Topik : BIOTEKNOLOGI

1. Title:The use of DNA markers for rapid improvement of crops in Africa
View Article: African Crop Science Journal. 2000-. 8- (1-). 99-108
CD Volume:297
Print Article: Pages: 99-108
Author(s):Thottappilly G Mignouna H D Omitogun O G
Author Affiliation:Biotechnology Research Unit, International Institute of Tropical Agriculture (IITA), Oyo Road, PMB 5320, Ibadan, Nigeria
Language:English
Language of Summary:french
Abstract:Genetic engineering and biotechnology are providing new tools for genetic improvement of food crops. Molecular DNA markers are some of these tools which can be used in various fields of plant breeding and germplasm management. For example, molecular markers have been used to confirm the identity of hybrids in breeding programmes. Another application of molecular markers is in determining phylogenetic relationships in related species. Information on phylogenetic relationships is useful in facilitating introgression of desirable traits from wild relatives to cultivated crop species. Molecular markers are also being used to construct genetic maps. A genetic map is a collection of genetic markers that have been grouped according to their linkage. Breeders can use DNA maps to carry out marker-assisted selection. This technique enables plants carrying desirable traits such as pest and disease resistance to be selected while still in the seedling stage. Ultimately, this enables the cloning of the genes to be used for crop improvement. The polymerase chain reaction (PCR) has become a popular technique for molecular genome mapping and the diagnosis of plant pathogens. The technique ensures amplification of specific DNA sequences by the use of primers and the enzyme Taq DNA polymerase. Restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNAs (RAPDs), microsatellites and amplified fragment length polymorphisms (AFLPs) are some of the most useful molecular markers for DNA fingerprinting. For viral, fungal and bacterial DNA fingerprinting and diagnosis as well as strain differentiation of rhizobia, PCR-RAPD and cDNA probes can be applied alongside with monoclonal antibodies
Descriptors:biotechnology. plant-breeding. genetic-markers. microsatellites. monoclonal-antibodies. plant-pathogens. polymerase-chain-reaction. restriction-fragment-length-polymorphism. random-amplified-polymorphic-DNA. crops. gene-mapping. diagnosis
Geographic Locator:Africa
Identifiers:amplified fragment length polymorphism
Subject Codes:FF020. WW000. FF610. ZZ395
Supplementary Info:19 ref
ISSN:1021-9730
Year:2000
Journal Title:African Crop Science Journal

2. Title:Rent creation and distribution from biotechnology innovations: the case of Bt cotton and herbicide-tolerant soybeans in 1997
View Article: Agribusiness (New York) 2000. 16 (1). 21-32
CD Volume:332
Print Article: Pages: 21-32
Author(s):Falck Zepeda J B Traxler G Nelson R G

Author Affiliation:Department of Agricultural Economics and Rural Sociology, 204 Comer Hall, Auburn University, Auburn, AL 36849, USA
Language:English
Abstract:The economic welfare from the second year planting of Bt cotton in 1997 is evaluated. Estimates for the economic surplus generated by the first year commercial planting of herbicide tolerant soybeans are also presented. The estimation of economic welfare includes the welfare effect of the introduction of these technologies in foreign markets. Survey data of paired fields from commercial farms in several states of the USA, and data from industry reports for yield and cost charges formed the basis of the research
Descriptors:biotechnology. cotton. genetic-engineering. soyabeans. production-economics. economic-impact. yields. production-costs. herbicides. welfare-economics. transgenic-plants. grain-legumes
Geographic Locator:USA
Organism Descriptors:Fabaceae. Gossypium. Glycine-(Fabaceae)
Supplemental Descriptors:Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Malvaceae. Malvales. Papilionoideae. Fabaceae. North-America. America. Developed-Countries. OECD-Countries
Subject Codes:EE145. FF020. FF005. EE110. WW000
Supplementary Info:20 ref
ISSN:0742-4477
Year:2000
Journal Title:Agribusiness

3. Title:The source of comparative advantage in the biotechnology industry: a real options approach
View Article: Agribusiness (New York) 2000. 16 (1). 56-67
CD Volume:332
Print Article: Pages: 56-67
Author(s):Lavoie B F Sheldon I M
Author Affiliation:Department of Agricultural, Environmental and Development Economics, Ohio State University, 2120 Fyffe Road, Columbus, OH 43210, USA
Language:English
Abstract:Sources of heterogeneity within the process of research and development (R&D) investment, such as international differences in the maximum per-period rate of investment and level of regulatory uncertainty, as plausible explanations for US comparative advantage in biotechnology are assessed. Using dynamic stochastic simulation, the results presented in this article suggest US biotechnology firms may initiate more R&D projects, innovate earlier and more rapidly, persevere longer in the face of mounting R&D costs, and successfully complete more R&D projects than European firms
Descriptors:biotechnology. costs. investment. research-projects. market-competition. international-comparisons. agricultural-production. research. finance. terms-of-trade
Geographic Locator:Europe. USA
Supplemental Descriptors:North-America. America. Developed-Countries. OECD-Countries
Subject Codes:WW000. AA500. EE800
Supplementary Info:11 ref
ISSN:0742-4477
Year:2000
Journal Title:Agribusiness

4. Title:Is agricultural research still a public good?
View Article: Agribusiness (New York) 2000. 16 (1). 68-81
CD Volume:332
Print Article: Pages: 68-81
Author(s):Oehmke J F Weatherspoon D D Wolf C A Naseem A Maredia M Hightower A
Author Affiliation:Department of Agricultural Economics, Agriculture Hall, Michigan State University, East Lansing, MI 48824-1069, USA
Language:English
Abstract:Biotechnology is redefining the nature of agricultural research and intellectual property. In response, public agricultural research institutions are increasingly protecting their intellectual property and commercializing research results. This paper is a critical first step in understanding how increasingly private ownership of intellectual property affects the agribusiness environment and the evolving role of public agricultural research institutions. The innovative step is the development of a neo-Schumpeterian model which examines whether commercialization of public research maximizes social welfare. The model contains two types of research firms: large firms such as the major life-science companies; and small university-related firms (SMURFs). Results show that both large firms and SMURFs underinvest in research relative to the social optimum, that research investment can exhibit cyclical behavior, and that there is a continued, albeit diminished, role for public agricultural research as the life-science revolution progresses
Descriptors:agricultural-research. agribusiness. companies. institutions. investment. models. ownership. private-sector. public-sector. research-institutes. social-welfare. intellectual-property-rights
Geographic Locator:USA
Supplemental Descriptors:North-America. America. Developed-Countries. OECD-Countries
Subject Codes:WW000. AA500. EE800
Supplementary Info:17 ref
ISSN:0742-4477
Year:2000
Journal Title:Agribusiness
Copyright:Copyright CAB International

5. Title:Universities and agricultural biotechnology patent production
View Article: Agribusiness (New York) 2000. 16 (1). 82-95
CD Volume:332
Print Article: Pages: 82-95
Author(s):Foltz J Barham B Kim KwanSoo
Author Variant:Kim-K-S
Author Affiliation:Department of Agricultural and Resource Economics, U-4021, 1376 Storrs Road, Storrs, CT 06269, USA
Language:English
Abstract:Using patent data, this work provides an initial empirical investigation into university production of agricultural biotechnology patents. A methodology for understanding the university patent production process is developed and econometric models of university-owned agricultural biotechnology patents are tested on a series of explanatory variables. Of a total of 142 US universities, 53 were identified as having ag-biotech patents (1991-1998). The results demonstrate the importance of the US land grant university infrastructure, technology transfer offices, and star scientists
Descriptors:biotechnology. patents. agricultural-research. technology-transfer. universities
Geographic Locator:USA

Supplemental Descriptors:North-America. America. Developed-Countries. OECD-Countries
Subject Codes:WW000. AA500. EE120
Supplementary Info:23 ref
ISSN:0742-4477
Year:2000
Journal Title:Agribusiness
Copyright:Copyright CAB International

6. Title:An evaluation of risk analysis as applied to agricultural biotechnology (with a case study of GMO labeling)
View Article: Agribusiness (New York) 2000. 16 (1). 115-123
CD Volume:332
Print Article: Pages: 115-123
Author(s):Caswell J A
Author Affiliation:Department of Resource Economics, 235 Draper Hall, University of Massachusetts at Amherst, Amherst, MA 01003, USA
Language:English
Abstract:The current use by governments of risk analysis in making decisions about regulatory approval and labelling policies is evaluated. This includes an outline of the steps involved in the risk analysis process and the range of factors considered by different countries in making regulatory decisions regarding use of agricultural biotechnology. The evaluation will focus on the impacts of risk analysis approaches on the timing of introduction and the adoption rate (market share) of new agricultural biotechnologies. A case study of differences in policy for the labelling of genetically modified organisms on retail packages is presented in conclusion
Descriptors:biotechnology. agricultural-products. labelling. genetic-engineering. innovation-adoption. risk. regulation. decision-making. case-studies
Identifiers:genetically modified organism
Subject Codes:EE700. WW000
Supplementary Info:12 ref
ISSN:0742-4477
Year:2000
Journal Title:Agribusiness
Copyright:Copyright CAB International

7. Title:OWSimu: an object-oriented and Web-based simulator for plant growth
View Article: Agricultural Systems. 2000. 63 (1). 33-47
CD Volume:325
Print Article: Pages: 33-47
Author(s):Pan X Hesketh J D Huck M G
Author Affiliation:Biotechnology Center, University of Illinois, 330 ERML, 1201 W. Gregory Drive, Urbana, IL 61801, USA
Language:English
Abstract:OWSimu is a Java-based generic plant growth simulator. According to the principles of object-oriented design, Java classes were programmed for plant growth simulation as well as relevant input, output and user interfaces. The program was developed as a Java applet with a user-friendly graphical interface running on the Web. With a Java (JDK1.1)-embedded Web browser, users can link the run-time model and perform plant growth simulations at the authors website. OWSimu describes the growth of a typical plant that is free of pests and diseases. The program is currently able to simulate plant growth for more than a dozen crops and weeds under Illinois weather and three typical soil conditions. Additional data is needed to modify OWSimu so that it can have a better carbon balance model for different plant species and

accommodate different varieties within a selected plant species for use in a specific crop production management system. The program source code is highly reusable for further development and for other crop modelling work
Descriptors:crops. weeds. models. growth-models. simulation-models. computer-software. growth
Geographic Locator:USA. Illinois
Supplemental Descriptors:North-America. America. Developed-Countries. OECD-Countries. East-North-Central-States-of-USA. North-Central-States-of-USA. USA. Corn-Belt-States-of-USA
Subject Codes:ZZ100. FF060. FF500. FF005
Supplementary Info:27 ref
ISSN:0308-521X
Year:2000
Journal Title:Agricultural Systems

8. Title:Global change and food and forest production: future scientific challenges
View Article: Agriculture, Ecosystems & Environment. 2000. 82 (1/3). 3-14
CD Volume:375
Print Article: Pages: 3-14
Author(s):Gregory P J Ingram J S I
Author Affiliation:Department of Soil Science, The University of Reading, PO Box 233, Whiteknights, Reading RG6 6DW, UK
Conference Title:Special issue: Food and forestry: global change and global challenges. Selected papers from the GCTE Focus 3 Conference, Reading, UK, September 1999
Language:English
Abstract:Production of food and forest products will need to increase to meet the world's projected demand. This challenge can be met by either extensification or intensification but, with little new land available for agriculture in many regions of rapid population growth, intensification will be pre-eminent. Global, average cereal yields will need to rise from the current 2.9 to 4.2 Mg ha-1 by 2025. The task of increasing production will be made more complex by the additional and interactive effects of changes in climate, atmospheric composition, land use and other global change drivers. However, increasing production with existing technologies will, itself, enhance these major drivers of global change and have other substantial impacts. The global change agenda relating to food and forest products considers research into impacts, adaptation and mitigation. Adaptation and mitigation need to be considered together to harness new technologies (including the use of biotechnology and computer-assisted management schemes) and integrate them with existing technologies in production systems. Better economic, finance and trade policies will also be necessary to allow more open trade of food and forest products. These factors, together with the positive effects that increased atmospheric CO2 concentration will have on yield will reduce the degree of intensification required to meet demand, thereby mitigating some of the unfavourable environmental consequences. However, there are several social and biophysical management issues associated with intensification that have proven intractable to past research approaches that urgently require resolution. Further research on improving nutrient use efficiency and other aspects of agronomic practice is clearly needed both to increase production and reduce harmful effects on other ecosystems. The effects of fluctuations of weather in the short term on agricultural production systems also warrant further study so that the longer term effects of climate

variability and change can be better managed. Multidisciplinary research and interdisciplinary approaches to modelling will be required to apply knowledge both from individual crops to agricultural systems and from plot-scale research to regional food supply issues
Descriptors:food-production. forest-products. food-supply. forestry. intensive-silviculture. intensive-farming. intensive-production. intensification. agriculture. crop-yield. production-possibilities. climatic-change. land-use. change. impact. research. appropriate-technology. agricultural-economics. forest-economics. international-trade. agricultural-production. farming-systems. population-growth. adaptation. extensive-farming. extensive-production
Identifiers:extensification. mitigation
Subject Codes:KK110. EE110. EE116. EE600. EE112. UU200. EE120. PP500. PP300
Supplementary Info:49 ref
ISSN:0167-8809
Year:2000
Journal Title:Agriculture, Ecosystems & Environment

9. Title:Differential aluminium tolerance of Portuguese rye populations and North European rye cultivars
View Article: Agronomie. 2000. 20 (1). 93-99
CD Volume:336
Print Article: Pages: 93-99
Author(s):Pinto Carnide O Guedes Pinto H
Author Affiliation:Department of Genetics and Biotechnology, University of Tras-os-Montes and Alto Douro, Ap. 202, 5001 Vila Real Codex, Portugal
Language:English
Language of Summary:french
Abstract:Seven Portuguese rye populations and 11 European rye varieties were grown at different aluminium concentrations. The results obtained reveal that Portuguese rye populations are more tolerant than the European cultivars, with most of them being even better than the Al-tolerant cv. Dank Zlote, used as a tester
Descriptors:aluminium. rye. acid-soils. toxic-substances. soil-pH. cereals
Geographic Locator:Portugal
Organism Descriptors:Secale-cereale
Supplemental Descriptors:Secale. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Southern-Europe. Europe. Mediterranean-Region. Developed-Countries. European-Union-Countries. OECD-Countries
Subject Codes:FF020. FF800. FF005
Supplementary Info:22 ref
ISSN:0249-5627
Year:2000
Journal Title:Agronomie

10. Title:Evaluation and characterisation of a collection of wild Spanish populations of the genera Elymus and Thinopyrum using morphological and agronomical traits
View Article: Agronomie. 2000. 20 (1). 111-122
CD Volume:336
Print Article: Pages: 111-122
Author(s):Nieto Lopez R M Casanova C Soler C
Author Affiliation:Department of Plant Breeding and Biotechnology, I.N.I.A, La Canaleja, PO Box 1045, 28800 Alcala de Henares (Madrid), Spain
Language:English
Language of Summary:french

Abstract:A collection of 29 wild Spanish populations of the genera Elymus and Thinopyrum was characterised using 22 morphological and agronomical characteristics. Field studies were performed over two years, 1994 and 1995. Frequencies were calculated for qualitative and quantitative traits. Pearson's product-moment correlation coefficient was used to analyse inter-population variation using frequency data. Means and coefficients of variation were calculated for quantitative characteristics. Analysis of variance was performed for each species to study differences between intra- and inter-populational variability. Similar degrees of variability were observed between quantitative and qualitative traits in all the species studied (T. junceum [E. farctus], T. junceiforme [E. farctus], E. caninus and E. hispanicus). Differences in variability were found at the level of species and population
Descriptors:plant-morphology. genetic-variation. plant-genetic-resources. evaluation. fodder-plants
Geographic Locator:Spain
Identifiers:Thinopyrum junceum. Thinopyrum junceiforme. Elymus hispanicus
Organism Descriptors:Thinopyrum. Elymus. Elymus-caninus. grasses. Poaceae
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Elymus. Southern-Europe. Europe. Mediterranean-Region. Developed-Countries. European-Union-Countries. OECD-Countries. Thinopyrum
Subject Codes:PP720. FF020. FF007
Supplementary Info:19 ref
ISSN:0249-5627
Year:2000
Journal Title:Agronomie

11. Title:Optimal population size for RFLP-assisted cultivar identification in alfalfa (Medicago sativa L.)
View Article: Agronomie. 2000. 20 (2). 233-240
CD Volume:336
Print Article: Pages: 233-240
Author(s):Labombarda P Pupilli F Arcioni S
Author Affiliation:Istituto di Ricerche sul Miglioramento Genetico delle Piante Foraggere, via Madonna Alta 130, 06128, Perugia, Italy
Language:English
Language of Summary:french
Abstract:The ability of RFLP markers to distinguish between 2 heterogeneous alfalfa ecotypes, Vogherese and Maremmana, was correlated with the number of plants sampled in either single-plant or bulk analyses. Independent subsample populations of 20 and 50 plants were compared for variance component partitioning and band frequencies in 20-, 50- and 100-plant subpopulations of Maremmana. Homogeneity within 3 independent bulks of the same size as given above was taken as a measure of bulk optimal size. A minimum of 50 plants is required for both single-plant and bulk analyses; however, for a large majority of bands analysed, no significant differences were detected for their frequency among populations of 20, 50 and 100 plants, with the exception of 6 bands out of 48. One ecotype-specific marker was found through bulk analysis. Results are discussed in relation to the improvement of RFLP methodology for cultivar identification in alfalfa
Descriptors:cultivar-identification. ecotypes. methodology. restriction-fragment-length-polymorphism. variety-classification. fodder-plants. fodder-legumes. biotechnology. lucerne
Organism Descriptors:Medicago-sativa. Medicago. Fabaceae
Supplemental Descriptors:Medicago. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. FF007. WW000
Supplementary Info:20 ref
ISSN:0249-5627
Year:2000
Journal Title:Agronomie
Copyright:Copyright CAB International

12. Title:The privatization of food: corporate control of biotechnology
View Article: Agronomy Journal. 2000. 92 (4). 803-806
CD Volume:297
Print Article: Pages: 803-806
Author(s):Jordan M C
Author Affiliation:Cereal Research Centre, Agriculture and Agri-Food Canada, 195 Dafoe Road, Winnipeg MB, R3T 2M9, Canada
Language:English
Descriptors:biotechnology. foods. industry
Subject Codes:WW000. FF020. EE110
Supplementary Info:6 ref
ISSN:0002-1962
Year:2000
Journal Title:Agronomy Journal
Copyright:Copyright CAB International

13. Title:Surplus Distribution from the Introduction of a Biotechnology Innovation
View Article: American Journal of Agricultural Economics. 82 (2) 2000. 360-69
CD Volume:302
Print Article: Pages: 360-369
Author(s):Falck Zepeda J B Traxler G Nelson R G
Author Affiliation:Auburn U. Auburn U. Auburn U
Language:English
Abstract:We examine the distribution of welfare from the introduction of Bt cotton in the United States in 1996. The welfare framework explicitly recognizes that research protected by intellectual property rights generates monopoly profits, and makes it possible to partition these rents among consumers, farmers, and the innovating input firms. We calculate a total increase in world surplus of ST0.3 million for 1996. Of this total, the largest share (59%) went to U.S. farmers. The gene developer, Monsanto, received the next largest share (21%), followed by U.S. consumers the rest of the world (6%), and the germplasm supplier, Delta and Pine Land Company (5%)
Descriptors:Agricultural R&D; Agricultural Technology; Agricultural Extension Services. Intellectual Property Rights: National and International Issues patents, copyrights)
Geographic Locator:U.S.
Subject Codes:EE110. EE450
ISSN:0002-9092
Year:2000
Journal Title:American Journal of Agricultural Economics
Copyright:Record from the EconLit database, _Copyright (c)_2001 American Economic Association, is used with permission

14. Title:Lessons from genetically engineered animal models. VIII. Absorption and secretion of ions in the gastrointestinal tract
View Article: American Journal of Physiology. 2000. 278 (2). G185-G190
CD Volume:311
Print Article: Pages: G185-G190
Author(s):Shull G E Miller M L Schultheis P J

Author Affiliation:Department of Molecular Genetics, Biochemistry, and Microbiology, University of Cincinnati College of Medicine, Cincinnati, Ohio, 45267, USA
Language:English
Abstract:In this review, we discuss gene knockout studies, in mice, of the secretory isoform of the Na+-K+-2Cl- cotransporter, isoforms 1, 2, and 3 of the Na+/H+ exchanger, and the colonic H+-K+-ATPase. This approach is leading to a clearer understanding of the functions of these transporters
Descriptors:animal-models. digestive-system. targeted-mutagenesis. genes. digestive-tract. ion-transport. uncertainty. reviews. mineral-absorption. genetic-engineering. transgenics. adenosinetriphosphatase. sodium. potassium. chloride. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000. VV140
Supplementary Info:30 ref
ISSN:0002-9513
Year:2000
Journal Title:American Journal of Physiology
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15. Title:Spontaneous mutation in the db gene results in obesity and diabetes in CD-1 outbred mice
View Article: American Journal of Physiology. 2000. 278 (2). R320-R330
CD Volume:311
Print Article: Pages: R320-R330
Author(s):Brown J A Chua S C Jr Liu ShunMei Andrews M T Vandenbergh J G
Author Variant:Liu-S-M
Author Affiliation:Department of Zoology, North Carolina State University, Raleigh 27695-7617, USA
Language:English
Abstract:Five allelic mutants of the diabetes (db) gene have been previously described in mice and rats causing obesity, infertility and varying degrees of diabetes. We have identified a new, spontaneous mutation resulting in obesity and diabetes in a colony of CD-1 outbred mice. Genetic complementation studies indicated that the new mutation was an allele of the diabetes locus. Sequence analysis of cDNA fragments showed a deletion of one G residue located in exon 12 of the leptin receptor (Lepr) gene. The mutation, Leprdb-NCSU, results in a frameshift and reduces Lepr transcript levels 10-fold. Mutant mice drank up to 4 times more water and were up to 2 times heavier than wild-type mice. Blood glucose and plasma insulin and leptin concentrations were sexually dimorphic among affected mice, suggesting an effect of sex steroids. Mortality of affected males was 100% by 5 months of age; affected females survived up to 10 months of age
Descriptors:diabetes. mutations. obesity. complementary-DNA. insulin. leptin. receptors. genes. mortality. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000
Supplementary Info:36 ref
ISSN:0002-9513
Year:2000
Journal Title:American Journal of Physiology
Copyright:Copyright CAB International

16. Title:Lessons from genetically engineered animal models X. Trefoil peptide and EGF receptor/ligand transgenic mice
View Article: American Journal of Physiology. 2000. 278 (4). G501-G506
CD Volume:312
Print Article: Pages: G501-G506
Author(s):Giraud A S
Author Affiliation:Department of Medicine, University of Melbourne, Western Hospital, Footscray 3011, Australia
Language:English
Abstract:This review highlights some of the major findings obtained using genetically engineered mice pertinent to the epidermal growth factor receptor and its ligands, particularly the major gut ligand transforming growth factor- alpha and the trefoil peptides
Descriptors:transgenics. epidermal-growth-factor. receptors. digestive-system. digestive-tract. growth-factors. intestines. ligands. mutations. peptides. transforming-growth-factor. genes. reviews. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000
Supplementary Info:35 ref
ISSN:0002-9513
Year:2000
Journal Title:American Journal of Physiology
Copyright:Copyright CAB International

17. Title:Influences of IGF-I gene disruption on the cellular profile of the diaphragm
View Article: American Journal of Physiology. 2000. 278 (4). E707-E715
CD Volume:312
Print Article: Pages: E707-E715
Author(s):Fournier M Lewis M I
Author Affiliation:Division of Pulmonary/Critical Care Medicine, Burns and Allen Research Institute, Cedars-Sinai Medical Center, University of California, Los Angeles School of Medicine, Los Angeles, California 90048, USA
Language:English
Abstract:The effect of targeted disruption of the Igf1 gene on diaphragm cellularity was studied in 2-month-old homozygous mutant [IGF-I(-/-)] mice and their wild-type littermates. Diaphragm fibre types were classified histochemically. Diaphragm fibre cross-sectional areas were determined from digitized muscle sections, and fibre succinate dehydrogenase activity was determined histochemically using a microdensitometric procedure. An acidic ATPase reaction was used to visualize capillaries. Myosin heavy chain isoforms were identified by SDS-PAGE and their proportions were determined by scanning densitometry. The body weight of IGF-I(-/-) animals was 32% of that of wild-type littermates. Diaphragm fibre type proportions were unchanged between the groups. The cross-sectional areas of types I, IIa, and IIx diaphragm fibres of IGF-I(-/-) mutants were 63, 68 and 65% respectively of those of wild-type animals ($P<0.001$). The diaphragm thickness and the number of fibres spanning its entire thickness were reduced by 36 and 25% respectively in IGF-I(-/-) mice ($P<0.001$). Succinate dehydrogenase activity was significantly increased in all 3 types of diaphragm fibres of IGF-I(-/-) mutants ($P<0.05$). The number of capillaries per fibre was reduced approx equal to 30% in IGF-I(-/-) animals, whereas the capillary density was preserved. The proportions of myosin heavy chain isoforms were similar between the groups. It is suggested that muscle hypoplasia reflects the importance of IGF-I on

cell proliferation, differentiation and apoptosis (alone or in combination) during development, although reduced cell size highlights the importance of IGF-I on rate and/or maintenance of diaphragm fibre growth in the postnatal state. Reduced capillarity may result from both direct and indirect influences on angiogenesis. Improved oxidative capacity may reflect compensatory mechanisms in IGF-I(-/-) mutants
Descriptors:diaphragm. capillaries. targeted-mutagenesis. genes. muscle-fibres. hypoplasia. insulin-like-growth-factor. muscles. mutants. myosins. succinate-dehydrogenase. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. LL400. LL600
Supplementary Info:50 ref
ISSN:0002-9513
Year:2000
Journal Title:American Journal of Physiology
Copyright:Copyright CAB International

18. Title:Production and characterization of "second generation" somatic hybrids derived from protoplast fusion between interspecific somatohaploid and dihaploid Solanum tuberosum L
View Article: American Journal of Potato Research. 2000-. 77- (3-). 149-159
CD Volume:297
Print Article: Pages: 149-159
Author(s):Rokka V M Valkonen J P T Tauriainen A Pietila L Lebecka R Zimnoch Guzowska E Pehu E
Author Affiliation:Agricultural Research Centre of Finland, Plant Production Research, Crops and Soil, Myllytie 10, FIN-31600 Jokioinen, Finland
Language:English
Abstract:Protoplasts were fused to produce somatic hybrids between a triploid (2n = 3x = 32-34) interspecific somatohaploid between Solanum brevidens and S. tuberosum, and a dihaploid (2n = 2x = 24) anther-derived line of S. tuberosum cv. Van Gogh. A total of 265 plants were regenerated from protoplast fusion derived calli and their hybridity was verified using fusion partner specific RAPD markers. These "second generation" somatic hybrids were aneuploid pentaploids (2n = 5x = 51-65) with a 2C DNA content ranging from 3.36 to 4.43 pg, which corresponded to the sum of the 2C values of each of the fusion partners (somatohaploid: 2.22 pg; and the dihaploid line of cv. Van Gogh: 1.87 pg). Most of the "second generation" somatic hybrids were vigorous, but variable in morphology. They were extremely resistant to potato leaf roll virus and they had tolerance of potato virus Y infection derived from the somatohaploid fusion partner. Even though most of the "second generation" hybrids tuberized, the tuber morphology was variable and most were poorly shaped. In Erwinia soft rot (E. carotovora subsp. atroseptica) resistance tests, the tubers showed a higher level of resistance than the tetraploid S. tuberosum cultivars, the dihaploid S. tuberosum fusion partners, and the hexaploid somatic hybrids between S. brevidens and S. tuberosum. The "second generation" somatic hybrids were all male sterile and failed to produce berries or seeds
Descriptors:hybrids. interspecific-hybridization. protoplasts. protoplast-fusion. tubers. plant-morphology. plant-diseases. plant-pathogens. disease-resistance. plant-pathogenic-bacteria. somatic-hybridization. haploidy. root-crops. biotechnology. potatoes
Organism Descriptors:Solanum-tuberosum. Erwinia-carotovora-subsp.-atroseptica. Solanum-brevidens. potato-Y-potyvirus. potato-leaf-roll-luteovirus. plant-viruses

Supplemental Descriptors:Solanum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Erwinia-carotovora. Erwinia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. potyvirus-group. plant-viruses. viruses. plant-pathogens. pathogens. luteovirus-group
Subject Codes:FF005. FF170. FF020. WW000. FF610. HH600
Supplementary Info:48 ref
ISSN:1099-209X
Year:2000
Journal Title:American Journal of Potato Research

19. Title:Expression of the chicken lysozyme gene in potato enhances resistance to infection by Erwinia carotovora subsp. atroseptica
View Article: American Journal of Potato Research. 2000-. 77- (3-). 191-199
CD Volume:297
Print Article: Pages: 191-199
Author(s):Serrano C Arce Johnson P Torres H Gebauer M Gutierrez M Moreno M Jordana X Venegas A Kalazich J Holuigue L
Author Affiliation:Departamento de Genetica Molecular y Microbiologia, Facultad de Ciencias Biologicas, Pontificia Universidad Catolica de Chile, P.O. Box 114-D, Santiago, Chile
Language:English
Language of Summary:spanish
Abstract:Infection of potato plants and tubers with the bacterium Erwinia carotovora subsp. atroseptica produces blackleg and soft rot diseases, which cause significant losses to crops and stored potatoes. In order to obtain resistance against this bacterium, the gene chly encoding the enzyme lysozyme from chicken was introduced into potato plants (cv. Desiree) via Agrobacterium-mediated transformation. Sixty-three and 69 transgenic potato clones were evaluated in the greenhouse for resistance to blackleg and soft rot diseases, respectively. Results reported in this paper indicate that 21%-29% of the potato clones showed increased resistance to infection by the bacterium E. c. subsp. atroseptica T7, as revealed by a reduced severity of blackleg or soft rot symptoms. Nine clones showing different levels of resistance were selected for further molecular analysis. The number of copies of the transgene integrated in the plant genome of these clones was estimated by Southern blot analysis. The level of transgene expression, detected by Northern blot analysis, correlated with the level of resistance detected in these clones
Descriptors:disease-resistance. genetic-transformation. transgenic-plants. potatoes. plant-diseases. plant-pathogens. plant-pathogenic-bacteria. bacterial-diseases. lysozyme. gene-expression. root-crops. biotechnology. poultry
Organism Descriptors:fowls. Erwinia-carotovora-subsp.-atroseptica. Solanum-tuberosum
Supplemental Descriptors:Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. Erwinia-carotovora. Erwinia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. Solanum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. FF610. HH600
Supplementary Info:42 ref
ISSN:1099-209X
Year:2000
Journal Title:American Journal of Potato Research

20. Title:Effects of increasing amounts of Lupinus albus seeds without or with whole egg powder in the diet of growing pigs on performance
View Article: Animal Feed Science and Technology. 2000. 83 (2). 89-101
CD Volume:332
Print Article: Pages: 89-101
Author(s):Nevel C van Seynaeve M Voorde G van de Smet S de Driessche E van Wilde R de
Author Variant:van-Nevel-C. van-de-Voorde-G. de-Smet-S. van-Driessche-E. de-Wilde-R
Author Affiliation:Laboratory of Protein Chemistry, Institute for Molecular Biology and Biotechnology, Vrije Universiteit Brussel, Paardenstraat, 65, B-1640 Sint-Genesius-Rode, Belgium
Language:English
Abstract:The effect of including L. albus seeds 150 or 300 g/kg of feed in the diet was investigated in a growth trial with 42 Belgian Native x Pietrain pigs (23.8 kg liveweight). Parameters studied were growth, feed utilization, digestibility of nutrients, and slaughter and carcass characteristics. Spray-dried whole egg powder, a specific inhibitor of lectins in L. albus seeds was also added (50 g/kg of feed), with the aim of verifying whether the unfavourable effects of high levels of lupin seeds could be neutralized. Feeding the diet containing lupin seeds 300 g/kg lowered average daily gain from 727 to 674 g and feed intake from 2.32 to 2.05 kg; feed conversion ratio remained unaltered. The presence of whole egg powder in the lupin seed diets did not abolish the negative effects. Apparent faecal digestibility of most nutrients in the diets was not influenced by addition of lupin seeds or egg powder, except for the crude fat fraction, whereas the digestibility coefficient increased from 0.51 to 0.61. Crude fibre digestibility also increased, but only at the lowest lupin seed level. Carcass weight and dressing percentage were lower in the groups fed the highest lupin seed level. Fatty acid profile of backfat was determined and slightly higher proportions of C18:1 were observed when lupin seeds were fed. Possible reasons accounting for the lower performance of animals receiving lupin seeds are discussed, thought the exact reason could not be derived from this experiment
Descriptors:pig-feeding. performance. feeding. feed-conversion-efficiency. liveweight-gain. feed-intake. lupins. seeds. backfat. carcass-quality. carcass-weight. digestibility. lectins. nutrients. utilization
Organism Descriptors:Lupinus-albus. pigs. Lupinus
Supplemental Descriptors:Lupinus. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL520. LL500. RR000
Supplementary Info:33 ref
ISSN:0377-8401
Year:2000
Journal Title:Animal Feed Science and Technology

21. Title:Pathogenicity of fungi associated with melon vine decline and selection strategies for breeding resistant cultivars
View Article: Annals of Applied Biology. 137 (2). October, 2000. 141-151
CD Volume:356
Print Article: Pages: 141-151
Author(s):Iglesias A Pico B Nuez F
Author Affiliation:Biotechnology Department (Genetics), Polytechnic University of Valencia, Camino de Vera 14, 46022, Valencia
Language:English

Language of Summary:English (EN)
Abstract:Melon Vine Decline is a severe rot root disease of increasing world-wide importance. In Eastern Spain it is related to the presence of Acremonium cucurbitacearum and Monosporascus cannonballus. The strong influence of environmental conditions on the progress of this disease has made its study difficult. A field screening of Cucumis melo accessions has been conducted over four years. Simultaneously, the pathogenicity of isolates of the two fungi recovered from the screening field was studied. These were more aggressive than other Spanish and American isolates. Percentage of vine decay was scored, together with root damage, the latter being evaluated by using four scoring systems based on root characteristics and disease severity. Root inspection allowed the selection of resistance sources, even when aboveground symptoms did not appear, due to the lack of environmental stresses at time of fruit maturity. The root damage scoring systems provided for each genotype a measure of the potential risk of suffering vine decline if environmental stresses occur during fruit maturity. The accession C. melo var. agrestis Pat 81 consistently exhibited high field resistance level, expressed as a higher percentage of symptomless plants, together with a significant delay in symptoms appearance. The F1 hybrids derived from the cross Pat 81 X C. melo susceptible varieties showed an intermediate level of resistance between the parents, suggesting a partial dominance gene action. The high resistance level found in Pat 81, and also in its derived hybrids, against the aggressive isolates found in this area, makes it promising for breeding melon varieties resistant to melon vine decline
Descriptors:plant breeding: disease resistance. Pest Assessment Control and Management. melon vine decline: fungal disease
Geographic Locator:Spain (Europe, Palearctic region)
Organism Descriptors:Acremonium cucurbitacearum (Fungi Imperfecti or Deuteromycetes): plant pathogen; Cucumis melo (Cucurbitaceae): host; Cucumis melo var. agrestis x Cucumis melo (Cucurbitaceae): host; Monosporascus cannonballus (Ascomycetes): plant pathogen
Supplemental Descriptors:Ascomycetes: Fungi, Plantae; Cucurbitaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Angiosperms; Dicots; Fungi; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants
Subject Codes:Pest Assessment Control and Management
ISSN:0003-4746
Year:2000
Journal Title:Annals of Applied Biology

22. Title:Genetic diversity and evolution of closteroviruses
View Article: Annual Review of Phytopathology. Webster-Robert-K. Shaner-Gregory. van-Alfen-Neal-K. (Authors) 38. (4139 El Camino Way: Annual Reviews) 293-324
CD Volume:298
Print Article: Pages: 293-324
Author(s):Karasev Alexander V
Author Affiliation:Department of Microbiology and Immunology, Biotechnology Foundation Laboratories at Thomas Jefferson University, 1020 Locust Street, Philadelphia, PA, 19107: AKarasev@hendrix.jci.tju.edu
Language:English
Language of Summary:English (EN)
Abstract:No Abstract available

Descriptors:Book Chapter. Molecular Genetics (Biochemistry and Molecular Biophysics); Evolution and Adaptation; Infection; Systematics and Taxonomy
Organism Descriptors:aphids (Homoptera): disease vector; closteroviruses (Closterovirus): plant pathogen; mealybug (Homoptera): disease vector; whitefly (Homoptera): disease vector
Supplemental Descriptors:Closterovirus: Plant Viruses, Viruses, Microorganisms; Homoptera: Insecta, Arthropoda, Invertebrata, Animalia. Animals; Arthropods; Insects; Invertebrates; Microorganisms; Plant Viruses; Viruses
Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Evolution and Adaptation; Infection; Systematics and Taxonomy
ISSN:0066-4286
Year:2000
Journal Title:Annual Review of Phytopathology

23. Title:Pathways and regulation of sulfur metabolism revealed through molecular and genetic studies
View Article: Annual Review of Plant Physiology and Plant Molecular Biology. 2000. 51. 141-165
CD Volume:298
Print Article: Pages: 141-165
Author(s):Leustek T Martin M N Bick J A Davies J P
Author Affiliation:Biotechnology Center for Agriculture and the Environment, Rutgers University, New Brunswick, New Jersey 08901-8520, USA
Language:English
Abstract:This review focuses on recent advances in the field of plant sulfur metabolism. Topics discussed include sulfate transport, sulfate assimilation, and metabolism of glutathione and glutathione S-conjugates
Descriptors:sulfur. glutathione. sulfates. metabolism. translocation. reviews
Subject Codes:FF061. FF060
Supplementary Info:141 ref
ISSN:1040-2519
Year:2000
Journal Title:Annual Review of Plant Physiology and Plant Molecular Biology

24. Title:Removal of ammonium-N from a recirculation aquacultural system using an immobilized nitrifier
View Article: Aquacultural Engineering. 21 (3). Jan., 2000. 139-150
CD Volume:332
Print Article: Pages: 139-150
Author(s):Kim Sung Koo Kong Insoo Lee Byung Hun Kang Limseok Lee Min Gyu Suh Kuen Hack
Author Affiliation:Department of Biotechnology and Bioengineering, Pukyong National University, Pusan, 608-737
Language:English
Language of Summary:English (EN)
Abstract:Various immobilization methods were evaluated for the removal of ammonium-N from recirculating aquacultural water. Ba-alginate, Ca-alginate, carrageenan, and agar beads were prepared with nitrifer consortium from the activated sludge of a sewage treatment facility in Sooyoung, Pusan, South Korea. Batch bioreactor tests for the determination of the effectiveness of the immobilized nitrifier and the optimum hydraulic retention time (HRT) were carried out. The nitrifiers immobilized in Ba-alginate and Ca-alginate showed the most effective nitrification, while those immobilized in the carrageenan and agar

beads showed reduced activities. Ninety five percent of the ammonia (20 mg/l) added to the batch bioreactor was nitrified in 6 h when immobilized Ba-alginate or Ca-alginate nitrifiers were used. In order to apply the immobilized nitrifier to an aquaculture facility, a continuous bioreactor was used with synthetic aquacultural water containing 2 mg/l ammonia. Using immobilized Ba-alginate and Ca-alginate beads, 94 and 87% of loaded ammonia were removed with in 3.4 h of HRT, respectively. The amounts of ammonia removal per day were in the range of 2.8-82 g ammonia/m3 per day depending on HRT. The highest ammonia removal rate of 82 g/m3 per day was observed when HRT was 0.3 h (18 min)

Descriptors:activated sludge; aerobic biofilteration; agar bead; immobilization; immobilized nitrifier; optimum hydraulic retention time; recirculation aquacultural system; sewage treatment facility. Aquaculture. ammonia removal; ammonium-nitrogen; barium-alginate; calcium- alginate; carrageenan

Geographic Locator:Sooyoung (South Korea, Asia, Palearctic region): Pusan

Subject Codes:Aquaculture

ISSN:0144-8609

Year:2000

Journal Title:Aquacultural Engineering

25. Title:Mass production of Rhodopseudomonas palustris as diet for aquaculture

View Article: Aquacultural Engineering. 23 (4). October, 2000. 281-293

CD Volume:332

Print Article: Pages: 281-293

Author(s):Kim Joong Kyun Lee Bum Kyu

Author Affiliation:Major of Biotechnology, Division of Food Science and Biotechnology, Pukyong National University, 599-1 Daeyeon-Dong Nam- Gu, Pusan, 608-737

Language:English

Language of Summary:English (EN)

Abstract:Three different types of anaerobic fermentations were used for the mass production of the photosynthetic bacterium Rhodopseudomonas palustris as diet for aquaculture. The optimum agitation speed and malate concentration were 300 r.p.m. and 0.2% in the modified MYC medium, respectively. In batch fermentations of R. palustris, the maximum number of viable cells was 1.1 X 1010 c.f.u. ml-1 with 2.65 g l-1 of DCW, and the maximum specific growth rate and biomass productivity were estimated to be 0.12 h-1 and 55 mg l-1 h-1, respectively. Crude protein content of R. palustris was about 72- 74%. The composition of stearic acid and oleic acid of R. palustris was superior to those of Chlorella and yeasts, while that of other fatty acids tested was not. The amino acid profiles of the protein hydrolysate compared favorably with Food Agricultural Organization (FAO) guidelines. The biomass productivities from fed-batch experiments were found to be 50, 47 and 49 mg l-1 h-1 for linear, exponential, and sigmoidal feeding strategy, respectively. The maximum biomass productivity was found to be 112 mg l-1 h-1 in chemostat. Compared to growth in batch cultures, continuous fermentation yielded two times higher biomass productivity

Descriptors:agitation speed; anaerobic fermentations; biomass productivity; diet; growth rate; mass production. Aquaculture. malate

Organism Descriptors:Rhodopseudomonas palustris (Purple Nonsulfur Bacteria): aquaculture species, diet item

Supplemental Descriptors:Purple Nonsulfur Bacteria: Purple Bacteria, Anoxygenic Phototrophic Bacteria, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms

Subject Codes:Aquaculture

ISSN:0144-8609
Year:2000
Journal Title:Aquacultural Engineering

26. Title:Substrate specificity of lignin peroxidase and a S168W variant of manganese peroxidase
View Article: Arch Biochem Biophys 2000 Jan 1;373(1):147-53
CD Volume:332
Print Article: Pages: 147-153
Author(s):Timofeevski SL Nie G Reading NS Aust SD
Author Affiliation:Biotechnology Center, Utah State University, Logan, Utah, 84322-4705, USA
Abstract:Lignin peroxidase (LiP) and manganese peroxidase (MnP) are structurally similar heme-containing enzymes secreted by white-rot fungi. Unlike MnP, which is only specific for Mn(2+), LiP has broad substrate specificity, but it is not known if this versatility is due to multiple substrate-binding sites. We report here that a S168W variant of MnP from Phanerochaete chrysosporium not only retained full Mn(2+) oxidase activity, but also, unlike native or recombinant MnP, oxidized a multitude of LiP substrates, including small molecule and polymeric substrates. The kinetics of oxidation of most nonpolymeric substrates by the MnP variant and LiP were similar. The stoichiometries for veratryl alcohol oxidation by these two enzymes were identical. Some readily oxidizable substrates, such as guaiacol and ferrocyanide, were oxidized by MnP S168W and LiP both specifically and nonspecifically while recombinant MnP oxidized these substrates only nonspecifically. The functional similarities between this MnP variant and LiP provide evidence for the broad substrate specificity of a single oxidation site near the surface tryptophan
Descriptors:Amino Acid Sequence. Base Sequence. Catalytic Domain. Comparative Study. DNA Primers. Isoenzymes. Kinetics. Molecular Sequence Data. Oxidation-Reduction. Peroxidases. Phanerochaete. Recombinant Proteins. Sequence Homology, Amino Acid. Substrate Specificity. Support, Non-U.S. Gov't. Tryptophan. Variation (Genetics)
Geographic Locator:UNITED STATES
ISSN:0003-9861
Year:2000
Journal Title:Archives of Biochemistry and Biophysics

27. Title:Spontaneous porphyria of the Long-evans cinnamon rat: an animal model of Wilson's disease
View Article: Arch Biochem Biophys 2000 Mar 15;375(2):240-50
CD Volume:332
Print Article: Pages: 240-250
Author(s):Nakayama K Takasawa A Terai I Okui T Ohyama T Tamura M
Author Affiliation:Department of Clinical Pathology, Division of Biotechnology, Hokkaido Institute of Public Health, North 19 West 12, Kita-ku, Sapporo, 060-0819, Japan. VZB03673@nifty.ne.jp
Abstract:To confirm and extend our previous microspectrophotometric observations of 30-week-old male Long-Evans Cinnamon (LEC) rats, an animal model of human Wilson's disease, we analyzed the porphyrin patterns of the organs, urine, and plasma of LEC rats. Abnormal accumulation of porphyrins, especially highly carboxylated porphyrins (uro- and heptaporphyrin), in the kidneys and liver was seen in male and female LEC rats aged 30 weeks and also in 10-week-old rats, before the onset of spontaneous hepatic dysfunction. Accumulation of copper and iron in the kidneys was not observed in the 10-week-old rats. Massive accumulation of porphyrins was observed only in the kidneys of the 30-

week-old male LEC rat, indicating that this symptom is related to sex and age. Renal accumulation of porphyrins was reflected in the rate of urinary porphyrin excretion. Hepatic accumulation of porphyrins appeared to be independent of sex and age. These results indicate that neither renal nor hepatic porphyrin accumulation is the result of renal deposition of metals or of spontaneous hepatic dysfunction and that porphyrinuria in the LEC rat is closely related to the renal accumulation of porphyrins. In contrast to these organs, a reduction in the porphyrin levels was observed in the brain of the LEC rat. This was independent of sex and age. The present work stresses the existence of an abnormal heme metabolism in the LEC rat, and thus, the necessity to study the heme metabolism in human Wilson's disease is strongly suggested

Descriptors:Aging. Animal. Bone Marrow. Brain Chemistry. Chromatography, High Pressure Liquid. *Disease Models, Animal. Female. Heme. Hepatolenticular Degeneration. Human. Kidney. Liver. Male. Microscopy, Fluorescence. Porphyria. Porphyrins. Rats. Rats, Inbred LEC. Sex Characteristics. Spleen

Geographic Locator:UNITED STATES

ISSN:0003-9861
Year:2000
Journal Title:Archives of Biochemistry and Biophysics

28. Title:Disruption of interkringle disulfide bond of plasminogen kringle 1-3 changes the lysine binding capability of kringle 2, but not its antiangiogenic activity

View Article: Arch Biochem Biophys 2000 Mar 15;375(2):359-63
CD Volume:332
Print Article: Pages: 359-363

Author(s):Lee H Kim HK Lee JH You WK Chung SI Chang SI Park MH Hong YK Joe YA
Author Affiliation:Mogam Biotechnology Research Institute, Yongin, 449-910, Korea

Abstract:Kringle 1-3 of human plasminogen is a potent inhibitor of endothelial cell proliferation. To understand a possible role for the unique cystine bridge between kringle 2 and kringle 3, we disrupted the interkringle disulfide bond by mutating Cys(169) and Cys(297) to serine residues. The yield of the mutant during the refolding process was decreased significantly. Anti-endothelial cell proliferative activity of the mutant was similar to that of the wild type. There was no significant difference in in vivo antiangiogenic activity between the wild type and the mutant in chorioallantoic membrane assay. However, in the mutant, the weak lysine binding capability of kringle 2 was not detected and its mobility in nonreducing sodium dodecyl sulfate-polyacrylamide gel electrophoresis is different from that of the wild type. These results support the notion that the overall antiangiogenic function of angiostatin is mediated by individual kringles, and suggest that the lysine binding capability of kringle 2 is likely not important for the antiangiogenic activity of kringle 1-3

Descriptors:Amino Acid Substitution. Angiogenesis Inhibitors. Animal. Cattle. Cell Division. Chick Embryo. Chorion. Cysteine. Disulfides. Electrophoresis, Polyacrylamide Gel. Endothelium, Vascular. Human. Kringles. Ligands. Lysine. Mutation. *Neovascularization, Physiologic. Plasminogen. Protein Binding. Protein Folding. Recombinant Proteins. Support, Non-U.S. Gov't. Thermodynamics

Geographic Locator:UNITED STATES

ISSN:0003-9861
Year:2000
Journal Title:Archives of Biochemistry and Biophysics

29. Title:Molecular modeling and substrate specificity of discrete cruzipain-like and cathepsin L-like cysteine proteinases of the human blood fluke Schistosoma mansoni
View Article: Arch Biochem Biophys 2000 Aug 1;380(1):46-55
CD Volume:333
Print Article: Pages: 46-55
Author(s):Brady CP Brinkworth RI Dalton JP Dowd AJ Verity CK Brindley PJ
Author Affiliation:School of Biotechnology, Dublin City University, Dublin, Ireland
Abstract:Adult Schistosoma mansoni blood flukes express two discrete cysteine proteinases, SmCL1 and SmCL2, both of which are related to the cathepsin L-like enzymes of the C1 family of peptidases. Our previous phylogenetic analysis indicated that SmCL1 is more closely related to cruzipain from the parasitic protozoa Trypanosoma cruzi than to human cathepsin L, whereas the converse situation applies with SmCL2. To characterize their catalytic subsites and substrate specificities, we have now developed three-dimensional (3D) homology models of SmCL1 and SmCL2 using the structure of cruzipain and cathepsin L. Eisenberg analysis of the 3D models revealed self-compatibility scores of 90.1 and 96.1 out of a possible score of 97.6 for SmCL1 and SmCL2, respectively, verifying the accuracy and utility of the models. Substrate preferences of recombinant SmCL1 and SmCL2 at positions P3, P2, and P1 conformed to the substrate specificity predicted by the models. In particular, SmCL1 and SmCL2 both exhibited high affinity (k(cat)/K(m)) for substrates with hydrophobic residues at P2 including Z-Leu-Arg-NHMec (773.4 and 548.5 mM(-1) s(-1), respectively), Boc-Val-Leu-Lys-NHMec (116.8 and 306.5 mM(-1) s(-1)), and Z-Phe-Arg-NHMec (38.9 and 113.4 mM(-1) s(-1)). SmCL1 exhibited only a low affinity for the cathepsin B diagnostic substrate Z-Arg-Arg-NHMec while SmCL2 failed to cleave this substrate. The substrate specificities of SmCL1 and SmCL2 were clearly differentiated with H-Leu-Val-Tyr-NHMec and Suc-Leu-Tyr-NHMec since SmCL1 cleaved both efficiently (k(cat)/K(m) values of 51.9 and 41.1 mM(-1) s(-1), respectively), whereas SmCL2 cleaved neither. The 3D models revealed that this difference in specificity was due to restrictions imposed on the S3 subsite of SmCL2 as a result of insertion of two amino acids vicinal to residue 60
Descriptors:Amino Acid Sequence. Amino Acids. Animal. Catalysis. Cathepsins. Cysteine Endopeptidases. Kinetics. Models, Molecular. Molecular Sequence Data. Protein Binding. Protein Structure, Tertiary. Recombinant Proteins. Schistosoma mansoni. Sequence Homology, Amino Acid. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:UNITED STATES
ISSN:0003-9861
Year:2000
Journal Title:Archives of Biochemistry and Biophysics

30. Title:Intact human ceruloplasmin is required for the incorporation of iron into human ferritin
View Article: Arch Biochem Biophys 2000 Sep 1;381(1):119-26
CD Volume:333
Print Article: Pages: 119-126
Author(s):Van Eden ME Aust SD
Author Affiliation:Biotechnology Center, Utah State University, Logan 84322-4705, USA
Abstract:We have previously reported several studies on the loading of iron into ferritin by ceruloplasmin using proteins from rats. Loading iron into human ferritin using human serum ceruloplasmin is complicated by the fact that human ceruloplasmin is very susceptible to proteolysis (T. P. Ryan, T. A. Grover, and S. D. Aust, 1992, Arch. Biochem Biophys. 293,

1-8). The present study investigated the effect of proteolysis on the ability of human ceruloplasmin to load iron into human ferritin. SDS-PAGE revealed one major band with an apparent molecular weight of 116 kDa for a proteolytically degraded form of ceruloplasmin versus a 132-kDa band for an intact form of the enzyme. Both forms of the enzyme possessed ferroxidase activity, although that of the proteolytically degraded enzyme was approximately twofold less than that of the intact enzyme (4.9 nmol (min)-1 vs 8.3 nmol (min)-1). Only the intact form of ceruloplasmin was able to catalyze iron loading into ferritin without altering the physical characteristics of the ferritin protein during the process. Abnormal migration in nondenaturing PAGE gels, as well as a decrease in the amount of detectable ferritin protein, was observed when ferritin was incubated with iron alone or with proteolytically degraded ceruloplasmin and iron. It was concluded that the structural integrity of ceruloplasmin is required for the enzyme to effectively catalyze iron loading into ferritin

Descriptors:Animal. Catalysis. Ceruloplasmin. Electrophoresis, Polyacrylamide Gel. Ferritin. Human. In Vitro. Iron. Molecular Weight. Peptide Fragments. Rats. Recombinant Proteins. Support, Non-U.S. Gov't. Support, U.S. Gov't, P.H.S.

Geographic Locator:UNITED STATES

ISSN:0003-9861
Year:2000
Journal Title:Archives of Biochemistry and Biophysics

31. Title:Coexpression of genetically engineered fused enzyme between yeast NADPH-P450 reductase and human cytochrome P450 3A4 and human cytochrome b5 in yeast

View Article: Arch Biochem Biophys 2000 Sep 1;381(1):164-70
CD Volume:333
Print Article: Pages: 164-170

Author(s):Hayashi K Sakaki T Kominami S Inouye K Yabusaki Y
Author Affiliation:Biotechnology Laboratory, Sumitomo Chemical Company, Ltd., Hyogo, Japan

Abstract:Human hepatic cytochrome P450 3A4 (CYP3A4) was expressed in yeast Saccharomyces cerevisiae. While the expression level was high as compared with other human hepatic cytochrome P450s, CYP3A4 showed almost no catalytic activity toward testosterone. Coexpression of CYP3A4 with yeast NADPH-P450 reductase did not give a full activity. Low monooxygenase activity of CYP3A4 was attributed to the insufficient reduction of heme iron of CYP3A4 by NADPH-P450 reductase. To enhance the efficiency of electron transfer from NADPH-P450 reductase to CYP3A4, a fused enzyme was constructed between CYP3A4 and yeast NADPH-P450 reductase. The rapid reduction of the heme iron of the fused enzyme by NADPH was observed. The fused enzyme showed a high testosterone 6beta-hydroxylation activity with a sigmoidal velocity saturation curve. However, the coupling efficiency between NADPH utilization and testosterone 6beta-hydroxylation was only 10%. Finally, coexpression of the fused enzyme and human cytochrome b5 was examined. A significant decrease in the Km value and a remarkable increase in the coupling efficiency were observed. Substrate-induced spectra revealed that the dissociation constant of the fused enzyme for testosterone significantly decreased with coexpression of human cytochrome b5. These results strongly suggest that human cytochrome b5 directly interacts with the CYP3A4 domain of the fused enzyme and modifies the tertiary structure of substrate binding pocket, resulting in tight binding of the substrate and high coupling efficiency

Descriptors:Base Sequence. Cytochrome P-450. Cytochrome b5. DNA Primers. Human. Hydroxylases. Hydroxylation. In Vitro. Kinetics. Microsomes. NADH,

NADPH Oxidoreductases. NADPH-Ferrihemoprotein Reductase. Protein Engineering. Recombinant Fusion Proteins. Saccharomyces cerevisiae. Substrate Specificity. Testosterone
Geographic Locator:UNITED STATES
ISSN:0003-9861
Year:2000
Journal Title:Archives of Biochemistry and Biophysics

32. Title:Amorpha-4,11-diene synthase of Artemisia annua: cDNA isolation and bacterial expression of a terpene synthase involved in artemisinin biosynthesis
View Article: Arch Biochem Biophys 2000 Nov 15;383(2):178-84
CD Volume:333
Print Article: Pages: 178-184
Author(s):Chang YJ Song SH Park SH Kim SU
Author Affiliation:School of Agricultural Biotechnology and the Research Center for New Biomaterials in Agriculture, Seoul National University, Suwon, Korea
Abstract:Artemisia annua, an indigenous plant to Korea, contains an antimalarial sesquiterpene, artemisinin. The first committed step of artemisinin biosynthesis is the cyclization of farnesyl diphosphate by a sesquiterpene synthase to produce an amorphane-type ring system. The aims of this research were to molecularly clone and express amorpha-4,11-diene synthase for metabolic engineering. PCR amplification of genomic DNA with a pair of primers, designed from the conserved regions of sesquiterpene synthases of several plants, produced a 184-bp DNA fragment. This fragment was used in Northern blot analysis as a probe, showing approximately 2.2 kb of a single band. Its sequence information was used to produce 2106 bp of a full-length cDNA sequence including 1641 bp of open reading frame for 546 amino acids (kcs12) through a rapid amplification of cDNA ends (RACE). The deduced amino acid sequence displayed 36% identity with 5-epi-aristolochene synthase of Nicotiana tabacum. A soluble fraction of Escherichia coli harboring kcs12 catalyzed the cyclization of farnesyl diphosphate to produce a sesquiterpene, which was identified through GC-MS analysis as amorpha-4,11-diene
Descriptors:Alkyl and Aryl Transferases. Amino Acid Sequence. Artemisia. Blotting, Northern. Blotting, Southern. DNA, Complementary. Electrophoresis, Polyacrylamide Gel. Escherichia coli. Mass Fragmentography. Molecular Sequence Data. Polyisoprenyl Phosphates. Polymerase Chain Reaction. Protein Engineering. Sequence Homology, Amino Acid. Sesquiterpenes. Support, Non-U.S. Gov't. Tobacco
Geographic Locator:United States
ISSN:0003-9861
Year:2000
Journal Title:Archives of Biochemistry and Biophysics

33. Title:Production of recombinant human apoferritin heteromers
View Article: Arch Biochem Biophys 2000 Dec 1;384(1):116-22
CD Volume:333
Print Article: Pages: 116-122
Author(s):Grace JE Van Eden ME Aust SD
Author Affiliation:Biotechnology Center, Utah State University, Logan 84322, USA
Abstract:We are interested in learning how iron is safely inserted and stored in ferritin. Recombinant DNA technology has considerable potential in determining the functional roles of the two ferritin subunits (H and L). In previous studies, we have observed that recombinant rat H ferritin was repressive to cell growth in both prokaryotic and eukaryotic expression systems (Guo et al., Biochem. Biophys. Res.

Commun. 242, 39-45 (1998)). This results in the protein being expressed at very low levels. This problem was partially bypassed by the use of an inducible expression system, which utilizes T7 RNA polymerase dependent expression of the gene, induced by isopropyl beta-D-thiogalactopyranoside (IPTG). Simultaneously expressing the H and L ferritin genes in this system resulted in only a narrow range of ferritin heteromers, which predominantly consisted of the L subunit. Addition of rifampicin to cultures, 1 h following the induction of protein synthesis by IPTG, increased the production of the H subunit and thus increased the range of ferritin H:L subunit ratios. Simultaneous expression of the H and L ferritin genes in Escherichia coli grown in a deficient medium with minimal iron and with the addition of rifampicin resulted in the production of a range of recombinant human apoferritin heteromers that could be separated based on their subunit composition

Descriptors:Apoferritin. Ceruloplasmin. Chromatography, Ion Exchange. Dimerization. Enzyme Inhibitors. Escherichia coli. Human. Protein Engineering. Recombinant Proteins. Rifampin. Support, U.S. Gov't, P.H.S.. Transfection

Geographic Locator:United States

ISSN:0003-9861

Year:2000

Journal Title:Archives of Biochemistry and Biophysics

34. Title:Structural basis of the synergistic inhibition of glycogen phosphorylase a by caffeine and a potential antidiabetic drug

View Article: Arch Biochem Biophys 2000 Dec 15;384(2):245-54

CD Volume:333

Print Article: Pages: 245-254

Author(s):Tsitsanou KE Skamnaki VT Oikonomakos NG

Author Affiliation:Institute of Biological Research and Biotechnology, The National Hellenic Research Foundation, Athens, Greece

Abstract:Caffeine, an allosteric inhibitor of glycogen phosphorylase a (GPa), has been shown to act synergistically with the potential antidiabetic drug (-)(S)-3-isopropyl 4-(2-chlorophenyl)-1,4-dihydro-1-ethyl-2-methyl-pyridine-3,5,6-tricarboxyl ate (W1807). The structure of GPa complexed with caffeine and W1807 has been determined at 100K to 2.3 A resolution, and refined to a crystallographic R value of 0.210 (Rfree = 0.257). The complex structure provides a rationale to understand the structural basis of the synergistic inhibition between W1807 and caffeine. W1807 binds tightly at the allosteric site, and induces substantial conformational changes both in the vicinity of the allosteric site and the subunit interface which transform GPa to the T'-like state conformation already observed with GPa-glucose-W1807 complex. A disordering of the N-terminal tail occurs, while the loop of polypeptide chain containing residues 192-196 and residues 43'-49', from the symmetry related subunit, shift to accommodate W1807. Caffeine binds at the purine inhibitor site by intercalating between the two aromatic rings of Phe285 and Tyr613 and stabilises the location of the 280s loop in the T state conformation

Geographic Locator:United States

ISSN:0003-9861

Year:2000

Journal Title:Archives of Biochemistry and Biophysics

35. Title:Probiotics in animal nutrition

View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (Special iss.). 12-26

CD Volume:297

Print Article: Pages: 12-26
Author(s):Lopez J
Author Affiliation:Dept. de Zootecnia, Universidade Federal RGS., Porto Alegre 90001-970, Brazil
Document Editor:Aumaitre-A. Lee-B-D. Ha-J-K
Conference Title:Proceedings of 2000 International Symposium Recent Advances in Animal Nutrition, Seoul, Korea, 20-22 April 2000
Language:English
Abstract:This review discusses the advantages of using probiotics in animal nutrition. The characteristics and mode of action of probiotics such as lactic acid bacteria, yeasts, and enzymes were discussed and how biotechnology has played a major role in their use in animal feeding
Descriptors:feed-additives. probiotics. reviews. livestock. enzyme-preparations
Organism Descriptors:Bacillus-subtilis. Lactobacillus. Saccharomyces-cerevisiae. Streptococcus. yeasts. Aspergillus
Supplemental Descriptors:Bacillus. Bacillaceae. Firmicutes. bacteria. prokaryotes. Lactobacillaceae. Saccharomyces. Endomycetales. Ascomycotina. Eumycota. fungi. Streptococcaceae. Deuteromycotina
Subject Codes:LL500. WW000. RR130
Supplementary Info:46 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences
Copyright:Copyright CAB International

36. Title:Role of xylan degrading enzymes in fiber digestion in ruminants
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (Special iss.). 149-157
CD Volume:297
Print Article: Pages: 149-157
Author(s):Ha J K Kam D K Jeon H S Lee S S
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Document Editor:Aumaitre-A. Lee-B-D. Ha-J-K
Conference Title:Proceedings of 2000 International Symposium Recent Advances in Animal Nutrition, Seoul, Korea, 20-22 April 2000
Language:English
Abstract:Recent developments in microorganisms are described in this review. Topics covered are; substrates, enzyme activity, xylanase and esterase genes, expression of heterologous genes in ruminal bacteria, and synergism among hemicellulose-degrading enzymes
Descriptors:digestion. fibre. rumen-microorganisms. xylan. xylanolytic-microorganisms. reviews
Identifiers:xylan endo-1,2-. xylosidase
Organism Descriptors:Beta
Supplemental Descriptors:Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:LL500. RR000. ZZ394
Supplementary Info:33 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences
Copyright:Copyright CAB International

37. Title:Recent advances in cloning technology in the pig - review
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (2). 258-264
CD Volume:297
Print Article: Pages: 258-264

Author(s):Miyoshi K Sato E
Author Affiliation:Laboratory of Animal Reproduction, Graduate School of Agricultural Science, Tohoku University, 1-1 Tsutsumidori-amamiyamachi, Aoba-ku, Sendai 981-8555, Japan
Language:English
Abstract:This review discusses recent advances in the production of cloned pigs by nuclear transfer of cultured cells
Descriptors:animal-cloning. clones. embryos. oocytes. reviews. biotechnology
Identifiers:nuclear transfer
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:WW000. LL220
Supplementary Info:69 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

38. Title:Isolation and genetic transformation of primordial germ cell (PGC)-derived cells from cattle, goats, rabbits and rats
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (5). 587-594
CD Volume:297
Print Article: Pages: 587-594
Author(s):Lee C K Moore K Scales N Westhusin M Newton G Im K S Piedrahita J A
Author Affiliation:Department of Animal Science, Texas A&M University, College Station, TX 77843, USA
Language:English
Abstract:At present embryonic stem (ES) cells with confirmed pluripotential properties are only available in the mouse. Recently, we were able to isolate, culture and genetically transform primordial germ cell (PGC)-derived cells from pig embryos and demonstrate their ability to contribute to chimera development in the pig. In order to determine whether the system we developed could be used to isolate embryonic germ (EG) cells from other mammalian species, we placed isolated PGCs from cattle, goats, rabbits and rats in culture. Briefly, PGCs were isolated from fetuses of cow (day 30-50), goat (day 25), rabbit (day 15-18) and rat (day 11-12), and plated on STO feeder cells in Dulbecco's modified Eagle's medium (DMEM):Ham's F10 medium (1:1) supplemented with 0.01 mM nonessential amino acids, 2 mM L-glutamine, 0.1 mM beta -mercaptoethnol, soluble recombinant human stem cell factor (SCF; 40ng/ml), human basic fibroblast growth factor (bFGF; 20ng/ml) and human leukemia inhibitory factor (LIF; 20ng/ml). For maintenance of the cells, colonies were passed to fresh feeders every 7-10 days. In all species tested, we were able to obtain and maintain colonies with ES-like morphology. Their developmental potential was tested by alkaline phosphatase (AP) staining and in vitro differentiation assay. For genetic transformation, cells were electroporated with a construct containing the green fluorescent protein (GFP) under the control of the cytomegalovirus (CMV) promoter. GFP-expressing colonies were detected in cattle, rabbits and rats. These results suggest that PGC-derived cells from cattle, goats, rabbits and rats can be isolated, cultured, and genetically transformed, and provide the basis for analyzing their developmental potential and their possible use for the precise genetic modification of these species
Descriptors:genetic-transformation. alkaline-phosphatase. amino-acids. chimaeras. embryos. growth-factors. in-vitro. enzymes. culture-media.

embryonic-stem-cells. in-vitro-culture. isolation. techniques. biotechnology
Organism Descriptors:cattle. goats. rabbits. rats. mice. pigs
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Capra. Leporidae. Lagomorpha. small-mammals. Muridae. rodents. Sus-scrofa. Sus. Suidae. Suiformes
Subject Codes:LL240. WW000. LL250
Supplementary Info:46 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

39. Title:Effect of superovulatory regimens on ovarian response and embryo production in fine wool sheep in tropics
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (5). 595-599
CD Volume:297
Print Article: Pages: 595-599
Author(s):Naqvi S M K Gulyani R Pareek S R
Author Affiliation:Division of Physiology, Central Sheep & Wool Research Institute, Avikanagar, Via-Jaipur, Rajasthan 304-501, India
Language:English
Abstract:Fine wool sheep (n=18, Rambouillet and Bharat Merino) maintained in a tropical environment (Avikanagar, India) were allocated to three treatment groups. Oestrus was induced with two injections of PGF2 alpha (10 mg im) given 10 days apart. Superovulation treatment started 2 days prior to the second injection of PGF2 alpha . Each ewe was treated with a total dose of 25 units FSH (Super-OV) i.m. every 12 h over 3 days; Group 2 were also injected i.m. with 200 IU PMSG at the first injection of FSH; Group 3 was treated as in Group 2 and also with GnRH (4 micro g Buserelin) at the onset of oestrus. The ewes in oestrus were mated with a fertile ram. Ovarian examination and recovery of embryos and ova were performed at laparoscopy and laparotomy on day 3 or 4 after mating. Data for onset of oestrus, duration of oestrus, number of corpora lutea (CL), number of unovulated large follicle (LF), embryo recovery rate, embryo quality and fertilization were recorded for the 3 groups. Ewes in Group 1 came into oestrus later ($P<0.05$; 50.0 plus or minus 7.29 h) than the ewes in Groups 2 (24.5 plus or minus 3.58 h) and 3 (32.5 plus or minus 3.58 h). The duration of oestrus, ovarian size and ovarian response (number of CL and LF) did not differ significantly among the 3 groups. The proportion of ewes with a superovulatory response (more than or equal to 2 CL) was the lowest (50%) in Group 1 treated with FSH alone but ova/embryo recovery (100%) and fertilization (100%) was significantly ($P<0.05$) higher than in Group 2 (58.3 and 85.7%, respectively) and Group 3 (48.6 and 50%, respectively). It is concluded that in tropical fine wool sheep, there is no difference in the 3 treatments for yield of good quality embryos but ovarian response and ovulation rate increased on additional use of PMSG and GnRH respectively to FSH alone
Descriptors:embryos. ovaries. tropics. oestrus. ewes. fertilization. FSH. GnRH. ova. ovulation. ovulation-rate. PMSG. superovulation. biotechnology
Organism Descriptors:sheep
Supplemental Descriptors:Ovis. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. WW000
Supplementary Info:21 ref
ISSN:1011-2367

Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences
Copyright:Copyright CAB International

40. Title:The effects of dimethyl-sulfoxide added to the fertilization medium on the motility and the acrosome reaction of spermatozoa and the subsequent development of oocytes in bovine
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (6). 739-747
CD Volume:297
Print Article: Pages: 739-747
Author(s):Tsuzuki Y Duran D H Sawamizu M Ashizawa K Fujihara N
Author Affiliation:Laboratory of Animal Reproduction, Faculty of Agriculture, Miyazaki University, Miyazaki 889-2192, Japan
Language:English
Abstract:This experiment was conducted to evaluate the influence of dimethyl-sulfoxide (DMSO; 0, 5, 50, 100 and 500 micro M) on the motility and acrosome reaction of frozen-thawed spermatozoa from 3 bulls (A, B and C). The developmental capacity of cattle embryos fertilized in a medium containing DMSO at various concentrations was also examined. DMSO had negligible effects on sperm motility and acrosome reaction in all 3 bulls. The development rates from the 2-cell to the 16-cell stage on the 3rd day after fertilization in medium with 50, 100 and 500 micro M DMSO with semen from bull B and up to the blastocyst stage after fertilization in medium containing 5, 50, 100 and 500 micro M DMSO with semen from bull A were significantly higher ($P<0.05$) than those of the control (0 micro M DMSO) group for each bull. The rates of blastocysts formed per cleaved embryo for the 5 to 500 micro M DMSO groups for bull A and the 5 to 100 micro M DMSO groups for bull C were significantly higher ($P<0.05$) than those for their 0 micro M groups respectively. These results indicate that DMSO at micromolar level used for in vitro fertilization might stimulate the development of embryos for some bulls
Descriptors:acrosome. acrosome-reaction. fertilization. motility. oocytes. spermatozoa. blastocyst. embryos. bulls. dimethyl-sulfoxide. in-vitro. embryonic-development. biotechnology
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. LL600. WW000
Supplementary Info:45 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences
Copyright:Copyright CAB International

41. Title:Glucose and its role in generating reactive oxygen species required for mouse sperm fertilizing ability
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (6). 748-756
CD Volume:297
Print Article: Pages: 748-756
Author(s):Lin S C Chen M C Huang A J Salem B Li K C Chou K
Author Affiliation:Department of Animal Science, National Ilan Institute of Technology, Ilan, Taiwan
Language:English
Abstract:Effects of xanthine (X), xanthine oxidase (XO), catalase (C), H2O2 and carbohydrates on sperm capacitation, acrosome reaction and fertilizing ability in vitro were examined. Glucose alone, but not fructose, supported the maximum rate of sperm capacitation and acrosome reaction.

In combination with X, XO and C (XXOC) or H2O2, fructose alone also supported maximum capacitation, acrosome reaction and fertilization. Insufficient or excessive amounts of H2O2 decreased sperm capacitation and the acrosome reaction. In order to understand how glucose generates H2O2 or other reactive oxygen species in sperm cells, 6-aminonicotinamide, an inhibitor of the pentose-phosphate pathway and apocynin, an inhibitor of NADPH oxidase, were added to sperm suspensions in glucose-containing medium. Sperm capacitation, acrosome reaction and fertilization were consequently inhibited by either one of these compounds. These inhibitory effects were nullified by addition of XXOC. These results support the hypothesis that glucose, in addition to being a substrate for glycolysis, facilitates sperm capacitation and the acrosome reaction by generating reactive oxygen species through glucose-6-phosphate dehydrogenase and NADPH oxidase

Descriptors:fertilization. fertilizing-ability. spermatozoa. acrosome. acrosome-reaction. capacitation. carbohydrates. catalase. fructose. glycolysis. in-vitro. inhibition. xanthine-oxidase. glucose. hydrogen-peroxide. xanthine. biotechnology

Organism Descriptors:mice

Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals

Subject Codes:LL250. LL600. WW000

Supplementary Info:32 ref

ISSN:1011-2367

Year:2000

Journal Title:Asian-Australasian Journal of Animal Sciences

42. Title:A study of the milking and reproduction performances of grazing indigenous cattle at a semi urban area of Bangladesh

View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (6). 837-841

CD Volume:297

Print Article: Pages: 837-841

Author(s):Islam S S Ashraf A Islam A B M M

Author Affiliation:Discipline of Biotechnology, Khulna University, Khulna-9208, Bangladesh

Language:English

Abstract:The study was conducted in a semi urban area of Bangladesh between October 1998 and January 1999. It was based on a field survey by a prepared questionnaire. Various milking and reproduction performance were analysed. The effects of grazing time were significant on age at weaning (AW) (P<0.001), age at first oestrus (AFH) (P<0.001), age at first conception (AF conception) (P<0.001), age at first calving (AF calving) (P<0.001), postpartum oestrus period (PPHP) (P<0.001), calving interval (CI) (P<0.001), lactation length (LL) (P<0.001) and total lactational production (TLP) (P<0.001). The effects of concentrate feed were significant on AW (P<0.01), AFH (P<0.01), AF conception (P<0.001), AF calving (P<0.001), PPHP (P<0.001) CI (P<0.001), LL (P<0.001) and TLP (P<0.001). The effects of management level were significant on AW (P<0.001), PPHP (P<0.01), CI (P<0.001), daily milk yield (DMY) (P<0.05) and TLP (P<0.001). The overall mean values were 251.88 plus or minus 2.97 days for AW, 37.29 plus or minus 0.33 months for AFH, 38.43 plus or minus 0.34 months for AF conception, 47.62 plus or minus 0.34 months for AF calving, 1.30 plus or minus 0.02 number of services per conception (NSPC), 191.57 plus or minus 3.92 days for PPHP, 17.02 plus or minus 0.15 months for CI, 2.49 plus or minus 0.06 kg for DMY, 247.23 plus or minus 3.51 days for LL and 590.40 plus or minus 15.00 kg for TLP

Descriptors:lactation-duration. grazing-time. milking. reproduction. age-at-first-calving. age-at-first-conception. reproductive-performance. calving. calving-interval. conception. lactation. milk. milk-yield. questionnaires. weaning. farm-surveys. concentrates. oestrus. animal-husbandry. tropics
Geographic Locator:Bangladesh
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. South-Asia. Asia. Least-Developed-Countries. Developing-Countries. Commonwealth-of-Nations
Subject Codes:LL110. LL250. LL520
Supplementary Info:15 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

43. Title:Improvements in nuclear transfer procedures will increase commercial utilization of animal cloning - review
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (6). 856-860
CD Volume:297
Print Article: Pages: 856-860
Author(s):Stice S L Gibbons J Rzucidlo S J Baile C A
Author Affiliation:Department of Animal and Dairy Science, University of Georgia, Athens, GA 30602, USA
Language:English
Abstract:The potential applications of cloning by nucleus transfer in the production of transgenic livestock are described. Problems with these techniques are discussed
Descriptors:animal-cloning. reviews. transgenics. nuclei. embryos. livestock. biotechnology
Subject Codes:WW000. LL250. LL240
Supplementary Info:26 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

44. Title:Effect of oviductal cell co-culture on cleavage and development of buffalo IVF embryos
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (7). 894-896
CD Volume:297
Print Article: Pages: 894-896
Author(s):Yadav P S Khanna S Hooda O K Sethi R K
Author Affiliation:Central Institute for Research on Buffaloes, Sirsa Road, Hisar, Haryana, India
Language:English
Abstract:In the present study the cleavage and development of buffalo embryos was studied with homologous (buffalo) and heterologous (goat) oviductal cell co-culture systems. The cleavage rate improved significantly ($P<0.01$) in both homologous and heterologous co-culture as compared with controls (55.3, 46.8 and 11.4% respectively). The morula formation rate using homologous and heterologous oviductal cells also increased significantly as compared with the control group (43.6, 21.9 and 1.9% respectively). There was no blastula formation in the control group, but addition of oviductal cells either from homologous or heterologous species significantly increased blastula formation (9.5, 12.5%). The

cleavage rate and embryo development was slightly better (non-significant) in homologous as compared to heterologous oviductal cell culture. It was concluded that the use of oviductal cell co-culture (homologous and heterologous species) have significantly improved cleavage and development of buffalo embryos in vitro
Descriptors:culture-techniques. embryos. embryonic-development. fertilization. germ-cells. in-vitro. slaughter. morula. oviducts. biotechnology
Organism Descriptors:buffaloes
Supplemental Descriptors:Bubalus. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. WW000. ZZ900
Supplementary Info:13 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

45. Title:Effects of GnRH on the plasma FSH, LH and estradiol levels at estrus induced with injection of PGF2 alpha and eCG in prepubertal buffaloes (Bubalus bubalis)
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (7). 897-900
CD Volume:297
Print Article: Pages: 897-900
Author(s):Singh C Madan M L
Author Affiliation:National Dairy Research Institute, Karnal 132 001, Haryana, India
Language:English
Abstract:The experiment was conducted to study the effect of GnRH administration at induced oestrus on pituitary and ovarian response in buffalo heifers. Eight Murrah river buffaloes from the herd of the National Dairy Research Institute (Haryana, India) of 12 to 13 months of age were treated with PGF2 alpha and equine chorionic gonadotropin (eCG). GnRH (Fertagyl; 200 micro g) was injected intravenously at oestrus in four heifers (treated group) while saline (2 ml) was injected intravenously in the remaining four heifers (control group). Blood was collected through a jugular catheter to estimate plasma FSH, LH and oestradiol level. The pretreatment plasma FSH, LH and estradiol values ranged from 8.46 plus or minus 1.97 to 12.31 plus or minus 1.30 ng/ml, 0.87 plus or minus 0.21 to 1.19 plus or minus 0.29 ng/ml and 19.09 plus or minus 2.38 to 20.24 plus or minus 1.00 pg/ml respectively. The plasma oestradiol concentration increased significantly ($P<0.05$) within 24 h after eCG administration and reached peak levels of 154.09 plus or minus 17.28 pg/ml and 181.95 plus or minus 31.82 pg/ml at oestrus in treatment and control groups respectively. The plasma FSH and LH concentrations did not increase during follicular development after eCG administration while initial significant ($P<0.05$) increases in both plasma FSH and LH concentrations occurred within 5 and 10 min, reaching peak levels of 110.06 plus or minus 23.56 ng/ml and 13.15 plus or minus 3.13 ng/ml respectively within 90 min after GnRH injection. A sharp and significant decline in plasma oestradiol concentration (59.27 plus or minus 8.78 pg/ml) associated with synchronized ovulation within 24 h after GnRH injection was recorded. The observations suggest that the hypophysis of immature buffaloes treated with eCG have gonadotropins awaiting the releasing factor to evoke release of gonadotropin during the follicular phase to induce synchronized ovulation
Descriptors:estradiol. oestrus. FSH. GnRH. LH. heifers. pituitary. Murrah. ovaries. ovulation. hypothalamic-releasing-hormones. chorionic-gonadotropin. prostaglandins. gonadotropins. tropics. biotechnology

Geographic Locator:India
Organism Descriptors:buffaloes
Supplemental Descriptors:Bubalus. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations
Subject Codes:LL250. LL600. WW000
Supplementary Info:14 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences
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46. Title:Effect of caffeine, cAMP and cattle seminal plasma on freezability of buffalo bull semen
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (7). 901-905
CD Volume:297
Print Article: Pages: 901-905
Author(s):Singh P Raina V S
Author Affiliation:Artificial Insemination Laboratory, National Dairy Research Institute, Karnal 132 001, India
Language:English
Abstract:An experiment was conducted to investigate the effect of caffeine, cAMP and cattle seminal plasma on preservation of semen at ultra low temperature (-196 deg C). Each semen sample was divided into 4 parts equal in volume and sperm concentration; 3 were treated with caffeine, or cAMP, or cattle seminal plasma (CSP) and the 4th was kept as control. Sperm motility, abnormal spermatozoa, live-dead count and acrosomal damage were studied at different stages of freeze preservation; just after dilution, at 5 deg C, at glycerolisation, before freezing, just after freezing, 24 h of storage, and a week of storage. Sperm motility (58.39, 61.33, 52.00 and 50.39%), non-eosinophilic spermatozoa (72.55, 69.98, 63.31 and 67.64%), abnormal spermatozoa (5.71, 4.98, 8.04 and 5.66%) and acrosomal damage (13.28, 13.33, 14.80 and 14.65%) were observed in cAMP, caffeine, CSP and control respectively, at every stage of freeze preservation. It is concluded that freezability of buffalo semen can be improved through the addition of caffeine followed by cAMP and CSP
Descriptors:caffeine. semen. cryopreservation. seminal-plasma. motility. semen-preservation. spermatozoa. c-AMP. semen-diluent-additives. freezing. biotechnology
Geographic Locator:India
Organism Descriptors:buffaloes
Supplemental Descriptors:Bubalus. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations
Subject Codes:LL250. WW000. LL600. LL700
Supplementary Info:24 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences
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47. Title:Possible application of animal reproductive researches to the restoration of endangered and/or extinct wild animals. Review
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (7). 1026-1034
CD Volume:297
Print Article: Pages: 1026-1034

Author(s):Fujihara N Xi Y M
Author Affiliation:Animal Resource Science Section, Division of Bioresource and Bioenvironmental Sciences, Graduate School, Kyushu University, Fukuoka 812-8581, Japan
Language:English
Abstract:In this review, most recently developed methods for improving reproduction performance of domesticated animals such as cattle, pigs and chicken have been considered to be also usable for restoring some sorts of endangered and/or extinct wild animals in the very near future. Especially, the techniques for in vitro storage of gametes obtained from dead animals shortly after the death, probably 24 h following the sacrifice are also available for obtaining some of experimental specimens. In case of the endangered animals, nobody will be allowed to use any tissues from the living animals, therefore, the use of skin tissues from these bodies is another possibility of restoring the living animals. Regarding the use of skin tissues, the most highly usable tools must be the cloning techniques for reviving rare cells from the living body. Most possible techniques for cloning cells is nuclear transfer from rare species to highly relative species, and this is the case of germ cells, e.g., primordial germ cells (PGC) of avian species. One of the possibilities is the nuclear transfer of Crested Ibis (Nipponia nippon) to the PGC of fowls, resulting in the PGC with transferred nucleus from the ibis. In mammalian species, the same procedure as in the case of birds would be successful, e.g., the removed nucleus from Giant Pandas will be transferred to the cell, such as somatic cells or germ cells from black bears or lesser pandas, leading to the production of transnucleared cells in the body of female black bears. These two cases are most promising techniques for reviving endangered animals in the world, particularly in Asian countries, mainly in China. It is concluded that the production of cloned animals carrying transnucleared cells from endangered animals, such as Giant Pandas and Crested Ibis, may be reproduced gradually in the near future. Scientists are, therefore, required to convert the paradigm from domestic animals to wild animals, including endangered and/or extinct animals
Descriptors:wild-animals. poultry. animal-breeding. clones. animal-cloning. domestic-animals. gametes. germ-cells. in-vitro. reproduction. endangered-species. wild-birds. reviews. cryopreservation. research. biotechnology
Geographic Locator:China
Identifiers:nuclear transfer
Organism Descriptors:cattle. fowls
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. East-Asia. Asia. Developing-Countries
Subject Codes:LL250. LL240. WW000. YY200. PP710
Supplementary Info:4 pp. of ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

48. Title:DNA fingerprinting of red jungle fowl, village chicken and broilers
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (8). 1040-1043
CD Volume:297
Print Article: Pages: 1040-1043
Author(s):Mohd Azmi M L Ali A S Kheng W K

Author Affiliation:Faculty of Veterinary Medicine, Universiti Putra Malaysia, 43400 UPM, Serdang, Selangor DE, Malaysia
Language:English
Abstract:The genomic mapping of Red Jungle Fowl (Gallus gallus) from Malaysia, Malaysian local village chickens, and broilers was carried out by random amplified polymorphic DNA (RAPD) technique. Two different sets of arbitrary primers were used (Operon OPA01-20 and Genemed GM01-50). All the genomes of the three types of chickens were amplified with OPA01-20 primers. The genomes of the Red Jungle Fowl and local village chickens were further amplified with GM01-50 primers. Analysis of the results based on band sharing (BS) and the molecular size of individually amplified DNA fragments showed that Red Jungle Fowl and local village chickens had a similarity of 66% with Operon primers 01-20, there was a similarity of 64% between local village chicken and broiler, and 63% when DNA bands between Red Jungle Fowl and broiler were compared. With GM01-50, the BS between Red Jungle Fowl and local village chicken increased to 72%. The results showed that the local village chicken is more closely related to Red Jungle Fowl than to broiler. On the other hand, broiler is 1% closer in genetic distance to local village chicken than to Red Jungle Fowl. The results also indicated that primers like OPA-7, 8 and 9 can be used as type specific DNA markers for these three species of chickens
Descriptors:broilers. DNA. genetic-distance. genomes. genetic-polymorphism. tropics. random-amplified-polymorphic-DNA. types. biotechnology. poultry
Geographic Locator:Malaysia
Organism Descriptors:fowls. Gallus-gallus. jungle-fowls
Supplemental Descriptors:Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. South-East-Asia. Asia. Developing-Countries. Threshold-Countries. ASEAN-Countries. Commonwealth-of-Nations
Subject Codes:LL240. WW000
Supplementary Info:20 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

49. Title:Effects of PGF2 alpha and GnRH during different ovarian status at onset of puberty in Murrah buffalo heifers (Bubalus bubalis)
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (8). 1059-1062
CD Volume:297
Print Article: Pages: 1059-1062
Author(s):Singh C Madan M L
Author Affiliation:National Dairy Research Institute, Karnal-132001, Haryana, India
Language:English
Abstract:The objective of the investigation was to study the effect of intramuscular PGF2 alpha and GnRH on oestrus behaviour and ovarian response in Murrah buffalo heifers. Twelve Murrah buffalo heifers at 32 months of age that had not exhibited behavioural oestrus symptom were included in the experiment which was performed between July and September (year not given). Four heifers were in follicular phase (plasma estradiol 57.05 plus or minus 12.52 pg/ml), another 4 heifers were in luteal phase (plasma progesterone 2.24 plus or minus 0.25 ng/ml) while the ovaries of the remaining 4 heifers were inactive (estradiol 23.70 plus or minus 1.66 pg/ml and progesterone 0.32 plus or minus 0.06 ng/ml). PGF2 alpha (25 mg, Lutalyse, administered by

intramuscular injection) and GnRH (200 micro g, Fertagyl, administered intravenously) was administered to each heifer at intervals of 10 days. The plasma progesterone concentration decreased within 48 h after PGF2 alpha injection; this was followed by follicular growth, oestrus and ovulation. GnRH administration induced follicular growth, elevation of plasma estradiol concentration with subsequent exhibition of behavioural oestrus in 2 out of 4 heifers with inactive ovaries. The observation reveals that Murrah buffalo heifers at 32 months of age have developed receptors for PGF2 alpha and GnRH on ovarian and pituitary tissue respectively and respond to the single injection of PGF2 alpha and GnRH similarly to mature cycling animals
Descriptors:GnRH. Murrah. ovaries. sexual-maturity. estradiol. oestrus. ovulation. pituitary. progesterone. receptors. prostaglandins. biotechnology
Organism Descriptors:buffaloes
Supplemental Descriptors:Bubalus. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. LL600. WW000
Supplementary Info:13 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

50. Title:A study of some economic traits of indigenous cattle and their crossbreeds in southern Bangladesh
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (9). 1189-1192
CD Volume:297
Print Article: Pages: 1189-1192
Author(s):Ashraf A Islam S S Islam A B M M Ali S Z
Author Affiliation:Discipline of Biotechnology, Khulna University, Khulna-9208, Bangladesh
Language:English
Abstract:The experiment was conducted on 69 cows to identify the quantitative variations of some economic traits of 5 genetic groups as Local x Friesian F1, Local x Sahiwal F1, Local (indigenous zebu type), Local x Sindhi F1, and Local x Hariana F1. The traits studied were age at weaning, age at first heat, age at first conception, services per conception, daily milk yield, lactation length, lactation yield and postpartum heat period. The records on milking and reproduction performances of cows and heifers were obtained from farm register and by interviewing the farmers. The lowest age at weaning, age at first heat and age at first conception were 5.37 plus or minus 0.24, 27.17 plus or minus 1.72 and 27.83 plus or minus 1.82 months respectively in Local x Hariana F1. Services per conception were lowest in Local x Sahiwal F1 (1.08 plus or minus 0.18) although not significantly affected by farms, genetic groups and farm x genetic groups interaction. Average daily milk yield was highest in Local x Friesian F1 (5.81 plus or minus 0.40 kg). Lactation duration and lactation yield were highest in Local x Sahiwal F1 (299.38 x 9.74 days and 1863.00 plus or minus 141.00 kg respectively). Average postpartum heat period was lowest in Local x Sindhi F1 (3.19 plus or minus 0.38 months). Least squares ANOVA showed that farm had effect (P<0.001) on age at weaning, age at first heat, age at first conception and postpartum heat period. There was insignificant effect of farm on services per conception, daily milk yield, lactation duration and lactation yield, whereas genetic groups had a significant effect for all the traits under review except services per conception. Farm x genetic groups interaction was

insignificant for all of the traits under consideration except age at weaning
Descriptors:performance-traits. reproductive-performance. milk-yield. conception. age-at-first-conception. age-at-first-calving. age-at-first-mating. lactation-duration. reproduction. crossbreeding. cattle-breeds. tropics. Friesian. Sahiwal. Red-Sindhi. Hariana. genotypes. lactation. breed-differences. crossbreds. postpartum-period. performance. cows. heifers. genotype-environment-interaction
Geographic Locator:Bangladesh
Identifiers:native breeds
Organism Descriptors:cattle. zebu
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. South-Asia. Asia. Least-Developed-Countries. Developing-Countries. Commonwealth-of-Nations
Subject Codes:LL240. LL110. LL250
Supplementary Info:14 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

51. Title:Imc-415 gene expression in the proliferation and cell death phases of mammary epithelial cells
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (9). 1201-1204
CD Volume:297
Print Article: Pages: 1201-1204
Author(s):Ha S H Lee D Y Kho Y J Baik M G Choi Y J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea Republic
Language:English
Abstract:We examined expression patterns of imc-415 gene in mammary gland and in HC11 mammary epithelial cells in culture. mRNA levels of imc-415 gene were higher at pregnancy and involution stages of mouse mammary gland compared with lactation period. Expression of imc-415 gene was induced with serum starvation or treatment with Fas monoclonal antibody in HC11 mammary epithelial cells in culture
Descriptors:mammary-glands. epithelium. messenger-RNA. gene-expression. genes. involution. pregnancy. tissue-culture. mast-cells
Identifiers:mouse lactation
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL600. LL250. WW000
Supplementary Info:15 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

52. Title:Effects of replacing spray dried plasma protein with spray dried porcine intestine hydrolysate on ileal digestibility of amino acids and growth performance in early-weaned pigs
View Article: Asian-Australasian Journal of Animal Sciences. 2000. 13 (12). 1738-1742
CD Volume:297
Print Article: Pages: 1738-1742
Author(s):Kim J H Chae B J Kim Y G

Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Language:English
Abstract:A study was conducted to determine the ileal digestibility (ID) of amino acids and feeding values of spray dried plasma protein (SDPP) and spray dried porcine intestine hydrolysate (SDPI) in early-weaned pigs. Twelve pigs aged 18 days old (Landrace x Yorkshire x Duroc; 5.83 plus or minus 0.51 kg BW) were cannulated in the terminal ileum for determination of ID of amino acids. Ninety pigs (6.28 plus or minus 0.1 kg, 18 days old) were also employed for a feeding trial during phase I period. Treatments were: (1) 6% SDPP, (2) 6% SDPI and (3) 3% SDPP+3% SDPI. The apparent and true ID values of the essential amino acids except leucine, methionine and valine were lower (P<0.01) in SDPI than in SDPP. The average apparent ID of essential amino acids in SDPP and SDPI were 75.63 and 71.30%, and the average true ID of essential amino acids 84.83 and 80.51%, respectively. The ADG and feed conversion ratio in piglets fed the 6% SDPP diet were better (P<0.01) than in those fed the 6% SDPI diet. When 3% of SDPP was replaced by SDPI, however, the growth rate and efficiency of pigs were comparable to those in pigs fed 6% SDPP. In conclusion, SDPP can be partially replaced by SDPI without any detrimental effect on growth performance in early-weaned pigs
Descriptors:blood-protein. early-weaning. essential-amino-acids. feed-conversion-efficiency. ileum. liveweight-gain. piglets. protein-digestibility. protein-hydrolysates. protein-supplements. supplementary-feeding
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL510. LL520
Supplementary Info:17 ref
ISSN:1011-2367
Year:2000
Journal Title:Asian-Australasian Journal of Animal Sciences

53. Title:Plant regeneration from mature embryo-derived callus of Australian rice (Oryza sativa L.) varieties
View Article: Australian Journal of Agricultural Research. 2000. 51 (2). 305-312
CD Volume:324
Print Article: Pages: 305-312
Author(s):Azria D Bhalla P L
Author Affiliation:Plant Molecular Biology and Biotechnology Laboratory, Institute of Land and Food Resources, University of Melbourne, Parkville, Victoria 3010, Australia
Language:English
Abstract:In vitro plant regeneration from callus induced from embryos of mature seeds of 4 Australian varieties (Amaroo, Millin, Pelde and Langi) of rice was studied. Observations of callus induction on Murashige and Skoog (MS) and N6 media indicated that MS medium supplemented with 0.5-2.0 mg/L of 2,4-D is suitable for callus formation from the varieties tested. Comparison of shoot initiation on medium containing BAP [benzyladenine], BAP + NAA, and thidiazuron (TDZ) + NAA indicated that these varieties prefer BAP + NAA or TDZ + NAA in the shoot initiation medium. Partial desiccation, resulting in up to 20% loss of fresh weight of callus, significantly increased the regeneration frequency of the 4 rice varieties tested. The varieties showed varied response to number of shoots produced per callus. Regenerated shoots were rooted on plant growth regulator free medium. The plants regenerated were

phenotypically normal and fertile. Our study showed that callus derived from mature embryos of these rice varieties are amenable to multiple shoot formation, and could be used for genetic transformation studies
Descriptors:callus. rice. regeneration. 2,4-D. desiccation. embryo-culture. plant-growth-regulators. NAA. benzyladenine. thidiazuron. cereals. biotechnology. auxins. cytokinins
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. FF170. WW000
Supplementary Info:31 ref
ISSN:0004-9409
Year:2000
Journal Title:Australian Journal of Agricultural Research
Copyright:Copyright CAB International

54. Title:Two genetic linkage maps of mungbean using RFLP and RAPD markers
View Article: Australian Journal of Agricultural Research. 2000. 51 (4). 415-425
CD Volume:324
Print Article: Pages: 415-425
Author(s):Lambrides C J Lawn R J Godwin I D Manners J Imrie B C
Author Affiliation:CSIRO Tropical Agriculture, St. Lucia, Brisbane, Qld 4067, Australia
Language:English
Abstract:Two genetic linkage maps of mung bean (Vigna radiata) derived from the cross BerkenxACC 41 are reported. The F2 map constructed from 67 individuals consisted of 110 markers (52 RFLP and 56 RAPD) that grouped into 12 linkage groups. The linked markers spanned a total map distance of 758.3 cM. A recombinant inbred (RI) population derived from the 67 F2 individuals was used for the generation of an additional linkage map. The RI map, composed entirely of RAPD markers, consisted of 115 markers in 12 linkage groups. The linked markers spanned a total map distance of 691.7 cM. Using a framework set of RFLP markers, the F2 map was compared with another F2 mung bean map constructed in Minnesota. In general, the order of these markers was consistent between maps. Segregation distortion was observed for some markers. 14.5% (16/110) of mapped F2 markers and 24% (28/115) of mapped RI markers segregated with distorted ratios. Segregation distortion occurred in each successive generation after the F2. The regions of distortion identified in the Australian maps did not coincide with regions of the Minnesota map
Descriptors:linkage. restriction-fragment-length-polymorphism. gene-mapping. mung-beans. random-amplified-polymorphic-DNA. grain-legumes. biotechnology
Geographic Locator:Australia
Organism Descriptors:Vigna-radiata. Fabaceae
Supplemental Descriptors:Vigna. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries
Subject Codes:FF005. WW000. FF020
Supplementary Info:26 ref
ISSN:0004-9409
Year:2000
Journal Title:Australian Journal of Agricultural Research
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55. Title:Association of the Leu127 variant of the bovine growth hormone (bGH) gene with increased yield of milk, fat, and protein in Australian Holstein-Friesians

View Article: Australian Journal of Agricultural Research. 2000. 51 (4). 515-522
CD Volume:324
Print Article: Pages: 515-522
Author(s):Shariflou M R Moran C Nicholas F W
Author Affiliation:Department of Animal Sciences, University of Sydney, NSW 2006, Australia
Language:English
Abstract:The occurrence of the Leu127/Val127 variants of the bovine growth hormone (bGH) gene and their effect on milk production traits was investigated in Australian Holstein-Friesian cattle. 384 animals, from 4 herds belonging to the University of Sydney at Camden (New South Wales, Australia) were genotyped for the Leu127/Val127 variants, with RFLP methodology, using PCR and AluI digestion of PCR products (AluI-RFLP). Alleles Leu127 and Val127 occurred with frequencies of 82% and 18% respectively. The quantitative effect of this polymorphic site on milk-production traits was estimated from lactation data recorded between 1986 and 1996 and test-day data. Results from the 2 data sets consistently showed that the Leu127 allele is associated with higher yield of milk, fat and protein and is dominant to Val127. The average effects of the gene substitution are 95 litres for milk yield, 7 kg for fat yield, and 3 kg for protein yield per lactation. This locus may be directly responsible for quantitative variation or it may be a marker for a closely linked quantitative trait locus (QTL) for milk-production traits in Australian dairy cattle. In either case, it will be useful as an aid to selection for improvement of milk production traits. As the Leu127 allele is dominant, selection of AI sires homozygous for the Leu127 allele (Leu127/Leu127) will result in maximum benefit without the need for genotyping cows
Descriptors:somatotropin. milk. milk-fat. alleles. cows. dairy-cattle. Holstein-Friesian. lactation. milk-yield. genetic-polymorphism. milk-composition. restriction-fragment-length-polymorphism. genes. biotechnology
Geographic Locator:Australia
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries
Subject Codes:LL240. LL110. WW000
Supplementary Info:32 ref
ISSN:0004-9409
Year:2000
Journal Title:Australian Journal of Agricultural Research

56. Title:Genetic variability in a collection of Stagonospora nodorum isolates from Western Australia
View Article: Australian Journal of Agricultural Research. 2000. 51 (6). 679-684
CD Volume:324
Print Article: Pages: 679-684
Author(s):Murphy N E Loughman R Appels R Lagudah E S Jones M G K
Author Affiliation:WA State Agricultural Biotechnology Centre, Murdoch University, Murdoch, WA 6150, Australia
Language:English
Abstract:Stagonospora nodorum [Phaeosphaeria nodorum] isolates were collected from the Western Australian grain-belt during 1993. These isolates and a subset of isolates taken from a single location were used to assay the level of variation within the pathogen population. The isolates were compared using anonymous nuclear DNA markers. Three low copy-number and a single high copy-number RFLP probe were used to generate

polymorphisms. The collection exhibited a high genotypic diversity for the high copy-number probe, a result consistent with the high level of sexual reproduction previously found in the fungal population. The high level of genotypic diversity was consistent with previous international studies. There was no evidence of differentiation between the total collection of isolates and the subset of isolates taken from the single location. Further work needs to be undertaken to determine if the aggressiveness of the pathogen is influenced by the host genotype

Descriptors:plant-pathogens. restriction-fragment-length-polymorphism. plant-pathogenic-fungi. plant-diseases. fungal-diseases. genetic-diversity. cereals. plant-pathology

Geographic Locator:Australia. Western-Australia

Identifiers:isolates. Stagonospora nodorum. Phaeosphaeria nodorum. Phaeosphaeria. Coelomycetes. mitosporic fungi. Phaeosphaeriaceae

Organism Descriptors:Stagonospora

Supplemental Descriptors:Deuteromycotina. Eumycota. fungi. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Australia. Stagonospora. Dothideales. Ascomycotina

Subject Codes:FF610. FF005. ZZ395

Supplementary Info:15 ref

ISSN:0004-9409

Year:2000

Journal Title:Australian Journal of Agricultural Research

57. Title:Effect of sulfur fertilisation on oil accumulation, acetyl-CoA concentration, and acetyl-CoA carboxylase activity in the developing seeds of rapeseed (Brassica campestris L.)

View Article: Australian Journal of Agricultural Research. 2000. 51 (8). 1023-1029

CD Volume:324

Print Article: Pages: 1023-1029

Author(s):Altaf Ahmad Ishrat Khan Abdin M Z

Author Variant:Ahmad-A. Khan-I

Author Affiliation:Centre for Biotechnology, Faculty of Science, Hamdard University, New Delhi-110 062, India

Language:English

Abstract:The effect of sulfur (S) fertilizer application on oil accumulation, acetyl-CoA concentration, and activity of acetyl-CoA carboxylase (EC 6.4.1.2) was determined in the developing seeds of rapeseed (Brassica campestris cv. Pusa Gold) grown in the field with and without S. The period between 14 and 35 days after flowering (DAF) was identified as the active period of oil accumulation in the developing seeds of rapeseed. The accumulation of oil was preceded by a marked rise in acetyl-CoA carboxylase activity and acetyl-CoA concentration, which declined rapidly when oil accumulation reached a plateau. Starch and soluble sugar content decreased, while protein content increased during the period of active oil accumulation in the developing seeds (i.e. 14-35 DAF). Sulfur application significantly ($P<0.05$) enhanced the oil accumulation in the developing seeds at all the growth stages except at 7 DAF. The increase in the oil content was 13.0-52.0% with S application compared with the control treatment. Sulfur also increased acetyl-CoA concentration, acetyl-CoA carboxylase activity, and soluble protein, sugar, and starch content in the developing seeds. It is suggested that the increase in the oil content with S fertilizer application may be associated with increases in acetyl-CoA carboxylase activity through the enhancement of acetyl-CoA concentration. Further, the increased sugar content due to S application provided enough carbon sources for oil biosynthesis

Descriptors:plant-nutrition. sulfur. sulfur-fertilizers. oils. rape. seeds. seed-development. acetyl-coenzyme-A. acetyl-CoA-carboxylase. enzymes. enzyme-activity. sugars. chemical-composition. plant-composition
Organism Descriptors:Brassica-campestris. Brassica-napus-var.-oleifera
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica-napus
Subject Codes:FF061. FF060. FF040. FF005. JJ700
Supplementary Info:34 ref
ISSN:0004-9409
Year:2000
Journal Title:Australian Journal of Agricultural Research
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58. Title:In vitro propagation of Epacris impressa (Epacridaceae) and the effects of clonal material
View Article: Australian Journal of Botany. 2000. 48 (2). 215-221
CD Volume:324
Print Article: Pages: 215-221
Author(s):Anthony J McLean C B Lawrie A C
Author Affiliation:Department of Applied Biology and Biotechnology, RMIT University, GPO Box 2476V, Melbourne, Vic. 3001, Australia
Language:English
Abstract:A system of micropropagation has been developed for Epacris impressa (pink heath), floral emblem of Victoria, Australia. Only explants from glasshouse-grown plants treated with 1.2 g L-1 mancozeb were established successfully in vitro. Shoot material was very sensitive to surface-sterilization, with 0.5% NaOCl for 5 min being optimal. Multiple shooting was induced optimally on Woody Plant Medium (WPM) with 12-25 micro M of the cytokinin 2iP [isopentenyladenine]. Inclusion of the auxin IBA induced callus and reduced shooting. Rooting in vitro was greatest (up to 40%) with half-strength WPM and 16 micro M IBA. Clones from individual plants varied in multiple shooting response to 2iP (0-49 micro M) and root induction response to auxins (IBA and NAA, 0-43 micro M). These results suggest that explant materials are the main determinant of success in in vitro propagation and that they require individual optimization of treatments to maximize shoot and root formation
Descriptors:auxins. explants. IBA. micropropagation. NAA. ornamental-woody-plants. tissue-culture. plant-growth-regulators. isopentenyladenine. ornamental-plants. cytokinins
Identifiers:Epacris impressa. Epacris
Organism Descriptors:Epacridaceae
Supplemental Descriptors:Ericales. dicotyledons. angiosperms. Spermatophyta. plants. Epacridaceae
Subject Codes:FF003. FF160. FF170
Supplementary Info:26 ref
ISSN:0067-1924
Year:2000
Journal Title:Australian Journal of Botany
Copyright:Copyright CAB International

59. Title:Efficient organogenesis of an Australian passionfruit hybrid (Passiflora edulis x Passiflora edulis var. flavicarpa) suitable for gene delivery
View Article: Australian Journal of Botany. 2000. 48 (5). 673-680
CD Volume:324
Print Article: Pages: 673-680
Author(s):Hall R M Drew R A Higgins C M Dietzgen R G

Author Affiliation:Queensland Agricultural Biotechnology Centre, Department of Primary Industries, Gehrmann Laboratories, University of Queensland, St Lucia, Qld 4072, Australia
Language:English
Abstract:An efficient regeneration protocol based on organogenesis from cotyledon explants and suitable for gene delivery has been developed for an Australian passionfruit hybrid. Multiple shoots were regenerated from 30-day-old cotyledon explants on Murashige and Skoog (MS) medium containing benzyladenine (BAP) and coconut water. Media pulsing experiments were conducted to investigate the effect on organogenesis of exposure time of the explants to MS containing 10 micro M BAP and 10% (v/v) coconut water, i.e. passionfruit regeneration medium (PRM). Continuous exposure of these explants to PRM maximized the number of shoots produced to 12.1 per explant. However, periods on hormone-free medium improved the appearance of the shoots and increased the number of explants with shoots from 75 to 84.6%. Further, shoots exposed for 7 days to half-strength MS supplemented with 10 micro M NAA produced twice as many plantlets than those on half-strength MS alone. Transient GUS histochemical assays indicated delivery of the uidA gene via Agrobacterium tumefaciens
Descriptors:in-vitro-regeneration. hybridization. tissue-culture. organogenesis. culture-media. benzyladenine. plant-growth-regulators. NAA. genetic-transformation. genetic-engineering. gene-expression. transgenic-plants. reporter-genes. passion-fruits
Organism Descriptors:Passiflora-edulis. Agrobacterium-tumefaciens. plants
Supplemental Descriptors:Passiflora. Passifloraceae. Violales. dicotyledons. angiosperms. Spermatophyta. plants. Agrobacterium. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF020. WW000. FF003. FF170
Supplementary Info:24 ref
ISSN:0067-1924
Year:2000
Journal Title:Australian Journal of Botany

60. Title:Shoot mineral composition and yield of wheat genotypes grown on a sodic and a non-sodic soil
View Article: Australian Journal of Experimental Agriculture. 2000. 40 (1). 69-78
CD Volume:324
Print Article: Pages: 69-78
Author(s):Liu C Y Paull J G Rathjen A J
Author Affiliation:Grain BioTech Australia Pty Ltd., SABC, Division of Biological Science and Biotechnology, Murdoch University, Murdoch, WA 6150, Australia
Language:English
Abstract:A collection of wheat lines including 49 overseas and 35 Australian lines, plus Triticum durum cv. Yallaroi, was grown in a 3-replicate randomised block design experiment at 2 sites (Two Wells and Roseworthy Campus, South Australia) during the 1994 growing season (June-December 1994). The aim of this investigation was to determine if elemental nutrients could be implicated in response to soil sodicity tolerance of wheat. Large grain yield differences and mineral concentrations were evident among different varieties including those from Australia. Several mineral concentrations in shoot, including manganese, potassium, sodium, phosphorus, boron, zinc and copper, taken up by these plants were correlated significantly with grain yield. The detrimental effects of sodium and boron concentrations on grain yields were less for local varieties than the overseas lines, because of lower

average shoot concentrations and lower coefficients of variation associated with the Australian varieties. The grain yield reduction at a sodic site appeared to be due to both soil physical changes and nutritional changes, with the combined effects of nutrient deficiencies and toxicities accounting for 23% of the variation. Except for the large differences of boron and sodium concentrations, there appeared to be a similar magnitude of variability between the overseas wheat collection and the Australian wheats. The present study confirmed that the tetraploid and hexaploid wheats differ in sodium concentration or potassium: sodium ratio, in addition to other nutrient changes including potassium, manganese, magnesium and copper. However, sodium concentration (or potassium: sodium ratio) and boron were not sufficient enough to explain the variability in grain yield of all the Australian wheats studied, suggesting that other factors detrimental to wheat production in sodic soils need to be identified
Descriptors:genotypes. wheat. yields. boron. copper. deficiency. magnesium. manganese. nutrient-deficiencies. nutrients. phosphorus. potassium. sodic-soils. soil. varieties. cultivars. yield-losses. zinc. mineral-uptake. mineral-nutrition. cereals
Geographic Locator:Australia. South-Australia
Organism Descriptors:Triticum. Triticum-durum. Triticum-aestivum
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Australia
Subject Codes:FF020. FF005. FF061
Supplementary Info:34 ref
ISSN:0816-1089
Year:2000
Journal Title:Australian Journal of Experimental Agriculture

61. Title:Response of lentil to Rhizobium leguminosarum bv. viciae strains at different levels of nitrogen and phosphorus
View Article: Australian Journal of Experimental Agriculture. 2000. 40 (1). 93-98
CD Volume:324
Print Article: Pages: 93-98
Author(s):Shah N H Hafeez F Y Arshad M Malik K A
Author Affiliation:National Institute for Biotechnology and Genetic Engineering (NIBGE), PO Box 577, Jhang Road, Faisalabad, Pakistan
Language:English
Abstract:In a field experiment at Faisalabad, Pakistan, on a soil deficient in N and available P that had a very low indigenous population of lentil (Lens culinaris) rhizobia, lentils were seed inoculated with 1 exotic and 3 local strains of R. leguminosarum bv. viciae and given 0:0, 20:20,
Descriptors:phosphorus-fertilizers. nitrogen-fertilizers. application-rates. seed-inoculation. nodulation. biomass-production. returns. nutrient-uptake. mineral-uptake. nitrogen. phosphorus. lentils
Geographic Locator:Pakistan
Organism Descriptors:Lens-culinaris. Rhizobium-leguminosarum
Supplemental Descriptors:Lens. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Rhizobium. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations
Subject Codes:FF005. JJ100. JJ700. FF100. EE110. FF061
Supplementary Info:22 ref
ISSN:0816-1089
Year:2000

Journal Title:Australian Journal of Experimental Agriculture

62. Title:Whole-plant growth and N allocation in transgenic rice plants with decreased content of ribulose-1,5-bisphosphate carboxylase under different CO2 partial pressures
View Article: Australian Journal of Plant Physiology. 2000. 27 (1). 1-12
CD Volume:324
Print Article: Pages: 1-12
Author(s):Makino A Harada M Kaneko K Mae T Shimada T Yamamoto N
Author Affiliation:Department of Applied Plant Science, Graduate School of Agricultural Sciences, Tohoku University, Tsutsumidori-Amamiyamachi, Sendai 981-8555, Japan
Language:English
Abstract:Growth of transgenic rice (Oryza sativa) with an antisense gene to the small subunit of Rubisco was analysed under 36 and 100 Pa CO2 during a 14-h photoperiod (1000 micro mol quanta m-2 s-1). Two lines of the antisense plants were used; one with 65% wild-type Rubisco and the other with 40% wild-type Rubisco. The plants were grown hydroponically for 70 d. The final biomass of the antisense plants grown in 36 Pa CO2 was much smaller than that of the wild-type plant. However, several compensation phenomena were found in the antisense plants. Increased biomass allocation to leaf blades and preferential N investment in leaf blades were observed. Leaf senescence was also delayed. Elevated CO2 levels up to 100 Pa caused the antisense plants to achieve a size similar to that of the wild-type plant. However, although the antisense plant with 65% wild-type Rubisco was selected as a plant with optimal Rubisco content for CO2-saturated photosynthesis, its final biomass was not greater than that of the wildtype plant. This may have been caused by a relatively strong Rubisco-antisense effect during the early stage of growth (21-42 d). N-use efficiency for growth after d 42 was greater in the selected antisense plant. Thus, improvement of N-use efficiency at the level of a single leaf did not necessarily lead to greater production of biomass at the whole-plant level
Descriptors:rice. transgenic-plants. biomass. photoperiod. photosynthesis. senescence. genetic-transformation. antisense-DNA. nitrogen. ribulose-bisphosphate-carboxylase. use-efficiency. carbon-dioxide-enrichment. cereals. biotechnology
Organism Descriptors:Oryza. Oryza-sativa
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Oryza
Subject Codes:FF020. FF005. FF060. WW000
Supplementary Info:44 ref
ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology

63. Title:Sucrose phosphate synthase and sucrose synthase activity during maturation of internodal tissue in sugarcane
View Article: Australian Journal of Plant Physiology. 2000. 27 (1). 81-85
CD Volume:324
Print Article: Pages: 81-85
Author(s):Botha F C Black K G
Author Affiliation:Institute for Plant Biotechnology, University of Stellenbosch, Private Bag X1, Matieland 7602, South Africa
Language:English
Abstract:In sugarcane cv. N19, the sucrose accumulation rate sharply increased between internodes 3 and 11. In the older internodes, sucrose-phosphate

synthase (SPS, EC 2.4.1.14) activity was at least 3 times higher than the soluble sucrose synthase (SuSy, EC 2.4.1.13) activity. A highly significant positive correlation was found between SPS activity and sucrose content. In contrast, no significant correlation was observed between SuSy and sucrose content. When radio-labelled glucose was fed to internodes with a high sucrose accumulation rate, label was equally distributed in the hexose moieties of sucrose. This clearly indicates that SPS is the major sucrose synthesis activity in the culm of sugarcane. Different kinetic forms of SPS apparently exist in the internodal tissue at different stages of development
Descriptors:maturation. sucrose. sucrose-synthase. hexosyltransferases. enzyme-activity. sugarcane. internodes. metabolism. biosynthesis. stems. growth-stages
Identifiers:sucrose-phosphate synthase
Organism Descriptors:Saccharum-officinarum. Saccharum
Supplemental Descriptors:Saccharum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060
Supplementary Info:34 ref
ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology

64. Title:Variation in puroindoline polypeptides in Australian wheat cultivars in relation to grain hardness
View Article: Australian Journal of Plant Physiology. 2000. 27 (2). 153-158
CD Volume:324
Print Article: Pages: 153-158
Author(s):Turnbull K M Gaborit T Marion D Rahman S
Author Affiliation:CSIRO Plant Industry, PO Box 1600, Canberra, ACT 2601, Australia
Language:English
Abstract:The sequence of the puroindoline-b gene from 15 Australian wheat cultivars was determined. Sequence variation was observed in the WPTKWWKGGCE motif of the deduced puroindoline-b protein sequence. Previously, it has been suggested that this sequence is crucial in determining grain hardness. In this study, no correlation was found between the variation in this sequence and the hardness or softness of the cultivar. The amounts of puroindoline-a and puroindoline-b protein in a selection of hard and soft Australian wheat cultivars were also determined using ELISA techniques. Both soft and hard cultivars had variable amounts of puroindoline-a and puroindoline-b. In particular, it is notable that the hard cultivars Cook and Diaz contained high amounts of puroindoline-a and puroindoline-b and also contained the puroindoline-b sequence previously reported to be associated with grain softness. These results suggest that if the puroindoline proteins are involved in determining grain softness or hardness they do so as part of a multi-component mechanism
Descriptors:cultivars. grain. polypeptides. wheat. ELISA. hard-seeds. nucleotide-sequences. cereals. biotechnology
Geographic Locator:Australia
Identifiers:puroindoline
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries
Subject Codes:FF020. FF005. FF040. WW000
Supplementary Info:22 ref

ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology
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65. Title:Differential expression of soluble acid invertase genes in the shoots of high-sucrose and low-sucrose species of Saccharum and their hybrids
View Article: Australian Journal of Plant Physiology. 2000. 27 (3). 193-199
CD Volume:324
Print Article: Pages: 193-199
Author(s):Zhu Y J Albert H H Moore P H
Author Affiliation:Hawaii Agriculture Research Center (YJZ) and USDA, Agriculture Research Service (HHA & PHM), 99-193 Aiea Heights Drive, Aiea, HI 96701, USA
Language:English
Abstract:The hydrolytic activity of soluble acid invertase [beta -fructofuranosidase] (SAI) is strongly correlated to sucrose accumulation in sugarcane (Saccharum spp.). Plants exhibiting SAI activity above a low threshold level do not accumulate high concentrations of sucrose. The present work investigates the basis for the difference in SAI activity observed between high- and low-sucrose-accumulating sugarcane lines. SAI-encoding cDNAs were isolated from two high- and one low-sucrose lines. All of these cDNAs were highly similar, with deduced proteins at least 98% identical. Expression of SAI in the stem of sugarcane was developmentally regulated, with relatively larger pools of SAI protein and mRNA in the apex and young internodes, which declined rapidly in the maturing internodes where sucrose accumulation occurs. This developmental pattern, while qualitatively similar, was quantitatively quite different between low- and high-sucrose lines. SAI protein and mRNA pools started substantially higher, declined later, and stabilized at a significantly higher level in a low-sucrose line than in a high-sucrose line. These data indicate that differences in SAI activity between high- and low-sucrose sugarcane lines are due, at least in part, to differences in the level of expression of essentially identical SAI genes
Descriptors:genes. hybrids. internodes. messenger-RNA. sucrose. sugarcane. gene-expression. sugar-crops. biotechnology
Identifiers:beta -fructofuranosidase
Organism Descriptors:Saccharum-officinarum. Saccharum
Supplemental Descriptors:Saccharum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. FF060
Supplementary Info:35 ref
ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology
Copyright:Copyright CAB International

66. Title:Agrobacterium-mediated transformation of Australian rice cultivars Jarrah and Amaroo using modified promoters and selectable markers
View Article: Australian Journal of Plant Physiology. 2000. 27 (3). 201-210
CD Volume:324
Print Article: Pages: 201-210
Author(s):Upadhyaya N M Surin B Ramm K Gaudron J Schunmann P H D Taylor W Waterhouse P M Wang MingBo
Author Variant:Wang-M-B
Author Affiliation:CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Language:English

Abstract:Agrobacterium-mediated transformation of Australian elite rice cultivars, Jarrah and Amaroo, was performed using binary vectors with improved promoters and selectable markers. Calli derived from mature embryos were used as target tissues. The binary vectors contained hph (encoding hygromycin resistance) or bar (encoding herbicide resistance) as the selectable marker gene and uidA (gus) or sgfpS65T as the reporter gene driven by different promoters. Use of Agrobacterium strain AGL1 carrying derivatives of an improved binary vector pWBVec8, wherein the CaMV35S driven hph gene is interrupted by the castor bean catalase 1 intron, produced a 4-fold higher number of independent transgenic lines compared to that produced with the use of strain EHA101 carrying the binary vector pIG121-Hm wherein the CaMV35S driven hph is intronless. The Ubiquitin promoter produced 30-fold higher beta -glucuronidase (GUS) activity (derivatives of binary vector pWBVec8) in transgenic plants than the CaMV35S promoter (pIG121-Hm). The two modified SCSV promoters produced GUS activity comparable to that produced by the Ubiquitin promoter. Progeny analysis (R1) for hygromycin resistance and GUS activity with selected lines showed both Mendelian and non-Mendelian segregation. Lines showing very high levels of GUS activity in T0 showed a reduced level of GUS activity in their T1 progeny, while lines with moderate levels of GUS activity showed increased levels in T1 progeny. Stable heritable green fluorescent protein (GFP) expression was also observed in few transgenic plants produced with the binary vector pTO134 which had the CaMV35S promoter-driven selectable marker gene bar and a modified CaMV35S promoter-driven reporter gene sgfpS65T
Descriptors:rice. genetic-transformation. catalase. herbicide-resistance. genetic-markers. transgenic-plants. ubiquitin. promoters. gene-expression. cereals. biotechnology
Identifiers:beta -glucuronidase. selectable markers. hygromycin
Organism Descriptors:Oryza-sativa. Agrobacterium. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF020. FF005. WW000
Supplementary Info:45 ref
ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology

67. Title:Xanthophyll cycle, light energy dissipation and electron transport in transgenic tobacco with reduced carbon assimilation capacity
View Article: Australian Journal of Plant Physiology. 2000. 27 (4). 289-300
CD Volume:324
Print Article: Pages: 289-300
Author(s):Ruuska S A Caemmerer S von Badger M R Andrews T J Price G D Robinson S A
Author Variant:von-Caemmerer-S
Author Affiliation:Molecular Plant Physiology Group, Research School of Biological Sciences, Australian National University, GPO Box 475, Canberra ACT 2601, Australia
Language:English
Abstract:The effects of reduced CO2 assimilation capacity on the leaf pigment composition and the dissipation of light energy were studied using transgenic tobacco (Nicotiana tabacum cv. W38). Two plant types were used: anti-SSu plants with reduced amounts of Rubisco and anti-GAPDH plants with reduced activity of chloroplast glyceraldehyde 3-phosphate dehydrogenase. A moderate reduction in the photosynthetic capacity

increased the de-epoxidation state of the xanthophyll-cycle pigments. In contrast, there was no large effect on the leaf pigment composition and the ratio of the xanthophyll cycle pigments to chlorophyll, and total carotenoids increased only in the most severe transgenic plants. The light induction of photosynthesis, fluorescence quenching and de-epoxidation of the xanthophyll cycle pigments were also followed in wild-type and anti-SSu plants. Anti-SSu plants maintained high nonphotochemical quenching and increased xanthophyll de-epoxidation in the light but the reduction state of QA remained high. For both wild-type and anti-SSu plants, the electron transport rate estimated from chlorophyll a fluorescence appeared to be much higher than that required to support the observed rate of CO2 assimilation and photorespiration during the early phase of photosynthetic induction. However, the two estimates converged with the onset of steady-state photosynthesis

Descriptors:photosynthesis. electron-transfer. tobacco. transgenic-plants. carotenoids. chlorophyll. chloroplasts. fluorescence. pigments. ribulose-bisphosphate-carboxylase. glyceraldehyde-3-phosphate-dehydrogenase. genetic-transformation. gene-expression. stimulant-plants. biotechnology

Organism Descriptors:Nicotiana. Nicotiana-tabacum

Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Nicotiana

Subject Codes:FF060. WW000. FF020

Supplementary Info:2 pp. of ref

ISSN:0310-7841

Year:2000

Journal Title:Australian Journal of Plant Physiology

68. Title:Expression patterns of cytoplasmic pyruvate, orthophosphate dikinase of rice (C3) and maize (C4) in a C3 plant, rice

View Article: Australian Journal of Plant Physiology. 2000. 27 (4). 343-347

CD Volume:324

Print Article: Pages: 343-347

Author(s):Nomura M Sentoku N Tajima S Matsuoka M

Author Affiliation:Faculty of Agriculture, Kagawa University, Miki, Kita, Kagawa 761-0795, Japan

Language:English

Abstract:Two types of mRNAs are transcribed from the C4-type pyruvate, orthophosphate dikinase gene (Pdk) with different sizes, which encode chloroplastic and cytoplasmic forms of the enzyme. The two transcripts are produced by two independent promoters and this unusual dual promoter system is also found in the C4-like Pdk gene of the C3 plant, rice. In order to elucidate the expression pattern of the cytoplasmic transcript from the maize C4-type and rice C4-like Pdk genes, we have produced chimaeric constructs with the beta -glucuronidase (GUS) reporter gene under the control of the cytoplasmic promoters and introduced the constructs into rice. Both cytoplasmic promoters directed GUS expression in non-photosynthetic organs, such as endosperm and roots, in transgenic rice plants, while expression was low in photosynthetic organs. These results indicate that the organ-specific localization of the cytoplasmic enzyme is similar in C3 and C4 plants. The results also suggest the possibility that the cytoplasmic enzyme has a similar function(s) in non-photosynthetic organs both in C3 and C4 plants

Descriptors:maize. pyruvic-acid. rice. messenger-RNA. gene-expression. genetic-transformation. cereals. biotechnology

Identifiers:pyruvate,orthophosphate dikinase

Organism Descriptors:Zea-mays. Oryza-sativa. Oryza
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Oryza
Subject Codes:FF060. FF020. WW000
Supplementary Info:25 ref
ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology
Copyright:Copyright CAB International

69. Title:Characterisation of a methionine-rich storage protein cDNA from perilla (Perilla frutescens) seeds
View Article: Australian Journal of Plant Physiology. 2000. 27 (7). 701-707
CD Volume:324
Print Article: Pages: 701-707
Author(s):Jin UnHo Jin ByungRae Lee JinWoo Cho YoungSu Kwon OChang Kim YoungKil Chung ChungHan
Author Variant:Jin-U-H. Jin-B-R. Lee-J-W. Cho-Y-S. Kwon-O-C. Kim-Y-K. Chung-C-H
Author Affiliation:Division of Biotechnology, Faculty of Life Sciences and Resources, Dong-A University, Pusan 604-714, Korea Republic
Language:English
Abstract:We have cloned and characterized a cDNA (PrLeg) coding for a methionine-rich storage protein, which is reported for the first time in P. frutescens var. japonica seeds, homologous to the 11S legumin-like storage proteins. The most significant feature of the PrLeg precursor protein is that it has the highest content of methionine residues among the 11S legumin-like storage proteins examined so far. Another feature is that the deduced amino acid sequences of the PrLeg protein are phylogenetically close to the sequence groups derived from evolutionally ancient states of the 11S legumin-like storage proteins. In contrast, with the exception of sesame, relatively low phylogenetic relationships were determined between the PrLeg sequence group and those derived from plants such as soyabean, pea, broad bean, rape, pumpkin, rice, coffee and citrus. Southern blot analysis suggested that there may be several copy numbers of the PrLeg genes, and their seed-specific expression patterns at the transcriptional level were confirmed by northern hybridization analysis
Descriptors:complementary-DNA. seeds. plant-protein. plant-composition. chemical-composition. proteins. genes. hybridization. methionine. phylogenetics. chemotaxonomy
Organism Descriptors:Perilla-frutescens
Supplemental Descriptors:Perilla. Lamiaceae. Lamiales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF040. ZZ380
Supplementary Info:28 ref
ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology
Copyright:Copyright CAB International

70. Title:Interaction between phloem proteins and viral movement proteins
View Article: Australian Journal of Plant Physiology. 2000. 27 (8/9). 801-806
CD Volume:324
Print Article: Pages: 801-806
Author(s):Shalitin D Wolf S
Author Affiliation:Department of Field Crops, Vegetables and Genetics and the Otto Warburg Center for Agricultural Biotechnology, Hebrew University of Jerusalem, Rehovot 76100, Israel
Language:English

Abstract:Following the finding that viral movement proteins (MPs) can exert an effect on sugar metabolism and resource allocation at sites distant from their expression, we suggested that the MPs interfere with an element(s) involved in the plant's endogenous long-distance signal network. To provide experimental support for this hypothesis, several unique procedures were employed to identify interactions between viral MPs and phloem sap proteins (PSPs) collected from cut petioles of squash (Cucurbita pepo subsp. pepo cv. B26) and melon (Cucumis melo cv. Hales Best Jumbo) plants. Far-western experiments with blotted PSPs, using both bacteria-overexpressed and in vitro-translated cucumber mosaic virus (CMV)- and tobacco mosaic virus (TMV)-MPs, revealed that the 2 virally encoded proteins react specifically with more than 1 PSP. Moreover, isolation of the naturally folded phloem protein in an affinity column containing a TMV-MP-maltose-binding protein indicated, once again, an interaction between the viral protein and similar PSPs. Two melon PSPs with molecular masses of 8 and 23 kDa were found to specifically interact with both the CMV- and TMV-MPs. The possible effects of this interaction in terms of altering the process of phloem transport and resource allocation are discussed
Descriptors:binding-proteins. melons. phloem. plant-proteins. viral-proteins. movement-proteins. translocation. sugars
Identifiers:Bromoviridae
Organism Descriptors:cucumber-mosaic-cucumovirus. Cucumis-melo. Cucurbita-pepo. tobacco-mosaic-tobamovirus. plant-viruses
Supplemental Descriptors:cucumovirus-group. plant-viruses. viruses. plant-pathogens. pathogens. Cucumis. Cucurbitaceae. Violales. dicotyledons. angiosperms. Spermatophyta. plants. Cucurbita. tobamovirus-group
Subject Codes:FF003. FF060. ZZ394. FF610
Supplementary Info:25 ref
ISSN:0310-7841
Year:2000
Journal Title:Australian Journal of Plant Physiology

71. Title:A recombinant Eimeria protein inducing interferon- gamma production: comparison of different gene expression systems and immunization strategies for vaccination against coccidiosis
View Article: Avian Diseases. 2000. 44 (2). 379-389
CD Volume:298
Print Article: Pages: 379-389
Author(s):Lillehoj H S Choi K D Jenkins M C Vakharia V N Song K D Han J Y Lillehoj E P
Author Affiliation:Immunology and Disease Resistance Laboratory, Livestock and Poultry Sciences Institute, BARC-East, Building 1040, U.S. Department of Agriculture, Beltsville, MD 20705, USA
Language:English
Language of Summary:spanish
Abstract:A rabbit antiserum against an 18 to 27 kDa native protein fraction (F3) from Eimeria acervulina merozoites identified a cDNA (3-1E) containing a 1086-bp insertion with an open reading frame of 170 amino acids (predicted molecular weight, 18 523; GenBank accession number AF113613). The recombinant 3-1E cDNA expressed in Escherichia coli produced a 60 kDa fusion protein and a 23 kDa protein after factor Xa treatment of the fusion protein. Both proteins were reactive with the F3 antiserum by Western blot analysis. A rabbit antiserum against a synthetic peptide deduced from the amino acid sequence of the 3-1E cDNA reacted with a 27-kDa recombinant 3-1E protein expressed in Sf9 insect cells and a 20-kDa native protein expressed by E. acervulina sporozoites and Eimeria tenella sporozoites and merozoites. By

immunofluorescence staining, a monoclonal antibody produced against the recombinant 3-1E protein reacted with sporozoites and merozoites of E. acervulina, E. tenella, and Eimeria maxima. Spleen lymphocytes from E. acervulina-immune chickens showed antigen-specific proliferation and interferon (IFN)- gamma production upon stimulation with the recombinant 3-1E protein, indicating that the protein activates cell-mediated immunity during coccidiosis. Immunization of fowls with either the E. coli- or Sf9-expressed recombinant 3-1E protein with adjuvant, or direct injection of the 3-1E cDNA, induced protective immunity against live E. acervulina. Simultaneous injection of the recombinant 3-1E protein, or the 3-1E cDNA, with cDNAs encoding fowl IFN- gamma or interleukin (IL)-2/15 further enhanced protective immunity. These results indicate that the recombinant E. acervulina 3-1E cDNA or its polypeptide product may prove useful as vaccines against avian coccidiosis

Descriptors:coccidiosis. immunization. interferon. recombinant-proteins. vaccination. vaccines. recombinant-vaccines. protozoal-infections. biotechnology. poultry

Organism Descriptors:Eimeria-acervulina. Eimeria-maxima. Eimeria-tenella. fowls

Supplemental Descriptors:Eimeria. Eimeriidae. Eucoccidiorida. Apicomplexa. Protozoa. invertebrates. animals. Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata

Subject Codes:HH600. LL822. WW000. LL650

Supplementary Info:20 ref

ISSN:0005-2086

Year:2000

Journal Title:Avian Diseases

72. Title:Processing of cassava waste for improved biomass utilization

View Article: Bioresource Technology. 71 (1). Jan., 2000. 63-69

CD Volume:326

Print Article: Pages: 63-69

Author(s):Sriroth Klanarong Chollakup Rungsima Chotineeranat Sunee Piyachomkwan Kuakoon Oates Christopher G

Author Affiliation:Department of Biotechnology, Faculty of Agro-Industry, Kasetsart University, Bangkok

Language:English

Language of Summary:English (EN)

Abstract:Cassava (Manihot esculenta Crantz) pulp is the solid waste produced as a consequence of starch production. This pulp contains a high starch content (50-60% dry basis), causing an environmental problem with disposal. In order to recover this starch, physical or biological treatment of the material must be employed. Pulp was treated either by sonication or incubation with a multi-enzyme mixture of cellulase and pectinase. Both methods were found to improve efficiency of starch extraction by disrupting the complex structure of polysaccharides associated with and entrapping starch granules. In the enzymatic treatment, the content of cellulase and pectinase for high efficiency of starch extraction determined as the yield of liberated starch was investigated using Response Surface Methodology. Use of either cellulase or pectinase alone failed to effectively improve starch extraction. Cellulase concentration seemed to have a greater effect on efficiency of starch yield than pectinase concentration. Treatment of pulp with 15 Novo cellulase units (NCU) of cellulase and 122.5 polygalacturonase (PG) units of pectinase per g dry pulp for 60 min resulted in 40% starch recovery. Quality characteristics of the liberated starch, including paste viscosity (measured by Rapid Visco Analysis) and thermal properties (measured by Differential Scanning

Calorimetry) were comparable to a primary starch obtained by root extraction. Susceptibility of the liberated starch to alpha- amylase was inferior to that of a primary starch. Cellulase and pectinase, however, increased alpha-amylase susceptibility of the starch remaining in the pulp
Descriptors:biomass utilization; pulp waste processing; solid waste; starch production; waste disposal. Waste Management (Sanitation). alpha-amylase; cellulase; pectinase; polygalacturonase; polysaccharides; starch
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae)
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

73. Title:Nutrient digestibility and intestinal enzyme activity of Clarias batrachus (Linn.) juveniles fed on dried fish and chicken viscera incorporated diets
View Article: Bioresource Technology. 71 (2). Jan., 2000. 97-101
CD Volume:326
Print Article: Pages: 97-101
Author(s):Giri S S Sahoo S K Sahu A K Mukhopadhyay P K
Author Affiliation:Central Institute of Freshwater Aquaculture, Bhubaneswar, Orissa, 751002
Language:English
Language of Summary:English (EN)
Abstract:A feeding trial was conducted for 56 days to study the effect of replacement of fish meal by dried fish and chicken viscera, and a combination of oil cakes, in the diet of Clarias batrachus juveniles. The nutritional values of these by-products were studied through a digestibility experiment. No significant difference in nutrient digestibility was observed in different diets. Even 19.59% lipid in the diet of catfish did not affect the nutrient digestibility. Both amylolytic and proteolytic enzymes in the intestine of juveniles were studied. A decreased protease activity due to replacement of animal protein by plant protein and a decreased ($P < 0.01$) aspartate aminotransferase (ASAT) activity could be observed after inclusion of 22% of dried fish viscera in the diet of the catfish. Though body lipid content increased in fish fed a high level of lipid, fat-free body composition did not vary among the fish fed on different diets
Descriptors:bioresource technology; biotechnology; chicken viscera: fish feed; diets; dried fish: fish feed; feeding trials; fish feeding. Aquaculture; Nutrition; Waste Management (Sanitation). enzymes; gut enzymes: functions; lipids; nutrients: digestibilities
Organism Descriptors:Clarias batrachus (Osteichthyes); fish (Pisces). intestine: digestive system
Supplemental Descriptors:Osteichthyes: Pisces, Vertebrata, Chordata, Animalia; Pisces: Vertebrata, Chordata, Animalia. Animals; Chordates; Fish; Nonhuman Vertebrates; Vertebrates
Subject Codes:Aquaculture; Nutrition; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

74. Title:Surface properties of granular activated carbons from agricultural by-products and their effects on raw sugar decolorization
View Article: Bioresource Technology. 71 (2). Jan., 2000. 103-112
CD Volume:326
Print Article: Pages: 103-112
Author(s):Ahmedna M Marshall W E Rao R M
Author Affiliation:Department of Food Science, LAES, Louisiana State University Agricultural Center, Baton Rouge, LA, 70803-4200
Language:English
Language of Summary:English (EN)
Abstract:Granular activated carbons (GACs) were produced from sugarcane bagasse combined with one of two binders (corn syrup, coal tar) by physical activation and from pecan shells by physical and chemical activation. GACs were evaluated for their physical (hardness, bulk density), chemical (ash, pH), surface (surface area, pore size distribution, surface chemistry), and adsorption properties (molasses color removal, sugar decolorization) and compared with two commercial reference carbons. Results showed that larger surface area, a well-developed macro- and mesoporosity, and a minimal surface charge were desirable in GACs designed for sugar decolorization. Steam activation of pecan shells carbon was the only by-product-activation combination that produced GAC with all the above three desirable characteristics of a good sugar decolorizer. Chemical activation of pecan shells yielded GACs with high surface area and adequate pore size distribution but with large surface charge. In contrast, sugarcane bagasse-based GACs exhibited low surface areas and unsatisfactory physical/chemical properties
Descriptors:agricultural byproducts: utilization; bioresource technology; biotechnology; food processing; raw sugar: decolorization; surface chemistry. Bioprocess Engineering; Foods; Waste Management (Sanitation). activated carbons: applications, granular, production; sugars
Subject Codes:Bioprocess Engineering; Foods; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

75. Title:Production of granular activated carbons from select agricultural by-products and evaluation of their physical, chemical and adsorption properties
View Article: Bioresource Technology. 71 (2). Jan., 2000. 113-123
CD Volume:326
Print Article: Pages: 113-123
Author(s):Ahmedna M Marshall W E Rao R M
Author Affiliation:Department of Food Science, LAES, Louisiana State University Agricultural Center, Food Science Building, Baton Rouge, LA, 70803-4200
Language:English
Language of Summary:English (EN)
Abstract:Representative samples of soft, low density, group 1 (rice straw, rice hulls, sugarcane bagasse) and hard, high density, group 2 agricultural by-products (pecan shells) were converted into granular activated carbons (GACs). GACs were produced from group 1 and 2 materials by physical activation or from group 2 materials by chemical activation. Carbons were evaluated for their physical (hardness, bulk density), chemical (ash, conductivity, pH), surface (total surface area), and adsorption properties (molasses color removal, sugar decolorization) and compared with two commercial reference carbons. The results show

that the type of by-product, binder, and activation method determine the properties of GACs. Regardless of the binder, sugarcane bagasse showed a better potential than rice straw or rice hulls as precursor of GACs with the desirable properties of a sugar decolorizing carbon. Pecan shells produced GACs that were closest to the reference carbons in terms of all the properties investigated
Descriptors:agricultural byproducts: utilization; bioresource technology; biotechnology; food processing; raw sugar: decolorization; surface chemistry. Bioprocess Engineering; Foods; Waste Management (Sanitation). activated carbons: adsorption capacities, applications, granular, physicochemical properties, production; sugars
Subject Codes:Bioprocess Engineering; Foods; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

76. Title:Degradation of spent casings with commercial cellulases
View Article: Bioresource Technology. 71 (2). Jan., 2000. 125-131
CD Volume:326
Print Article: Pages: 125-131
Author(s):Sanders D A Belyea R L Taylor T A
Author Affiliation:Department of Animal Science, University of Missouri, Columbia, MO, 65211
Language:English
Language of Summary:English (EN)
Abstract:Spent casings (SC) are a coproduct of the frankfurter/sausage processing industries: traditional disposal methods (landfills and land application) are becoming costly or limited. Reusing SC as food for animals could provide a disposal alternative. The objective was to determine if ruminal bacteria or commercial cellulases could degrade SC. The cellulases of ruminal bacteria were unable to degrade SC. One cellulase (C3) was very effective in degrading cellulosic substrates; it degraded SC approximately 95% by 6 h and 98% by 12 h into glucose, but the glucose concentration was low (about 2.5 mM). Activity of C3 was greatest at a pH of 4.0 and a temperature of 56-60degreeC; particle size and pigmentation of SC did not affect degradation. Spent casings could be reused as animal feed, but a bioprocessing approach is needed to increase glucose concentration and remove water before this would be feasible
Descriptors:bioresource technology; biotechnology; food processing; spent casings: degradation; waste disposal. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Foods; Waste Management (Sanitation). commercial cellulases: applications; glucose
Organism Descriptors:bacteria (Bacteria)
Supplemental Descriptors:Bacteria: Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Foods; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

77. Title:Alkali-treated straw and insoluble straw xanthate as low cost adsorbents for heavy metal removal - preparation, characterization and application
View Article: Bioresource Technology. 71 (2). Jan., 2000. 133-142
CD Volume:326

Print Article: Pages: 133-142
Author(s):Kumar Anupama Rao N N Kaul S N
Author Affiliation:Wastewater Technology Division, National Environmental Engineering Research Institute, Nehru Marg, Nagpur, 440020
Language:English
Language of Summary:English (EN)
Abstract:Heavy metal removal using alkali-treated straw (ATS) and insoluble straw xanthate (ISX) is reported. Insoluble straw xanthate consisting of 4.1% total sulfur is also applied for the removal of various metal ions simultaneously. Potentiometric data of alkali- treated straw and xanthated straw indicated polyfunctionality of these materials. Diffuse Reflectance IR (DRIFT) spectra of ISX exhibited peaks characteristic of xanthate groups on straw. Removal of Cr3+ from aqueous solutions using ATS and ISX followed the Langmuir adsorption model and both the materials have shown significant chromium removal efficiencies (>80%). In the case of chromate and dichromate, pore adsorption preceded the surface adsorption. Detailed spectroscopic (DRIFT & EPR) and sodium release studies conducted using ISX suggest that Cr3+ is removed through the adsorption-exchange mechanism involving alkoxide or xanthate groups. Xanthate groups bind Cr3+ aqua complex through unidentate monosulfur chelation
Descriptors:alkali-treated straw: applications; bioresource technology; biotechnology; insoluble straw xanthate: applications, characterization, preparation. Methods and Techniques; Pollution Assessment Control and Management. heavy metals: removal; sulfur
Subject Codes:Methods and Techniques; Pollution Assessment Control and Management
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

78. Title:Anaerobic pre-treatment of slaughterhouse wastewater using fixed- film reactors
View Article: Bioresource Technology. 71 (2). Jan., 2000. 143-149
CD Volume:326
Print Article: Pages: 143-149
Author(s):del Pozo R Diez V Beltran S
Author Affiliation:Department of Biotechnology and Food Science, Faculty of Food Science and Technology and Chemistry Science, University of Burgos, Pza. Misael Banuelos s/n, 09001, Burgos
Language:English
Language of Summary:English (EN)
Abstract:The aim of this work was to study the performance of anaerobic fixed-film reactors with non-random support, for poultry slaughterhouse wastewater pre-treatment, including the influence of operating conditions. The work was carried out with two labscale reactors, one upflow and the other downflow, both equipped with vertical corrugated PVC tubes as support and a recirculation circuit. Both reactors were operated at 35degreeC. COD removal efficiencies ranging from 85% to 95% were achieved for organic loading rates of 8 kg COD m-3 d-1, while the highest organic loading rates (35 kg COD m-3 d-1) led to efficiencies of 55-75%. The reactors did not show destabilization after 12 h shock loads of 50 kg COD m-3 d-1. Reactor stability was easily achieved under intermittent operation, with weekend breaks, after which the reactors rapidly returned to their optimal performance. The influences of the hydraulic retention time, temperature, the recirculation ratio and flow direction were alsostudied

Descriptors:bioresource technology; biotechnology; chemical oxygen demand: removal; food processing; slaughterhouse wastewater: anaerobic pretreatment. Bioprocess Engineering; Waste Management (Sanitation)
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

79. Title:Influence of media-packing ratio on performance of anaerobic hybrid reactors
View Article: Bioresource Technology. 71 (2). Jan., 2000. 151-157
CD Volume:326
Print Article: Pages: 151-157
Author(s):Wu M Wilson F Tay J H
Author Affiliation:School of Civil and Structural Engineering, Nanyang Technological University, No. 1a-13 Nanyang Ave., CSE Blk N1, Singapore, 639798
Language:English
Language of Summary:English (EN)
Abstract:In this study, the influence of media-packing ratio on the performances of anaerobic hybrid reactors (AHRs) at low, medium and high organic loading rates was evaluated by conducting COD profile, granulation and tracer studies. Four laboratory upflow anaerobic hybrid reactors, each with a total unpacked volume of 7.85 1, with varying packing depths, were operated at organic loading rates from 1 to 24 g COD/1 d. The media-packing ratios were 75%, 60%, 40% and 20% of the total reactor height in the AHRs. Three types of soluble COD profiles along the reactor height were observed when the organic loading rate was gradually increased. When operated at 1 and 2 g COD/1 d the COD profiles along the reactor height from bottom to top showed a plug-flow regime. From 4 to 12 g COD/1 d the COD profiles were distorted in the reactors with 20%, 40% and 60% packing, while at 16 g COD/1 d and above the COD profile indicated homogeneity in each reactor, suggesting a perfectly-mixed regime. The distortedCOD profiles were considered to be caused by the non- ideal flow pattern prevalent in the reactors. The dead-space volume and the bypass flowrate due to short-circuiting were determined using the Cholette and Cloutier model. A 'distortion index' (DI), which was calculated from the ratio of the average COD value of the sludge bed over the average COD value of the reactor, was used to describe distortion of the COD profile. The distortion index correlated well with the short-circuiting fraction
Descriptors:bioresource technology; biotechnology; chemical oxygen demand; media-packing ratio; sludge blankets. Bioprocess Engineering; Waste Management (Sanitation)
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

80. Title:Effects of oxygen concentration and moisture content of refuse on nitrification, denitrification and nitrous oxide production
View Article: Bioresource Technology. 71 (2). Jan., 2000. 159-165
CD Volume:326
Print Article: Pages: 159-165
Author(s):Hwang Sunjin Hanaki Keisuke

Author Affiliation:Environmental R and D Department, Environmental Engineering Group, EBARA Co., 4-2-1 Honfujisawa, Fujisawa-shi, 251-8502
Language:English
Language of Summary:English (EN)
Abstract:The purposes of this study were to evaluate the potential production of nitrous oxide (N2O), which is known as a greenhouse gas, to identify the reaction responsible for it and to examine the effects of oxygen and moisture content on nitrification, denitrification and N2O production. Applying a tracer method using a 15N-isotope into an oxygen controllable reactor with artificial refuse proved that biological denitrification was a main source of released N2O even when the oxygen of the bulk atmosphere was as high as 15%. Calculating the mass balance for nitrogenous compounds showed that only denitrification occurred as the sole microbial process when the bulk oxygen was 0-5%. With increasing oxygen above 5% nitrification also began to occur simultaneously with denitrification. As the bulk space of the refuse became aerobic, the total amount of N2 produced from denitrification decreased but the proportion of N2O in the (N2 + N2O) increased. Denitrification was the main source ofreleased N2O when the moisture content was between 40-60% and oxygen 10%. The amounts of nitrification, denitrification and N2 production increased as the moisture content increased
Descriptors:bioresource technology; biotechnology; denitrification; global warming; nitrification; refuse: chemistry, conversion. Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation). greenhouse gases: production; nitrogen: production; nitrous oxide: production; oxygen
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

81. Title:Effect of organic solvents on a chloroperoxidase biotransformation
View Article: Bioresource Technology. 71 (2). Jan., 2000. 167-172
CD Volume:326
Print Article: Pages: 167-172
Author(s):Loughlin Wendy A Hawkes David B
Author Affiliation:School of Science, Griffith University, Nathan Campus, Griffith, QLD
Language:English
Language of Summary:English (EN)
Abstract:The effect of organic solvents on the chlorination activity of chloroperoxidase (CPO) was identified for use in biotransformations with CPO. CPO was found to chlorinate monochlorodimedon (MCD) in the presence of organic solvents with log P values less than 0. The relative rates of chlorination with chloride ion in the presence of H2O2, buffer and 2.5-20% of either dimethyl sulfoxide, N,N-dimethyl formamide, methanol or acetonitrile, were in the range of 10-58% of that in buffer (pH 2.8) at the same reactant concentrations. The presence of such organic solvents was found to alter CPO catalysis by altering the protein conformation and the local environment at the active site. CPO did not display chlorination activity in the presence of organic solvents which had log P values greater than 0
Descriptors:biohalogenation; bioresource technology; biotechnology; biotransformations: solvent effects. Enzymology (Biochemistry and

Molecular Biophysics); Bioprocess Engineering. chloroperoxidase [EC 1.11.1.10]: applications, enzymatic characteristics; monochlorodimedon: chlorination; organic solvents
Organism Descriptors:Caldariomyces fumago (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

82. Title:Nitrogen excretion by farm livestock with respect to land spreading requirements and controlling nitrogen losses to ground and surface waters. Part 1: Cattle and sheep
View Article: Bioresource Technology. 71 (2). Jan., 2000. 173-181
CD Volume:326
Print Article: Pages: 173-181
Author(s):Smith K A Frost J P
Author Affiliation:ADAS Wolverhampton, Woodthorne, Wolverhampton, WV6 8TQ
Language:English
Language of Summary:English (EN)
Abstract:In this paper, published and unpublished information on excretion by dairy cattle, beef cattle and sheep is reviewed. A number of factors are known to affect both the amount and N content of livestock excreta, most notably animal liveweight, diet and water intake and, for adults, whether in lactation or not. Relationships between liveweight and the volume and N output of excreta have been used to derive estimates for 'standard' outputs for a range of adult and young stock; in the case of breeding stock, allowing for the lactation period. An alternative approach for estimating N excretion, via nitrogen balance calculations, was undertaken for a number of livestock categories and provides some validation of the standards, increasing confidence in their application. These standards are now incorporated into the guidelines already in place for Nitrate Vulnerable Zones in England and Wales and in the recently revised Code of Good Agricultural Practice for the Protection of Water
Descriptors:bioresource technology; biotechnology; land spreading requirements; manure; water pollution. Pollution Assessment Control and Management; Waste Management (Sanitation). nitrate: leaching; nitrogen: excretion, losses
Geographic Locator:UK (Europe, Palearctic region)
Organism Descriptors:cattle (Bovidae); sheep (Bovidae). feces: digestive system; urine: excretory system
Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

83. Title:Nitrogen excretion by farm livestock with respect to land spreading requirements and controlling nitrogen losses to ground and surface waters. Part 2: Pigs and poultry
View Article: Bioresource Technology. 71 (2). Jan., 2000. 183-194

CD Volume:326
Print Article: Pages: 183-194
Author(s):Smith K A Charles D R Moorhouse D
Author Affiliation:ADAS Wolverhampton, Woodthorne, Wolverhampton, WV6 8TQ
Language:English
Language of Summary:English (EN)
Abstract:In this paper, published and some unpublished information on excretion by pigs and poultry is reviewed. Well established relationships between feed and water intake and faecal and urinary output in fattening pigs have been adapted, using modern growth curves and typical commercial feeding practice, to make estimates of excretal output for a range of growing and finishing pigs and, also, breeding sows. Nitrogen (N) outputs were then estimated from typical excretal N content. For poultry, estimates were based on empirical data available from a range of production related studies and, for broilers and turkeys, a metabolic model relating litter output to liveweight, feed inputs and feed conversion. An alternative approach of estimating N excretion, via N balance calculations, was undertaken for fattening pigs and sows and for the major poultry categories, and provides some validation of the estimated standards, increasing confidence in their application. These standards are now incorporated into the guidelines already in place for Nitrate Vulnerable Zones in England and Wales and in the recently revised Water Code
Descriptors:bioresource technology; biotechnology; feed conversion; land spreading requirements; manure; water pollution. Pollution Assessment Control and Management; Waste Management (Sanitation). nitrate: leaching; nitrogen: excretion, losses
Geographic Locator:UK (Europe, Palearctic region)
Organism Descriptors:pig (Suidae); poultry (Aves). feces: digestive system; urine: excretory system
Supplemental Descriptors:Aves: Vertebrata, Chordata, Animalia; Suidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Birds; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

84. Title:Co-composting of spent pig litter and sludge with forced-aeration
View Article: Bioresource Technology. 72 (1). March , 2000. 1-7
CD Volume:326
Print Article: Pages: 1-7
Author(s):Tiquia S M Tam N F Y
Author Affiliation:Department of Food, Agricultural and Biological Engineering, Agricultural Research and Development Center (OARDC), Ohio State University, Wooster, OH
Language:English
Language of Summary:English (EN)
Abstract:Co-composting spent pig (Sus scrofa L.) litter (a mixture of partially decomposed pig manure and sawdust) with pig sludge (the sludge that settled at the bottom of the primary sedimentation tank in treating slurries) was evaluated as a means to reduce the volume of wastes and to produce a stable organic soil amendment. Three piles with forced-aeration were established by mixing 2:1 wet (v/v) ratio of spent litter and pig sludge. Composting process parameters monitored over 91 days included some physical, chemical, and biological properties of the

spent litter-sludge mixture. The efficiency of composting at the top location of the forced-aeration piles was slower than the middle, bottom and surface locations. The top location took 63 days to return to ambient level. It took 49 days for the middle and bottom locations, and only 28 days were needed for that in the surface location. The variations in temperature at different locations of the forced-aeration piles were also reflected in differences in some chemical and biological parameters. The top location had the lowest total aerobic heterotroph numbers, suggesting that the microbial activity was slower. Moreover, this zone also had the lowest germination index and highest concentrations of NH4+-N and water-extractable Cu and Zn during the first 49 days of composting, indicating that the elimination of phytotoxicity and the composting rate was slower than the middle, bottom and surface locations. However, these differences were evident only during the first 49 days of composting. By day 63, the spent litter-sludge at the top location had similar properties with that of the other three locations

Descriptors:agriculture; bioresource technology; biotechnology; phytotoxicity; sludges: treatment; soils; spent pig litter: treatment; temperature. Methods and Techniques; Waste Management (Sanitation); Soil Science

Organism Descriptors:bacteria (Bacteria); microorganisms (Microorganisms); pig (Suidae); plants (Plantae)

Supplemental Descriptors:Bacteria: Microorganisms; Microorganisms; Plantae; Suidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Bacteria; Chordates; Eubacteria; Mammals; Microorganisms; Nonhuman Mammals; Nonhuman Vertebrates; Plants; Vertebrates

Subject Codes:Methods and Techniques; Waste Management (Sanitation); Soil Science

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

85. Title:Influence of organic and mineral fertilisers on soil biological and physical properties

View Article: Bioresource Technology. 72 (1). March , 2000. 9-17
CD Volume:326
Print Article: Pages: 9-17

Author(s):Marinari S Masciandaro G Ceccanti B Grego S
Author Affiliation:Dipartimento di Agrobiologia Agrochimica, University of Tuscia, Viterbo

Language:English
Language of Summary:English (EN)

Abstract:The aim of this research was to study in a field experiment the influence of different fertiliser applications on soil biological and physical properties. Vermicompost (VC) from biological sludge, stabilised dairy manure or mineral nitrogen fertiliser (NH4NO3) were applied to a corn crop (Zea mays L.) at 200 kg N ha-1. Soil enzyme activity (acid phosphatase, dehydrogenase and protease BAA) and CO2 production were measured as indices of soil biological activity. These measures of metabolic activity were correlated to soil physical properties such as soil porosity. The soluble fractions of C and N were taken as indicators of fertiliser effects on soil fertility. There were positive correlations between soil porosity, enzymatic activity and CO2 production in organic and mineral treatments. The addition of organic fertilisers improved soil physical and biological properties. The increase in macropores, ranging from 50-500 mum, in soil treated with organic fertilisers was mainly due to an increase in elongated pores,

which are considered very important both in soil-water-plant relationships and in maintaining a good soil structure. Organic treatments stimulated soil biological activity probably due to an enrichment of soil organic matter. Mineral fertiliser enhanced soil porosity by increasing regular and irregular pores and caused a priming effect of native soil organic matter

Descriptors:bioresource technology; biotechnology; manure; soils: biological properties, physical properties. Agronomy (Agriculture); Soil Science. carbon; enzymes; mineral fertilizers: uses; nitrogen; organic fertilizers: uses

Organism Descriptors:Zea mays [corn] (Gramineae)

Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Agronomy (Agriculture); Soil Science

ISSN:0960-8524

Year:2000

Journal Title:Bioresource Technology

86. Title:Economic feasibility of producing ethanol from lignocellulosic feedstocks

View Article: Bioresource Technology. 72 (1). March , 2000. 19-32

CD Volume:326

Print Article: Pages: 19-32

Author(s):Kaylen Michael Van Dyne Donald L Choi Youn Sang Blase Melvin

Author Affiliation:Department of Agricultural Economics, University of Missouri, 200 Mumford Hall, Columbia, MO

Language:English

Language of Summary:English (EN)

Abstract:A mathematical programming model is built to analyze the economic feasibility of producing ethanol from lignocellulosic feedstocks. The optimal size of an ethanol plant is determined by the trade-off between increasing transportation costs for feedstocks versus decreasing average plant costs as the plant size increases. The ethanol plant is modeled under the assumption that it utilizes recent technological advancements in dilute acid hydrolysis. Potential feedstocks include energy crops, crop residues and woody biomass. It is found that the recent technological advancements appear to make ethanol competitive with gasoline, but only if higher valued chemicals are produced as co-products with the ethanol. The low cost and chemical composition of crop residues make them attractive as a feedstock

Descriptors:bioresource technology; biotechnology; crop residues: conversions; economics; industrial alcohol production; mathematical models: applications. Bioprocess Engineering. ethanol: production; lignocellulose: conversion

Organism Descriptors:microorganisms (Microorganisms)

Supplemental Descriptors:Microorganisms. Microorganisms

Subject Codes:Bioprocess Engineering

ISSN:0960-8524

Year:2000

Journal Title:Bioresource Technology

87. Title:Characterisation of NaOH-extracted humic acids during composting of a biowaste

View Article: Bioresource Technology. 72 (1). March , 2000. 33-41

CD Volume:326

Print Article: Pages: 33-41

Author(s):Veeken Adrie Nierop Klaas de Wilde Vinnie Hamelers Bert
Author Affiliation:Department of Agricultural, Environmental and Systems Technology, Wageningen Agricultural University, 6700 EV, Wageningen
Language:English
Language of Summary:English (EN)
Abstract:Changes in amount and characteristics of humic acids (HA) were studied during the composting of a biowaste in an 80 l composting device. HA was extracted by NaOH, purified with HCl-HF and dialysed. Freeze-dried HA was characterised by UV-285, elemental analysis, 13C NMR and pyrolysis-GC/MS. Composting of biowaste resulted in the degradation of 65% of the organic matter. The amount of HA decreased in the initial stage of composting but started to increase again after 20 days. At the start, HA was mainly composed of aliphatic compounds which were replaced by aromatic compounds during composting. Characterisation of HA revealed that the contribution of the condensation route was significant for HA formation during composting. Maturity indexes based on NaOH-extracted HA were inappropriate and moreover, beneficial effects of compost amendments to soils cannot be studied by organic matter analysis of bulk compost, but the amount and characteristics of available HA should be determined
Descriptors:bioresource technology; biotechnology; biowastes: treatment. Biochemistry and Molecular Biophysics; Methods and Techniques; Waste Management (Sanitation); Soil Science. humic acids: characterization, sodium hydroxide-extracted; sodium hydroxide: uses
Subject Codes:Biochemistry and Molecular Biophysics; Methods and Techniques; Waste Management (Sanitation); Soil Science
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

88. Title:Isolation of thermotolerant, osmotolerant, flocculating Saccharomyces cerevisiae for ethanol production
View Article: Bioresource Technology. 72 (1). March , 2000. 43-46
CD Volume:326
Print Article: Pages: 43-46
Author(s):Sree N Kiran Sridhar M Suresh K Banat I M Venkateswar Rao L
Author Affiliation:Department of Microbiology, Osmania University, Hyderabad, AP, 500 007
Language:English
Language of Summary:English (EN)
Abstract:Four thermotolerant, osmotolerant, flocculating alcohol producing cultures of Saccharomyces cerevisiae were isolated from soil samples collected from a thermal power plant in India. All the isolates grew at 44degreeC but VS1 and VS3 were better than the other two. Maximum ethanol yields obtained from 150 g/l glucose were 75 and 60 g/l using culture VS3 at 30degreeC and 40degreeC, respectively. Growth and ethanol production were decreasing at 44degreeC so higher temperatures were not tested, but the isolates could tolerate temperatures above 44degreeC. All cultures belonged to class IV flocculating yeasts and were able to tolerate up to 350 g/l glucose. These cultures have economical importance for use in alcohol production during hot seasons in countries such as India
Descriptors:bioresource technology; biotechnology; flocculation; industrial alcohol production; osmotolerance; product yield; temperature effects; thermotolerance. Bioprocess Engineering. ethanol: production; glucose
Organism Descriptors:Saccharomyces cerevisiae (Ascomycetes)
Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants

Subject Codes:Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

89. Title:Biodegradation of tetrachloroethylene in upflow anaerobic sludge blanket reactor
View Article: Bioresource Technology. 72 (1). March , 2000. 47-54
CD Volume:326
Print Article: Pages: 47-54
Author(s):Prakash S M Gupta S K
Author Affiliation:Center for Environmental Science and Engineering, Indian Institute of Technology, Powai, Mumbai, 400 076
Language:English
Language of Summary:English (EN)
Abstract:The laboratory study using upflow anaerobic sludge blanket (UASB) reactor in high strength wastewater containing tetrachloroethylene (PCE) was carried out to develop granular sludge in the presence of PCE (2 mg/l) and to assess the potential of UASB reactor in treating PCE containing wastewater. The granules of 0.25-4 mm size were observed after 82 days having mostly Methanothrix and Methanosarcina bacteria. Influent PCE concentration of 5-50 mg/l decreased to less than 0.23 mg/l (98.5 +- 1% removal) in most cases. The trichloroethylene (TCE), cis-1,2-dichloroethylene (cis- DCE), vinyl chloride (VC) and ethylene were formed on dehalogenation of PCE. Under steady state operation conditions the COD removal of 94 +- 2% and biogas production of 0.559-0.508 m3/kg CODrem with methane content of 64 +- 2% was achieved. The maximum PCE dechlorination rate (qmax), was 14.28 mg PCE/g VSS d and the half velocity coefficient, (Ks), was 0.417 mg PCE/l under steady state conditions. The UASB reactor may prove to be a potential wastewater treatment process for PCE containing wastewater
Descriptors:biodegradation; bioresource technology; biotechnology; chemical oxygen demand; dechlorination; dehalogenation; granular sludges: treatment; wastewaters: treatment. Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation). tetrachloroethylene: degradation, pollutant; volatile organic compounds
Organism Descriptors:Methanosarcina (Methanosarcinaceae); Methanothrix (Methanosarcinaceae); bacteria (Bacteria)
Supplemental Descriptors:Bacteria: Microorganisms; Methanosarcinaceae: Methanomicrobiales, Methanogenic Archaeobacteria, Archaeobacteria, Bacteria, Microorganisms. Archaeobacteria; Bacteria; Eubacteria; Microorganisms
Subject Codes:Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

90. Title:Influence of phase separation, leachate recycle and aeration on treatment of municipal solid waste in simulated landfill cells
View Article: Bioresource Technology. 72 (1). March , 2000. 55-66
CD Volume:326
Print Article: Pages: 55-66
Author(s):O'Keefe D M Chynoweth D P
Author Affiliation:Department of Agricultural and Biological Engineering, Institute of Food and Agricultural Science, University of Florida, 1 Frazier Rogers Hall, Gainesville, FL

Language:English
Language of Summary:English (EN)
Abstract:Decomposition in landfills is erratic and influenced primarily by moisture, inoculum, oxygen and accumulation of inhibitory fermentation products. These parameters may be optimized for decomposition by use of controlled landfill cells or bioreactors. This work evaluated the effect of combined-phase and two-phase anaerobic digestion of municipal solid waste (MSW) in laboratory leachbed (LB) cells. Phase separation resulted in increased rates of decomposition and greater process stability. Leachate recycle with an upflow sludge anaerobic reactor resulted in improvement of performance in a LB reactor which was attributed to removal of inhibitory fermentation products and buffering of acids in the leachate. The effects of aeration and leachate flooding of the LB were also studied. Intermittent aeration of the LB enhanced phase separation but inhibition of methanogenesis was not sustainable beyond six days. Conversion of organic matter was similar in the anaerobic and aerated LBs
Descriptors:aeration; bioresource technology; biotechnology; fermentation; landfill design; landfills: decomposition, simulated cells; leachate recycle; methanogenesis; municipal solid wastes: treatment methodology; phase separation. Bioprocess Engineering; Waste Management (Sanitation). methane
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

91. Title:Adjustment of the composting process for mushroom cultivation based on initial substrate composition
View Article: Bioresource Technology. 72 (1). March , 2000. 67-74
CD Volume:326
Print Article: Pages: 67-74
Author(s):Straatsma Gerben Gerrits Jan P G Thissen Jac T N M Amsing Jos G M Loeffen Hennie Van Griensven Leo J L D
Author Affiliation:Mushroom Experimental Station, 5960 AA, Horst
Language:English
Language of Summary:English (EN)
Abstract:The feasibility of adjusting individual composting processes to be able to produce the desired mass of compost of the required composition was evaluated. Data sets from experiments in tunnels were constructed and analyzed. Total mass and dry matter contents at the start and at the end of composting contained much statistical error. Error was propagated into the calculated central parameter of the process, the loss of dry matter. Water loss was estimated based on dry matter loss, heat generation and evaporation in a model. Estimated and actual losses from individual processes almost lacked correlation but the averages were rather similar. It is not the model but the error in input data that prevent the accurate prediction of the losses of water and of total matter. Moreover, error masked any correlation between the loss of dry matter and processing parameters. A model cannot be successfully applied to adjust an individual composting process. Compost producers should focus on getting the composition of the substrate constant at the start of processing. Adjusting an individual process is not a very reliable option
Descriptors:bioresource technology; biotechnology; dry matter loss; statistical error; substrates: initial composition; total matter; water loss.

Horticulture (Agriculture); Waste Management (Sanitation).
lignocellulose: degradation
Organism Descriptors:Agaricus [mushroom] (Basidiomycetes); mushrooms (Basidiomycetes)
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Horticulture (Agriculture); Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

92. Title:Post-mortem examination and analysis of anaerobic filters
View Article: Bioresource Technology. 72 (1). March , 2000. 75-84
CD Volume:326
Print Article: Pages: 75-84
Author(s):Jawed Mohammad Tare Vinod
Author Affiliation:Department of Civil Engineering, University of Durban-Westville, Durban, 4000
Language:English
Language of Summary:English (EN)
Abstract:This paper presents post-mortem examination and analysis of downflow (DAF) and upflow anaerobic filter (UAF) operated under similar sets of operating and environmental conditions but varying organic loads for more than 20 months. It can be observed from performance studies of these filters that the COD removal, methane gas production and COD methanisation do not differ significantly at 95% confidence level. However, the post-mortem analysis revealed that considerable filter volumes (42% in DAF and 49% in UAF) were occupied by retained biomass leading to significant reduction in operating HRT (hydraulic retention time) towards the end of the study period. Retained biomass (suspended as well as retained in packing media) in the filter was observed to have considerable black, brown-black and brown granular solid fractions. The brown granules were spongy in nature. The deposition of sludge solids in DAF packing media was observed to be uneven as compared to UAF. Solids were simply held-up or retained in the packing media. Solids retained in DAF packing media were mostly composed of black granules (3-5 mm in size) whereas solids retained in UAF packing media were brown-black granules (2-3 mm in size). The retained granular solids in DAF packing media appeared to be more compact as compared to that in UAF. The estimated concentration of retained solids in DAF packing media was 76.39 g TS/L that was significantly higher than that in UAF (69.91 g TS/L)
Descriptors:anaerobic processes: applications; biomass; bioresource technology; biotechnology; chemical oxygen demand; wastewaters: treatment methodology. Bioprocess Engineering; Equipment, Apparatus, Devices and Instrumentation; Methods and Techniques; Waste Management (Sanitation)
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Equipment, Apparatus, Devices and Instrumentation; Methods and Techniques; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

93. Title:Inactivation of indicator bacteria in wastewater by chlorine: A kinetics study
View Article: Bioresource Technology. 72 (1). March , 2000. 85-93

CD Volume:326
Print Article: Pages: 85-93
Author(s):Hassen Abdennaceur Heyouni Abderrahim Shayeb Hedi Cherif Mohamed Boudabous Abdellatif
Author Affiliation:Laboratoire Environnement, Institut National de Recherche Scientifique et Technique, Cite Mahrajene, Tunis
Language:English
Language of Summary:English (EN)
Abstract:The aim of this study was to characterise the kinetics of chlorine consumption and of inactivation of indicator bacteria in secondary wastewater using a batch laboratory reactor. In this time-course study, different concentrations of chlorine, used as NaOCl, were injected into the reactor, the levels of the different forms of residual chlorine were measured, and the numbers of faecal coliforms and faecal streptococci were determined. The results of the kinetics of chlorine consumption showed that monochloramines and trichloramines were the more important forms of residual chlorine as compared to free chlorine and dichloramines. The high contents of trichloramines indicated that the reaction of chlorine with ammoniacal nitrogen was very fast and that the transformation of chlorine into trichloramines was carried out in a time shorter than 1 min. Experimental results showed that the application of the model of Chick-Watson in its original form was not representative of the kinetics of inactivation of faecal coliforms and faecal streptococci. Modification of this model, in considering an initial reduction just at the contact of water with chlorine, improved the results of adjustment of the model. The same findings are valid for the model of Collins-Selleck in considering a value m imposed to the concentration of residual chlorine, since it appeared clearly that the concentration of chlorine influenced the output of disinfection more than did the time of contact
Descriptors:bioresource technology; biotechnology; disinfection; mathematical models: applications; wastewaters: treatment methodology. Models and Simulations (Computational Biology); Methods and Techniques; Waste Management (Sanitation). ammonia nitrogen; chlorine: disinfectant, uses
Organism Descriptors:bacteria (Bacteria): bioindicator, inactivation
Supplemental Descriptors:Bacteria: Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Models and Simulations (Computational Biology); Methods and Techniques; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

94. Title:The effects of coirpith compost on the growth and quality of leaves of the mulberry plant Morus alba L
View Article: Bioresource Technology. 72 (1). March , 2000. 95-97
CD Volume:326
Print Article: Pages: 95-97
Author(s):Prince W SPM Sivakumar S Ravi V Subburam V
Author Affiliation:Department of Environmental Sciences, Bharathiar University, Coimbatore, TN, 641 046
Language:English
Language of Summary:English (EN)
Abstract:The effects of addition of coirpith compost (CPC) (5-25 g/3 kg of soil) on the above-ground (plant height, number of branches and leaves, leaf area and weight of the leaves), and below-ground (root length, number of roots and weight of the roots) parameters and the quality of leaves

(chlorophyll and nitrogen) were studied. The responses of the various parameters to addition of increasing quantities of CPC were different. Compost at 5 g or more per 3 kg soil produced a significant increase over the control in the number of roots. At 10 g compost or more the length of roots and nitrogen content of leaves were increased, while 15 g or more increased the wet and dry weights of roots. At 20 g or 25 g the plant height and wet and dry weights of leaves were increased, whereas only 25 g compost increased leaf chlorophyll and the number of branches and leaves. Excepting individual leaf area, which did not show a statistically significant increase even with the 25 g compost treatment, all parameters recorded the greatest response at 25 g compost. Considering the influence in increasing the growth and quality of leaves, CPC supplementation is recommended for mulberry cultivation

Descriptors:bioresource technology; biotechnology; coirpith compost: applications. Horticulture (Agriculture); Waste Management (Sanitation). chlorophyll; nitrogen

Organism Descriptors:Morus alba [mulberry] (Moraceae). leaves: growth, quality

Supplemental Descriptors:Moraceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Horticulture (Agriculture); Waste Management (Sanitation)

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

95. Title:Methanogenesis of carbohydrates and their fermentation products by syntrophic methane producing bacteria isolated from freshwater sediments

View Article: Bioresource Technology. 72 (3). May, 2000. 199-205
CD Volume:326
Print Article: Pages: 199-205

Author(s):Tabassum Romana Rajoka M Ibrahim
Author Affiliation:National Institute for Biotechnology and Genetic Engineering (NIBGE), Jhang Road, Faisalabad

Language:English
Language of Summary:English (EN)

Abstract:Anaerobic conversion of substrates namely cellulose, cellobiose, glucose, volatile fatty acids, and methanol with a co-culture of fermentative, acidogenic, acetogenic, and methanogenic organisms isolated from freshwater sediments was performed. Maximum reduction of volatile solids (VS) was from cellulose, cellobiose and glucose followed by methanol and other compounds with a product yield coefficient (Yp/s) of 0.59 m3/kg VS consumed with a volumetric productivity (Qp) of 15.7 mmol/l/d after 12 d fermentation of cellulose. Maximum methane content in the gas mixture was 86.1% with an average of 82.5 +- 3.6%. Batch culture methane production characteristics were analyzed and compared. The maximum values of Yp/s from cellobiose, glucose, methanol, formate, acetate, propionate, and butyrate were 4.0, 2.2, 0.71, 0.22, 0.90, 1.6 and 1.43 mmol/M substrate used and are higher than those values reported in the literature

Descriptors:freshwater sediment. Bioprocess Engineering; Waste Management (Sanitation). acetate; acetogens; butyrate; carbohydrates: methanogenesis; cellobiose; fermentation endproducts; formate; glucose; methanol; propionate; volatile fatty acids

Organism Descriptors:methanogenic bacteria (Methanogenic Archaeobacteria): syntrophic

Supplemental Descriptors:Methanogenic Archaeobacteria: Archaeobacteria, Bacteria, Microorganisms. Archaeobacteria; Bacteria; Microorganisms

Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

96. Title:Physical removal of textile dyes from effluents and solid-state fermentation of dye-adsorbed agricultural residues
View Article: Bioresource Technology. 72 (3). May, 2000. 219-226
CD Volume:326
Print Article: Pages: 219-226
Author(s):Nigam P Armour G Banat I M Singh D Marchant R
Author Affiliation:Biotechnology Research Group, School of Applied Biological and Chemical Sciences, University of Ulster, Coleraine, Co., Londonderry, BT52 1SA
Language:English
Language of Summary:English (EN)
Abstract:Three agricultural residues, wheat straw, wood chips and corn-cob shreds were tested for their ability to adsorb individual dyes and dye mixtures in solutions. Up to 70-75% colour removal was achieved from 500 ppm dye solutions at room temperature using corn-cob shreds and wheat straw. Increasing the temperature had little effect on the adsorption capacity of the residues. The resulting dye-adsorbed residues were found to be suitable substrates for solid-state fermentation (SSF) by two white-rot fungi; Phanerochaete chrysosporium and Coriolus versicolor. Both strains grew uninhibited and produced a maximum protein content of 16, 25 and 35 g and 19, 23 and 50 g in SSF of 100 g dry weight wood chips, corn-cob shreds and wheat straw, respectively, supplemented with ammonical nitrogen to give a C:N ratio of 20:1. This approach provides preliminary results for the remediation of textile effluent and the conversion of agricultural residues into soil conditioner
Descriptors:corn cob shreds: agricultural residue, dye absorbing ability, substrate; wheat straw: agricultural residue, dye absorbing ability, substrate; wood chips: agricultural residue, dye absorbing ability, substrate. Bioprocess Engineering; Waste Management (Sanitation). textile dyes: physical removal
Organism Descriptors:Coriolus versicolor (Basidiomycetes); Phanerochaete chrysosporium (Basidiomycetes)
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology
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97. Title:Bioconversion of starch to ethanol in a single-step process by coculture of amylolytic yeasts and Saccharomyces cerevisiae 21
View Article: Bioresource Technology. 72 (3). May, 2000. 261-266
CD Volume:326
Print Article: Pages: 261-266
Author(s):Verma G Nigam Poonam Singh Dalel Chaudhary Kamla
Author Affiliation:Biotechnology Research Group, School of Applied Biological and Chemical Sciences, University of Ulster, Coleraine, BT52 1SA
Language:English
Language of Summary:English (EN)
Abstract:Ethanol production by a coculture of Saccharomyces diastaticus and Saccharomyces cerevisiae 21 was 24.8 g/l using raw unhydrolysed starch in a single-step fermentation. This was 48% higher than the yield

obtained with the monoculture of S. diastaticus (16.8 g/l). The maximum ethanol fermentation efficiency was achieved (93% of the theoretical value) using 60 g/l starch concentration. In another coculture fermentation with E. capsularis and S. cerevisiae 21, maximum ethanol yield was 16.0 g/l, higher than the yield with the monoculture of Endomycopsis capsularis. In batch fermentations using cocultures maximum ethanol production occurred in 48 h of fermentation at 30degreeC using 60 g/l starch. Fermentation efficiency was found lower in a two-step process using alpha- amylase and glucoamylase-treated starch

Descriptors:Bioprocess Engineering; Methods and Techniques. alpha-amylase; ethanol; glucoamylase; starch: single-step bioconversion

Organism Descriptors:Endomycopsis capsularis (Ascomycetes); Saccharomyces cerevisiae 21 [distillers yeast] (Ascomycetes)

Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants

Subject Codes:Bioprocess Engineering; Methods and Techniques

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

98. Title:Growth of inoculated white-rot fungi and their interactions with the bacterial community in soil contaminated with polycyclic aromatic hydrocarbons, as measured by phospholipid fatty acids

View Article: Bioresource Technology.. 73 (1). May, 2000. 29-36
CD Volume:326
Print Article: Pages: 29-36

Author(s):Andersson B E Welinder L Olsson P A Olsson S Henrysson T
Author Affiliation:Department of Biotechnology, Center for Chemistry and Chemical Engineering, Lund University, SE-221 00, Lund

Language:English
Language of Summary:English (EN)

Abstract:The objective of this study was to examine the possibility of measuring the growth of three white-rot fungi in soil contaminated with polycyclic aromatic hydrocarbons (PAHs), by estimating the soil levels of the phospholipid fatty acid (PLFA) 18:2omega6,9. The effect of the fungi on the PAH concentration and on the indigenous bacterial population in the soil was monitored. As shown by visual examination, the fungi investigated, Pleurotus ostreatus, Phanerochaete chrysoporium and Hypholoma fasciculare, grew well in autoclaved soil, whilst only H. fasciculare grew in non-autoclaved soil. In these reactors, there was also detected an increase in the PLFA 18:2omega6,9. However, the interpretation of the PLFA data was somewhat disturbed since 18:2omega6,9 also was found to be present in the birch wood used as a fungal substrate. In autoclaved soil, P. ostreatus and P. chrysosporium were found to exhibit a PAH- degrading capability, with the total PAH concentration decreasing from 209 +- 35 and 186 +- 2 to 149 +- 6 and 109 +- 6 mg/kg dry weight (dw) soil, respectively, during the 10 week incubation period. No PAH-degradation could be detected in any treatment using non-autoclaved soil. In the autoclaved soil, the total level of bacterial specific PLFAs in all fungal treatments, and in a control using added ground birch sticks, was found to be lowered. In the non-autoclaved soil, 6 out of 9 selected bacterial PLFAs exhibited a significant change between the treatments, but the overall total content of bacterial PLFAs did not change. The present study has shown that it is possible to measure fungal growth in a PAH- contaminated soil derived from a former gasworks plant by estimating the levels of the PLFA 18:2omega6,9. The inoculated fungi affected the indigenous

bacteria, as shown by estimating the level of bacterial specific PLFAs. Finally, fungal PAH-degradation could be detected in autoclaved soil but not in non-autoclaved soil

Descriptors:fungal-bacterial interaction. Bioprocess Engineering; Methods and Techniques; Pollution Assessment Control and Management; Waste Management (Sanitation); Soil Science. phospholipid fatty acid: fungal growth indicator; polycyclic aromatic hydrocarbon: pollutant, soil contaminant

Organism Descriptors:Hypholoma fasciculare (Basidiomycetes): bioremediation agent, white- rot fungus; Phanerochaete chrysosporium (Basidiomycetes): bioremediation agent, white-rot fungus; Pleurotus ostreatus (Basidiomycetes): bioremediation agent, white-rot fungus; bacteria (Bacteria): indigenous, soil; birch wood (Betulaceae): fungal substrate

Supplemental Descriptors:Bacteria: Microorganisms; Basidiomycetes: Fungi, Plantae; Betulaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Bacteria; Dicots; Eubacteria; Fungi; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants

Subject Codes:Bioprocess Engineering; Methods and Techniques; Pollution Assessment Control and Management; Waste Management (Sanitation); Soil Science

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

99. Title:Nitrite accumulation in an attapulgas clay biofilm reactor by fulvic acids

View Article: Bioresource Technology.. 73 (1). May, 2000. 91-93
CD Volume:326
Print Article: Pages: 91-93

Author(s):Zhang Shao Yuan Wang Ju Si Jiang Zhao Chun Chen Mei xue
Author Affiliation:Environmental Biotechnology, TNO Institute, 7300 AH, Apeldoorn

Language:English
Language of Summary:English (EN)

Abstract:As a result of seriously polluted raw water sources, some water-treatment plants in China are intending to apply the biofilm process as a pretreatment prior to the traditional drinking water- treatment systems. These polluted raw waters contain higher total organic matter and ammonium than unpolluted waters. It has been reported that synthetic organic matter can cause nitrite accumulation. However, there have been few reports about the influence of fulvic acids on nitrification. Fulvic acids are the main part of the natural organic matter in waters, and nitrite is a toxic substance which has been paid attention to recently, especially in the treatment of drinking water, so it is necessary to study the effect of fulvic acids on the nitrification process. In this experiment, a so-called 'attapulgas clay' biofilm reactor was set up, in which attapulgas clay was packed as the support medium for biological growth. After 40 days start-up, a multi- species biofilm developed in the reactor. The influence of fulvic acids on nitrite accumulation was investigated. Nitrite accumulation in the biofilm process was related to fulvic acids loadings. When the fulvic acids loading was less than 0.002 kg (TOC)/hcntdotm3, no nitrite build-up; but when the loading was in the range of 0.002-0.02 kg (TOC)/hcntdotm3, nitrite built up and the concentration of nitrite could reach as high as 11.4 mg/l. When the loading was above 0.07 kg (TOC)/hcntdotm3, the nitrification process was completely inhibited

Descriptors:nitrification process. Bioprocess Engineering; Freshwater Ecology (Ecology, Environmental Sciences); Pollution Assessment Control and Management; Waste Management (Sanitation). fulvic acids; nitrite: accumulation, toxin
Geographic Locator:China (Palearctic region)
Organism Descriptors:microorganism (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Freshwater Ecology (Ecology, Environmental Sciences); Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

100. Title:Production of exocellular pigment by the marine diatom Haslea ostrearia Simonsen in a photobioreactor equipped with immersed ultrafiltration membranes
View Article: Bioresource Technology. 73 (2). June, 2000. 197-200
CD Volume:326
Print Article: Pages: 197-200
Author(s):Rossignol Nathalie Jaouen Pascal Robert Jean Michel Quemeneur Francis
Author Affiliation:Cnt. de Rech. et de Trans. de Tech., Laboratorie de Genie des Procedes, ISOMer - Institut des Substances et Organismes de la Mer, Boulevard de l'Universite, F-44602, Saint-Nazaire Cedex
Language:English
Language of Summary:English (EN)
Abstract:A new photobioreactor coupled with an ultrafiltration system (immersed membranes) was investigated for the continuous culture of the microalga Haslea ostrearia in order to improve pigment (marennine) production and recovery. The system presents a commercial interest, because energetic costs were minimized, and the cells were not submitted to any shear stress due to pumping or circulation. To obtain this, since the photobioreactor was of cylindrical type, a membrane module was placed at the bottom of the reactor and the hydrostatic pressure (the height of the water column) used as driving force both for the permeation and periodical backflushing steps. The production of biomass and marennine was stable for a three-week period, with marennine specific productivity apprxeq30-35 mg 10-9 cell day-1, marennine concentration apprxeq3 times higher than in a conventional batch photobioreactor. The permeation flux obtained was acceptable (3-10 l h-1 m-2, 3 kPa, 15degreeC), but for such applications, this type of integrated process needs further improvements. Owing to its simple design, the concept "photobioreactor - ultrafiltration with immersed membranes" has good possibilities in biotechnology and aquaculture for continuous extraction of exocellular metabolites
Descriptors:biomass. Aquaculture; Bioprocess Engineering; Equipment, Apparatus, Devices and Instrumentation. exocellular pigment: production; marennine: production, recovery
Organism Descriptors:Haslea ostrearia (Chrysophyta): marine diatom
Supplemental Descriptors:Chrysophyta: Algae, Plantae. Algae; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Aquaculture; Bioprocess Engineering; Equipment, Apparatus, Devices and Instrumentation
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

101. Title:A comparison of mesophilic and thermophilic anaerobic upflow filters
View Article: Bioresource Technology. 73 (3). July, 2000. 201-205
CD Volume:326
Print Article: Pages: 201-205
Author(s):Ahn J H Forster CF
Author Affiliation:School of Civil Engineering, Birmingham University, Edgbaston, Birmingham, B15 2TT
Language:English
Language of Summary:English (EN)
Abstract:Two anaerobic filters, one mesophilic (35degreeC) and one thermophilic (55degreeC), were operated with a starch-based feed at a series of organic loading rates. At loading rates up to 8.3 kg COD m-3 d-1, there was no difference in the performance of the two types of reactor, measured in terms of the removal of soluble COD (SCOD) and gas production. At the higher loading rates of 12.4 and 17 kg COD m-3 d-1, the thermophilic filter gave the better performance; a SCOD removal of 93% compared to 78% at the former loading rate and one of 88% compared to 55% at the latter one. The daily methane production from the mesophilic digester was also lower; 3.19 ld-1 compared to 4.98 ld-1 for the thermophilic digester at the loading rate of 12.4 kg COD m-3 d-1 and 2.24 ld-1 compared to 6.18 ld-1 at the loading rate of 17 kg COD m-3 d-1. The volatile fatty acid concentration in the effluent from the mesophilic filter also increased from <50 mg acetate l-1 to 254 and 464 mg acetate l-1 at the two higher loading rates
Descriptors:bioresource technology; biotechnology; chemical oxygen demand; Meeting Abstract. Bioprocess Engineering; Waste Management (Sanitation). acetate; methane
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

102. Title:Larvicidal and repellent actions of Dalbergia sissoo Roxb. (F. Leguminosae) oil against mosquitoes
View Article: Bioresource Technology. 73 (3). July, 2000. 207-211
CD Volume:326
Print Article: Pages: 207-211
Author(s):Ansari M A Razdan R K Tandon Mamta Vasudevan Padma
Author Affiliation:Centre for Rural Development and Technology, Indian Institute of Technology, Delhi, Hauz Khas, New Delhi, 110016
Language:English
Language of Summary:English (EN)
Abstract:Studies were carried out to evaluate the larvicidal, growth inhibitor and repellent actions of D. sissoo oil against Anopheles stephensi, Aedes aegypti and Culex quinquefasciatus under laboratory conditions. Pure oil was applied at 0.4-5 ml/m2 on a water surface. This showed that larvicidal activity was directly proportional to dosages. One hundred percent mortality of Cx. quinquefasciatus immatures was observed within 24 h at 4 ml/m2, followed by Ae. aegypti (90%) and An. stephensi (60%), and pupation was totally inhibited. Adults which emerged from exposure to a sublethal dosage (2 ml/m2) either did not lay eggs (Ae. aegypti) or hatch (Cx. quinquefasciatus and An. stephensi). The oil also showed strong repellent action when 1 ml oil was applied on exposed parts of human volunteers. They were protected from mosquito bites for 8- 11 h. The protection (91.6 +- 2%) obtained

with sissoo oil was comparable to that with commercial Mylol oil (93.8 +- 1.2%) consisting of di-butyl and dimethyl phthalates
Descriptors:bioresource technology; biotechnology; laboratory conditions; Meeting Abstract. Pest Assessment Control and Management. shisham oil: insecticide, larvicidal action, mosquitocide, repellent action
Organism Descriptors:Dalbergia sissoo [shisham] (Leguminosae); human (Hominidae); mosquitoes (Diptera): pest
Supplemental Descriptors:Diptera: Insecta, Arthropoda, Invertebrata, Animalia; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Arthropods; Chordates; Dicots; Humans; Insects; Invertebrates; Mammals; Plants; Primates; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Pest Assessment Control and Management
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

103. Title:Sludge treatment and reuse as soil conditioner for small rural communities
View Article: Bioresource Technology. 73 (3). July, 2000. 213-219
CD Volume:326
Print Article: Pages: 213-219
Author(s):Kuai Linping Doulami Farida Verstraete Willy
Author Affiliation:Laboratory of Microbial Ecology and Technology(LabMET), Center for Environmental Sanitation, Genth University, Coupure L 653, B- 9000, Gent
Language:English
Language of Summary:English (EN)
Abstract:An alternative method for on-site treatment of sewage sludge for small-scale wastewater treatment installations was developed. Primary Domestic Sludge (PDS) at 40 g dry matter per liter of suspension was supplemented with 10 g of the super-absorbent (SA). The mixture obtained in a matter of minutes was of crumbly consistency without leakage of free water. These crumbs were spread on cardboard supported by an undulated plate. After air drying for 1-2 weeks, depending on the ambient air temperature and humidity, the water content of the crumbs decreased from 96% to 8.5%. The dried residue was used to treat a new volume of primary domestic sludge. This cycle was repeated for more than 15 times and the SA remained active. The technical skills and the costs related to convert PDS to an air-dry residue by means of this SA-based process, appear appropriate for a family or a small community. The final product of the sludge treatment process contained about 50% (w/w) organic material in a stabilised form. It was rich in N and P and it had a high hygienic quality. Greenhouse tests growing maize showed that this final product had soil improving properties
Descriptors:bioresource technology; biotechnology; hygiene; sewage sludge: reuses, treatment; small rural communities; small-scale wastewater treatment facilities; soil conditioners; Meeting Abstract. Waste Management (Sanitation); Soil Science
Subject Codes:Waste Management (Sanitation); Soil Science
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

104. Title:Biosynthesis of L-lysine by Corynebacterium glutamicum grown on fish silage

View Article: Bioresource Technology. 73 (3). July, 2000. 221-225
CD Volume:326
Print Article: Pages: 221-225
Author(s):Coello Nereida Brito Lysbeth Nonus Maurice
Author Affiliation:Institute of Experimental Biology, Central University of Venezuela, (UCV), Caracas, 1041-A
Language:English
Language of Summary:English (EN)
Abstract:The microbial utilization of fish silage as a fermentation substrate for the extracellular production of L-lysine by Corynebacterium glutamicum ATCC 21543 was studied in Erlenmeyer baffled flasks. When culture media were supplemented with fish silage at 40 g/l the concentrations of biomass and L-lysine attained 10 and 30 g/l, respectively after 72 h of fermentation. Kinetic fermentation data, the specific rate of L-lysine production and the product yield reached maximum values of 0.096 g/g h and 0.30 g/g, respectively, when yeast extract was replaced by fish silage in culture media. Statistical analysis showed that there was not a significant difference (P > 0.05) between yeast extract (20 g/l) and fish silage (40 g/l) kinetic fermentation data
Descriptors:bacterial growth conditions; bioresource technology; biotechnology; fish silage: bacterial growth substrate; industrial fermentations; product yield; statistical analyses; Meeting Abstract. Bioprocess Engineering. L-lysine: biosynthesis
Organism Descriptors:Corynebacterium glutamicum (Irregular Nonsporing Gram-Positive Rods)
Supplemental Descriptors:Irregular Nonsporing Gram-Positive Rods: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

105. Title:Distribution of lipases in the Gramineae. Partial purification and characterization of esterase from Avena fatua
View Article: Bioresource Technology. 73 (3). July, 2000. 227-234
CD Volume:326
Print Article: Pages: 227-234
Author(s):Mohamed Magda A Mohamed Tarek M Mohamed Saleh A Fahmy Afaf S
Author Affiliation:Department of Molecular Biology, National Research Centre, Tahrir St., Dokki, Cairo
Language:English
Language of Summary:English (EN)
Abstract:The activity levels of esterase, lipid acylhydrolase and lipase were quantitatively screened in 23 species and cultivars of Gramineae. Their activity levels expressed as units g-1 seeds, were found to range from 10 to 123 for esterase, 0.28 to 7.67 for lipid acylhydrolase and 13.1 to 93.9 for lipase. Avena fatua, one of the grass species, exhibited the highest levels of esterase and lipase and could be potentially a good starting material for preparation of lipases. A. fatua esterase has been partially purified and characterized. Four isoenzymes, EI, EII, EIII and EIV, were separated by ion exchange chromatography. Esterases EII and EIII had Km values of 0.52 and 0.38 mM and a pH optimum at 9.0 with half maximal activities at pHs 8.5, 10 and 8, 10.5, respectively. Esterases EII and EIII had optimum activities at temperatures of 75degreeC and 65degreeC with activation energies of 3.3 and 4.3 kcal mol-1, respectively. The enzymes were thermally stable as

esterases EII and EIII retaining 39% and 23% of their activities at 90degreeC, respectively. Esterases EII and EIII were stimulated by Ba2+ and Ca2+ but were inhibited by Mn2+ and Zn2+. A. fatua esterases exhibited optimum storage stability and were stable at high temperatures and alkaline pH. They possessed high affinity toward substrate and were resistant to inhibition by most divalent cations that were examined. These are important properties when considering the industrial application of these enzymes
Descriptors:bioresource technology; biotechnology; Meeting Abstract. Enzymology (Biochemistry and Molecular Biophysics). esterases: applications, distribution; industrial enzymes: applications; lipases [EC 3.1.1.3]: applications, distribution
Organism Descriptors:Avena fatua (Gramineae); Gramineae (Gramineae); grasses (Gramineae)
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

106. Title:Evaluation of combination treatments of sodium hydroxide and steam explosion for the production of cellulase-systems by two T. reesei mutants under solid-state fermentation conditions
View Article: Bioresource Technology. 73 (3). July, 2000. 235-245
CD Volume:326
Print Article: Pages: 235-245
Author(s):Awafo V A Chahal D S Simpson B K
Author Affiliation:Department of Food Science and Agricultural Chemistry, McGill University, 21, 111 Lakeshore Road, Macdonald Campus, Sainte Anne de Bellevue, PQ, H9X 3V9
Language:English
Language of Summary:English (EN)
Abstract:A central composite orthogonal design model was used to optimize pretreatment and culture conditions for the production of cellulase-systems by T. reesei QMY-1 and MCG 80 using wheat straw as carbon source. The model was capable of predicting conditions for maximum filter paper activity (FPA) and beta-glucosidase activity (betaGA). Statistical analysis showed close agreement between the experimental FPA and betaGA activities and predicted values. Maximum FPA of 9.88 IU/ml and 8.38 IU/ml were obtained for T. reesei MCG 80 and T. reesei QMY-1, respectively, using 4% NaOH pretreatment and initial culture pH 6, under solid-state fermentation conditions. The cellulase-systems produced were capable of hydrolyzing over 80% delignified wheat straw. Combination of NaOH pretreatment with steam explosion did not enhance the activity of the cellulase-systems of the two mutants
Descriptors:bioresource technology; biotechnology; industrial fermentation; solid-state fermentation conditions; Meeting Abstract. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering. cellulase systems: production; enzymes; sodium hydroxide: treatment
Organism Descriptors:Trichoderma reesei (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering
ISSN:0960-8524
Year:2000

Journal Title:Bioresource Technology

107. Title:Fertilisation of potted geranium with a municipal solid waste compost
View Article: Bioresource Technology. 73 (3). July, 2000. 247-249
CD Volume:326
Print Article: Pages: 247-249
Author(s):Ribeiro H M Vasconcelos E dos Santos J Q
Author Affiliation:Departmento de Quimica Agricola e Ambiental, Instituto Superior de Agronomia, 1349-017, Lisboa
Language:English
Language of Summary:English (EN)
Abstract:A greenhouse pot study was conducted to evaluate the use of a municipal solid waste compost (MSWC) as a fertilizer for potted geranium (Pelargonium X hortorum Bailey) cv. Meridonna. MSWC was mixed with a peat-based growing-media at rates of 0%, 10%, 20%, 30%, 40% and 50% by volume. Plants grew in those mixes for 90 days, with no additional fertilization. MSWC increased the electrical conductivity (saturated extract) of the growth-media linearly from 1.4 mS cm-1 at 0% to 12 mS cm-1 at 50% MSWC. 10% and 20% MSWC promoted the highest plant growth, although these plants showed low leaf concentrations of nitrogen and phosphorus. The lowest yield was obtained at 0% MSWC caused by a low level of available nutrients in the growth-media. Application rates of MSWC >20% reduced plant growth as a consequence of the high level of salts, and rates gtoreq40% resulted in high levels of copper. The results of this experiment showed that potassium, magnesium, calcium and micronutrients requirements of geranium were provided with 20% MSWC, indicating that this crop could be grown in peat-based substrates with 15-20% of MSWC, as long as adequate amounts of nitrogen and phosphorus were being provided
Descriptors:bioresource technology; biotechnology; greenhouse pot study; municipal solid waste composts: agricultural applications, fertilizers; Meeting Abstract. Horticulture (Agriculture); Waste Management (Sanitation). copper; nitrogen; phosphorus
Organism Descriptors:Pelargonium sp. [geranium] (Geraniaceae). leaves
Supplemental Descriptors:Geraniaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

108. Title:Application of a statistical technique to the production of ethanol from sugar beet molasses by Saccharomyces cerevisiae
View Article: Bioresource Technology. 73 (3). July, 2000. 251-255
CD Volume:326
Print Article: Pages: 251-255
Author(s):Ergun Mubeccel Mutlu S Ferda
Author Affiliation:Chemical Engineering Department, Faculty of Architecture and Engineering, Gazi University, 06570 Maltepe, Ankara
Language:English
Language of Summary:English (EN)
Abstract:In this work, a statistical model which can be used to describe the rate of ethanol production from sugar beet molasses by Saccharomyces cerevisiae was developed. Total sugar concentration, pH, and ammonium dihydrogen phosphate (NH4H2PO4) concentration were chosen as a 23-factorial experimental design and the effects of these factors on

ethanol production were examined in repeated shake flask cultures according to the Box-Wilson experimental design method. With the use of the developed model a maximum ethanol production of 1.06 g dm-3 h-1 was obtained when sugar concentration, pH, ammonium dihydrogen phosphate concentration, were 1.6 g dm-3, 4.51, 0.72 g dm-3, respectively
Descriptors:bioresource technology; biotechnology; experimental design; industrial ethanol production; industrial fermentations; statistical model: applications; sugar beet molasses: conversion; Meeting Abstract. Bioprocess Engineering. ethanol: production
Organism Descriptors:Saccharomyces cerevisiae (Ascomycetes)
Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

109. Title:A simple method for production of pure silica from rice hull ash
View Article: Bioresource Technology. 73 (3). July, 2000. 257-262
CD Volume:326
Print Article: Pages: 257-262
Author(s):Kalapathy U Proctor A Shultz J
Author Affiliation:Department of Food Science, University of Arkansas, 272 Young Ave, Fayetteville, AR, 72704
Language:English
Language of Summary:English (EN)
Abstract:Rice hull ash (RHA), a waste product of the rice industry is rich in silica. A simple method based on alkaline extraction followed by acid precipitation was developed to produce pure silica xerogels from RHA, with minimal mineral contaminants. The silica gels produced were heated to 80degreeC for 12 h to obtain xerogels. Silica and mineral contents of xerogels were determined by energy dispersive X-ray (EDX) and inductively-coupled plasma (ICP) emission spectrometers, respectively. Xerogels produced from RHA had 93% silica and 2.6% moisture. The major impurities of silica produced from RHA at an extraction yield of 91% were Na, K, and Ca. Acid washing prior to extraction resulted in silica with a lower concentration of Ca (<200 ppm). However, final water washing of the xerogel was more effective in producing silica with lower overall mineral content (Na < 200 ppm and K < 400 ppm). X-ray diffraction patterns revealed the amorphous nature of silica xerogel. Fourier transform infrared (FTIR) data indicated the presence of siloxane and silanol groups
Descriptors:bioresource technology; biotechnology; rice hull ash: conversion, waste product; Meeting Abstract. Chemistry; Methods and Techniques; Waste Management (Sanitation). minerals; silica: production methodology, pure form; xerogels
Subject Codes:Chemistry; Methods and Techniques; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

110. Title:Nitrogen and phosphorus removal from urban wastewater by the microalga Scenedesmus obliquus
View Article: Bioresource Technology. 73 (3). July, 2000. 263-272
CD Volume:326
Print Article: Pages: 263-272
Author(s):Martinez M E Sanchez S Jimenez J M El Yousfi F Munoz L

Author Affiliation:Departamento de Ingenieria Quimica, Instituto de Biotecnologia, Universidad de Granada, Granada
Language:English
Language of Summary:English (EN)
Abstract:The removal of phosphorus and nitrogen by the freshwater alga Scenedesmus obliquus, cultured in urban wastewater, previously submitted to secondary sewage treatment, was studied under different conditions of stirring and temperature. In all cases, the amount of NH3 lost, as well as biomass productivity and its biochemical composition, were evaluated. The specific growth rates proved greatest in the stirred cultures, the highest mu value being 0.0438 h-1 at 30degreeC. The stirring increased biomass productivity (PB) in the linear growth phase after exponential growth, with the optimum appearing at 25degreeC. For the temperatures studied stirring was not necessary to provide the highest percentage of P elimination (%Pmax), but did reduce the time needed to reach that percentage (tmax). The highest %Pmax value, 98%, within the shortest time period, tmax = 94.33 h, was found in the culture with stirring at 25degreeC. Ammonium removal was determined by two factors - the consumption of ammonium for growth and elimination by desorption as ammonia. The highest percentage of ammonium removal (%Nmax), 100%, resulted at the final culture time (tf) of 188.33 h, in the stirred culture at 25degreeC. The biochemical composition of the biomass gave the normal values for this microalga reported by other authors. The protein content was notably low, around 11.8% by weight, and the polyunsaturated- fatty-acid content was high. The N:P ratio of the culture medium was 12.9. Finally, we proposed a dilution factor for the treated wastewater (f) to be dumped in order to regulate operation conditions and time for an optimal removal of nitrogen and phosphorus
Descriptors:algal growth conditions; biomass; bioresource technology; biotechnology; urban wastewater samples: mineral removal, treatment; Meeting Abstract. Bioprocess Engineering; Waste Management (Sanitation). nitrogen: removal; phosphorus: removal
Organism Descriptors:Scenedesmus obliquus (Chlorophyta): microalga
Supplemental Descriptors:Chlorophyta: Algae, Plantae. Algae; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

111. Title:A cellulase-poor, thermostable, alkalitolerant xylanase produced by Bacillus circulans AB 16 grown on rice straw and its application in biobleaching of eucalyptus pulp
View Article: Bioresource Technology. 73 (3). July, 2000. 273-277
CD Volume:326
Print Article: Pages: 273-277
Author(s):Dhillon Ashita Gupta J K Jauhari B M Khanna S
Author Affiliation:Microbial Biotechnology, Tata Energy Research Institute, Habitat Place, Lodhi Road, Darbari Seth Block, New Delhi, 110003
Language:English
Language of Summary:English (EN)
Abstract:Bacillus circulans AB 16 isolated from a garbage dump produced appreciable quantities (19.28 IU/ml) of extracellular thermophilic xylanase, but negligible quantities of cellulase, when grown on 0.3% xylan. The optimum pH for the enzyme was 6.0-7.0, but it was stable over a wide range of pH (5.0-9.0). The optimum temperature was 80degreeC. The organism produced 20.6 IU/ml of xylanase in shake flask

on rice straw, an inexpensive lignocellulosic biomass. Glucose, fructose, xylose and other sugars induced enzyme levels only in the range 0.82-2.52 IU/ml. The crude enzyme produced on rice straw showed good thermal and pH stability, retaining 67% activity after 1 h at 70degreeC, pH 9 and 84.5% activity after 2 h at 65degreeC, pH 9. The enzyme had a half-life of 24 h at 70degreeC, pH 7. When the xylanase from B. circulans AB 16 was used in the prebleaching of eucalyptus Kraft pulp the amount of chlorine was reduced by 20% without any decrease in brightness. The viscosity of xylanase-treated pulp was 9.5-9.7 cp, whereas that of the pulp treated exclusively with chlorine was 9.2 cp

Descriptors:Kraft pulps; bacterial growth characteristics; bioresource technology; biotechnology; Meeting Abstract. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering. cellulases; xylanase: alkalitolerant, applications, production, thermostabile; xylans

Organism Descriptors:Bacillus circulans (Endospore-forming Gram-Positives): strain-AB 16

Supplemental Descriptors:Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms

Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

112. Title:Partial purification of proteins involved in the bioconversion of arteannuin B to artemisinin

View Article: Bioresource Technology. 73 (3). July, 2000. 279-282
CD Volume:326
Print Article: Pages: 279-282

Author(s):Dhingra Vikas Rajoli Chakrapani Narasu M Lakshmi
Author Affiliation:School of Biotechnology, Institute of Post Graduate Studies and Research, Jawaharlal Nehru Technological University, Mahaveer Marg, Hyderabad, 500028

Language:English
Language of Summary:English (EN)

Abstract:Artemisinin is an important antimalarial drug that is presently being used for controlling the resurgence of malaria. Attempts have been made to partially purify the proteins involved in the bioconversion of arteannuin B to artemisinin by affinity chromatography and precipitation techniques. Our studies indicate that a Tris-HCl buffer system is better than a phosphate buffered saline buffer system. Highest specific activity (0.1 units/mg) with crude cell-free extract has been obtained with this system. A threefold and fivefold increase in specific activity was observed when the proteins were partially purified by acetone precipitation and affinity chromatography, respectively. This is the first report on the study of proteins involved in the bioconversion of arteannuin B to artemisinin

Descriptors:large-scale drug production. Biochemistry and Molecular Biophysics; Bioprocess Engineering; Pharmacology. arteannuin B: bioconversion; artemisinin: antimalarial agent, pharmaceutical, production; proteins: applications, partial purification

Organism Descriptors:Artemisia annua (Compositae)

Supplemental Descriptors:Compositae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering; Pharmacology

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

113. Title:Laccase production by some white rot fungi under different nutritional conditions
View Article: Bioresource Technology. 73 (3). July, 2000. 283-285
CD Volume:326
Print Article: Pages: 283-285
Author(s):Arora Daljit Singh Gill Paramjit Kaur
Author Affiliation:Microbiol Technology Lab, Department of Microbiology, Guru Nanak Dev University, Amritsar, PU, 143005
Language:English
Language of Summary:English (EN)
Abstract:The role of laccase in ligninolysis has been disputed but it still seems to have an important place in the reactions. Trametes versicolor has been the organism of choice for laccase production. The present paper reports laccase production by Phlebia fascicularia, P. floridensis and Dichomitus squalens. Enzyme production in mineral salts broth, malt extract broth and in the presence of various supplements showed that P. floridensis and D. squalens were better laccase producers than T. versicolor. Different lignin preparations and natural agricultural residues gave the best enzyme production, except with T. versicolor. The studies underline the need to explore more organisms to fully exploit the potential of laccase-producing fungi
Descriptors:bioresource technology; biotechnology; industrial enzyme production; lignolysis; nutritional conditions; Meeting Abstract. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Nutrition. laccases: applications, production, uses
Organism Descriptors:Dichomitus squalens (Basidiomycetes); Phlebia fascicularia (Basidiomycetes); Phlebia floridensis (Basidiomycetes); Trametes versicolor (Basidiomycetes); fungi (Fungi)
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae; Fungi: Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Nutrition
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

114. Title:Developments at the Second International Symposium on Anaerobic Digestion of Solid Waste (Barcelona, 15-19 June 1999)
View Article: Bioresource Technology. 73 (3). July, 2000. 287-289
CD Volume:326
Print Article: Pages: 287-289
Author(s):Verstraete W Van Lier J Pohland F Tilche A Mata Alvarez J Ahring B Hawkes D Cecchi F Moletta R Noike T
Author Affiliation:Department of Chemical Engineering, Marti i Franques 1, Plta. 6, E-08028, Barcelona
Language:English
Language of Summary:English (EN)
Abstract:No Abstract available
Descriptors:bioresource technology; biotechnology; Meeting Report. Bioprocess Engineering; Waste Management (Sanitation). carbon dioxide: emissions, production
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms

Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

115. Title:Biotechnological potential of agro-industrial residues. I: Sugarcane bagasse
View Article: Bioresource Technology. 74 (1). Aug., 2000. 69-80
CD Volume:326
Print Article: Pages: 69-80
Author(s):Pandey Ashok Soccol Carlos R Nigam Poonam Soccol Vanete T
Author Affiliation:Biotechnology Division, Regional Research Laboratory, CSIR, Trivandrum, 695 019
Language:English
Language of Summary:English (EN)
Abstract:Advances in industrial biotechnology offer potential opportunities for economic utilization of agro-industrial residues such as sugarcane bagasse. Sugarcane bagasse, which is a complex material, is the major by-product of the sugar cane industry. It contains about 50% cellulose, 25% hemicellulose and 25% lignin. Due to its abundant availability, it can serve as an ideal substrate for microbial processes for the production of value-added products. Attempts have been made to produce from bagasse substrate protein- enriched animal feed, enzymes, amino acids, organic acids and compounds of pharmaceutical importance, etc. Often, a pre-treatment process has resulted in improved substrate utilization by the microbes. Application of solid-state fermentation technology could be an attractive possibility for such bioconversions. This article reviews the recent developments on processes and products developed for the value addition of sugarcane bagasse through the biotechnological means. Emphasis has been given on more recent developments of the past 8-10 years
Descriptors:agro-industrial residues; bioconversions; protein-enriched animal feed: animal feed. Agronomy (Agriculture); Bioprocess Engineering. amino acids; bagasse substrate; cellulose; enzymes; hemicellulose; lignin; organic acids; protein; sugarcane bagasse
Organism Descriptors:microbe (Microorganisms); sugarcane (Gramineae): crop
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Microorganisms. Angiosperms; Microorganisms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

116. Title:Biotechnological potential of agro-industrial residues. II: Cassava bagasse
View Article: Bioresource Technology. 74 (1). Aug., 2000. 81-87
CD Volume:326
Print Article: Pages: 81-87
Author(s):Pandey Ashok Soccol Carlos R Nigam Poonam Soccol Vanete T Vandenberghe Luciana P S Mohan Radjiskumar
Author Affiliation:Biotechnology Division, Regional Research Laboratory, CSIR, Trivandrum, 695 019
Language:English
Language of Summary:English (EN)
Abstract:Advances in industrial biotechnology offer potential opportunities for economic utilization of agro-industrial residues such as cassava

bagasse. Cassava bagasse, which is a fibrous material, is the by-product of the cassava-processing industry. It contains about 30-50% starch on dry weight basis. Due to its rich organic nature and low ash content, it can serve as an ideal substrate for microbial processes for the production of value added products. Attempts have been made to produce several products such as organic acids, flavour and aroma compounds, and mushrooms from cassava bagasse. Solid-state fermentation has been mostly employed for bioconversion processes. This paper reviews the developments in processes and products developed for the value addition of cassava bagasse through biotechnological means

Descriptors:agro-industrial residues; bioconversions. Agronomy (Agriculture); Bioprocess Engineering. aroma compounds; cassava bagasse; enzymes; flavor compounds; hemicellulose; organic acids; starch

Organism Descriptors:cassava (Euphorbiaceae); mushroom (Basidiomycetes)

Supplemental Descriptors:Basidiomycetes: Fungi, Plantae; Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Fungi; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants

Subject Codes:Agronomy (Agriculture); Bioprocess Engineering

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

117. Title:Upflow biological aerated filters for the treatment of flushed swine manure

View Article: Bioresource Technology. 74 (3). Sept., 2000. 181-190
CD Volume:326
Print Article: Pages: 181-190

Author(s):Westerman P W Bicudo J R Kantardjieff A

Author Affiliation:Department of Biological and Agricultural Engineering, North Carolina State University, Raleigh, NC, 27695-7625

Language:English
Language of Summary:English (EN)

Abstract:A pilot plant with capacity to treat up to 8 m3/day of supernate from settled flushed swine wastes was monitored for 12 months. The main system is composed of two upflow aerated biofilters connected in series. The aerated biofilters, operated under warm weather conditions (average temperature of 27degreeC), were able to remove about 88% of biochemical oxygen demand (BOD), 75% of chemical oxygen demand (COD), and 82% of total suspended solids (SS) with loading of 5.7 kg COD/m3/day of biofilter media. The total Kjeldahl nitrogen (TKN), total ammonia nitrogen (NH3-N), and total nitrogen (Total-N) reductions averaged 84%, 94% and 61%, respectively, during warm weather, with a significant portion of the NH3-N being converted to nitrite plus nitrate nitrogen (NO2 + NO3-N). At higher organic loading (over 9 kg COD/m3/day) during September, the biofilters had only slightly lower percentage removal rates. Operation at lower temperatures (average of 10degreeC) resulted in lower performances. The COD, TKN, NH3-N, and Total-N removal averaged 56%, 49%, 52%, and 29%, respectively, in December through March. The COD mass removal rate was linear with loading rate over the range of approximately 2-12 kg COD/m3/day of filter. A mass balance average for the 12 months indicated that about 30% of the influent volume, 35% of Total-N and 60% of total phosphorus (Total- P) are removed with the biofilter backwash. Management and utilization of the backwash are important factors in implementing this type of system on farms. The unaccounted-for nitrogen was about 24% and could have been lost as ammonia volatilization or possibly through denitrification within the biofilm

Descriptors:biochemical oxygen demand; biofilms; biotechnology; chemical oxygen demand; flushed swine manure: treatment methodology. Bioprocess Engineering; Equipment, Apparatus, Devices and Instrumentation; Waste Management (Sanitation). nitrogen
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Equipment, Apparatus, Devices and Instrumentation; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

118. Title:Production of endo-1,4-beta-glucanase by a biocontrol fungus Cladorrhinum foecundissimum
View Article: Bioresource Technology. 75 (1). October, 2000. 95-97
CD Volume:326
Print Article: Pages: 95-97
Author(s):Kumar R Dahiya J S Singh D Nigam P
Author Affiliation:Biotechnology Research Group, School of Applied Biological and Chemical Sciences, University of Ulster, Coleraine, BT52 1SA
Language:English
Language of Summary:English (EN)
Abstract:The biocontrol fungus Cladorrhinum foecundissimum isolated from the soil collected from the canola field in Vegreville, Alberta, Canada, was studied for the production of endo-1,4-beta-glucanase enzyme. The production of the enzyme was significantly stimulated in cellulose-containing medium. Relatively high levels of enzyme activity were produced on L-sorbose and xylan, while moderate enzyme activity was detected using as substrates carboxymethylcellulose, laminarin and cellobiose. Maximum mycelial growth occurred in 8 d of cultivation while maximum enzyme yield was achieved in 9-10 d of fermentation
Descriptors:canola field; maximum mycelial growth. Bioprocess Engineering; Infection; Methods and Techniques; Waste Management (Sanitation); Soil Science. carboxymethylcellulose: substrate; cellobiose: substrate; endo-1,4- beta-glucanase: production; l-sorbose; laminarin: substrate; xylan
Organism Descriptors:Cladorrhinum foecundissimum (Fungi Imperfecti or Deuteromycetes): biocontrol agent, soil isolate; Rhizoctonia solani (Fungi Imperfecti or Deuteromycetes): soil-borne pathogen
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Infection; Methods and Techniques; Waste Management (Sanitation); Soil Science
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

119. Title:Inactivation of Vibrio cholerae during anaerobic digestion of human night soil
View Article: Bioresource Technology. 75 (2). November, 2000. 149-151
CD Volume:326
Print Article: Pages: 149-151
Author(s):Kunte D P Yeole T Y Ranada D R
Author Affiliation:Division of Microbial Sciences, Agharkar Research Institute, G.G. Agarkar Road, Pune, 411 004
Language:English
Language of Summary:English (EN)

Abstract:The fate of Vibrio cholerae was studied during anaerobic digestion of human night soil (HNS). In an experimental digester (VFAsimeq8000 mg/l and pHsimeq6.4), counts of V. cholerae declined rapidly and the counts were below detectable limits within 20 d. In the control digester (VFAsimeq500 mg/l and pH 7.6), a four log reduction in count was achieved, however, the pathogen was not completely eliminated. T90 values for the experimental and control digesters were 1.53 and 2.63 d, respectively
Descriptors:bacterial inactivation mechanisms; biotechnology; human night soil: anaerobic digestion. Methods and Techniques; Microbiology; Waste Management (Sanitation). volatile fatty acids: analysis
Organism Descriptors:Vibrio cholerae (Vibrionaceae); human (Hominidae)
Supplemental Descriptors:Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Vibrionaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Animals; Bacteria; Chordates; Eubacteria; Humans; Mammals; Microorganisms; Primates; Vertebrates
Subject Codes:Methods and Techniques; Microbiology; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

120. Title:Influence of earthworm-processed pig manure on the growth and yield of greenhouse tomatoes
View Article: Bioresource Technology. 75 (3). December, 2000. 175-180
CD Volume:326
Print Article: Pages: 175-180
Author(s):Atiyeh R M Arancon N Edwards C A Metzger J D
Author Affiliation:Soil Ecology Laboratory, 105 Botany and Zoology Building, The Ohio State University, 1735 Neil Avenue, Columbus, OH, 43210
Language:English
Language of Summary:English (EN)
Abstract:The effects of earthworm-processed pig manure (vermicompost) on germination, growth, and yields of tomato (Lycopersicon esculentum Mill.) plants were evaluated under glasshouse conditions. Tomatoes were germinated and grown in a standard commercial greenhouse container medium (Metro-Mix 360), substituted with 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, and 100% (by volume) pig manure vermicompost. The control consisted of Metro-Mix 360 alone without vermicompost. Plants were grown for 158 days and were frequently supplied with a complete mineral nutrient solution. The germination rates of tomato seeds increased significantly upon substitution of Metro-Mix 360 with 20%, 30%, and 40% vermicompost. Seedlings grown in 100% pig manure vermicompost were significantly shorter, had fewer leaves, and weighed less than those in Metro-Mix 360 controls. Incorporation of 10% or 50% vermicompost into Metro-Mix 360 increased the dry weights of tomato seedlings significantly compared to those grown in the Metro-Mix 360 controls. The largest marketable yield was in the substitution of Metro-Mix 360 with 20% vermicompost (5.1 kg/plant). The average weight of a tomato fruit in substitution of Metro-Mix 360 with 20% vermicompost was 12.4% greater than that in the Metro-Mix 360 control. Substitution of Metro-Mix 360 with 10%, 20%, and 40% vermicompost reduced the proportions of fruits that were non-marketable, and produced more large size (diameter > 6.4 cm) than small size (diameter < 5.8 cm) tomato fruits. There was no significant difference in overall tomato yields between Metro-Mix 360 and 100% pig manure vermicompost. Some of the growth and yield enhancement resulting from substitution of Metro-Mix 360 with pig manure vermicompost could be attributed to the

high mineral N concentration of the pig manure vermicompost. However, other factors might have also been involved since all plants were frequently supplied with all required nutrients. These factors need to be investigated in future studies
Descriptors:bioresource technology; biotechnology; pig manure: agricultural uses, earthworm-processed; plant germination; plant growth; plant yield. Horticulture (Agriculture); Nutrition; Waste Management (Sanitation)
Organism Descriptors:Lycopersicon esculentum [tomato] (Solanaceae): seedling; earthworm (Oligochaeta)
Supplemental Descriptors:Oligochaeta: Annelida, Invertebrata, Animalia; Solanaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Annelids; Dicots; Invertebrates; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Nutrition; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

121. Title:Extraction and purification of lactic acid from silages
View Article: Bioresource Technology. 75 (3). December, 2000. 181-187
CD Volume:326
Print Article: Pages: 181-187
Author(s):Danner H Madzingaidzo L Holzer M Mayrhuber L Braun R
Author Affiliation:Department for Environmental Biotechnology, IFA-Tulln, Konrad Lorenz Strasse 20, A-3430, Tulln
Language:English
Language of Summary:English (EN)
Abstract:Various silages with different contents of organic acids were used to evaluate the possibilities of recovery of lactic acid from grass silages. Press extraction yields of lactic acid from silage preparations ranged from 31 to 96 g lactate perkg silage dry matter (g LA/kg DM). The crude liquid press extract was pre-treated with ultrafiltration membranes followed by purification with mono-polar electrodialysis (ED). Low current densities, high energy consumption at 1.47-1.76 kWh/kg lactate and the high levels of organics and minerals (8 g/l) limit the possible applications of the resulting product to low-grade applications such as animal feed additive or road-de-icers
Descriptors:animal feed additives; bioresource technology; biotechnology; product yields; silages: uses. Biochemistry and Molecular Biophysics; Bioprocess Engineering; Foods; Methods and Techniques. lactic acid: extraction, purification; organic acids: extraction, purification; road deicers
Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering; Foods; Methods and Techniques
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

122. Title:Bacterial concentration reduction in swine waste amended livestock feed using a single-screw dry-extrusion process
View Article: Bioresource Technology. 75 (3). December, 2000. 189-195
CD Volume:326
Print Article: Pages: 189-195
Author(s):Kelley Timothy R Walker Paul M

Author Affiliation:Health Sciences Department, Environmental Health Program, Illinois State University, 322 Felmley Hall, Normal, IL, 61790-5220
Language:English
Language of Summary:English (EN)
Abstract:A study was conducted to determine the efficiency of a dry- extrusion process to reduce or eliminate bacterial contamination of swine waste amended livestock feed. Separated swine waste solids were mixed with ground corn and soybean hulls and dry-extruded at temperatures of 110-135degreeC for no more than 30 s to produce animal feed. Swine waste, pre- and post-extrusion livestock feed, and commercial swine feed samples were collected aseptically and analysed for total coliform, Escherichia coli, fecal coliform, heterotrophic, and non-specific anaerobic/facultative bacteria using standard culturing techniques. Selected pre-extrusion feed samples were inoculated with liquid cultures of Bacillus stearothermophilus to test efficiency of the dry-extrusion process to eliminate heat-resistant spore-forming bacteria. Bacterial concentrations recovered from post-extrusion livestock feed were significantly reduced from other sample types analysed. Based on these data, it is apparent that a single-screw, dry-extrusion process can consistently disinfect animal feed. However, careful monitoring of the extrusion process may be necessary for consistent sterilization
Descriptors:bioresource technology; biotechnology; livestock feeds: preparation; sterilization/disinfection; swine waste: bacterial concentration reduction. Foods; Methods and Techniques; Microbiology; Waste Management (Sanitation)
Organism Descriptors:bacteria (Bacteria); swine (Suidae)
Supplemental Descriptors:Bacteria: Microorganisms; Suidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Bacteria; Chordates; Eubacteria; Mammals; Microorganisms; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Foods; Methods and Techniques; Microbiology; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

123. Title:Steam- or carbon dioxide-activated carbons from almond shells: Physical, chemical and adsorptive properties and estimated cost of production
View Article: Bioresource Technology. 75 (3). December, 2000. 197-203
CD Volume:326
Print Article: Pages: 197-203
Author(s):Toles Christopher A Marshall Wayne E Wartelle Lynda H McAloon Andrew
Author Affiliation:ARS, Southern Regional Research Center, USDA, 1100 Robert E. Lee Boulevard, New Orleans, LA, 70179-0687
Language:English
Language of Summary:English (EN)
Abstract:A series of steam- or carbon dioxide (CO2)-activated, granular activated carbons (GACs) were made from almond shells using six different activation or activation/oxidation conditions for each series. Unoxidized/oxidized pairs of GACs were compared among treatments and to two commercial GACs in order to determine the relative value of the carbons. Comparative terms included yield, surface area, attrition, surface charge, copper ion (Cu2+) uptake, adsorption of a mixture of six polar and non-polar organic compounds and an estimated cost of carbon production. Of the six conditions investigated for steam activation, two treatments consisting of a 1 h pyrolysis at either 700degreeC or 800degreeC, followed by a 2 h

activation at 800degreeC with the introduction of water at a rate of 7.0 ml/min were the best overall performing unoxidized/oxidized pairs in terms of copper or organics adsorption, respectively. Of the six conditions investigated for carbon dioxide activation, a treatment consisting of a 1 h pyrolysis at 700degreeC, followed by a 2 h activation at 800degreeC using a 75% CO2/25% N2 gas mixture was the best overall performing unoxidized/oxidized pair. Our estimated costs of production indicate that steam-activated, unoxidized and oxidized carbons appear to be the most economical GACs to manufacture and also the most economical for removal of copper ions and organic compounds

Descriptors:almond shells: conversion processes; bioresource technology; biotechnology; process economics. Biochemistry and Molecular Biophysics; Bioprocess Engineering. activated carbons: carbon dioxide-activated, granular, preparation, steam-activated; carbon dioxide; copper ions: removal; organic compounds: removal

Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering

ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

124. Title:Effect of antibiotics on psychrophilic anaerobic digestion of swine manure slurry in sequencing batch reactors

View Article: Bioresource Technology. 75 (3). December, 2000. 205-211
CD Volume:326
Print Article: Pages: 205-211

Author(s):Masse D I Lu D Masse L Droste R L
Author Affiliation:Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Route 108 East, Lennoxville, Quebec, J1M 1Z3

Language:English
Language of Summary:English (EN)

Abstract:The effect of antibiotics on the psychrophilic anaerobic digestion (PAD) of swine manure slurry in sequencing batch reactors (SBRs) was investigated. Six antibiotics, tylosin, lyncomycin, tetracycline, sulphamethazine, penicillin and carbadox, were individually added to the pig diet at their maximum prescribed level. Manure slurries collected from pigs receiving control and medicated diets were individually fed to pairs of SBRs at organic loading rates (OLRs) ranging from 2.2 to 3.5 g total chemical oxygen demand (TCOD) per litre of bioreactor initial sludge volume per day. Three mixtures of slurries from pigs fed on individual antibiotics were also tested at OLRs varying between 2.5 and 3.2 g TCOD/l/d. The presence of penicillin and tetracycline in manure slurries reduced methane production by 35% and 25%, respectively. However, the slurries from pigs receiving the other antibiotics and the slurry mixtures did not significantly affect ($P > 0.05$) methane production. In addition, the presence of individual and combined antibiotics did not have noticeable adverse effects on process stability and treatment efficiency. Total and soluble COD (TCOD and SCOD) reduction, total and volatile solids (TS and VS) removal, pH and volatile fatty acid (VFA) concentrations in experimental units were not statistically different ($P > 0.05$) than in the controls. In all bioreactors, the TCOD, SCOD, TS and VS removal exceeded 62%, 76%, 65% and 75%, respectively

Descriptors:bioresource technology; biotechnology; pig diets; swine manure slurries: psychrophilic anaerobic digestion; total chemical oxygen demand: analysis. Bioprocess Engineering; Waste Management (Sanitation). antibiotics: process effects; volatile fatty acids: analysis

Organism Descriptors:bacteria (Bacteria); pig (Suidae)

Supplemental Descriptors:Bacteria: Microorganisms; Suidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Bacteria; Chordates; Eubacteria; Mammals; Microorganisms; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

125. Title:Use of vegetable oils and fatty acid methyl esters in the production of spherical activated carbons
View Article: Bioresource Technology. 75 (3). December, 2000. 213-218
CD Volume:326
Print Article: Pages: 213-218
Author(s):Gryglewicz S Grabas K Gryglewicz G
Author Affiliation:Institute of Chemistry and Technology of Petroleum and Coal, Wroclaw University of Technology, ul. Gdanska 7/9, 50-344, Wroclaw
Language:English
Language of Summary:English (EN)
Abstract:The possibility of using vegetable oils, i.e., rapeseed oil, soybean oil, linseed oil, tung oil, castoroil and dehydroxylated castor oil, and the fatty acid methyl esters (FAMEs) obtained from them, for the agglomeration of bituminous coals was investigated. Both vegetable oils and FAMEs were found to be suitable bridging liquids for the production of spherical agglomerates-precursor of spherical activated carbons. By replacing the petroleum and coal derivatives commonly used in coal granulation with liquids of natural origin the environmental nuisance in the production of activated carbon can be reduced. Coal agglomerates produced using vegetable oils and FAME, and subjected to carbonisation and activation with steam became spherical activated carbons characterised by well-developed porous structures, marked mechanical strength, and good sorption properties determined by the standard tests of methylene blue and iodine adsorption from aqueous solutions
Descriptors:bioresource technology; biotechnology; bituminous coal agglomeration. Biochemistry and Molecular Biophysics; Bioprocess Engineering. fatty acid methyl esters: industrial uses; spherical activated carbons: industrial uses, production; vegetable oils: industrial uses
Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

126. Title:Purification and properties of a milk-clotting enzyme produced by Penicillium oxalicum
View Article: Bioresource Technology. 75 (3). December, 2000. 219-222
CD Volume:326
Print Article: Pages: 219-222
Author(s):Hashem Amal M
Author Affiliation:Department of Natural and Microbial Products Chemistry, National Research Centre, 12622 Tahrir Street, Dokki, Cairo
Language:English
Language of Summary:English (EN)
Abstract:Partial purification of milk-clotting and caseinase enzymes, produced by Penicillium oxalicum, was achieved by fractional precipitation with acetone, ethanol and methanol. Of the fractions obtained by three

precipitants, the 60-70% ethanol fraction was the most promising enzyme fraction and possessed the highest milk- clotting activity, which reached about ninefold that of the culture filtrate. Purification of the milk-clotting enzyme by DEAE- cellulose column chromatography afforded a rennin-like enzyme component that showed no proteolytic activity. The enzyme activity was maximum at pH 4.0-5.0 and 65degreeC. In absence of substrate and up to 50degreeC, the enzyme showed good stability and retained 80% of its original activity after 20 min. Cu2+, Co2+ and Mg2+ had stimulating effects on enzyme activity. Ascorbic acid, sodium lauryl sulphate, cysteine hydrochloride, cystine and EDTA had partial inhibitory effects on the enzyme
Descriptors:bioresource technology; biotechnology; food processing; milk: clotting, dairy product. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Foods. chemical precipitants: uses; milk-clotting enzyme: enzymatic properties, molecular properties, pH, production, purification, temperature
Organism Descriptors:Penicillium oxalicum (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Foods
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

127. Title:Co-composting of barley wastes and solid poultry manure
View Article: Bioresource Technology. 75 (3). December, 2000. 223-225
CD Volume:326
Print Article: Pages: 223-225
Author(s):Guerra Rodriguez E Vazquez M Diaz Ravina M
Author Affiliation:Dpto Quimica Analitica, Area Tecnologia de los Alimentos, Universidad de Santiago de Compostela, Escuela Politecnica Superior, 27002, Lugo
Language:English
Language of Summary:English (EN)
Abstract:The transformation of barley wastes and solid poultry manure to a fertiliser using a co-composting process is reported in this work. Determinations of chemical and physicochemical parameters as well as biological tests were performed. The co-compost was mature in 103 days. The final pH of the co-compost was 8.72 and the C/N ratio was 13. The percentage of germination obtained using the co-compost varied with the seeds used. It was 186% for ryegrass seeds, 85.74% for wheat seeds and 103% for barley seeds
Descriptors:barley wastes: treatment methodology; bioresource technology; biotechnology; brewing; solid poultry manure: treatment methodology. Agriculture; Methods and Techniques; Waste Management (Sanitation)
Organism Descriptors:barley (Gramineae); ryegrass (Gramineae); wheat (Gramineae)
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agriculture; Methods and Techniques; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

128. Title:Irrigating short rotation coppice with landfill leachate: Constraints to productivity due to chloride

View Article: Bioresource Technology. 75 (3). December, 2000. 227-229
CD Volume:326
Print Article: Pages: 227-229
Author(s):Stephens W Tyrrel S F Tiberghien J E
Author Affiliation:Institute of Water and Environment, Cranfield University, Silsoe, Bedford, MK45 4DT
Language:English
Language of Summary:English (EN)
Abstract:A pot-based experiment was conducted to determine the effect of different chloride concentrations (0-422 mmol l-1) on the growth of transplanted saplings of Salix viminalis (clone Q683). Chloride had a very rapid effect on the growth and development of the willow plants and on evapotranspiration (ETa). The degree of reduction in ETa of willows was directly related to chloride concentration and, in the short term, evaporative demand. Sustainable growth and development of willow is unlikely at chloride concentrations greater than 70 mmol l-1. Further investigations into the management of solute accumulation in the root zone are required in order to develop effective landfill leachate irrigation strategies for trees
Descriptors:bioresource technology; biotechnology; landfill leachates: uses; plant development; plant growth characteristics; pot-based experiment: results; short rotation coppice: irrigation. Agriculture; Waste Management (Sanitation). chloride
Organism Descriptors:Salix viminalis (Salicaceae): seedling. root
Supplemental Descriptors:Salicaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agriculture; Waste Management (Sanitation)
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

129. Title:Production of citric acid from molasses integrated with in-situ product separation by ion-exchange resin adsorption
View Article: Bioresource Technology. 75 (3). December, 2000. 231-234
CD Volume:326
Print Article: Pages: 231-234
Author(s):Wang Jianlong Wen Xianghua Zhou Ding
Author Affiliation:State Key Joint Laboratory of Environment Simulation and Pollution Control, Department of Environmental Engineering, Tsinghua University, Beijing, 100084
Language:English
Language of Summary:English (EN)
Abstract:A novel method of citric acid production from beet molasses was developed, in which an anion-exchange resin packed-column was connected to a fermenter for separation of citric acid from fermentation broth. The experimental results indicated that, as compared with conventional batch, the new fermentation techniques increased the citric acid productivity and sugar conversion from 0.338 g/l h and 82.2% to 0.543 g/l h and 94.8%, respectively
Descriptors:bioresource technology; biotechnology; product yields. Bioprocess Engineering; Methods and Techniques. citric acid: production; molasses: conversions; sugars: conversions
Organism Descriptors:Aspergillus niger (Fungi Imperfecti or Deuteromycetes): strain-W1-2
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Methods and Techniques
ISSN:0960-8524

Year:2000
Journal Title:Bioresource Technology

130. Title:Production of surfactant from Bacillus subtilis ATCC 21332 using potato substrates
View Article: Bioresource Technology. 75 (3). December, 2000. 235-240
CD Volume:326
Print Article: Pages: 235-240
Author(s):Fox Sandra L Bala Greg A
Author Affiliation:Biotechnology Department, Idaho National Engineering and Environmental Laboratory, Bechtel BWXT Idaho, LLC, MS 2203, Idaho Falls, ID, 83415-2203
Language:English
Language of Summary:English (EN)
Abstract:Surfactin, a lipopeptide biosurfactant, produced by Bacillus subtilis is known to reduce the surface tension of water from 72 to 27 mN/m. Potato substrates were evaluated as a carbon source for surfactant production by B. subtilis ATCC 21332. An established potato medium, simulated liquid and solid potato waste media, and a commercially prepared potato starch in a mineral salts medium were evaluated in shake flask experiments to verify growth, surface tension reduction, and carbohydrate reduction capabilities. Total carbohydrate assays and glucose monitoring indicated that B. subtilis was able to degrade potato substrates to produce surfactant. Surface tensions dropped from 71.3 +- 0.1 to 28.3 +- 0.3 mN/m (simulated solid potato medium) and to 27.5 +- 0.3 mN/m (mineral salts medium). A critical micelle concentration (CMC) of 0.10 g/l was obtained from a methylene chloride extract of the simulated solid potato medium
Descriptors:bioresource technology; biotechnology; potato substrates: uses. Biochemistry and Molecular Biophysics; Bioprocess Engineering. bacterial biosurfactants: industrial production, microbial production, uses; surfactin: industrial production, microbial production, uses
Organism Descriptors:Bacillus subtilis (Endospore-forming Gram-Positives): strain-ATCC 21332
Supplemental Descriptors:Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

131. Title:Production of activated carbon from prosopis (Prosopis juliflora)
View Article: Bioresource Technology. 75 (3). December, 2000. 241-243
CD Volume:326
Print Article: Pages: 241-243
Author(s):Kailappan R Gothandapani L Viswanathan R
Author Affiliation:Department of Agricultural Processing, College of Agricultural Engineering, Tamil Nadu Agricultural University, Coimbatore, 641 003
Language:English
Language of Summary:English (EN)
Abstract:Activated carbon was produced from prosopis (Prosopis juliflora), a wild thorny plant grown in wastelands, by chemical activation using zinc chloride. The process variables: activation temperature, level of zinc chloride required and activation duration of 600degreeC, 50% and 30 min, respectively, yielded 56.9% of activated carbon. The methylene blue adsorbed and zinc chloride recovery were 23 ml and 52.9%,

respectively for the activated carbon produced from prosopis at the optimum levels of process variables. The characteristics of the activated carbon produced from prosopis indicated its suitability in the oil, food and pharmaceutical industries
Descriptors:bioresource technology; biotechnology; chemical activation: applications; process variables. Biochemistry and Molecular Biophysics; Bioprocess Engineering. activated carbon: industrial production; zinc chloride
Organism Descriptors:Prosopis juliflora (Leguminosae)
Supplemental Descriptors:Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

132. Title:Production of citric acid by immobilized Aspergillus niger using a rotating biological contactor (RBC)
View Article: Bioresource Technology. 75 (3). December, 2000. 245-247
CD Volume:326
Print Article: Pages: 245-247
Author(s):Wang Jianlong
Author Affiliation:Department of Environmental Science and Engineering, State Key Joint Laboratory of Environment Simulation and Pollution Control, Tsinghua University, Beijing, 100084
Language:English
Language of Summary:English (EN)
Abstract:Production of citric acid by Aspergillus niger was studied in a rotating biological contactor (RBC) consisting of plastic disks mounted on a horizontal shaft with polyurethane foam (PUF), as a porous biomass support, attached on each side of the RBC disks. Mycelia of A. niger formed the biofilm of immobilized cells on the surface of the PUF. The RBC-PUF system was operated with a rotational speed of 10 rev/min during the stage of biofilm formation. The mature biofilm was exposed to the fermentation medium and the air space alternately. The results showed that the volumetric productivity obtained with the RBC-PUF system (0.896 g/l h) was almost three times higher than that obtained with a stirred- tank fermenter (0.33 g/l h). The immobilized biofilm was active for over 8-cycle periods of citric acid production with repetitive use without loss of bioactivity
Descriptors:biomass; bioresource technology; biotechnology; microbial biofilms. Bioprocess Engineering. citric acid: industrial production, microbial production
Organism Descriptors:Aspergillus niger (Fungi Imperfecti or Deuteromycetes). mycelia
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

133. Title:Lysine production by Bacillus laterosporus from various carbohydrates and seed meals
View Article: Bioresource Technology. 75 (3). December, 2000. 249-252
CD Volume:326

Print Article: Pages: 249-252
Author(s):Umerie S C Ekwealor I A Nwagbo I O
Author Affiliation:Department of Science Technology, Nnamdi Azikiwe University, Awka, Anambra State
Language:English
Language of Summary:English (EN)
Abstract:Production of the essential amino acid, L-lysine, by a soil isolate identified as Bacillus laterosporus was assessed in batch fermentation. Carbon sources including cassava, yam, millet, corn, plantain, sweet potato and sorghum starches, and nitrogen sources including ammonium sulphate, blood meal, defatted and non-defatted cowpea, bambara groundnut, groundnut, cotton seed and soyabean meals were used. In a shake flask fermentation using the various carbon sources, and ammonium sulphate as the nitrogen source, millet gave the highest yield (3.0 g/l) of lysine. The effect of various nitrogen sources at 1.0% (w/v) concentration on lysine production using millet as the carbon source showed that soyabean produced the highest lysine yield (5.67 g/l). The lysine yields were higher for the defatted nitrogen sources than for the non- defatted ones or ammonium sulphate
Descriptors:bioresource technology; biotechnology; industrial amino acid productin; product yield; seed meals: uses. Bioprocess Engineering. carbohydrates: conversions, uses; lysine: microbial production
Organism Descriptors:Bacillus laterosporus (Endospore-forming Gram-Positives)
Supplemental Descriptors:Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Bioprocess Engineering
ISSN:0960-8524
Year:2000
Journal Title:Bioresource Technology

134. Title:A leaf-section bioassay for evaluating rice stem borer resistance in transgenic rice containing a synthetic cry1Ab gene from Bacillus thuringiensis Berliner
View Article: Bulletin of Entomological Research. 2000. 90 (2). 179-182
CD Volume:299
Print Article: Pages: 179-182
Author(s):Ye G Y Shu Q Y Cui H R Hu C Gao M W Xia Y W Cheng X Altosaar I
Author Affiliation:College of Agriculture and Biotechnology, Zhejiang University, Hangzhou 310029, China
Language:English
Abstract:A leaf section bioassay and a whole-plant bioassay were evaluated for determining resistance of transgenic rice to Scirpophaga incertulas. The two methods gave similar results, particularly when both larval mortality and leaf area consumed were used as the criteria for assessing resistance in the leaf-section bioassay, which is simpler and more rapid than the whole-plant bioassays
Descriptors:bioassays. rice. transgenic-plants. insect-pests. plant-pests. pest-resistance. genetic-transformation. cereals. agricultural-entomology
Organism Descriptors:Bacillus-thuringiensis. Oryza. Scirpophaga-incertulas. Oryza-sativa. arthropods
Supplemental Descriptors:Bacillus. Bacillaceae. Firmicutes. bacteria. prokaryotes. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Scirpophaga. Pyralidae. Lepidoptera. insects. arthropods. invertebrates. animals. Oryza
Subject Codes:FF620. ZZ900. HH600. FF020. FF005. WW000
Supplementary Info:6 ref
ISSN:0007-4853

Year:2000
Journal Title:Bulletin of Entomological Research
Copyright:Copyright CAB International

135. Title:Intellectual property rights: implications for the canola sector and publicly funded research
View Article: Canadian Journal of Agricultural Economics. 2000. 48 (2). 175-194
CD Volume:317
Print Article: Pages: 175-194
Author(s):Carew R
Author Affiliation:Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, British Columbia V0H 1Z0, Canada
Language:English
Language of Summary:french
Abstract:This paper reviews various vehicles to protect intellectual property in Canada including Plant Breeders' Rights and reviews changes in inventive activity and research in the rape sector. The experience to date, following implementation of the Canadian Plant Breeders' Rights Act, indicates that for crop agriculture, the majority of plant protection certificates were granted to rape, followed by potato and soyabean. Several rape protection certificates consisted of hybrid varieties that were developed by private breeders. Ten private companies accounted for most of the plant protection certificates issued for rape. For rape patents, over 200 were filed in Canada during the 1986-97 period. Biotechnology patents numbered slightly over 100, with most of them comprising new plants, hybrid processes, nucleotide sequences, polypeptides, plant promoters, regulators and methods to produce improved fatty acid profiles. A large proportion of patent owners were transnational corporations or joint venture operations that controlled the distribution of identity preserved products from seed to end user. The paper highlights how publicly funded research has responded to greater investments in private plant breeding and suggests what policies may be necessary to ensure that maximum public benefits are achieved as a result of strengthened intellectual property right protection
Descriptors:rape. intellectual-property-rights. biotechnology. patents. plant-breeding. breeders'-rights. research. public-sector. private-sector
Geographic Locator:Canada
Organism Descriptors:Brassica-napus. Brassica-napus-var.-oleifera
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica-napus. North-America. America. Developed-Countries. Commonwealth-of-Nations. OECD-Countries
Subject Codes:FF005. FF020. DD500. WW000. AA500
Supplementary Info:27 ref
ISSN:0008-3976
Year:2000
Journal Title:Canadian Journal of Agricultural Economics
Copyright:Copyright CAB International

136. Title:Adoption of biotechnology in Thailand and the threat of intellectual property piracy
View Article: Canadian Journal of Agricultural Economics. 2000. 48 (4). 597-606
CD Volume:357
Print Article: Pages: 597-606
Author(s):Kerr W A Yampoin R
Author Variant:Revadee-Yampoin
Author Affiliation:Department of Agricultural Economics, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan S7N 5A8, Canada

Conference Title:Proceedings of the 2000 Annual Meeting of the Canadian Agricultural Economics Society
Language:English
Abstract:This paper examines the question of property rights in biotechnology from a broad perspective and then briefly discusses the challenges Thailand faces in putting a regulatory regime for biotechnology in place
Descriptors:biotechnology. genetic-engineering. intellectual-property-rights. patents. regulations
Geographic Locator:Thailand
Supplemental Descriptors:South-East-Asia. Asia. Developing-Countries. ASEAN-Countries
Subject Codes:DD500. WW000. EE110. EE120
Supplementary Info:9 ref
ISSN:0008-3976
Year:2000
Journal Title:Canadian Journal of Agricultural Economics

137. Title:Polyclonal antisera to epacrid mycorrhizae and to Hymenoscyphus ericae display specificity
View Article: Canadian Journal of Botany. 78 (7). July, 2000. 841-850
CD Volume:298
Print Article: Pages: 841-850
Author(s):Parry R A McLean C B Alderton M R Coloe P J Lawrie A C
Author Affiliation:Department of Applied Biology and Biotechnology, RMIT University, Melbourne, VIC, 3000
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Three polyclonal antisera produced in mice were used to investigate specificity and cross-reactivity between ericaceous and epacridaceous mycorrhizal fungi. One antiserum was to a culture of Hymenoscyphus ericae (Read) Korf and Kernan, the fungal endophyte of Calluna vulgaris (L.) Hull (Ericaceae). The other two were to peloton preparations from roots of Epacris impressa Labill. (Epacridaceae) from two sites (Cranbourne and Grampians) in Victoria, Australia. By immunofluorescence, all three antisera recognised H. ericae but not Oidiodendron griseum Roback, suggesting a serological relationship with the former endophyte. They also recognised 10 of the 12 fungal isolates tested, from mycorrhizal roots of E. impressa (Cranbourne), and all 4 isolates from Astroloma pinifolium (R. Br.) Benth. (Epacridaceae) (Grampians). Furthermore, none of the antisera recognised any of the nine common soil-inhabiting fungi selected for screening. Antisera recognised only unmelanized hyphae on epacrid and other plant roots taken from the wild. With plants from Cranbourne, all antisera except the Grampians antiserum recognised hyphae only on epacrid roots, demonstrating specificity. Hyphae on other plant roots were not recognised by any of the antisera. With plants from the Grampians, all antisera recognised some hyphae on both epacrid and other plant roots, except in two instances. The immunogold labelling indicates that the antisera are specific for fungi and do not recognise the plant. Since the fungal isolate forms true mycorrhizal structures, this suggests that there is a serological similarity between fungi forming epacrid mycorrhiza and those (H. ericae) forming ericoid mycorrhiza
Descriptors:polyclonal antisera specificity. Infection; Methods and Techniques
Organism Descriptors:Astroloma pinifolium (Epacridaceae); Calluna vulgaris (Ericaceae); Epacris impressa (Epacridaceae); Hymenoscyphus ericae

(Ascomycetes): endophyte, mycorrhizae; Oidiodendron griseum (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Ascomycetes: Fungi, Plantae; Epacridaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Ericaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Angiosperms; Dicots; Fungi; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants
Subject Codes:Infection; Methods and Techniques
ISSN:0008-4026
Year:2000
Journal Title:Canadian Journal of Botany

138. Title:Evidence for plasmid-mediated chemotaxis of Pseudomonas putida towards naphthalene and salicylate
View Article: Canadian Journal of Microbiology.. 46 (1). Jan., 2000. 1-6
CD Volume:299
Print Article: Pages: 1-6
Author(s):Samanta Sudip K Jain Rakesh K
Author Affiliation:Institute of Microbial Technology, Environmental Biotechnology Laboratory, Sector-39A, Chandigarh, 160036
Language:English
Language of Summary:English (EN); French (FR)
Abstract:A naphthalene (Nap) and salicylate (Sal) degrading microorganism, Pseudomonas putida RKJ1, is chemotactic towards these compounds. This strain carries a 83 kb plasmid. A 25 kb EcoRI fragment of the plasmid contains the genes responsible for Nap degradation through Sal. RKJ5, the plasmid-cured derivative of RKJ1, is neither capable of degradation nor is chemotactic towards Nap or Sal. The recombinant plasmid pRKJ3, which contained a 25 kb EcoRI fragment, was transferred back into the plasmid-free wild-type strain RKJ5, and the transconjugant showed both degradation and chemotaxis. The recombinant plasmid pRKJ3 was also transferred into motile, plasmid- free P. putida KT2442. The resulting transconjugant (RKJ15) showed chemotaxis towards both Nap and Sal. Two mutant strains carrying deletions in pRKJ3 (in KT2442) with phenotypes Nap- Sal+ and Nap- Sal-, were also tested for chemotaxis. It was found that the Nap- Sal+ mutant strain showed chemotaxis towards Sal only, whereas the Nap- Sal- mutant strain is non-chemotactic towards both the compounds. These results suggest that the metabolism of Nap and Sal may be required for the chemotactic activity
Descriptors:plasmid-encoded chemotaxis. Behavior; Molecular Genetics (Biochemistry and Molecular Biophysics); Metabolism. naphthalene: substrate; salicylate: substrate
Organism Descriptors:Pseudomonas putida (Pseudomonadaceae): chemotaxis, strain-KT2442, strain-KT2442/pLAFR3, strain-KT2442/pRKJ1, strain-RKJ1, strain-RKJ15, strain-RKJ17, strain-RKJ18, strain-RKJ5, strain-RKJ5/pRKJ3
Supplemental Descriptors:Pseudomonadaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Behavior; Molecular Genetics (Biochemistry and Molecular Biophysics); Metabolism
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

139. Title:Diversity in the yeast Cryptococcus albidus and related species as revealed by ribosomal DNA sequence analysis

View Article: Canadian Journal of Microbiology.. 46 (1). Jan., 2000. 7-27
CD Volume:299
Print Article: Pages: 7-27
Author(s):Fonseca Alvaro Scorzetti Gloria Fell Jack W
Author Affiliation:Biotechnology Unit, Faculty of Sciences and Technology, New University of Lisbon, Quinta da Torre, 2825-114, Caparica
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Evidence accumulated from studies based on physiological, biochemical, and molecular characteristics has pointed to the heterogeneity of the ubiquitous anamorphic basidiomycetous yeast species Cryptococcus albidus (Saito) Skinner, with its current varieties and synonyms. The taxonomic status of this species has not been reappraised because different studies, mostly involving limited numbers of strains, have not been integrated. To assess species diversity within the clade containing Cryptococcus albidus and other phylogenetically related Cryptococcus and Filobasidium species, we determined ribosomal DNA (rDNA) sequences of 69 strains from the 5' end of the 26S gene, D1/D2 region, and in some cases, the non-coding ITS2 region. Analysis of the sequence data together with available physiological, biochemical, and molecular characteristics, showed the segregation of C. albidus into at least 12 species, leading to the elevation of former varieties to the rank of species (C. aerius, C. diffluens), the reinstatement of synonyms (C. liquefaciens, C. terricola), and the proposal of new species (C. arrabidensis, C. chernovii, C. cylindricus, C. oeirensis, C. phenolicus, C. saitoi, C. uzbekistanensis, C. wieringae). The overall analyses of the results argue in favour of the use of rDNA sequence data to improve species delineation when integrated with other available physiological and molecular characteristics
Descriptors:molecular systematics. Molecular Genetics (Biochemistry and Molecular Biophysics); Systematics and Taxonomy. ribosomal DNA; Cryptococcus 26S gene (Fungi Imperfecti or Deuteromycetes): D1/D2 region, ITS2 non-coding region; Cryptococcus albidus 26S gene (Fungi Imperfecti or Deuteromycetes): D1/D2 region, ITS2 non-coding region, ribosomal DNA; Filobasidium 26S gene (Basidiomycetes): D1/D2 region, ITS2 non-coding region
Organism Descriptors:Cryptococcus (Fungi Imperfecti or Deuteromycetes); Cryptococcus aerius (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus albidus (Fungi Imperfecti or Deuteromycetes): segregation into 12 species, ubiquitous anamorphic basidiomycetous yeast; Cryptococcus arrabidensis (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus chernovii (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus cylindricus (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus diffluens (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus liquefaciens (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus oeirensis (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus phenolicus (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus saitoi (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus terricola (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus uzbekistanensis (Fungi Imperfecti or Deuteromycetes): description, new species; Cryptococcus wieringae (Fungi Imperfecti or Deuteromycetes): description, new species; Filobasidium (Basidiomycetes). ribosome
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae; Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants

Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Systematics and Taxonomy
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

140. Title:Tween 80 enhanced TNT mineralization by Phanerochaete chrysosporium
View Article: Canadian Journal of Microbiology. 46 (2). Feb., 2000. 110-118
CD Volume:299
Print Article: Pages: 110-118
Author(s):Hodgson Jonathan Rho Denis Guiot Serge R Ampleman Guy Thiboutot Sonia Hawari Jalal
Author Affiliation:Biotechnology Research Institute, National Research Council Canada, 6100 Royalmount Avenue, Montreal, PQ, H4P 2R2
Language:English
Language of Summary:English (EN); French (FR)
Abstract:The effect of a nonionic surfactant (Tween 80) on 2,4,6-trinitrotoluene (TNT) mineralization by the white-rot fungus Phanerochaete chrysosporium strain BKM-F-1767, was investigated in a liquid culture at 20, 50, and 100 mg TNTcntdotL-1. The presence of 1% (w/v) Tween 80, at 20 mgcntdotL-1 TNT, added to a 4-d-old culture, allowed the highest TNT mineralization level, that is 29.3% after 24 d, which is two times more than the control culture, without Tween 80 (13.9%). The mineralization of TNT resumed upon additional Tween 80 supplementation, consequently, 39.0% of the TNT was respired on day 68. Orbital agitation of the fungal culture was found detrimental to TNT mineralization, with or without Tween 80 in the culture medium. The surfactant also stimulated the growth of P. chrysosporium without any notable effect on either the glycerol consumption rate or the extracellular LiP and MnP activity levels. Respirometric assays highlighted some differences between the oxygen uptake rate of the fungal culture supplemented with or without Tween 80
Descriptors:biodegradation; soil contamination; soil pollution; soils. Pollution Assessment Control and Management; Waste Management (Sanitation); Soil Science. 2,4,6-trinitrotoluene: explosive, mineralization, pollutant; Tween 80: nonionic surfactant, uses; enzymes
Organism Descriptors:Phanerochaete chrysosporium (Basidiomycetes)
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Pollution Assessment Control and Management; Waste Management (Sanitation); Soil Science
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

141. Title:Origin of p-cresol in the anaerobic degradation of trinitrotoluene
View Article: Canadian Journal of Microbiology. 46 (2). Feb., 2000. 119-124
CD Volume:299
Print Article: Pages: 119-124
Author(s):Shen C F Hawari J A Ampleman G Thiboutot S Guiot S R
Author Affiliation:Biotechnology Research Institute, National Research Council of Canada, 6100 Royalmount Avenue, Montreal, PQ, H4P 2R2
Language:English
Language of Summary:English (EN); French (FR)
Abstract:p-Cresol was repeatedly detected as a trace metabolite in anaerobic slurry reactors treating 2,4,6-trinitrotoluene (TNT)-contaminated soils. This study shows that p-cresol was not a metabolite of the

anaerobic degradation of TNT, by using a combination of analytical techniques and 13C-labelled TNT. Instead, p-cresol, an intermediate in the degradation pathway of some amino acids, was shown to be inhibited by TNT and its metabolites. The range and persistence of inhibition to p-cresol microbial degradation decreased with the level of amino-substitution of the derivatives. This explains why p- cresol accumulated within the TNT-treating anaerobic bioslurry, as it could not be further biodegraded in the presence of TNT
Descriptors:biodegradation; bioremediation; soil contamination; soil pollution; soils. Pollution Assessment Control and Management; Waste Management (Sanitation); Soil Science. 2,4,6-trinitrotoluene: explosive, mineralization, pollutant
Organism Descriptors:Phanerochaete chrysosporium (Basidiomycetes)
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Pollution Assessment Control and Management; Waste Management (Sanitation); Soil Science
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

142. Title:Molecular analysis and development of 16S rRNA oligonucleotide probes to characterize a diclofop-methyl-degrading biofilm consortium
View Article: Canadian Journal of Microbiology. 46 (2). Feb., 2000. 133-142
CD Volume:299
Print Article: Pages: 133-142
Author(s):Laramee Louise Lawrence John R Greer Charles W
Author Affiliation:Biotechnology Research Institute, National Research Council of Canada, 6100 Royalmount Avenue, Montreal, PQ, H4P 2R2
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Genomic DNA from nine individual bacteria, isolated from a diclofop-methyl-degrading biofilm consortium, was extracted for genetic characterization. The degradation of diclofop-methyl produces metabolites that are known intermediates or substrates for bacteria that degrade a variety of chlorinated aromatic compounds. Accordingly, oligonucleotide primers were designed from specific catabolic genes for chlorinated organic degradation pathways, and tested by PCR to determine if these genes are involved in diclofop- methyl degradation. DNA homology between the PCR products and the known catabolic genes investigated by Southern hybridization analysis and by sequencing, suggested that novel catabolic genes are functioning in the isolates. Specific fluorescent oligonucleotides were designed for two of the isolates, following 16S rDNA sequencing and identification of each of the isolates. These probes were successfully used for fluorescent in situ hybridization (FISH) studies of the two isolates in the biofilm consortium
Descriptors:biodegradation; catabolism; microbial biofilm consortium: applications. Pollution Assessment Control and Management. 16S ribosomal RNA oligonucleotide probes: applications, development, molecular analysis; DNA: genomic, isolation; diclofop- methyl: degradation, pesticide, pollutant; fluorescent oligonucleotides: applications; rDNA [ribosomal DNA]; rRNA [ribosomal RNA]: applications
Subject Codes:Pollution Assessment Control and Management
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

143. Title:Type I nitroreductases in soil enterobacteria reduce TNT (2,4,6-trinitrotoluene) and RDX (hexahydro-1,3,5-trinitro-1,3,5-triazine)
View Article: Canadian Journal of Microbiology.. 46 (3). March, 2000. 278-282
CD Volume:299
Print Article: Pages: 278-282
Author(s):Kitts Christopher L Green Chad E Otley Rebecca A Alvarez Marc A Unkefer Pat J
Author Affiliation:Environmental Biotechnology Institute, California Polytechnic State University, San Luis Obispo, CA, 93407
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Many enteric bacteria express a type I oxygen-insensitive nitroreductase, which reduces nitro groups on many different nitroaromatic compounds under aerobic conditions. Enzymatic reduction of nitramines was also documented in enteric bacteria under anaerobic conditions. This study indicates that nitramine reduction in enteric bacteria is carried out by the type I, or oxygen-insensitive nitroreductase, rather than a type II enzyme. The enteric bacterium Morganella morganii strain B2 with documented hexahydro-1,3,5-trinitro-1,3,5-triazine (RDX) nitroreductase activity, and Enterobacter cloacae strain 96-3 with documented 2,4,6-trinitrotoluene (TNT) nitroreductase activity, were used here to show that the explosives TNT and RDX were both reduced by a type I nitroreductase. Morganella morganii and E. cloacae exhibited RDX and TNT nitroreductase activities in whole cell assays. Type I nitroreductase, purified from E. cloacae, oxidized NADPH with TNT or RDX as substrate. When expression of the E. cloacae type I nitroreductase gene was induced in an Escherichia coli strain carrying a plasmid, a simultaneous increase in TNT and RDX nitroreductase activities was observed. In addition, neither TNT nor RDX nitroreductase activity was detected in nitrofurazone- resistant mutants of M. morganii. We conclude that a type I nitroreductase present in these two enteric bacteria was responsible for the nitroreduction of both types of explosive
Descriptors:aerobic conditions; anaerobic conditions; nitramine reduction; soil microbiology. Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics); Metabolism. 2,4,6-trinitrotoluene [TNT]: explosive, substrate; NADPH; hexahydro-1,3,5-trinitro-1,3,5-triazine [RDX]; nitramine; nitramines; nitrofurazone; plasmid; type I nitroreductases: oxygen-insensitive; Enterobacter cloacae type I nitroreductase gene (Enterobacteriaceae)
Organism Descriptors:Enterobacter cloacae (Enterobacteriaceae): strain-96-3; Escherichia coli (Enterobacteriaceae); Morganella morganii (Enterobacteriaceae): nitrofurazone-resistant mutants, strain-B2
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics); Metabolism
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

144. Title:Development of a xylitol biosensor composed of xylitol dehydrogenase and diaphorase
View Article: Canadian Journal of Microbiology. 46 (4). April, 2000. 350-357
CD Volume:299
Print Article: Pages: 350-357

Author(s):Takamizawa Kazuhiro Uchida Shoji Hatsu Masahiro Suzuki Tohru Kawai Keiichi
Author Affiliation:Department of Bioprocessing, Faculty of Agriculture, Gifu University, 1-1, Yanagito, Gifu, 5011193
Language:English
Language of Summary:English (EN); French (FR)
Abstract:In preparation for the development of a xylitol biosensor, the xylitol dehydrogenase of Candida tropicalis IFO 0618 was partially purified and characterized. The optimal pH and temperature of the xylitol dehydrogenase were pH 8.0 and 50degreeC, respectively. Of the various alcohols tested, xylitol was the most rapidly oxidized, with sorbitol and ribitol being reduced at 65% and 58% of the xylitol rate. The enzyme was completely inactive on arabitol, xylose, glucose, glycerol, and ethanol. The enzyme's xylitol oxidation favored the use of NAD+ (7.9 U/mg) over NADP+ (0.2 U/mg) as electron acceptor, while the reverse reaction, D-xylulose reduction, favored NADPH (7.7 U/mg) over NADH (0.2 U/mg) as electron donor. The Km values for xylitol and NAD+ were 49.8 mM and 38.2 muM, respectively. For the generation of the xylitol biosensor, the above xylitol dehydrogenase and a diaphorase were immobilized on bromocyan-activated sephallose. The gel was then attached on a dissolved oxygen electrode. In the presence of vitamin K3, NAD+ and phosphate buffer, the biosensor recorded a linear response to xylitol concentration up to 3 mM. The reaction was stable after 15 min. When the biosensor was applied to a flow injection system, optimal operation pH and temperature were 8.0 and 30degreeC, respectively. The strengths and limitations of the xylitol biosensor are its high affinity for NAD+, slow reaction time, narrow linear range of detection, and moderate affinity for xylitol
Descriptors:biotechnology. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Methods and Techniques. NAD; NADH; NADPH; diaphorase: applications; enzymes: applications; xylitol: analysis; xylitol dehydrogenase: applications
Organism Descriptors:Candida tropicalis (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Methods and Techniques
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

145. Title:Effects of non-ionic surfactants on the uptake and hydrolysis of fluoresceindiacetate by alkane-oxidizing bacteria
View Article: Canadian Journal of Microbiology. 46 (4). April, 2000. 387-390
CD Volume:299
Print Article: Pages: 387-390
Author(s):Bruheim Per Eimhjellen Kjell
Author Affiliation:Department of Biotechnology, Faculty of Chemistry and Biology, Norwegian University of Science and Technology, Sem Selands Vei 6/8, N-7491, Trondheim
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Biological effects of non-ionic surfactants on alkane-oxidizing bacteria were studied by assessing their influence on the uptake of prefluorochrome fluoresceindiacetate (FDA) and its intracellular hydrolysis to fluorescein. Both decreasing and increasing rates of hydrolysis as a consequence of the presence of surfactants were observed. The surfactants influenced the uptake of FDA, but not its

intracellular hydrolysis. The effects of the surfacfants on the uptake rate depended strongly on the structure and physico-chemical properties of the surfactants. There was no qualitative or significant quantitative difference in surfactant susceptibility between induced (alkane grown) and non-induced bacteria (acetate grown), even though the induced cells possess greater cell surface hydrophobicity
Descriptors:biodegradation; cell surface hydrophobicities. Membranes (Cell Biology); Pollution Assessment Control and Management. alkanes: oxidation; fluoresceindiacetate: hydrolysis, uptake; non- ionic surfactants: physiological effects
Organism Descriptors:bacteria (Bacteria). cell surfaces: analysis
Supplemental Descriptors:Bacteria: Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Membranes (Cell Biology); Pollution Assessment Control and Management
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

146. Title:Community dynamics of a mixed-bacterial culture growing on petroleum hydrocarbons in batch culture
View Article: Canadian Journal of Microbiology. 46 (5). May, 2000. 441-450
CD Volume:299
Print Article: Pages: 441-450
Author(s):Van Hamme Jonathan D Odumeru Joseph A Ward Owen P
Author Affiliation:Microbial Biotechnology Laboratory, Department of Biology, University of Waterloo, Waterloo, ON, N2L 3G1
Language:English
Language of Summary:English (EN); French (FR)
Abstract:The effects of various hydrocarbon substrates, and a chemical surfactant capable of enhancing crude-oil biodegradation, on the community structure of a mixed-bacterial inoculum were examined in batch culture. Of 1000 TSA-culturable isolates, 68.6% were identified at the genus level or better by phospholipid fatty acid analysis over 7-day time course experiments. Cultures were exposed to 20 g/L Bow River crude oil with and without 0.625 g/L Igepal CO- 630 (a nonylphenol ethoxylate surfactant), 5 g/L saturates, 5 g/L aromatics, or 125 g/L refinery sludge. A group of six genera dominated the cultures: Acinetobacter, Alcaligenes, Ochrobactrum, Pseudomonas/Flavimonas, Stenotrophomonas, and Yersinia. Species from four of the genera were shown to be capable of hydrocarbon degradation, and counts of hydrocarbon degrading and total heterotrophic bacteria over time were nearly identical. Pseudomonas/Flavimonas and Stenotrophomonas normally dominated during the early portions of cultures, although the lag phase of Stenotrophomonas appears to have been increased by surfactant addition. Acinetobacter calcoaceticus was the most frequently isolated microorganism during exposure to the saturate fraction of crude oil. Regardless of substrate, the culture medium supported a greater variety of organisms during the latter portions of cultures. Understanding the community structure and dynamics of mixed bacterial cultures involved in treatment of heterogeneous waste substrates may assist in process development and optimization studies
Descriptors:bacterial communities; heterogeneous waste substrates: treatment; mixed bacterial cultures: community dynamics, growth characteristics; process development; process optimization. Microbiology; Pollution Assessment Control and Management; Waste Management (Sanitation).

chemical surfactants: degradation, pollutants; petroleum hydrocarbons: degradation, pollutants
Organism Descriptors:bacteria (Bacteria)
Supplemental Descriptors:Bacteria: Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Microbiology; Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

147. Title:Optimizing the expression of a monoclonal antibody fragment under the transcriptional control of the Escherichia coli lac promoter
View Article: Canadian Journal of Microbiology. 46 (6). June, 2000. 532-541
CD Volume:299
Print Article: Pages: 532-541
Author(s):Donovan Robert S Robinson Campbell W Glick Bernard R
Author Affiliation:Department of Chemical Engineering, University of Waterloo, Waterloo, ON, N2L 3G1
Language:English
Language of Summary:English (EN); French (FR)
Abstract:The expression of a monoclonal antibody Fab fragment in Escherichia coli strain RB791/pComb3, induced with either lactose or isopropyl-beta-D-thiogalactoside (IPTG), was compared to determine if lactose might provide an inexpensive alternative to induction with IPTG. Induction of Fab expression imposed a metabolic load on the recombinant cells, resulting in lower final cell yields compared to the non-induced controls. An IPTG concentration of 0.05 mM was sufficient to achieve maximal expression of soluble Fab protein when inducing in the early-, mid-, or late-log phases of batch cultures grown using either glucose or glycerol as a carbon source. The largest overall yield of Fab fragments when using 0.05 mM IPTG was achieved by increasing the final yield of cells through glycerol feeding following induction in late-log phase. Lactose was as effective as IPTG for inducing Fab expression in E. coli RB791/pComb3. The greatest overall level of Fab expression was found when cells grown on glycerol were induced with 2 g/L lactose in late-log phase. Since the cost of 0.05 mM of IPTG is significantly greater than the cost of 2 g/L lactose, lactose provides an inexpensive alternative to IPTG for inducing the expression of Fab fragments, and possibly other recombinant proteins, from the E. coli lac promoter
Descriptors:biomass; biotechnology; cell yields; gene transcription; lac promoter: transcriptional control. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering. lactose; monoclonal antibody fragment: expression optimization
Organism Descriptors:Escherichia coli (Enterobacteriaceae)
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

148. Title:Cometabolic biotransformation of nitrobenzene by 3-nitrophenol degrading Pseudomonas putida 2NP8
View Article: Canadian Journal of Microbiology. 46 (7). July, 2000. 643-652

CD Volume:299
Print Article: Pages: 643-652
Author(s):Zhao Jian Shen Ward Owen P
Author Affiliation:Microbial Biotechnology Laboratory, Department of Biology, University of Waterloo, Waterloo, ON, N2L 3G1
Language:English
Language of Summary:English (EN); French (FR)
Abstract:A strain of Pseudomonas putida (2NP8) capable of growing on both 2-nitrophenol and 3-nitrophenol, but not on nitrobenzene (NB), was isolated from municipal activated sludge. 2-Nitrophenol was degraded by this strain with production of nitrite. Degradation of 3-nitrophenol resulted in the formation of ammonia. Cells grown on 2-nitrophenol did not degrade nitrobenzene. A specific nitrobenzene degradation activity was induced by 3-nitrophenol. Ammonia, nitrosobenzene, and hydroxylaminobenzene have been detected as metabolites of nitrobenzene degradation by cells grown in the presence of 3-nitrophenol. These results indicated a NB cometabolism mediated by 3-nitrophenol nitroreductase
Descriptors:Enzymology (Biochemistry and Molecular Biophysics); Metabolism. 2-nitrophenol: degradation; 3-nitrophenol: degradation; 3- nitrophenol nitroreductase; ammonia: production; hydroxylaminobenzene; nitrite: production; nitrobenzene: cometabolic biotransformation
Organism Descriptors:Pseudomonas putida (Pseudomonadaceae): 3-nitrophenol degrading, strain-2NP8
Supplemental Descriptors:Pseudomonadaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Metabolism
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

149. Title:Characterization of the anti-cancer-cell parasporal proteins of a Bacillus thuringiensis isolate
View Article: Canadian Journal of Microbiology. 46 (10). October, 2000. 913-919
CD Volume:300
Print Article: Pages: 913-919
Author(s):Yamashita Satoko Akao Tetsuyuki Mizuki Eiichi Saitoh Hiroyuki Higuchi Kazuhiko Park Yu Shin Kim Ho San Ohba Michio
Author Affiliation:Biotechnology and Food Research Institute, Fukuoka Industrial Technology Centre, Aikawa-machi 1465-5, Kurume, Fukuoka, 839-0861
Language:English
Language of Summary:English (EN); French (FR)
Abstract:An unusual activity, associated with non-insecticidal and non-haemolytic parasporal inclusion proteins of a Bacillus thuringiensis soil isolate, designated 89-T-26-17, was characterized. The parasporal inclusion of this isolate was bipyramidal, rounded at both ends, containing proteins of 180, 150, 120, 100, and 88 kDa. No homologies with the Cry and Cyt proteins of B. thuringiensis were detected based on N-terminal sequences. Proteolytic processing of the inclusion proteins by proteinase K, trypsin, and chymotrypsin produced a major protein of 64 kDa exhibiting cytocidal activity against human leukaemic T cells and uterus cervix cancer (HeLa) cells. The protease-activated proteins showed no cytotoxicity to normal T cells
Descriptors:parasporal inclusion. Cell Biology. Cry: protein; chymotrypsin; proteinase K; trypsin

Organism Descriptors:Bacillus thuringiensis (Endospore-forming Gram-Positives): characterization, isolate-89-T-26-17; HeLa cell line (Hominidae). T cell: blood and lymphatics, immune system
Supplemental Descriptors:Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia. Animals; Bacteria; Chordates; Eubacteria; Humans; Mammals; Microorganisms; Primates; Vertebrates
Subject Codes:Cell Biology
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

150. Title:Isolation of a chitinase overproducing mutant of Streptomyces peucetius defective in daunorubicin biosynthesis
View Article: Canadian Journal of Microbiology. 46 (10). October, 2000. 956-960
CD Volume:300
Print Article: Pages: 956-960
Author(s):Vetrivel Kuzhandhaivel S Dharmalingam Kuppamuthu
Author Affiliation:Department of Genetic Engineering, School of Biotechnology, Madurai Kamaraj University, Madurai, 625 021
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Streptomyces peucetius, producer of the antitumor anthracycline antibiotic daunorubicin, was mutagenized, and mutants defective in daunorubicin biosynthesis were screened. One mutant (SPVI), which failed to produce daunorubicin, was found to overproduce an extracellular chitinase. Time course analyses of chitinase production and of the extracellular protein profile showed that the increase in activity is due to increased synthesis of the enzyme protein. The production of chitinase in SPVI was repressed by glucose as in the case of wild-type S. peucetius. PFGE analysis of VspI restriction fragments of S. peucetius and SPVI showed that there was no major alteration in the mutant genome. The hybridization pattern of S. peucetius and SPVI genomic DNA digested with various restriction enzymes was identical when probed with dnrUVJI genes of the S. peucetius daunorubicin cluster and chiA of Streptomyces lividans 66. The possible step affected in the daunorubicin biosynthetic pathway could be a polyketide synthase, since aklanonic acid, the earliest detectable intermediate in the daunorubicin pathway, was not synthesized in SPVI
Descriptors:daunorubicin pathway; extracellular protein profile. Enzymology (Biochemistry and Molecular Biophysics); Metabolism. DNA: digested, genomic; chitinase: overproduction; daunorubicin: antitumor anthracycline antibiotic, biosynthesis; glucose; Streptomyces lividans chiA gene (Streptomycetes and Related Genera); Streptomyces peucetius dnrUVJI genes (Streptomycetes and Related Genera)
Organism Descriptors:Streptomyces lividans (Streptomycetes and Related Genera); Streptomyces peucetius (Streptomycetes and Related Genera): isolation, mutant, mutant SPVI, wild-type
Supplemental Descriptors:Streptomycetes and Related Genera: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Metabolism
ISSN:0008-4166
Year:2000
Journal Title:Canadian Journal of Microbiology

151. Title:Value-added land values

View Article: Choices. The Magazine of Food, Farm, and Resources Issues. 2000. (No. 1). 18-23
CD Volume:318
Print Article: Pages: 18-23
Author(s):Jolly R W Lence S
Language:English
Abstract:New biotechnologies and associated organizational changes may affect farmland values and rental rates and, in so doing, influence the distribution of benefits and costs from these innovations along the agricultural value chain. The magnitudes of the resulting changes in the rental rates and values of farmland, as well as the distribution of benefits and costs, will depend on the characteristics of the innovations, the degree of competition within the input industry, and land tenure and ownership. Following an introduction, sections cover: determinants of land values; technological organizational changes and how they affect land values; input traits; and output traits. The importance of identifying the impacts of biotechnology and the accompanying organizational change of land values and rental rates is highlighted
Descriptors:biotechnology. land-prices. land-markets. value-added. valuation. innovation-adoption. innovations. technical-progress. returns. economic-impact. agricultural-land. land-ownership
Geographic Locator:USA
Supplemental Descriptors:North-America. America. Developed-Countries. OECD-Countries
Subject Codes:EE115. EE165. EE110. WW000
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Journal Title:Choices The Magazine of Food, Farm, and Resources Issues
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152. Title:Manipulation of the 1RS.1BL translocation in wheat by induced homoeologous recombination
View Article: Crop Science. 2000. 40 (1). 216-225
CD Volume:300
Print Article: Pages: 216-225
Author(s):Lukaszewski A J
Author Affiliation:Dep. of Botany and Plant Sciences, Univ. of California, Riverside CA 9252, USA
Language:English
Abstract:Centric translocations of the short arm of rye (Secale cereale) chromosome 1R are useful in wheat (Triticum aestivum) breeding because they confer resistance to several pests and diseases and improve yield. Their major disadvantage is in reduced bread making quality. To remedy this defect, rye chromosome arm 1RS in translocations 1RS.1BL and 1RS.1DL was induced by the ph1b mutation to recombine with the short arms of wheat group-1 chromosomes. Among 20 234 progeny screened, 139 primary recombinant chromosomes were recovered including 103 with 1BS, 22 with 1AS and 14 with 1DS. The Gli-1/Glu-3 loci of wheat were non-homoeoallelic to the Sec-1 locus of rye and were separated by about a 13-cM-long segment, which on the rye chromosome contained disease resistance loci Pm8, Lr26, Sr31 and Yr9. Pairs of primary recombinants 1RS-1BS with breakpoints flanking the storage protein loci were intercrossed and two types of secondary recombinant chromosomes 1RS were produced: a group of over 30 chromosomes where the Sec-1 locus was replaced by segments of 1BS of various lengths, and two chromosomes where 1.4- and 3.2-cM segments of 1BS introduced the Gli-1/Glu-3 loci. Selected chromosomes from each class were allowed to recombine within

the shared segments of 1RS separating the intercalary wheat segments and two tertiary recombinant chromosomes were recovered. Cytologically, these chromosomes appear as normal 1RS arms but each has two intercalary segments of 1BS, one introducing the Gli-1/Glu-3 loci and the second one removing the Sec-1 locus. Because the protein composition of the resulting translocation lines is identical to that of normal wheat, it is believed that these manipulations could eliminate the quality defect associated with the 1RS.1BL translocation

Descriptors:recombination. chromosome-translocation. wheat. chromosomes. disease-resistance. mutations. pests. rye. translocation-lines. gliadin. glutenins. breadmaking. baking-quality. quality. intergeneric-hybridization. plant-diseases. cereals. biotechnology. control. plant-pathology

Organism Descriptors:Triticum-aestivum. Secale-cereale. Secale. Triticum

Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Secale

Subject Codes:FF020. FF005. QQ050. QQ500

Supplementary Info:33 ref

ISSN:0011-183X

Year:2000

Journal Title:Crop Science

153. Title:Genetic diversity among elite sorghum inbred lines assessed with simple sequence repeats

View Article: Crop Science. 2000. 40 (1). 226-232

CD Volume:300

Print Article: Pages: 226-232

Author(s):Smith J S C Kresovich S Hopkins M S Mitchell S E Dean R E Woodman W L Lee M Porter K

Author Affiliation:Pioneer Hi-Bred International, Inc., Research Technology Services, 7300 NW 62nd Avenue - PO Box, 1004, Johnston, IA 50131-1004, USA

Language:English

Abstract:DNA markers are being increasingly utilized in cultivar development, quality control of seed production, measurement of genetic diversity for conservation management, varietal identity and to assist in maintenance of intellectual property protection (IPP). The use of simple sequence repeats (SSRs) for variety profiling can provide high discrimination, with excellent reproducibility at less cost than for restriction fragment length polymorphisms (RFLPs). The objective of this study was to evaluate the potential utility of SSR technology for applications in research, product development, seed production and genetic resource conservation management for sorghum. Fifty genetically diverse elite sorghum (Sorghum bicolor) inbreds were used to compare the discrimination abilities of 15 SSR primers with 104 RFLPs and to compare the associations among lines revealed by these molecular data and by pedigrees. RFLP data allowed all lines to be uniquely identified; two lines could not be distinguished by the SSR data. The mean polymorphism information content (PIC) values were 0.62 (RFLPs) and 0.58 (SSRs). Correlations for pairwise molecular profile distances with pedigree distances among the maintainer female (B) lines were 0.52 and 0.53 for RFLP and SSR data, respectively; data for the male parental restorer (R) lines were 0.41 and 0.47. This set of SSRs could be used to help genetic conservation management and to support IPP. Data from additional SSRs that collectively cover more of the genome will be required for applications to assist in breeding

Descriptors:discrimination. genetic-diversity. polymorphism. restriction-fragment-length-polymorphism. genetic-markers. variety-classification. cultivar-identification. cereals. biotechnology
Identifiers:simple sequence repeats
Organism Descriptors:Sorghum-bicolor
Supplemental Descriptors:Sorghum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. WW000
Supplementary Info:22 ref
ISSN:0011-183X
Year:2000
Journal Title:Crop Science

154. Title:Quantitative trait loci for antibiosis resistance to corn earworm in soybean
View Article: Crop Science. 2000. 40 (1). 233-238
CD Volume:300
Print Article: Pages: 233-238
Author(s):Rector B G All J N Parrott W A Boerma H R
Author Affiliation:USDA ARS, Insect Biology and Population Management Research Lab. P.O. Box 748, Tifton, GA 31793, USA
Language:English
Abstract:In more than 25 yr since the discovery of soyabean (Glycine max) resistance to defoliating insects, attempts to introgress this trait into elite germplasm have been relatively unsuccessful. Resistance to defoliating insects in soyabean is expressed as a combination of antibiosis (toxicity) and antixenosis (nonpreference). Both of these resistance modes are inherited quantitatively in soyabean. The objectives of this study were (i) to use restriction fragment length polymorphism (RFLP) maps to identify quantitative trait loci (QTLs) in soyabean for antibiosis against corn earworm (CEW; Helicoverpa zea), (ii) to determine the relative magnitude, gene action and genomic locations of these QTLs and (iii) to compare them to previously detected soyabean antixenosis QTLs. Restriction fragment length polymorphism maps were constructed in three soyabean F2 populations segregating for antibiosis against CEW: Cobb x PI171451, Cobb x PI227687 and Cobb x PI229358. Antibiosis was measured as larval weight gain in a detached leaf assay. The RFLP data were associated with insect bioassay data to detect QTLs for antibiosis in each cross. Variance component heritability estimates for antibiosis in the three crosses were 54, 42 and 62% in Cobb x PI171451, Cobb x PI227687 and Cobb x PI229358, respectively. An antibiosis QTL on Linkage Group (LG) M was detected in both Cobb x PI171451 and Cobb x PI229358 (R2 values of 28 and 22%, respectively). An antixenosis QTL was also significant at this location in the same two crosses. This was the only insect-resistance QTL that was detected for both antibiosis and antixenosis. Antibiosis QTLs were also detected on LGs F and B2 in Cobb x PI227687 (R2 = 33 and 12%, respectively) and LGs G and J in Cobb x PI229358 (R2 = 19% for each). Antibiosis was conditioned by the PI (resistant parent) allele at the QTLs on LGs G, M and B2, whereas the susceptible parent, Cobb, provided antibiosis alleles at the QTLs on LGs F and J
Descriptors:soyabeans. pest-resistance. quantitative-traits. alleles. gene-location. gene-mapping. assays. heritability. inheritance. linkage. polymorphism. restriction-fragment-length-polymorphism. genetics. antibiosis. varietal-resistance. insect-pests. grain-legumes. biotechnology. control. agricultural-entomology
Organism Descriptors:Glycine-max. Glycine-(Fabaceae). Helicoverpa. Helicoverpa-zea. Fabaceae. arthropods

Supplemental Descriptors:Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Noctuidae. Lepidoptera. insects. arthropods. invertebrates. animals. Helicoverpa
Subject Codes:FF020. FF005. FF620. HH600. WW000
Supplementary Info:44 ref
ISSN:0011-183X
Year:2000
Journal Title:Crop Science
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155. Title:Improvement of bacterial blight resistance of 'Minghui 63', an elite restorer line of hybrid rice, by molecular marker-assisted selection
View Article: Crop Science. 2000. 40 (1). 239-244
CD Volume:300
Print Article: Pages: 239-244
Author(s):Chen Sheng Lin X H Xu C G Zhang QiFa
Author Variant:Chen-S. Zhang-Q-F
Author Affiliation:National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan 430070, China
Language:English
Abstract:Minghui 63 is a restorer line widely used in hybrid rice production in China. However, this line has become increasingly susceptible to bacterial blight (BB), caused by Xanthomonas oryzae pv. oryzae, resulting in a rapid decline of its use in rice production. The objective of this study was to improve the BB resistance of Minghui 63 by introgressing Xa21, a broad-spectrum BB resistance gene, into Minghui 63 by molecular marker-assisted selection (MAS). A polymerase chain reaction (PCR)-based MAS system was established consisting of a marker that is a part of Xa21, a marker located at 0.8 centimorgans (cM) from the Xa21 locus on one side, and a marker at 3.0 cM from the gene on the other side. A total of 128 restriction fragment length polymorphism (RFLP) markers, evenly distributed on the 12 chromosomes, were used to recover the genetic background of Minghui 63. The resulting improved version of Minghui 63, or Minghui 63(Xa21), was exactly the same as the original except for a fragment of less than 3.8 cM in length surrounding the Xa21 locus. Both Minghui 63(Xa21) and its hybrid with Zhenshan 97A, referred to as Shanyou 63(Xa21), showed the same spectrum of BB resistance as the donor parent. Field examination of a number of agronomic traits showed that Minghui 63(Xa21) and Shanyou 63(Xa21) were identical to Minghui 63 and Shanyou 63, when there was no disease stress. Under heavily diseased conditions, Minghui 63(Xa21) showed significantly higher grain weight and spikelet fertility than Minghui 63, and Shanyou 63(Xa21) was significantly higher than Shanyou 63 in grains per panicle, grain weight and yield
Descriptors:rice. chromosomes. polymerase-chain-reaction. hybrid-seed-production. polymorphism. restriction-fragment-length-polymorphism. hybrid-varieties. yields. fertility. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Xanthomonas-oryzae. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF020. FF005. HH600. FF610. WW000
Supplementary Info:19 ref
ISSN:0011-183X
Year:2000
Journal Title:Crop Science
Copyright:Copyright CAB International

156. Title:RFLP mapping of QTLs influencing shoot regeneration from mature seed-derived calli in rice
View Article: Crop Science. 2000. 40 (1). 245-247
CD Volume:300
Print Article: Pages: 245-247
Author(s):Takeuchi Y Abe T Sasahara T
Author Affiliation:Laboratory of Plant Breeding, Faculty of Agriculture, Yamagata University, Tsuruoka 997-8555, Japan
Language:English
Abstract:This study focused on the mapping of quantitative trait loci (QTLs) related to shoot regeneration from mature seed-derived calli of rice (Oryza sativa) by restriction fragment length polymorphism (RFLP) markers. The F2 population from a cross between Norin 1 (japonica) and Tadukan (indica), which showed lower and higher shoot regeneration rates, respectively, was used for QTL interval mapping. The population was analysed for 103 RFLP markers distributed over the 12 rice chromosomes. The QTL with the largest effect on shoot regeneration, which accounted for about 19% of the total variation, was mapped on chromosome 2. A minor QTL on chromosome 4 exhibited a smaller effect, accounting for about 3% of the total variation in percentage shoot regeneration. No QTLs were detected on other chromosomes with the RFLP markers that were used in the present experiments. These results indicate that at least one major gene is associated with the percentage shoot regeneration, and agree with previous genetic studies, indicating that one dominant gene is associated with shoot regeneration
Descriptors:rice. callus. quantitative-traits. restriction-fragment-length-polymorphism. gene-mapping. regeneration. genetic-markers. genetics. tissue-culture. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. FF170. WW000
Supplementary Info:16 ref
ISSN:0011-183X
Year:2000
Journal Title:Crop Science
Copyright:Copyright CAB International

157. Title:Resistance to fusarium head blight in winter wheat: Heritability and trait associations
View Article: Crop Science. 40 (4). July-August, 2000. 1012-1018
CD Volume:301
Print Article: Pages: 1012-1018
Author(s):Buerstmayr Hermann Steiner Barbara Lemmens Marc Ruckenbauer Peter
Author Affiliation:Institute for Agrobiotechnology, Dep. of Biotechnology in Plant Production, IFA-Tulln, Konrad Lorenz Str. 20, A-3430, Tulln
Language:English
Language of Summary:English (EN)
Abstract:Fusarium head blight (FHB) or scab caused by Fusarium Link: Fr. spp. is a widespread disease of cereals, causing significant yield losses and contaminating cereal products with mycotoxins. The complex inheritance of resistance has hampered progress in breeding resistant, agronomically adapted cultivars. To streamline breeding for FHB resistance, we estimated genetic and environmental variance components and broad-sense heritability in two winter wheat (Triticum aestivum L.) populations, determined the association of FHB resistance with other traits (flowering date, plant height, and awnedness), and determined the level of maternal effects on FHB resistance. The moderately susceptible Austrian cultivar Capo was crossed with two resistant

lines, one from Hungary (UNG-226) and one from the Netherlands (SVP-72017). A hierarchical design was applied to develop recombinant F4-derived lines. Head blight resistance was measured by visual assessment of disease symptoms in artificially inoculated, mist-irrigated field experiments during 2 yr. Artificial inoculation and mist irrigation led to reproducible FHB infections. High broad-sense heritabilities (H > 0.75) were measured for FHB resistance, allowing for considerable progress by selection. The magnitude of additive genetic variance was greater than additive X additive epistatic variance. Despite a significant negative correlation between visual FHB symptoms and plant height (r = -0.37), the successful selection of short and FHB resistant genotypes should be feasible. In only one population, awned progeny showed slightly reduced FHB. Reciprocal effects were significant in one cross only. The development of FHB resistant cultivars should be possible by phenotypic selection under epidemic conditions, and should be largely independent of plant height, flowering date, awnedness, and genotype of the maternal parent within a cross

Descriptors:disease resistance: heritability, trait associations. Agronomy (Agriculture); Genetics; Infection. fusarium head blight: fungal disease

Organism Descriptors:Triticum aestivum [winter wheat] (Gramineae): grain crop

Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Agronomy (Agriculture); Genetics; Infection

ISSN:0011-183X
Year:2000
Journal Title:Crop Science

158. Title:Preliminary analysis of expressed sequence tags for sugarcane

View Article: Crop Science. 2000. 40 (6). 1769-1779
CD Volume:300
Print Article: Pages: 1769-1779

Author(s):Carson D L Botha F C
Author Affiliation:Biotechnology Dep., South African Sugar Association Exp. Stn, Private Bag X02, Mount Edgecombe 4300, South Africa

Language:English

Abstract:Sugarcane (Saccharum spp. hybrids), with its complex polyploid genome, is not well understood at the genetic level. Partial sequencing of anonymous cDNA clones is a widely used technique for gene identification. These partial cDNA sequences, or expressed sequence tags (ESTs) have potential application for the identification of important genes for genetic manipulation. This study aimed to initiate the preliminary development of an EST database for sugarcane and thereby gain some potentially useful information on sugarcane gene sequences. A non-directional cDNA library has been constructed from sugarcane leaf roll (meristematic region) tissue. Some 250 clones have been randomly selected, subjected to single-pass sequencing from the 5' end of the vector, and identified by sequence similarity searches against gene sequences in international databases. Of the 250 leaf roll clones, 26% exhibit similarity to known plant genes, 50% to non-plant genes, while 24% represent new gene sequences. Analysis of the identified clones indicated sequence similarity to a broad diversity of genes encoding proteins such as enzymes, structural proteins, and regulatory factors. A significant proportion of genes identified in the leaf roll were involved in processes related to protein synthesis and protein modification, as would be expected in meristematic tissues. These results present a successful application of EST analysis in

sugarcane and provide a preliminary indication of gene expression in leaf roll tissue
Descriptors:sugarcane. gene-expression. molecular-genetics. leaf-meristems
Organism Descriptors:Saccharum-officinarum. Saccharum
Supplemental Descriptors:Saccharum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:32 ref
ISSN:0011-183X
Year:2000
Journal Title:Crop Science
Copyright:Copyright CAB International

159. Title:Genetic engineering in the improvement of plants for phytoremediation of metal polluted soils
View Article: Environmental Pollution.. 107 (2). 2000. 225-231
CD Volume:333
Print Article: Pages: 225-231
Author(s):Karenlampi S Schat H Vangronsveld J Verkleij JAC van der Lelie D Mergeay M Tervahauta A I
Author Affiliation:Department of Biochemistry and Biotechnology, University of Kuopio, Kuopio, FIN-70211
Language:English
Language of Summary:English (EN)
Abstract:Metal concentrations in soils are locally quite high, and are still increasing due to many human activities, leading to elevated risk for health and the environment. Phytoremediation may offer a viable solution to this problem, and the approach is gaining increasing interest. Improvement of plants by genetic engineering, i.e. by modifying characteristics like metal uptake, transport and accumulation as well as metal tolerance, opens up new possibilities for phytoremediation. So far, only a few cases have been reported where one or more of these characteristics have been successfully altered; e.g. mercuric ion reduction causing improved resistance and phytoextraction, and metallothionein causing enhanced cadmium tolerance. These, together with other approaches and potentially promising genes for transformation of target plants are discussed
Descriptors:contaminated soil; plant metal accumulation; plant metal transport; plant metal uptake; soil pollution. Pollution Assessment Control and Management; Soil Science
Organism Descriptors:plant (Plantae): genetically engineered
Supplemental Descriptors:Plantae. Plants
Subject Codes:Pollution Assessment Control and Management; Soil Science
ISSN:0269-7491
Year:2000
Journal Title:Environmental Pollution

160. Title:Assessment of genetic relationships in Mentha species
View Article: Euphytica.. 111 (2). 2000. 121-125
CD Volume:310
Print Article: Pages: 121-125
Author(s):Khanuja S P S Shasany A K Srivastava Alka Kumar Sushil
Author Affiliation:Genetic Resources and Biotechnology Division, Central Institute of Medicinal and Aromatic Plants (CIMAP), Lucknow, 226015
Language:English
Language of Summary:English (EN)
Abstract:A set of 60 random primers was used to analyse 11 accessions from six taxa of Mentha developed by CIMAP. These accessions were maintained in

the national gene bank for medicinal and aromatic plants at CIMAP. A total of 630 bands could be detected as amplified products upon PCR amplification, out of which 589 were polymorphic (93.5%). Further analysis of these RAPD profiles for band similarity indices clearly differentiated five of the Mentha arvensis L. accessions from the rest. Among two accessions of Mentha spicata L. CIMAP/C33 could be distinguished from CIMAP/C32. Mentha X gracilis Sole cv. cardiaca showed a much higher similarity with Mentha spicata L. as well as Mentha arvensis L. which amongst themselves showed rather a greater distance indicating that Mentha X gracilis Sole cv. cardiaca might have evolved as a natural hybrid between M arvensis L. and M. spicata L.. In terms of uniqueness of amplified bands for developing RAPD markers, it was observed that at taxa level 298 bands were unique to one of the six taxa, singly amounting to 47.3% of total amplified fragments. Primers MAP 10 and 17 produced polymorphism only in case of M. spicata L. and Mentha spicata L. cv. viridis while MAP 08 produced polymorphic bands in all 4 other species than these two. Similarly unique patterns were observed differentiating all six species and could be used as RAPD markers for differentiating Mentha species

Descriptors:genetic relationship; phylogeny; plant breeding. Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Evolution and Adaptation; Systematics and Taxonomy. RAPD [random amplified polymorphic DNA]

Organism Descriptors:Mentha arvensis (Labiatae): industrial crop; Mentha spicata (Labiatae): industrial crop; Mentha x gracilis (Labiatae): cultivar-Cardiaca, industrial crop

Supplemental Descriptors:Labiatae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Evolution and Adaptation; Systematics and Taxonomy

ISSN:0014-2336
Year:2000
Journal Title:Euphytica

161. Title:Improvement of resistance to Fusarium head blight by recurrent selection in an intermating breeding spring wheat population using the dominant male-sterile gene ms2

View Article: Euphytica. 112 (1). 2000. 79-88
CD Volume:310
Print Article: Pages: 79-88
Author(s):Yang Z P Yang X Y Huang D C
Author Affiliation:Agro-Biotechnology Research Center, Shanghai Academy of Agricultural Sciences, Shanghai, 201106
Language:English
Language of Summary:English (EN)
Abstract:Four cycles of recurrent selection for FHB resistance were conducted in an intermating wheat breeding population using the dominant male-sterile gene ms2 during 1987-1991. Five cycles of phenotypic mass selection for male-sterile plants were evaluated using the soil-surface inoculation method in Experiment I. Experiment II evaluated changes in FHB scores during five cycles of progeny selection for fertile plants using the single-floret inoculation method. In Experiment I, the average level of FHB response increased to MR level in C4, compared to MS level in C0. The numbers of infected spikelets and diseased kernels decreased 0.32 and 2.68 per cycle, respectively. In Experiment II, the average level of FHB response increased to R level in C4F1. The numbers of infected spikelets and diseased kernels decreased 0.93 and 4.58 per

cycle, respectively. In both experiments, the largest selection gains were realized in the first cycle. The frequencies of R and MR individuals were increased significantly. The frequencies of individuals with FHB response equal and/or superior to Sumai 3 were increased to 5-8% in C4 and 25% in C4F1 after the fourth cycle. Agronomic traits tended to be slightly improved in selected populations. Compared to 2% in C0, about 34% of lines superior in both FHB resistance and agronomic traits in C4F1 were selected to enter the conventional breeding program for further evaluation. Sixty three semidwarf lines superior in both FHB resistance and yield potential were selected from the F5 generations derived from C1F1 to C4F1. From them, two resistant cultivars with high-yielding potential were developed and commercialized in the Lower Yangtze Valley. Recurrent selection appears to be highly effective and feasible in shifting the average FHB response of the intermating population in the desirable direction, thereby enhancing the frequency of resistant individuals

Descriptors:plant breeding. Agronomy (Agriculture); Genetics; Infection. Fusarium head blight: fungal disease. Triticum aestivum ms-2 gene (Gramineae): dominant male-sterile gene

Organism Descriptors:Triticum aestivum [wheat] (Gramineae): grain crop

Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Agronomy (Agriculture); Genetics; Infection

ISSN:0014-2336
Year:2000
Journal Title:Euphytica

162. Title:The development and use of microsatellite markers for genetic analysis and plant breeding with emphasis on bread wheat

View Article: Euphytica. 2000. 113 (3). 163-185
CD Volume:310
Print Article: Pages: 163-185

Author(s):Gupta P K Varshney R K
Author Affiliation:Molecular Biology Laboratory, Department of Agricultural Botany, Ch. Charan Singh University, Meerut-250 005, U.P., India

Language:English

Abstract:In recent years, a variety of molecular markers, based on microsatellites or simple sequence repeats (SSRs) have become the markers of choice, thus necessitating their development and use in a variety of plant systems. In this review, the basic principles underlying different hybridization-based (oligonucleotide fingerprinting) and PCR-based approaches (STMS, MP-PCR, AMP-PCR/ISSR/ASSR, RAMPs/dRAMPs, SAMPL), making use of microsatellites, have been outlined. Different methods for enrichment of genomic libraries for microsatellites are also outlined. Relevant literature on the subject, giving a summary of results obtained using each approach, has been reviewed and critically discussed. The review also includes a discussion on literature, which deals with the use of microsatellites in genome mapping, gene tagging, DNA fingerprinting, characterization of germplasm and cytogenetics research. The emphasis is on the bread wheat genome and a review of work done in the authors' own laboratory

Descriptors:genetic-analysis. wheat. DNA-fingerprinting. genomes. gene-mapping. microsatellites. polymerase-chain-reaction. reviews. genetic-markers. cereals. biotechnology

Organism Descriptors:Triticum-aestivum. Triticum

Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. WW000. FF005
Supplementary Info:7 pp. of ref
ISSN:0014-2336
Year:2000
Journal Title:Euphytica
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163. Title:Resistance to Septoria nodorum blotch in the Aegilops tauschii accession RL5271 is controlled by a single gene
View Article: Euphytica. 2000. 113 (3). 227-233
CD Volume:310
Print Article: Pages: 227-233
Author(s):Murphy N E A Loughman R Wilson R Lagudah E S Appels R Jones M G K
Author Affiliation:WA State Agriculture Biotechnology Centre, Division of Science and Engineering, Murdoch University, Murdoch, 6150, Perth, Australia
Language:English
Abstract:Septoria nodorum [Leptosphaeria nodorum] blotch is the most important leaf disease of wheat in Western Australia. A potentially useful source of resistance has been identified in an accession of Aegilops tauschii. To study the genetics of resistance of this source a cross was made between the resistant A. tauschii accession, RL5271, and a susceptible accession, CPI110889. The resistant parent took significantly longer to develop symptoms, developed significantly fewer lesions and expressed significantly lower levels of disease than the susceptible parent. The F1 mean response for disease severity indicated there was no complete dominance. The F3 families were classified using three approaches. In the first approach the individual F3 plant response was used to classify the F3 families. In the second approach the F3 family means and standard errors were used to classify the F3 families. In the final approach, Best Linear Unbiased Predictors of disease score and standard error for each F3 family derived from an REML analysis were used to classify the F3 families. The genotypic ratios generated by each of the approaches suggested that resistance is controlled by a single gene. The effectiveness of the resistance and its simple genetic control in A. tauschii accession RL5271 may be a useful resistance source for use in a bread wheat breeding programme
Descriptors:genetics. plant-pathogens. plant-diseases. disease-resistance. plant-pathogenic-fungi. genes. wild-relatives. cereals. wheat. control. plant-pathology
Organism Descriptors:Aegilops-tauschii. Leptosphaeria-nodorum. Triticum
Supplemental Descriptors:Aegilops. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Leptosphaeria. Dothideales. Ascomycotina. Eumycota. fungi
Subject Codes:FF020. FF005. HH600. FF610
Supplementary Info:26 ref
ISSN:0014-2336
Year:2000
Journal Title:Euphytica
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164. Title:AFLP markers distinguishing an early mutant of Flame seedless grape
View Article: Euphytica. 2000. 113 (3). 245-249
CD Volume:310
Print Article: Pages: 245-249
Author(s):Scott K D Ablett E M Lee L S Henry R J
Author Affiliation:Centre for Plant Conservation Genetics, Southern Cross University, Lismore, NSW 2480, Australia
Language:English

Abstract:Molecular markers have been frequently used to differentiate grape species and cultivars. There are fewer cases where molecular markers have been used to differentiate grape clones within a cultivar, or for the demarcation of somatic mutants from parental clones. This study reports the first successful utility of AFLPs for the differentiation of somatic mutants from their parental grapevine line, and discusses the potential for similar AFLP applications. The somatic mutant analysed demonstrates earlier bud burst characteristics than the Flame Seedless line from which it arose. Analysis of 64 AFLP primer combinations in silver stained polyacrylamide produced in excess of 3000 markers in Vitis vinifera, and provided two markers which differentiated the somatic mutant, from its parental line. One marker was 440 bp in length and was produced with primer combination EcoRI-AT and MseI-CTT. The second marker was 340 bp in length and generated with primer combination EcoRI-TC and MseI-CAC
Descriptors:mutants. clones. cultivars. differentiation. grapes. somatic-embryogenesis. mutations. genetic-markers. fruit-crops. biotechnology. fruits. temperate-fruits
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Vitis-vinifera. Vitis
Supplemental Descriptors:Vitis. Vitidaceae. Rhamnales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF003. WW000. FF170
Supplementary Info:17 ref
ISSN:0014-2336
Year:2000
Journal Title:Euphytica
Copyright:Copyright CAB International

165. Title:Anther culture of recalcitrant indica X Basmati rice hybrids
View Article: Euphytica. 114 (2). 2000. 93-101
CD Volume:310
Print Article: Pages: 93-101
Author(s):Bishnoi U Jain R K Rohilla J S Chowdhury V K Gupta K R Chowdhury J B
Author Affiliation:Department of Biotechnology and Molecular Biology, CCS Haryana Agricultural University, Hisar
Language:English
Language of Summary:English (EN)
Abstract:Fertile, green, di-haploid plants were obtained at high frequencies from several indica X Basmati rice F1 hybrids and/or F2 plant populations using an improved anther culture procedure. Anthers from cold-pretreated (10 degreeC for 10 d) panicles of six indica (HKR120, HKR86-3, HKR86-217, PR106, Gobind and CH2 double dwarf) and two Basmati rice (Basmati 370, Taraori Basmati) varieties and 14 heterotic indica X Basmati F1/F2 hybrids were cultured in modified agarose-solidified N6M, Heh5M and RZM media. Best callus induction frequencies (2.6-78%) were obtained in RZM medium containing 4% (w/v) maltose, 2,4-D, NAA and kinetin. F2 plants compared to F1 hybrids and parental rice varieties, were more responsive to anther culture. Androgenesis frequencies of 31-78% were obtained for indica X Basmati F2 plants in RZM medium in just 30 d which are comparable to or higher than that reported for japonica rice varieties and hybrids involving japonica rice parent(s). Agarose (1.0% w/v)-solidified MS medium containing 3.0% maltose, kinetin, BAP, and NAA, induced green shoot regeneration in 0-51% of the anther-derived calli depending upon the genotype. High plant regeneration frequencies (67-337 green plants per 1,000 anthers) were obtained from anther calli of several F1 hybrids (Gobind X Basmati 370 and HKR120 X Taraori Basmati) and F2 plants (Gobind X Basmati 370, Gobind X Taraori Basmati, HKR86-3 X Taraori Basmati). A sample of 498 plants obtained

from the above hybrids, were transferred to pots with >90% survival; 8-78% of these plants had >5% spikelet fertility and were diploid. In addition, 18% of the haploid plants could be diploidized by submerging in 0.1% colchicine solution for 16-18 h. The improved anther culture procedure reported here, resulted in several fold increase in the recovery of green plants from recalcitrant indica X Basmati rice hybrids compared to previous published procedures. The study may accelerate the introgression of desirable genes from indica into Basmati rice using anther culture as a breeding tool
Descriptors:plant breeding. Agronomy (Agriculture); Methods and Techniques
Organism Descriptors:Oryza sativa [rice] (Gramineae): Basmati hybrids, grain crop, indica types
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Methods and Techniques
ISSN:0014-2336
Year:2000
Journal Title:Euphytica

166. Title:Cross compatibility between Abelmoschus esculentus and A. moschatus
View Article: Euphytica. 114 (3). 2000. 175-180
CD Volume:310
Print Article: Pages: 175-180
Author(s):Akhond M Abdullah Yousuf Molla M Abul Hossain Islam M Obaidul Ali Mohammad
Author Affiliation:Biotechnology Division, Bangladesh Agricultural Research Institute, Gazipur, 1701
Language:English
Language of Summary:English (EN)
Abstract:Interspecific cross compatibility between cultivated and wild okra (Abelmoschus esculentus and A. moschatus) and pollen tube growth behaviour in the crosses among a local cultivar of A. esculentus, A. moschatus and their F1s were studied. Fruit set was observed in all the crosses except one and seed setting was absent in two of the crosses which set fruit. All seed produced were shrivelled but F1 plants were obtained from two crosses where cultivated okra was used as the seed parent. The F1 plants were perennial in nature with very low pollen viability and seed set. A high percentage of pollen germination and profuse pollen tube penetration in the style were observed in the cross A. esculentus X A. moschatus but low pollen tube penetration with abnormal pollen tubes was observed in the reciprocal cross. The number of pollen tubes was very low but they appeared to be normal in the backcross A. esculentus X F1, but were generally abnormal in the reciprocal cross. Both pre- and postzygotic barriers seemed to occur in crosses between the two species. The present studies indicate that these barriers can be overcome and desirable characters from A. moschatus transferred to cultivated okra using conventional hybridisation techniques
Descriptors:plant breeding. Horticulture (Agriculture); Genetics
Organism Descriptors:Abelmoschus esculentus [okra] (Malvaceae): vegetable crop; Abelmoschus moschatus [wild okra] (Malvaceae). pollen tube: reproductive system
Supplemental Descriptors:Malvaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Genetics
ISSN:0014-2336
Year:2000

Journal Title:Euphytica

167. Title:Induction of mutations for heat tolerance in potato by using in vitro culture and radiation
View Article: Euphytica. 114 (3). 2000. 205-209
CD Volume:310
Print Article: Pages: 205-209
Author(s):Das A Gosal S S Sidhu J S Dhaliwal H S
Author Affiliation:Department of Biotechnology, Punjab Agricultural University, Ludhiana, 141004
Language:English
Language of Summary:English (EN)
Abstract:Heat tolerant mutants were obtained in two commercial potato cultivars, 'Kufri Jyoti' and 'Kufri Chandramukhi' through in vitro mutagenesis of in vitro propagated plantlets. Gamma-irradiated (20 and 40 Gy) shoots were micropropagated for three cycles (M1V3). A large number of the micropropagated shoots produced microtubers at 28 degreeC. Microtubers induced at high temperature had distorted shape but showed normal germination in field. Under stress conditions of high temperature, the frequency of chlorophyll variants increased in the gamma irradiation-derived material, however, nearly 40% of the plants had normal leaf tissue, whereas control plants showed completely damaged leaves
Descriptors:heat tolerance; plant breeding. Horticulture (Agriculture); Genetics
Organism Descriptors:Solanum tuberosum [potato] (Solanaceae): cultivar-Kufri Chandramukhi, cultivar-Kufri Jyoti, vegetable crop
Supplemental Descriptors:Solanaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Genetics
ISSN:0014-2336
Year:2000
Journal Title:Euphytica

168. Title:Stability of flower colors due to anthocyanin-flavone copigmentation in Japanese garden iris, Iris ensata Thunb
View Article: Euphytica. 115 (1). 2000. 1-5
CD Volume:310
Print Article: Pages: 1-5
Author(s):Yabuya T Saito M Iwashina T Yamaguchi M
Author Affiliation:Applied Genetics and Biotechnology Division, Faculty of Agriculture, Miyazaki University, Miyazaki, 889-2192
Language:English
Language of Summary:English (EN)
Abstract:The fading of flower color in bluish purple and reddish purple cultivars of Iris ensata and the in vitro stability of malvidin 3RGac5G and petunidin 3RGac5G due to copigmentation with isovetixin under different pH conditions were examined. The bluish purple cultivars exhibited higher flower color stability than the reddish purple cultivars 2 days after anthesis. In the absence of isovitexin, malvidin 3RGac5G and petunidin 3RGac5G were not able to maintain color stability except at low pH. However, the color stability of malvidin 3RGac5G and petunidin 3RGac5G was increased by copigmentation with isovitexin under all pH conditions tested. Most remarkable was the stabilization of both anthocyanins due to the copigmentation at pH 4.2-6.2. Therefore, it can be concluded that the stability of flower color in the bluish purple cultivars of malvidin 3RGac5G and petunidin 3RGac5G type of I.

ensata is caused at least in part by the copigmentation between these anthocyanins and isovitexin
Descriptors:anthocyanin-flavone copigmentation; plant breeding. Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Genetics. isovetixin: pigment; malvidin: pigment; petunidin: pigment
Organism Descriptors:Iris ensata [Japanese garden iris] (Iridaceae): ornamental. flower: color stability, reproductive system
Supplemental Descriptors:Iridaceae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Genetics
ISSN:0014-2336
Year:2000
Journal Title:Euphytica

169. Title:Towards genetic transformation in the monocot Alstroemeria L
View Article: Euphytica. 115 (1). 2000. 17-26
CD Volume:310
Print Article: Pages: 17-26
Author(s):van Schaik C E van der Toorn C De Jeu M J Raemakers C J J M Visser R G F
Author Affiliation:Laboratory of Plant Breeding, Graduate School of Experimental Plant Sciences, Wageningen Agricultural University (WAU), 6700 AJ, Wageningen
Language:English
Language of Summary:English (EN)
Abstract:The successful application of plant biotechnology to Alstroemeria improvement will largely depend on the availability of an efficient regeneration/transformation system. Regeneration in Alstroemeria is accomplished from nodular embryogenic callus initiated from zygotic embryos. Histological studies of embryogenic callus initiation from 4-weeks old cultured ovules revealed that the outermost layers of the protoderm of the embryogenic nodules divided to form either a new nodule or a proembryo. Transient gene expression after particle bombardment of nodular embryogenic callus was optimised using DNA of pAHC25. The highest beta-glucuronidase expression was found when the GUS gene was under control of the maize ubiquitin promoter, the target tissue was placed 5 cm below the microcarrier launch assembly and when the rupture disc-breakage point was between 650- 900 psi. Kanamycin blocked regeneration of somatic embryos, however, did not block growth of nodular embryogenic callus. With phosphinothricin both callus growth and regeneration were blocked. Bombardment of nodular embryogenic callus with DNA of pAHC25 combined with selection on medium containing phosphinothricin resulted in putative transgenic chimeric. Friable calli were selected from nodular embryogenic callus and used to initiate suspensions. These cell suspensions were subjected to transformation by particle bombardment using DNA of pAHC25 and resulted in a stable transformed friable callus line after selection based on luciferase activity. Even after 2 years of maintenance this callus line was luciferase positive and the Polymerase Chain Reaction analysis demonstrated the presence of the introduced gene in this friable callus line
Descriptors:genetic engineering; plant breeding. Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques
Organism Descriptors:Alstroemeria (Liliaceae): ornamental crop

Supplemental Descriptors:Liliaceae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques
ISSN:0014-2336
Year:2000
Journal Title:Euphytica

170. Title:Factors affecting in vitro flowering and fruiting of green pea (Pisum sativum L.)
View Article: Euphytica. 115 (1). 2000. 65-73
CD Volume:310
Print Article: Pages: 65-73
Author(s):Franklin G Pius P K Ignacimuthu S
Author Affiliation:Plant Biotechnology, Department of Microbiology and Cell Biology, Indian Institute of Science, Bangalore, 560 012
Language:English
Language of Summary:English (EN)
Abstract:Multiple shoots were efficiently regenerated from cotyledonary node and shoot tip explants of Pisum sativum within 15 days on MS medium containing B5 vitamins and supplemented with 2.0 mgl-1 6-benzylaminopurine. The elongated shoots produced on the same medium were excised and transferred to MS medium containing half strength ammonium nitrate (8.25 gml-1) and supplemented with auxins (indole- 3-butyric acid or naphthalene acetic acid) either alone or in combinations with gibberellic acid. Rooting and flowering were observed on the 7th and 15th day after their transfer to rooting medium. The flowers self-fertilised in vitro and produced mature pods within 25 days of rooting. These seeds were germinable both in vitro and in vivo. In vitro seeds sown in pots under field conditions developed into flowering plants, and subsequently produced pods with viable seeds
Descriptors:plant breeding. Horticulture (Agriculture); Reproduction
Organism Descriptors:Pisum sativum [green pea] (Leguminosae): vegetable crop
Supplemental Descriptors:Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Reproduction
ISSN:0014-2336
Year:2000
Journal Title:Euphytica

171. Title:Salinity tolerant performance and genetic diversity of four rice varieties
View Article: Euphytica. 116 (2). 2000. 105-110
CD Volume:310
Print Article: Pages: 105-110
Author(s):Xie J H Zapata Arias F J Shen M Afza R
Author Affiliation:Plant Breeding Unit, FAO/IAEA Agriculture and Biotechnology Laboratory, International Atomic Energy Agency Laboratories, A- 2444, Seibersdorf: agcs@iaea.org
Language:English
Language of Summary:English (EN)
Abstract:The genetic diversity of three salinity tolerant rice varieties Pokkali, Nona-Bokra and Bicol was investigated using random amplified polymorphic DNAs (RAPDs). High yielding susceptible variety IR29 was used as check for comparison. The salinity performance of these

varieties were tested by using rapid screening techniques at seedling stage. One hundred primers tested of which 42 revealed differences between Pokkali & Nonabokra, 43 between Pokkali & Bicol and 50 between Nonabokra and Bicol. Polymorphism differences between IR29 - Pokkali, IR29 - NonaBokra and IR29 - Bicol were 47%, 53% and 31%, respectively. Four primers amplified specific fragments that appeared in all the three salt tolerant varieties but not in the salt susceptible variety IR 29. Primer UBC 9 (5'-CCTGCGCTTA-3') produced a prominent diagnostic fragment of approximately 1600 bp; primer UBC 244 (5'-CAGCCAACCG-3') generated a fragment of about 800 bp in the salt-tolerant varieties; primer UBC 251 (5'-CTTGACGGGG-3') amplified one polymorphic band of 1100 bp and primer UBC 267 (5'-CCATCTTGTG-3') yielded a relatively weak polymorphic band of 1100 bp

Descriptors:genetic diversity; plant breeding; salinity tolerance. Agronomy (Agriculture); Genetics

Organism Descriptors:Oryza sativa [rice] (Gramineae): cultivar-Bicol, cultivar-IR29, cultivar-Nona-Bokra, cultivar-Pokkali, grain crop

Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Agronomy (Agriculture); Genetics

ISSN:0014-2336
Year:2000
Journal Title:Euphytica

172. Title:Cytogeography and variation of stomatal size of Paspalum glaucescens (Gramineae; Paniceae) in Southern Brazil

View Article: Euphytica. 116 (3). 2000. 251-256
CD Volume:310
Print Article: Pages: 251-256

Author(s):Pozzobon M T Valls J F M
Author Affiliation:SAIN-Parque Rural, Embrapa Genetic Resources and Biotechnology (CENARGEN), 70770-900, Brasilia

Language:English
Language of Summary:English (EN)

Abstract:Paspalum glaucescens belongs to the informal group Plicatula, reproductively characterized by the dominance of tetraploid apomitic lines in most of its populations, with rare diploid, sexual counterparts. The species shows high phenotypic variation. Twenty nine Southern Brazilian accessions were cytologically and morphologically analysed. Most of the accessions were tetraploid (2n = 4x = 40). Meiotic study of three tetraploids showed their irregular behaviour. Eight accessions presented the diploid level (2n = 2x = 20). This can be considered a very high frequency of diploids in a member of the Plicatula group. While the tetraploids are concentrated at the highest elevations, diploids were detected mostly in the lowlands. Average stomatal sizes were quite distinct on different ploidy levels, being larger in tetraploids

Descriptors:cytogeography: ploidy; plant breeding. Molecular Genetics (Biochemistry and Molecular Biophysics); Cell Biology; Morphology

Geographic Locator:Brazil (South America, Neotropical region)

Organism Descriptors:Paspalum glaucescens (Gramineae): Paniceae. stomate: size variation

Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Cell Biology; Morphology

ISSN:0014-2336
Year:2000
Journal Title:Euphytica

173. Title:Incorporation of dairy ingredients into wheat bread: Effects on dough rheology and bread quality
View Article: European Food Research and Technology. 210 (6). 2000. 391-396
CD Volume:335
Print Article: Pages: 391-396
Author(s):Kenny Sheila Wehrle Karina Stanton Catherine Arendt Elke K
Author Affiliation:Food Science and Technology Department, National Food Biotechnology Centre, University College, Cork
Language:English
Language of Summary:English (EN)
Abstract:Dairy ingredients are used in breadmaking for their nutritional benefits and functional properties. The effects of the traditionally-used whole and skimmed milk powder, sodium caseinate, casein hydrolysate and three whey protein concentrates on dough rheology and bread quality were studied. Whole and skimmed milk powders improved sensory characteristics. Sodium caseinate and hydrolysed casein displayed beneficial functional properties in breadmaking including low proof time, high volume and low firmness. Both ingredients increased dough height measured with the rheofermentometer. Bread with 2% or 4% sodium caseinate added was rated highly in sensory evaluation. Incorporation of whey protein concentrates generally increased proof time, decreased loaf volume and decreased dough height measured with the rheofermentometer
Descriptors:skimmed milk product: bread ingredient, dairy product; wheat bread: bakery product, dough rheology, quality, sensory characteristics; whole milk powder: bread ingredient, dairy product. Foods. casein hydrolysate: food additive; sodium caseinate: food additive; whey protein concentrates: food additive
Subject Codes:Foods
ISSN:1438-2377
Year:2000
Journal Title:European Food Research and Technology

174. Title:Comparative properties of cakes prepared from rice flour and wheat flour
View Article: European Food Research and Technology. 211 (2). 2000. 117-120
CD Volume:335
Print Article: Pages: 117-120
Author(s):Varavinit Saiyavit Shobsngob Sujin
Author Affiliation:Department of Biotechnology, Faculty of Science, Mahidol University, Rama 6 Road, Bangkok, 10400
Language:English
Language of Summary:English (EN)
Abstract:The characteristics of butter cakes prepared from rice flour and wheat flour were compared. It was found that cake prepared from a mixture of rice flour, cross-linked rice flour and pregelatinized tapioca starch powder in the ratio 25:70:5 was similar to wheat flour butter cake. The pregelatinized tapioca starch acted as a binder to augment the rice starch, give the cake body and ensure that its texture was not too fragile. In this respect, it perfomed the same functions as wheat gluten in wheat flour. The modified rice flour provided good cake texture and overall properties similar to those of the cake prepared from wheat flour. Sensory evaluations on color, general appearance,

flavor, texture, taste and overall acceptability for cakes made from wheat flour and modified rice flour were not significantly different ($P < 0.05$)
Descriptors:mixed rice flour; rice flour butter cake; wheat flour butter cake; white flour. Foods
Subject Codes:Foods
ISSN:1438-2377
Year:2000
Journal Title:European Food Research and Technology

175. Title:Experimental manufacturing of kaddid, a salted dried meat product: Control of the microorganisms
View Article: European Food Research and Technology. 211 (3). 2000. 153-157
CD Volume:335
Print Article: Pages: 153-157
Author(s):Bennani L Faid M Bouseta A
Author Affiliation:Department of Food Microbiology and Biotechnology, Hassan II Institute of Agronomy and Veterinary Medicine, Rabat-Instituts, Rabat
Language:English
Language of Summary:English (EN)
Abstract:Trials of kaddid making were carried out in the laboratory by the traditional procedure. Batches of 6 kg each of sheep fresh meat were purchased directly from the slaughterhouse. The meats were sliced, salted, spiced and exposed to the sun for drying. The batches were sampled at different times to follow up the microbiological and physico-chemical properties. Determinations included the standard plate count, total and fecal coliforms, enterococci, staphylococci, Salmonella and Clostridium for the former and moisture, water activity, chlorides, total nitrogen, non protein nitrogen (NPN), total volatile nitrogen, fat content and the acid degree value (ADV) for the latter. Results indicated a considerable decrease in the moisture. The NPN increased slightly but the TVN did not show any change. The most relevant change was that of the ADV of fat. The microbiological characteristics showed a sharp increase during the first phase before salting and then a rapid decrease to low levels. Numbers were stabilized at less than 1 colony forming unit (cfu)/g for coliforms and enterococci and to around 100 cfu/g for staphylococci after 15-17 days drying. The same decreasing pattern was also observed for lipolytics and proteolytics
Descriptors:kaddid: meat product, microbiological properties, physico-chemical properties; moisture content. Foods. chlorides; fat; non protein nitrogen; total nitrogen; volatile nitrogen
Organism Descriptors:Clostridium (Endospore-forming Gram-Positives); Salmonella (Enterobacteriaceae); coliform (Enterobacteriaceae); enterococci (Gram-Positive Cocci); staphylococci (Micrococcaceae)
Supplemental Descriptors:Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Gram-Positive Cocci: Eubacteria, Bacteria, Microorganisms; Micrococcaceae: Gram-Positive Cocci, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Foods
ISSN:1438-2377
Year:2000
Journal Title:European Food Research and Technology

176. Title:Isolation of glutathione biosynthesis-deficient mutants of Saccharomyces cerevisiae and their use in baker's yeast production
View Article: European Food Research and Technology. 211 (6). 2000. 429-432
CD Volume:335
Print Article: Pages: 429-432
Author(s):Angelov Angel Hristozova Tsonka Roshkova Zlatka
Author Affiliation:Department of Biotechnology, Higher Institute of Food Industry, 26 Maritza Blvd, 4002, Plovdiv: anangel@plov.omega.bg
Language:English
Language of Summary:English (EN)
Abstract:Glutathione biosynthesis-deficient mutants of Saccharomyces cerevisiae 0511 were obtained by mutation under specific conditions. A total of 3388 strains were isolated and among them were found 46 mutants sensitive to methylglyoxal. The intracellular glutathione concentration of mutant strain S. cerevisiae 3033 was 0.0172 g/g dry weight, which was a decrease of > 76% compared to that of the parent. The growth of mutant strains S. cerevisiae 3033 and S. cerevisiae 1116 in the medium with glutathione present and absent was compared to that of the parent strain. The sensibility of the baker's yeast strains studied to antifoaming agents, butanol and acetic acid was also investigated. The relationship between glutathione presence in the cell and the sensitivity of strain S. cerevisiae 3033 to antifoaming agents and butanol was ascertained, while such a connection with the presence of acetic acid in the molasses medium used for baker's yeast cultivation was not observed. The higher sensitivity of strain S. cerevisiae 3033 to some chemical compounds in the molasses nutrition medium was shown
Descriptors:Foods. acetic acid: antifoaming agent; butanol: antifoaming agent; glutathione: biosynthesis; methylglyoxal
Organism Descriptors:Saccharomyces cerevisiae [baker's yeast] (Ascomycetes): fermentation agent, strain-0511, strain-3033
Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Foods
ISSN:1438-2377
Year:2000
Journal Title:European Food Research and Technology

177. Title:Characterization of a testicular 17 alpha ,20 beta -dihydroxy-4-pregnen-3-one (a spermiation-inducing steroid in fish) receptor from a teleost, Japanese eel (Anguilla japonica)
View Article: FEBS Letters. 2000. 465 (1). 12-17
CD Volume:327
Print Article: Pages: 12-17
Author(s):Todo T Ikeuchi T Kobayashi T Kajiura Kobayashi H Suzuki K Yoshikuni M Yamauchi K Nagahama Y
Author Affiliation:Laboratory of Reproductive Biology, National Institute for Basic Biology, Okazaki 444-8585, Japan
Language:English
Abstract:A cDNA encoding a nuclear 17 alpha ,20 beta -dihydroxy-4-pregnen-3-one (17 alpha ,20 beta -DP, a spermiation-inducing hormone in fish) receptor (DPR) was isolated from an eel testis cDNA library. The amino acid sequence of DPR shows high homology with those of human and fowl progesterone receptors. The affinity of the bacterial recombinant DPR ligand binding domain protein for 17 alpha ,20 beta -DP is higher than that of progesterone. In transfection experiments using COS7 cells, the DPR showed progestin-dependent activation of transcription. 17 alpha ,20 beta -DP was the most effective activator of transcription. These results indicate that the cDNA encodes a functional eel DPR, and show

that 17 alpha ,20 beta -DP has a nuclear receptor-mediated action in eel testes. The nucleotide sequence data reported will appear in the DDBJ/EMBL/GenBank nucleotide sequence databases with the accession number AB032075
Descriptors:steroids. testes. genes. complementary-DNA. nucleotide-sequences. receptors. biotechnology
Organism Descriptors:Anguilla-japonica
Supplemental Descriptors:Anguilla. Anguillidae. Anguilliformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms
Subject Codes:MM300. WW000. LL240. LL250
Supplementary Info:34 ref
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters
Copyright:Copyright CAB International

178. Title:Phosphatidyl serine exposure during apoptosis precedes release of cytochrome c and decrease in mitochondrial transmembrane potential
View Article: FEBS Lett 2000 Jan 7;465(1):47-52
CD Volume:327
Print Article: Pages: 47-52
Author(s):Denecker G Dooms H Van Loo G Vercammen D Grooten J Fiers W Declercq W Vandenabeele P
Author Affiliation:Department of Molecular Biology, Flanders Interuniversity Institute for Biotechnology and University of Gent, K.L. Ledeganckstraat 35, B-9000, Gent, Belgium
Abstract:Time kinetics of phosphatidyl serine (PS) exposure were compared to other apoptotic parameters following different apoptotic stimuli. Our data indicate that anti-Fas treatment of L929sAhFas cells results in rapid exposure of PS, which precedes decrease in mitochondrial transmembrane potential (DeltaPsi(m)) and release of cytochrome c, indicating that PS exposure occurs independently of these mitochondrial events. Also during TNF-, etoposide- or staurosporine-mediated apoptosis in PC60 RI/RII cells, PS-positive cells were observed before they had a decreased DeltaPsi(m). However, during growth factor depletion-induced death of 32D cells, both phenomena seemed to occur at the same time
Descriptors:Animal. Antigens, CD95. *Apoptosis. Cell Line. Comparative Study. Cytochrome c. Etoposide. Growth Substances. Human. Membrane Potentials. Mice. Mitochondria. Phosphatidylserines. Staurosporine. Support, Non-U.S. Gov't. Time Factors. Transfection. Tumor Necrosis Factor
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

179. Title:Effect of temperature on kinesin-driven microtubule gliding and kinesin ATPase activity
View Article: FEBS Lett 2000 Jan 21;466(1):59-62
CD Volume:327
Print Article: Pages: 59-62
Author(s):Bohm KJ Stracke R Baum M Zieren M Unger E
Author Affiliation:Institute of Molecular Biotechnology, Research Group of Molecular Cytology/Electron Microscopy, Beutenbergstrasse 11, D-07745, Jena, Germany. kboehm@imb-jena.de
Abstract:DeCuevas et al. [J. Cell Biol. 116 (1992) 957-965] demonstrated by circular dichroism spectroscopy for the kinesin stalk fragment that shifting temperature from 25 to 30 degrees C caused a conformational

transition. To gain insight into functional consequences of such a transition, we studied the temperature dependence of a full-length kinesin by measuring both the velocity of microtubule gliding across kinesin-coated surfaces and microtubule-promoted kinesin ATPase activity in solution. The corresponding Arrhenius plots revealed distinct breaks at 27 degrees C, corroborating the temperature-dependent conformational transition for a motility-competent full-length kinesin. Microtubules were found to glide up to 45 degrees C; at higher temperatures, kinesin was irreversibly damaged
Descriptors:Animal. Brain Chemistry. In Vitro. Kinesin. Microtubules. Molecular Motors. Movement. Protein Conformation. Support, Non-U.S. Gov't. Swine. Temperature. Thermodynamics
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

180. Title:Molecular cloning and characterization of a rice dehydroascorbate reductase
View Article: FEBS Letters. 2000. 466 (1). 107-111
CD Volume:327
Print Article: Pages: 107-111
Author(s):Urano J Nakagawa T Maki Y Masumura T Tanaka K Murata N Ushimaru T
Author Affiliation:Department of Biology, Faculty of Science, Shizuoka University, Shizuoka 422-8529, Japan
Language:English
Abstract:Plant dehydroascorbate reductase [glutathione dehydrogenase] (DHAR, EC 1.8.5.1), which re-reduces oxidized ascorbate to maintain an appropriate level of ascorbate, is very important, but no gene or cDNA for plant DHAR has been cloned yet. Here, we describe a cDNA for a rice glutathione-dependent DHAR (designated DHAR1). A recombinant Dhar1p produced in Escherichia coli was functional. The expression sequence tag database suggests that Dhar1p homologues exist in various plants. Furthermore, the rice Dhar1p has a low similarity to rat DHAR, although the rice enzyme has a considerably higher specific activity than the mammalian one. The mRNA level of DHAR1, the protein level of Dhar1p and the DHAR activity in rice seedlings were elevated by high temperature, suggesting the protection role of DHAR at high temperature
Descriptors:characterization. DNA-cloning. rice. complementary-DNA. gene-expression. genetic-engineering. genetic-transformation. heat. temperature. stress-response. seedlings. oxidoreductases. cereals. biotechnology
Identifiers:glutathione dehydrogenase (ascorbate)
Organism Descriptors:Oryza-sativa. Escherichia-coli. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF005. FF060. FF020. WW000
Supplementary Info:22 ref
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

181. Title:Cloning, expression and characterization of a novel four EF-hand Ca2+-binding protein from olive pollen with allergenic activity
View Article: FEBS Letters. 2000. 466 (1). 192-196
CD Volume:327
Print Article: Pages: 192-196

Author(s):Ledesma A Villalba M Rodriguez R
Author Affiliation:Departamento de Bioquimica y Biologia Molecular, Facultad de Quimica, Universidad Complutense, 28040 Madrid, Spain
Language:English
Abstract:A novel allergenic member of the family of Ca2+-binding proteins has been cloned from olive tree [Olea europaea] pollen. The isolated DNA codes for a protein of 171 amino acid residues, which displays four EF-hand sequence motifs. The encoded protein was overproduced in Escherichia coli and purified. The protein (18 795 Da), which binds Ca2+ and IgE antibodies from patients allergic to olive pollen, undergoes Ca2+-dependent conformational changes. It is retained on a phenyl-Sepharose column, which indicates the existence of regulatory EF-hand domains. This fact suggests its involvement in Ca2+-dependent signal transduction events of the pollen grain. This allergen could be considered as a member of a new subfamily of EF-hand Ca2+-binding proteins since it displays a low amino acid sequence similarity with the so far known proteins. The nucleotide sequence data for the cDNA clone have been submitted to the GenBank/EMBL database under accession no. AF078679
Descriptors:characterization. pollen. allergens. complementary-DNA. calcium. binding-proteins. olives. DNA-cloning. gene-expression. genetic-engineering. genetic-transformation. nucleotide-sequences. fatty-oil-plants. oil-plants. biotechnology
Organism Descriptors:Escherichia-coli. Olea-europaea
Supplemental Descriptors:Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. Olea. Oleaceae. Scrophulariales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000. VV055
Supplementary Info:34 ref
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

182. Title:Cross-talk between posttranscriptionally silenced neomycin phosphotransferase II transgenes
View Article: FEBS Letters. 2000. 467 (1). 41-46
CD Volume:327
Print Article: Pages: 41-46
Author(s):Houdt H van Kovarik A Montagu M van Depicker A
Author Variant:van-Houdt-H. van-Montagu-M
Author Affiliation:Department of Molecular Genetics, Flanders Interuniversity Institute for Biotechnology, Universiteit Gent, K.L. Ledeganckstraat 35, B-9000 Gent, Belgium
Language:English
Abstract:Tobacco plants containing a transgene locus with two chimaeric neomycin phosphotransferase II [kanamycin kinase] (nptII) genes in tail-to-tail orientation (locus 1) show post-transcriptional gene silencing. The silenced nptII transgenes of locus I can down-regulated the expression of homologous nptII transgenes in hybrid plants. The 3' region of the silenced nptII genes located in the centre of the inverted repeat locus 1 is extensively methylated. Moreover, 3' segments of in trans-inactivated transgenes also become methylated, suggesting cross-talk between homologous post-transcriptionally silenced genes. Our results are in accordance with the hypothesis that this cross-talk can be mediated by specially featured RNAs
Descriptors:genes. tobacco. DNA-methylation. genetic-transformation. transgenic-plants. gene-expression. reporter-genes. phosphotransferases. stimulant-plants. biotechnology

Identifiers:kanamycin kinase
Organism Descriptors:Nicotiana-tabacum. Nicotiana
Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:39 ref
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters
Copyright:Copyright CAB International

183. Title:Drug-induced hypomethylation of a posttranscriptionally silenced transgene locus of tobacco leads to partial release of silencing
View Article: FEBS Letters. 2000. 467 (1). 47-51
CD Volume:327
Print Article: Pages: 47-51
Author(s):Kovarik A Houdt H van Holy A Depicker A
Author Variant:van-Houdt-H
Author Affiliation:Institute of Biophysics, Academy of Sciences of the Czech Republic, Kralovopolska 135, 612 65 Brno, Czech Republic
Language:English
Abstract:The effect of DNA methylation upon post-transcriptional gene silencing (PTGS) has been investigated in transgenic tobacco lines showing PTGS and methylation of the neomycin phosphotransferase II [kanamycin kinase] (nptII) reporter genes. Application of the hypomethylation drugs dihydroxypropyladenine or 5-azacytidine resulted in approximately 30% reduced methylation of cytosines located in a non-symmetrical context in the 3' untranslated region of the nptII transgenes. The hypomethylation was accompanied by up to 12-fold increase in NPTII protein levels, suggesting that methylation of non-symmetrical motifs may account for an increased degree of PTGS. Models for the possible role of DNA methylation in PTGS are discussed
Descriptors:tobacco. reporter-genes. transgenic-plants. genetic-transformation. gene-expression. DNA-methylation. phosphotransferases. stimulant-plants. biotechnology
Identifiers:kanamycin kinase
Organism Descriptors:Nicotiana-tabacum. Nicotiana
Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. WW000. FF020
Supplementary Info:35 ref
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters
Copyright:Copyright CAB International

184. Title:Two carbohydrate recognition domains of Hyphantria cunea lectin bind to bacterial lipopolysaccharides through O-specific chain
View Article: FEBS Letters. 2000. 467 (1). 70-74
CD Volume:327
Print Article: Pages: 70-74
Author(s):Shin SangWoon Park DooSang Kim SunChang Park HoYong
Author Variant:Shin-S-W. Park-D-S. Kim-S-C. Park-H-Y
Author Affiliation:Insect Resources Laboratory, Korea Research Institute of Bioscience and Biotechnology, 52 Eoun-Dong, Yusong, Taejon 305-333, Korea Republic
Language:English
Abstract:We previously identified a novel lectin cDNA from Hyphantria cunea which encodes two carbohydrate recognition domains (CRD-N and CRD-C)

and is up-regulated following bacterial challenge. The lipopolysaccharide (LPS) binding activities of the recombinant CRD-N and CRD-C (rCRD-N and rCRD-C) were investigated by enzyme-linked immunosorbent assay. The LPS binding of rCRD-N and rCRD-C was pH-dependent: at pH below 6.0, they show a higher binding ability to LPS. The binding of the rCRD-N was inhibited by both D-mannose and N-acetyl-D-glucosamine, whereas the binding of the rCRD-C was inhibited only by D-mannose. The binding of both rCRD-N and rCRD-C to Escherichia coli was mainly mediated through the O-specific chain

Descriptors:binding. lectins. binding-proteins. immune-response. carbohydrates. lipopolysaccharides. agricultural-entomology

Organism Descriptors:Hyphantria-cunea. arthropods

Supplemental Descriptors:Hyphantria. Arctiidae. Lepidoptera. insects. arthropods. invertebrates. animals

Subject Codes:FF620. YY400

Supplementary Info:20 ref

ISSN:0014-5793

Year:2000

Journal Title:FEBS Letters

185. Title:Tumor necrosis factor-induced lethal hepatitis: pharmacological intervention with verapamil, tannic acid, picotamide and K76COOH

View Article: FEBS Lett 2000 Feb 11;467(2-3):201-5

CD Volume:327

Print Article: Pages: 201-205

Author(s):Van Molle W Vanden Berghe J Brouckaert P Libert C

Author Affiliation:Department of Molecular Biology, Flanders Interuniversity Institute for Biotechnology, University of Gent, K.L. Ledeganckstraat 35, B-9000, Gent, Belgium

Abstract:Tumor necrosis factor (TNF) induces hepatitis when injected in human beings or in rodents. The molecular mechanism by which TNF induces hepatic distress remains largely unknown, although induction of apoptosis of hepatocytes appears to be an essential step. In order to increase the therapeutic value of TNF, we have studied the protective activity of several molecules and found that four chemically totally different substances confer significant protection in the model of TNF-induced lethal hepatitis in mice sensitized with D-(+)-galactosamine (GalN), but not in mice sensitized with actinomycin-D (ActD) or against anti-Fas-induced lethal hepatitis. Verapamil, a calcium-channel blocker, tannic acid, picotamide, a thromboxane A(2) receptor antagonist, and K76COOH, an inhibitor, amongst others, of complement, protected significantly against induction of lethality, release of the liver-specific enzyme alanine aminotransferase (ALT) and induction of apoptosis in the liver after TNF/GalN, except for K76COOH, which paradoxically increased ALT values after challenge, and which also protected against TNF/GalN in complement-deficient mice. The data suggest that activation of platelets and neutrophils, as well as induction of inflammation occur in the TNF/GalN model, but not in the TNF/ActD or anti-Fas models, in which direct induction of apoptosis of hepatocytes may be more relevant. The protective activity of the drugs may lead to an increase in therapeutic value of TNF

Descriptors:Alanine Transaminase. Animal. Apoptosis. Astringents. Complement Inactivators. Dactinomycin. Disease Models, Animal. Galactosamine. Hepatitis, Toxic. Liver. Mice. Mice, Inbred C57BL. Mice, Inbred DBA. Phthalic Acids. Platelet Aggregation Inhibitors. Sesquiterpenes. Support, Non-U.S. Gov't. Tannic Acid. Tumor Necrosis Factor. Verapamil

Geographic Locator:NETHERLANDS

ISSN:0014-5793

Year:2000
Journal Title:FEBS Letters

186. Title:Trimeric ring-like structure of ArsA ATPase
View Article: FEBS Lett 2000 Mar 3;469(1):105-10
CD Volume:327
Print Article: Pages: 105-110
Author(s):Wang HW Lu YJ Li LJ Liu S Wang DN Sui S
Author Affiliation:State Key Laboratory of Biomembrane & Membrane Biotechnology, Department of Biological Sciences & Biotechnology, Tsinghua University, Beijing, PR China
Abstract:ArsA protein is the soluble subunit of the Ars anion pump in the Escherichia coli membrane which extrudes arsenite or antimonite from the cytoplasm. The molecular weight of the subunit is 63 kDa. In the cell it hydrolyzes ATP, and the energy released is used by the membrane-bound subunit ArsB to transport the substrates across the membrane. We have obtained two-dimensional crystals of ArsA in the presence of arsenite on negatively-charged lipid monolayer composed of DMPS and DOPC. These crystals have been studied using electron microscopy of negatively-stained specimens followed by image processing. The projection map obtained at 2.4 nm resolution reveals a ring-like structure with threefold symmetry. Many molecular assemblies with the same ring-shape and dimensions were also seen dispersed on electron microscopy grids, prepared directly from purified ArsA protein solution. Size-exclusion chromatography of the protein sample with arsenite present revealed that the majority of the protein particles in solution have a molecular weight of about 180 kDa. Based on these experiments, we conclude that in solution the ArsA ATPase with substrate bound is mainly in a trimeric form
Descriptors:Adenosinetriphosphatase. Arsenites. Bacterial Proteins. Chromatography, Gel. Crystallization. Escherichia coli. Image Processing, Computer-Assisted. Membrane Proteins. Microscopy, Electron. Phosphatidylcholines. Protein Conformation. Support, Non-U.S. Gov't. Support, U.S. Gov't, P.H.S.. Unithiol
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

187. Title:Proteins in the early golgi compartment of Saccharomyces cerevisiae immunoisolated by Sed5p
View Article: FEBS Lett 2000 Mar 10;469(2-3):151-4
CD Volume:327
Print Article: Pages: 151-154
Author(s):Cho JH Noda Y Yoda K
Author Affiliation:Department of Biotechnology, The University of Tokyo, Yayoi, Bunkyo-ku, Tokyo, Japan
Abstract:The yeast tSNARE Sed5p is considered to mainly reside in the early Golgi compartment at the steady state of its intracellular cycling. To better understand this compartment, we immunoisolated a membrane subfraction having Sed5p on the surface (the Sed5 vesicles). Immunoblot studies showed that considerable portions (20-30%) of the Golgi mannosyltransferases (Mnt1p, Van1p, and Mnn9p) were simultaneously recovered while the late Golgi (Kex2p) or endoplasmic reticulum (Sec71p) proteins were almost excluded. The N-terminal sequences of the polypeptides detectable by Coomassie blue staining indicated that the prominent components of the Sed5 vesicles include Anp1p, Emp24p, Erv25p, Erp1p, Ypt52p, and a putative membrane protein of unknown function (Yml067c)

Descriptors:Carrier Proteins. Electrophoresis, Polyacrylamide Gel. Fungal Proteins. Golgi Apparatus. Immunoblotting. Mannosyltransferases. Membrane Proteins. Saccharomyces cerevisiae. Sequence Analysis, Protein. Support, Non-U.S. Gov't. rab GTP-Binding Proteins
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

188. Title:Evidence for the existence of rhodanese (thiosulfate:cyanide sulfurtransferase) in plants: preliminary characterization of two rhodanese cDNAs from Arabidopsis thaliana
View Article: FEBS Lett 2000 Mar 24;470(2):147-50
CD Volume:327
Print Article: Pages: 147-150
Author(s):Hatzfeld Y Saito K
Author Affiliation:Chiba University, Faculty of Pharmaceutical Sciences, Laboratory of Molecular Biology and Biotechnology, Yayoi-cho 1-33, Inage-ku, Chiba, Japan
Abstract:The existence of rhodanese (thiosulfate:cyanide sulfurtransferase; EC 2.8.1.1) in plants has been highly controversial. We have isolated and characterized for the first time in plants two cDNAs encoding rhodanese isoforms in Arabidopsis thaliana, AtRDH1 and AtRDH2. Both cDNAs contained a full-length open reading frame, the expression of which increased the rhodanese activity of transgenic yeast. AtRDH1 protein was mitochondrial, while AtRDH2 was cytosolic. AtRDH1 and AtRDH2 genes originated from the duplication of a large genomic region in chromosome 1 which took place before the appearance of the Arabidopsis genus. Our results confirm the existence of rhodanese in plants
Descriptors:Amino Acid Sequence. Arabidopsis. Chromosomes. Cloning, Molecular. Conserved Sequence. Cytosol. DNA, Complementary. Expressed Sequence Tags. Gene Duplication. Genes, Plant. Introns. Isoenzymes. Mitochondria. Molecular Sequence Data. Open Reading Frames. Plant Proteins. Recombinant Fusion Proteins. Support, Non-U.S. Gov't. Thiosulfate Sulfurtransferase
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

189. Title:Chlorophyll fluorescence quenching in isolated light harvesting complexes induced by zeaxanthin
View Article: FEBS Lett 2000 Apr 7;471(1):71-4
CD Volume:327
Print Article: Pages: 71-74
Author(s):Wentworth M Ruban AV Horton P
Author Affiliation:Robert Hill Institute for Photosynthesis Research, Department of Molecular Biology and Biotechnology, University of Sheffield, Western Bank, Sheffield, UK
Abstract:Non-photochemical quenching of chlorophyll fluorescence in plants occurs in the light harvesting antenna of photosystem II and is regulated by the xanthophyll cycle. A new in vitro model for this process has been developed. Purified light harvesting complexes above the detergent critical micelle concentration have a stable high fluorescence yield but a rapidly inducible fluorescence quenching occurs upon addition of zeaxanthin. Violaxanthin was without effect, lutein and antheraxanthin induced a marginal response, whereas the violaxanthin analogue, auroxanthin, induced strong quenching. Quenching was not caused by aggregation of the complexes but was accompanied by a

spectral broadening and red shift, indicating a zeaxanthin-dependent alteration in the chlorophyll environment
Descriptors:Beta Carotene. Chlorophyll. Fluorescence. Photosynthetic Reaction Center, Plant. Spinach. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

190. Title:Scorpine, an anti-malaria and anti-bacterial agent purified from scorpion venom
View Article: FEBS Lett 2000 Apr 14;471(2-3):165-8
CD Volume:327
Print Article: Pages: 165-168
Author(s):Conde R Zamudio FZ Rodriguez MH Possani LD
Author Affiliation:Department of Molecular Recognition and Structural Biology, Institute of Biotechnology, National Autonomous University of Mexico, Avenida Universidad, 2001, P.O. Box 510-3, Cuernavaca, Mexico
Abstract:A novel peptide, scorpine, was isolated from the venom of the scorpion Pandinus imperator, with anti-bacterial activity and a potent inhibitory effect on the ookinete (ED(50) 0.7 microM) and gamete (ED(50) 10 microM) stages of Plasmodium berghei development. It has 75 amino acids, three disulfide bridges with a molecular mass of 8350 Da. Scorpine has a unique amino acid sequence, similar only to some cecropins in its N-terminal segment and to some defensins in its C-terminal region. Its gene was cloned from a cDNA library
Descriptors:Amino Acid Sequence. Animal. Anti-Infective Agents. Antimalarials. Bacillus subtilis. Base Sequence. Cloning, Molecular. Defensins. Disulfides. Dose-Response Relationship, Drug. Gametogenesis. Germ Cells. Klebsiella pneumoniae. Microbial Sensitivity Tests. Molecular Sequence Data. Molecular Weight. Peptides. Plasmodium berghei. Proteins. Scorpion Venoms. Scorpions. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

191. Title:Involvement of SH2-SH2-SH3 domain of phospholipase cgamma1 in NF-kappaB signaling
View Article: FEBS Lett 2000 Apr 21;472(1):45-9
CD Volume:328
Print Article: Pages: 45-49
Author(s):Kim BY Kang DO Oh WK Kim JH Choi YK Jang JS Suh PG Ryu SH Mheen TI Ahn JS
Author Affiliation:Korea Research Institute of Bioscience and Biotechnology, P.O. Box 115, Yusong, Taejon, South Korea
Abstract:To directly define the role of phospholipase Cgamma1 (PLCgamma1) in NF-kappaB activation, NF-kappaB promoted luciferase reporter gene plasmid (pNF-kappaB-Luc) was transfected into rat-3Y1 fibroblasts that overexpress whole PLCgamma1 (PLCgamma1-3Y1), src homology domains SH2-SH2-SH3 of PLCgamma1 (SH223-3Y1) and v-src (Src-3Y1). Transient transfection with pNF-kappaB-Luc remarkably increased the luciferase activity in all three transformants compared with normal rat-3Y1 cells. Pretreatment with inhibitors of protein tyrosine kinase reduced this increase in luciferase activity, but U73122 (a PLC inhibitor) did not. While PD98059, an inhibitor of mitogen activated protein kinase (MAPK), significantly reduced the luciferase activity, there was no effect by wortmannin and Ro-31-8220, inhibitors of phosphatidylinositol 3-kinase

(PI3K) and protein kinase C (PKC), respectively. This study shows a direct evidence that the SH2-SH2-SH3 region of PLCgamma1 contributes to the NF-kappaB signaling and that MAPK, but not PI3K and PKC, is involved in SH2-SH2-SH3 mediated NF-kappaB activation in these cells
Descriptors:3T3 Cells. Animal. Cell Line. Genes, Reporter. Isoenzymes. Luciferase. Mice. NF-kappa B. Phospholipase C. Rats. Signal Transduction. Support, Non-U.S. Gov't. Transfection. *src Homology Domains
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

192. Title:Nerve growth factor induces sphingomyelin accumulation in pheochromocytoma cells
View Article: FEBS Lett 2000 Apr 21;472(1):143-7
CD Volume:328
Print Article: Pages: 143-147
Author(s):Piccinotti A Benaglia G Bresciani R Zizioli D Presta M Preti A Marchesini S
Author Affiliation:Unit of Biochemistry, Department of Biomedical Sciences and Biotechnology, School of Medicine, University of Brescia, Via Valsabbina 19, 25123, Brescia, Italy. piccinot@med.unibs.it
Abstract:The pheochromocytoma cells are a well-known model for studying the nerve growth factor (NGF)-induced molecular changes during the differentiation process. The involvement of sphingomyelin (SM) was studied using the fluorescent analogue of ceramide, i.e. N-lissamine rhodaminyl-(12-aminododecanoyl) D-erythro-sphingosine (C12-LRh-Cer). This fluorescent analogue is metabolically active and can be used to follow the biosynthesis of SM in intact cells. NGF induces a 4-fold increase of fluorescent SM content in PC12 cells, when loaded with C12-LRh-Cer. Treatment of PC12 cells with actinomycin D or cycloheximide completely abolishes the NGF-induced elevation of SM. Inhibition of p140(trkA) receptor by AG-879 prevents extracellular signal-regulated kinase 1/2 phosphorylation and suppresses the increase of SM. Inhibition of protein kinase C (PKC), protein kinase A (PKA) and phosphatidylinositol 3-kinase does not have any effect on NGF-induced C12-LRh-SM accumulation. On the other hand, activation of PKA or PKC with simultaneous treatment with NGF has a synergistic effect on increase of SM content. The NGF-induced SM increase in PC12 cells is an effect promoted by other differentiating agents like dibutyryl cyclic AMP or fibroblast growth factor-2 but not by a mitogenic agent like epidermal growth factor
Descriptors:Animal. Cyclic AMP-Dependent Protein Kinases. Cycloheximide. Enzyme Activation. Enzyme Inhibitors. Mitogen-Activated Protein Kinases. Nerve Growth Factor. PC12 Cells. Phosphorylation. Protein Kinase C. Protein-Tyrosine Kinase. Rats. Receptor, trkA. Sphingomyelins. Support, Non-U.S. Gov't. Tyrphostins. p42 MAP Kinase
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

193. Title:Active site residue 297 of Aspergillus niger phytase critically affects the catalytic properties
View Article: FEBS Lett 2000 Apr 28;472(2-3):169-72
CD Volume:328
Print Article: Pages: 169-172

Author(s):Tomschy A Wyss M Kostrewa D Vogel K Tessier M Hofer S Burgin H Kronenberger A Remy R van Loon AP Pasamontes L
Author Affiliation:Biotechnology Department, Vitamins and Fine Chemicals Division, F. Hoffmann-La Roche Ltd, Business Unit VM4, Bldg. 241/865, CH-4070, Basel, Switzerland
Abstract:The wild-type phytases from the Aspergillus niger strains NRRL 3135 and T213 display a three-fold difference in specific activity (103 versus 32 U/mg protein), despite only 12 amino acid differences that are distributed all over the sequence of the protein. Of the 12 divergent positions, three are located in or close to the substrate binding site. Site-directed mutagenesis of these residues in A. niger T213 phytase showed that the R297Q mutation (R in T213, Q in NRRL 3135) fully accounts for the differences in catalytic properties observed. Molecular modelling revealed that R297 may directly interact with a phosphate group of phytic acid. The fact that this presumed ionic interaction - causing stronger binding of substrates and products - correlates with a lower specific activity indicates that product (myo-inositol pentakisphosphate) release is the rate-limiting step of the reaction
Descriptors:6-Phytase. Aspergillus niger. Binding Sites. Catalysis. Mutagenesis, Site-Directed. Protein Conformation
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

194. Title:The catalytic RNA of RNase P from Escherichia coli cleaves Drosophila 2S ribosomal RNA in vitro: a new type of naturally occurring substrate for the ribozyme
View Article: FEBS Lett 2000 Apr 28;472(2-3):187-90
CD Volume:328
Print Article: Pages: 187-190
Author(s):Hori Y Tanaka T Kikuchi Y
Author Affiliation:Division of Bioscience and Biotechnology, Department of Ecological Engineering, Toyohashi University of Technology, Tempaku-cho, Toyohashi, Aichi, Japan
Abstract:We have found that the catalytic RNA of RNase P of Escherichia coli (M1 RNA) can cleave 2S ribosomal RNA (2S rRNA) of Drosophila melanogaster at specific positions in vitro. The cleavage mainly occurred at two sites between nucleotides 11 and 12, and between 16 and 17 of 2S rRNA. Kinetic analyses of the reaction revealed that a dimer caused by intermolecular interaction of 2S rRNA may be the substrate for the cleavage between 11 and 12, while a simple monomer is the substrate for the cleavage between 16 and 17. Substrate recognition by M1 RNA is also discussed
Descriptors:Animal. Dimerization. Drosophila. Endoribonucleases. Escherichia coli. Nucleic Acid Conformation. RNA, Bacterial. RNA, Catalytic. RNA, Ribosomal. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

195. Title:Thrombin-induced inhibition of myoblast differentiation is mediated by Gbetagamma
View Article: FEBS Lett 2000 Apr 28;472(2-3):297-301
CD Volume:328
Print Article: Pages: 297-301
Author(s):Nagao M Kaziro Y Itoh H

Author Affiliation:Faculty of Bioscience and Biotechnology, Tokyo Institute of Technology, 4259 Nagatsuta-cho, Midori-ku, Yokohama, Japan
Abstract:Thrombin has been shown to inhibit skeletal muscle differentiation. However, the mechanisms by which thrombin represses myogenesis remain unknown. Since the thrombin receptor couples to G(i), G(q/11) and G(12), we examined which subunits of heterotrimeric guanine nucleotide-binding regulatory proteins (Galpha(i), Galpha(q/11), Galpha(12) or Gbetagamma) participate in the thrombin-induced inhibition of C2C12 myoblast differentiation. Galpha(i2) and Galpha(11) had no inhibitory effect on the myogenic differentiation. Galpha(12) prevented only myoblast fusion, whereas Gbetagamma inhibited both the induction of skeletal muscle-specific markers and the myotube formation. In addition, the thrombin-induced reduction of creatine kinase activity was blocked by the C-terminal peptide of beta-adrenergic receptor kinase, which is known to sequester free Gbetagamma. These results suggest that the thrombin-induced inhibition of muscle differentiation is mainly mediated by Gbetagamma
Descriptors:Animal. Cell Differentiation. Cell Line. G-Protein, Inhibitory Gi. GTP-Binding Proteins. Heterotrimeric GTP-Binding Proteins. Mice. Muscle, Skeletal. Proto-Oncogene Proteins. Rabbits. Rats. Support, Non-U.S. Gov't. Thrombin
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

196. Title:Identification of residues in the TPR domain of Ssn6 responsible for interaction with the Tup1 protein
View Article: FEBS Lett 2000 May 4;473(1):37-41
CD Volume:328
Print Article: Pages: 37-41
Author(s):Gounalaki N Tzamarias D Vlassi M
Author Affiliation:Institute of Molecular Biology and Biotechnology-Foundation of Research and Technology, Vassilika Vouton, P.O. Box 711 10, Heraklion, Crete, Greece
Abstract:Ssn6, a yeast protein that comprises 10 tandem tetratricopeptide repeat (TPR) motifs, associates with Tup1 repressor protein and acts as a transcriptional corepressor. In this report we identify point mutations in the TPR1 of Ssn6 that disrupt Tup1 interaction. Furthermore, we construct a 3D model of the TPR domain of Ssn6, which is responsible for Tup1 binding, based on the known structure of protein phosphatase 5. According to this model all selected mutations reduce the ability of Ssn6 to interact with Tup1 by affecting the structural integrity of TPR1 and/or the correct spatial arrangement of TPR1 relative to TPR2 and TPR3
Descriptors:Amino Acid Motifs. Amino Acid Sequence. Binding Sites. Crystallography, X-Ray. Electrostatics. Fungal Proteins. Gene Expression Regulation, Fungal. Models, Molecular. Molecular Sequence Data. Nuclear Proteins. Phosphoprotein Phosphatase. Point Mutation. Protein Binding. Protein Structure, Secondary. Protein Structure, Tertiary. Repetitive Sequences, Amino Acid. Repressor Proteins. *Saccharomyces cerevisiae. Sequence Alignment. Structure-Activity Relationship. Support, Non-U.S. Gov't. Two-Hybrid System Techniques
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

197. Title:Cd(II), Pb(II) and Zn(II) ions regulate expression of the metal-transporting P-type ATPase ZntA in Escherichia coli
View Article: FEBS Lett 2000 May 4;473(1):67-70
CD Volume:328
Print Article: Pages: 67-70
Author(s):Binet MR Poole RK
Author Affiliation:Department of Molecular Biology and Biotechnology, The University of Sheffield, Firth Court, Western Bank, Sheffield, UK
Abstract:ZntA is a cation-translocating ATPase which exports from Escherichia coli Cd(II) and Pb(II), as well as Zn(II). The metal-dependent ATP hydrolysis activity of purified ZntA was recently characterised and showed a specificity for Cd(II), Pb(II) and Zn(II). zntA expression has been reported to be up-regulated primarily by Zn(II), mediated by the regulatory protein ZntR, belonging to the MerR transcriptional regulator family. In contrast to previous claims, we now show, using a Phi(zntA-lacZ) monolysogen, that Cd(II) is the most effective inducer of zntA, which is also induced significantly by Pb(II). The Cd(II)- and Pb(II)-dependent transcriptional up-regulation of zntA is also mediated by ZntR
Descriptors:Adenosine Triphosphate. Adenosinetriphosphatase. Cadmium. Cations, Divalent. Drug Resistance, Microbial. Escherichia coli. Gene Dosage. Gene Expression Regulation, Bacterial. Genes, Bacterial. Hydrolysis. Lead. Microbial Sensitivity Tests. Mutation. Operon. Promoter Regions (Genetics). Substrate Specificity. Support, Non-U.S. Gov't. Transcription Factors. Up-Regulation (Physiology). Zinc
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

198. Title:A novel human processed gene, DAD-R, maps to 12p12 and is expressed in several organs
View Article: FEBS Lett 2000 May 12;473(2):233-6
CD Volume:328
Print Article: Pages: 233-236
Author(s):Kuittinen T Eggert A Lindholm P Horelli Kuitunen N Palotie A Maris JM Saarma M
Author Affiliation:Insitute of Biotechnology, Viikki Biocenter, P.O. Box 56 (Viikinkaari 9), FIN-00014 University of, Helsinki, Finland. tpkuitti@operoni.helsinki.fi
Abstract:A cDNA of a processed gene of human DAD-1 (defender against apoptotic cell death) was cloned from the human neuroblastoma cell line SH-SY5Y. The genomic sequence of this novel processed gene, DAD-R, lacked introns and was flanked by 8 bp terminal repeats. RT-PCR showed that the transcript is expressed predominantly in testis, ovaries, pancreas, lung and skeletal muscle. DAD-R has several possible initiation codons, one of them producing an open reading frame comprising 75% of the DAD-1 gene. We determined the chromosomal localization of DAD-R as 12p11.2-12p12.1, an area linked to familial synpolydactyly and frequently amplified in a variety of cancers, including those of testis, ovaries, pancreas and lungs
Descriptors:Amino Acid Sequence. Base Sequence. Chromosome Banding. Chromosome Mapping. Chromosomes, Human, Pair 12. DNA, Complementary. Female. Gene Expression. Human. In Situ Hybridization, Fluorescence. Male. Molecular Sequence Data. RNA, Messenger. Repressor Proteins. Reverse Transcriptase Polymerase Chain Reaction. Sequence Analysis, DNA. Sequence Homology, Amino Acid. Sequence Homology, Nucleic Acid. Support, Non-U.S. Gov't. Tissue Distribution. Tumor Cells, Cultured
Geographic Locator:NETHERLANDS

ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

199. Title:Novel Dictyostelium unconventional myosin, MyoM, has a putative RhoGEF domain
View Article: FEBS Lett 2000 May 26;474(1):16-22
CD Volume:328
Print Article: Pages: 16-22
Author(s):Oishi N Adachi H Sutoh K
Author Affiliation:Biotechnology Research Center, Teikyo University, 907 Nogawa, Miyamae-ku, Kawasaki-shi, Kanagawa 216-0001, Japan
Abstract:We have cloned a novel unconventional myosin gene myoM in Dictyostelium. Phylogenetic analysis of the motor domain indicated that MyoM does not belong to any known subclass of the myosin superfamily. Following the motor domain, two calmodulin-binding IQ motifs, a putative coiled-coil region, and a Pro, Ser and Thr-rich domain, lies a combination of dbl homology and pleckstrin homology domains. These are conserved in Rho GDP/GTP exchange factors (RhoGEFs). We have identified for the first time the RhoGEF domain in the myosin sequences. The growth and terminal developmental phenotype of Dictyostelium cells were not affected by the myoM(-) mutation. Green fluorescent protein-tagged MyoM, however, accumulated at crown-shaped projections and membranes of phase lucent vesicles in growing cells, suggesting its possible roles in macropinocytosis
Descriptors:Amino Acid Sequence. Animal. Base Sequence. Binding Sites. Calmodulin. Dictyostelium. Guanine Nucleotide Exchange Factors. Human. Indicators and Reagents. Luminescent Proteins. Molecular Sequence Data. Myosin. Phylogeny. Sequence Alignment. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

200. Title:Identification and light-induced expression of a novel gene of NADPH-protochlorophyllide oxidoreductase isoform in Arabidopsis thaliana
View Article: FEBS Lett 2000 Jun 2;474(2-3):133-6
CD Volume:328
Print Article: Pages: 133-136
Author(s):Oosawa N Masuda T Awai K Fusada N Shimada H Ohta H Takamiya K
Author Affiliation:Department of Biological Sciences, Faculty of Bioscience and Biotechnology, Tokyo Institute of Technology, Nagatsuta 4259, Midori-ku, 226-8501, Yokohama, Japan
Abstract:In Arabidopsis thaliana, we identified a novel gene of a NADPH-protochlorophyllide oxidoreductase (POR) isoform, which catalyzes the light-dependent protochlorophyllide a reduction in the chlorophyll (Chl) biosynthetic pathway. The deduced amino acid sequence of the novel POR isoform (PORC) showed significant identities (approximately 75%) with the previously isolated two POR isoforms of A. thaliana. Contrasting with these POR isoforms, the PORC transcript increased in etiolated seedlings by illumination, and was dominantly expressed in immature and mature tissues. The present results demonstrated that Chl biosynthesis and chloroplast biogenesis in A. thaliana are controlled by three POR isoforms, which are differentially controlled by light and development
Descriptors:Amino Acid Sequence. Arabidopsis. Cloning, Molecular. Enzyme Induction. Exons. Gene Expression Regulation, Developmental. *Gene Expression Regulation, Plant. Introns. Isoenzymes. *Light. Molecular

Sequence Data. Oxidoreductases. Phylogeny. RNA, Messenger. Sequence Alignment. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

201. Title:The active-site residue Cys-29 is responsible for the neutral-pH inactivation and the refolding barrier of human cathepsin B
View Article: FEBS Lett 2000 Jun 23;475(3):157-62
CD Volume:328
Print Article: Pages: 157-162
Author(s):Song J Xu P Xiang H Su Z Storer AC Ni F
Author Affiliation:Biomolecular NMR Laboratory and the Montr?eal Joint Centre for Structural Biology, Biotechnology Research Institute, National Research Council of Canada, Qu?ebec, H4P 2R2, Montr?eal, Canada
Abstract:Human cathepsin B, the most abundant lysosomal cysteine protease, has been implicated in a variety of important physiological and pathological processes. It has been known for a long time that like other lysosomal cysteine proteases, cathepsin B becomes inactivated and undergoes irreversible denaturation at neutral or alkaline pH. However, the mechanism of this denaturation process remains mostly unknown up to this day. In the present work, nuclear magnetic resonance spectroscopy was used to characterize the molecular origin of the neutral-pH inactivation and the refolding barrier of human cathepsin B. Two forms of human cathepsin B, the native form with Cys-29 at the active site and a mutant with Cys-29 replaced by Ala, were shown to have well-folded structures at the active and slightly acidic condition of pH 5. Surprisingly, while the native cathepsin B irreversibly unfolds at pH 7.5, the C29A mutant was found to maintain a stable three-dimensional structure at neutral pH conditions. In addition, replacement of Cys-29 by Ala renders the process of the urea denaturation of human cathepsin B completely reversible, in contrast to the opposite behavior of the wild-type cathepsin B. These results are very surprising in that replacement of one single residue, the active-site Cys-29, can eliminate the neutral-pH denaturation and the refolding barrier. We speculate that this finding may have important implications in understanding the process of pH-triggered inactivation commonly observed for most lysosomal cysteine proteases
Descriptors:Cathepsin B. Cysteine. Human. Hydrogen-Ion Concentration. Magnetic Resonance Spectroscopy. *Protein Folding. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

202. Title:Regulation of UDP-glucose:ceramide glucosyltransferase-1 by ceramide
View Article: FEBS Lett 2000 Jun 23;475(3):247-50
CD Volume:328
Print Article: Pages: 247-250
Author(s):Komori H Ichikawa S Hirabayashi Y Ito M
Author Affiliation:Department of Bioscience and Biotechnology, Graduate School of Bioresource and Bioenvironmental Sciences, Kyushu University, Higashi-ku, Fukuoka, Japan
Abstract:We report that the expression of mRNA and the activity of UDP-glucose:ceramide (Cer) glucosyltransferase-1 (GlcT-1) of human hepatoma Huh7 and mouse melanoma B16 cells increases after treatment with bacterial sphingomyelinase or upon addition of short-chain Cer. Interestingly, however, GlcT-1 gene transcription was not increased by

Cer when GlcT-1 cDNA was introduced with the CMV promoter in GlcT-1-deficient GM95 cells, suggesting that the normal promoter region of GlcT-1 gene is essential for the response. The conversion of C6-Cer to C6-GlcCer occurred much more rapidly in GlcT-1-overexpressing Huh7 cells than in mock transfectants. As a result, GlcT-1-overexpressing cells acquired a greater resistance to C6-Cer-mediated cell death
Descriptors:Animal. Ceramides. DNA, Complementary. Gene Expression Regulation, Enzymologic. Glucosyltransferases. Human. Mice. Promoter Regions (Genetics). RNA, Messenger. Support, Non-U.S. Gov't. Tumor Cells, Cultured
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

203. Title:Dual regulation of the T-type Ca2+ current by serum albumin and beta -estradiol in mammalian spermatogenic cells
View Article: FEBS Letters. 2000. 475 (3). 251-256
CD Volume:328
Print Article: Pages: 251-256
Author(s):Espinosa F Lopez Gonzalez I Munoz Garay C Felix R Vega Beltran J L de la Kopf G S Visconti P E Darszon A
Author Variant:de-la-Vega-Beltran-J-L
Author Affiliation:Department of Genetics and Molecular Physiology, Institute of Biotechnology, UNAM, Avenida Universidad 2001, Col. Chamilpa, P.O. Box 62100, Cuernavaca, Mor., Mexico
Language:English
Abstract:This study provides evidence for a novel mechanism of voltage-gated Ca2+ channel regulation in mammalian (mouse) spermatogenic cells by 2 agents that affect sperm capacitation and the acrosome reaction (AR). Patch-clamp experiments demonstrated that serum albumin induced an increase in Ca2+ T current density in a concentration-dependent manner, and significant shifts in the voltage dependence of both steady-state activation and inactivation of the channels. These actions were not related to the ability of albumin to remove cholesterol from the membrane. beta -estradiol significantly inhibited Ca2+ channel activity in a concentration-dependent and essentially voltage-independent fashion. In mature spermatozoa this dual regulation may influence capacitation and/or the AR
Descriptors:calcium. acrosome-reaction. spermatozoa. estradiol. serum-albumin
Identifiers:sperm capacitation
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL250. LL600
Supplementary Info:24 ref
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

204. Title:Bacterial protein translocase: a unique molecular machine with an army of substrates
View Article: FEBS Lett 2000 Jun 30;476(1-2):18-21
CD Volume:328
Print Article: Pages: 18-21
Author(s):Economou A

Author Affiliation:Institute of Molecular Biology and Biotechnology-FORTH and Department of Biology, University of Crete, P.O. Box 1527, Crete GR-711 10, Iraklio, Greece. aeconomo@imbb.forth.gr
Abstract:Secretion of most polypeptides across the bacterial plasma membrane is catalyzed by the Sec protein translocase. This complex molecular machine comprises a flexible transmembrane conduit coupled to a motor-like component and displays four activities: (a) it is a specific receptor at its cytoplasmic side for all secretory polypeptides, (b) it converts metabolic energy from ATP and proton gradients into mechanical motion, (c) it prevents substrates from folding in statu translocanti and (d) it binds and releases short segments of the polymeric substrate sequentially. Combination of these activities allows translocase to move processively along the length of the substrate. Substrates are thus gradually expelled from the membrane and are released for subsequent extracytoplasmic folding
Descriptors:Adenosinetriphosphatase. Bacteria. Bacterial Proteins. Carrier Proteins. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

205. Title:Chemical inhibitors: a tool for plant cell cycle studies
View Article: FEBS Lett 2000 Jun 30;476(1-2):78-83
CD Volume:328
Print Article: Pages: 78-83
Author(s):Planchais S Glab N Inze D Bergounioux C
Author Affiliation:Institute of Biotechnology, University of Cambridge, Tennis Court Road, Cambridge CB2 1ZT, UK. sp292@biotech.cam.ac.uk
Abstract:Synchrony provides a large number of cells at defined points of the cell cycle. Highly synchronised cells are powerful and effective tools for molecular analyses and for studying the biochemical events of the cell cycle in plants. Usually, plant cell suspensions can be synchronised by chemical agents, which arrest the cell cycle by acting on the driving forces of the cell cycle engine such as cyclin-dependent kinase activity, enzymes involved in DNA synthesis or proteolysis of cell cycle regulators or by acting on the cell cycle apparatus (mitotic spindle). The specificity, reversibility and efficiency of each type of cell cycle inhibitor are described and related to their mode of action
Descriptors:Cell Cycle. Cyclin-Dependent Kinases. Enzyme Inhibitors. *Plant Physiology. Plants. Support, Non-U.S. Gov't
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

206. Title:Kinetic model of ATP synthase: pH dependence of the rate of ATP synthesis
View Article: FEBS Lett 2000 Jul 7;476(3):113-7
CD Volume:328
Print Article: Pages: 113-117
Author(s):Jain S Nath S
Author Affiliation:Department of Biochemical Engineering and Biotechnology, Indian Institute of Technology, Hauz Khas, 110 016, New Delhi, India
Abstract:Recently, a novel molecular mechanism of torque generation in the F(0) portion of ATP synthase was proposed [Rohatgi, Saha and Nath (1998) Curr. Sci. 75, 716-718]. In this mechanism, rotation of the c-subunit was conceived to take place in 12 discrete steps of 30 degrees each due to the binding and unbinding of protons to/from the leading and

trailing Asp-61 residues of the c-subunit, respectively. Based on this molecular mechanism, a kinetic scheme has been developed in this work. The scheme considers proton transport driven by a concentration gradient of protons across the proton half-channels, and the rotation of the c-subunit by changes in the electrical potential only. This kinetic scheme has been analyzed mathematically and an expression has been obtained to explain the pH dependence of the rate of ATP synthesis by ATP synthase under steady state operating conditions. For a single set of three enzymological kinetic parameters, this expression predicts the rates of ATP synthesis which agree well with the experimental data over a wide range of pH(in) and pH(out). A logical consequence of our analysis is that DeltapH and Deltapsi are kinetically inequivalent driving forces for ATP synthesis

Descriptors:Adenosine Triphosphate. Chloroplasts. Electrochemistry. Escherichia coli. H(+)-Transporting ATP Synthase. Hydrogen-Ion Concentration. Kinetics. *Models, Biological. Protein Structure, Quaternary. Support, Non-U.S. Gov't

Geographic Locator:NETHERLANDS

ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

207. Title:Xanthophylls of the major photosynthetic light-harvesting complex of plants: identification, conformation and dynamics

View Article: FEBS Letters. 2000. 477 (3). 181-185
CD Volume:328
Print Article: Pages: 181-185

Author(s):Ruban A V Pascal A A Robert B
Author Affiliation:Department of Molecular Biology and Biotechnology, University of Sheffield, Western Bank, Firth Court, Sheffield S10 2TN, UK

Language:English

Abstract:The electronic transitions of lutein and neoxanthin in the major light-harvesting complex, LHCIIb, were identified for the first time in spinach. It was found that 0-0, 0-1 and 0-2 transitions of neoxanthin were located around 486, 457 and 430 nm, whilst those for lutein were dependent on the oligomerization state. For the monomer, the absorption bands of lutein were found at 495, 466 and 437 nm. Trimerization caused a decrease in lutein absorption and the parallel appearance of an additional absorption band around 510 nm, which was identified by resonance Raman excitation spectra to originate from lutein. Circular dichroism measurements together with analysis of the 1/4 resonance Raman region of xanthophylls suggested that this lutein molecule is distorted in the trimer. Oligomerization of trimers led to a specific distortion of the neoxanthin molecule. These observations suggest that the xanthophylls of LHCIIb sense the protein conformation and which may reflect their special role in the assembly and function of the light-harvesting antenna of higher plants

Descriptors:spinach. plant-composition. chemical-composition. xanthophyll. photosynthesis. chloroplasts. identification. absorption. measurement. xanthophylls. light. structure-activity-relationships. chemical-structure

Identifiers:neoxanthin
Organism Descriptors:Spinacia-oleracea
Supplemental Descriptors:Spinacia. Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF060. FF040
Supplementary Info:19 ref

ISSN:0014-5793
Year:2000

Journal Title:FEBS Letters

208. Title:Structure-based sequence alignment for the beta-trefoil subdomain of the clostridial neurotoxin family provides residue level information about the putative ganglioside binding site
View Article: FEBS Lett 2000 Sep 29;482(1-2):119-24
CD Volume:329
Print Article: Pages: 119-124
Author(s):Ginalski K Venclovas C Lesyng B Fidelis K
Author Affiliation:Biology and Biotechnology Research Program, Lawrence Livermore National Laboratory, Livermore, CA 94551, USA. kginal@icm.edu.pl
Abstract:Clostridial neurotoxins embrace a family of extremely potent toxins comprised of tetanus toxin (TeNT) and seven different serotypes of botulinum toxin (BoNT/A-G). The beta-trefoil subdomain of the C-terminal part of the heavy chain (H(C)), responsible for ganglioside binding, is the most divergent region in clostridial neurotoxins with sequence identity as low as 15%. We re-examined the alignment between family sequences within this subdomain, since in this region all alignments published to date show obvious inconsistencies with the beta-trefoil fold. The final alignment was obtained by considering the general constraints imposed by this fold, and homology modeling studies based on the TeNT structure. Recently solved structures of BoNT/A confirm the validity of this structure-based approach. Taking into account biochemical data and crystal structures of TeNT and BoNT/A, we also re-examined the location of the putative ganglioside binding site and, using the new alignment, characterized this site in other BoNT serotypes
Descriptors:Amino Acid Sequence. Botulinum Toxins. Clostridium. Comparative Study. Conserved Sequence. Models, Molecular. Molecular Sequence Data. *Protein Structure, Secondary. Sequence Alignment. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't. Support, U.S. Gov't, Non-P.H.S.. Tetanus Toxin
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

209. Title:NADPH:protochlorophyllide oxidoreductase from Synechocystis: overexpression, purification and preliminary characterisation
View Article: FEBS Lett 2000 Oct 13;483(1):47-51
CD Volume:329
Print Article: Pages: 47-51
Author(s):Heyes DJ Martin GE Reid RJ Hunter CN Wilks HM
Author Affiliation:Krebs Institute for Biomolecular Research and Robert Hill Institute for Photosynthesis, Department of Molecular Biology and Biotechnology, The University of Sheffield, S10 2TN, Sheffield, UK
Abstract:NADPH:protochlorophyllide oxidoreductase (POR) catalyses the light-dependent reduction of protochlorophyllide to chlorophyllide, a key regulatory reaction in the chlorophyll biosynthetic pathway. POR from the cyanobacterium Synechocystis has been overproduced in Escherichia coli with a hexahistidine tag at the N-terminus. This enzyme (His(6)-POR) has been purified to homogeneity and a preliminary characterisation of its kinetic and substrate binding properties is presented. Chemical modification experiments have been used to demonstrate inhibition of POR activity by the thiol-specific reagent N-ethyl maleimide. Substrate protection experiments reveal that the

modified Cys residues are involved in either substrate binding or catalysis
Descriptors:Chlorophyllides. Electrophoresis, Polyacrylamide Gel. Enzyme Inhibitors. Ethylmaleimide. Histidine. Kinetics. NADP. Oxidoreductases. Protein Binding. Protochlorophyllide. Recombinant Fusion Proteins. Spectrometry, Fluorescence. Substrate Specificity. Support, Non-U.S. Gov't. Synechocystis Group
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

210. Title:Quenching of singlet oxygen by carotenoids produced in escherichia coli - attenuation of singlet oxygen-mediated bacterial killing by carotenoids
View Article: FEBS Lett 2000 Nov 10;484(3):280-4
CD Volume:329
Print Article: Pages: 280-284
Author(s):Tatsuzawa H Maruyama T Misawa N Fujimori K Nakano M
Author Affiliation:Marine Biotechnology Institute (MBI), Kamaishi Laboratories, Japan. tatsuzawa06612@erc.ebara.co.jp
Abstract:We examined the viability of Escherichia coli transformants harboring various carotenoids synthesizing genes in a medium containing an enzymatic singlet oxygen generating system, which contained myeloperoxidase, hydrogen peroxide and Br(-) at pH 4.5. Singlet oxygen quenching activities of various carotenoids in phosphatidyl choline micelles in aqueous media were also studied using the same enzymatic singlet oxygen generating system. Viability of the transformants producing carotenoids was higher than that of the wild type E. coli in the singlet oxygen generation mixture. Of the transformants tested, the viability of zeaxanthin-diglucoside producing transformant was the highest. Carotenoids in increasing order of k(q) values were beta-carotene, a cyclic carotene<zeaxanthin with hydroxy groups < or =lycopene, an acyclic carotene<canthaxanthin and astaxanthin with keto groups <zeaxanthin-diglucoside. The k(q) value of zeaxanthin-diglucoside was 3.5 times higher than that of beta-carotene. These results suggest that orientation of the carotenoids in lipid layers of micelles and also in phospholipid membrane of bacteria is important for quenching of singlet oxygen. Furthermore, the viability of transformants producing lycopene and phytoene was almost as high as that of the transformant producing zeaxanthin-glucoside
Descriptors:Adenosine Triphosphate. Agrobacterium. Carotenoids. Electron Transport. Erwinia. Escherichia coli. Gene Transfer Techniques. Micelles. Oxidoreductases. Oxygen. Peroxidase. Phosphatidylcholines. Photochemistry
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

211. Title:NMR analysis of secondary structure and dynamics of a recombinant peptide from the N-terminal region of human erythroid alpha-spectrin
View Article: FEBS Lett 2000 Nov 17;485(1):81-6
CD Volume:329
Print Article: Pages: 81-86
Author(s):Park S Johnson ME Fung LW
Author Affiliation:Center for Pharmaceutical Biotechnology, Chicago, IL 60657-7173, USA

Abstract:We have studied the nuclear magnetic resonance solution secondary structure of the N-terminal region in human erythroid alpha-spectrin using a recombinant model peptide of alpha-spectrin consisting of residues 1-156. Pulsed field gradient diffusion coefficient measurements show that the model peptide exists as a monomer under the solution conditions used. The first 20 residues are in a random coil conformation, followed by a helix of 25 residues and then a random coil segment before the next helix. The random coil nature of this linker was confirmed by the presence of fast internal motion from (15)N relaxation measurements. The second, third and fourth helices are thought to form the triple helical bundle structural domain, consistent with previous studies. Our study shows that the N-terminal region of alpha-spectrin prior to the first structural domain forms a well behaved helix without its beta-spectrin partner
Descriptors:Amino Acid Sequence. Circular Dichroism. Erythrocytes. Human. Magnetic Resonance Spectroscopy. Molecular Sequence Data. Peptide Fragments. Protein Folding. *Protein Structure, Secondary. Recombinant Proteins. Spectrin. Support, Non-U.S. Gov't. Support, U.S. Gov't, Non-P.H.S.. Support, U.S. Gov't, P.H.S.
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

212. Title:Chloroplast development in Arabidopsis thaliana requires the nuclear-encoded transcription factor sigma B
View Article: FEBS Lett 2000 Nov 24;485(2-3):178-82
CD Volume:329
Print Article: Pages: 178-182
Author(s):Shirano Y Shimada H Kanamaru K Fujiwara M Tanaka K Takahashi H Unno K Sato S Tabata S Hayashi H Miyake C Yokota A Shibata D
Author Affiliation:Mitsui Plant Biotechnology Research Institute, Tsukuba, Ibaraki, Japan
Abstract:Development of plastids into chloroplasts, the organelles of photosynthesis, is triggered by light. However, little is known of the factors involved in the complex coordination of light-induced plastid gene expression, which must be directed by both nuclear and plastid genomes. We have isolated an Arabidopsis mutant, abc1, with impaired chloroplast development, which results in a pale green leaf phenotype. The mutated nuclear gene encodes a sigma factor, SigB, presumably for the eubacterial-like plastid RNA polymerase. Our results provide direct evidence that a nuclear-derived prokaryotic-like SigB protein, plays a critical role in the coordination of the two genomes for chloroplast development
Descriptors:Arabidopsis. Bacterial Proteins. Cell Nucleus. Chloroplasts. DNA, Plant. Fluorometry. Gene Expression. Light. Mutation. Phenotype. Plant Leaves. Plastids. Recombinant Proteins. Sigma Factor. Support, Non-U.S. Gov't. *Transcription Factors
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

213. Title:Identification of the Y985 and Y1077 motifs as SOCS3 recruitment sites in the murine leptin receptor
View Article: FEBS Lett 2000 Dec 1;486(1):33-7
CD Volume:329
Print Article: Pages: 33-37
Author(s):Eyckerman S Broekaert D Verhee A Vandekerckhove J Tavernier J

Author Affiliation:Flanders' Interuniversity Institute for Biotechnology, Department of Medical Protein Research, Ghent University, Faculty of Medicine and Health Sciences, Ghent, Belgium
Abstract:The leptin system provides a link between adipose mass and the central nervous system. The appetite suppressing effects of leptin are impaired in most obese patients and some mutant mice strains. Herein we describe how suppressor of cytokine signalling 3 (SOCS3), a potential mediator of this leptin resistance is recruited into the activated murine leptin receptor complex. Using a functional assay based on inhibition of leptin mediated reporter induction, and using phosphopeptide affinity chromatography we show binding of SOCS3 to the highly conserved phosphorylated Tyr-985 and Tyr-1077 motifs within the mouse leptin receptor
Descriptors:Amino Acid Motifs. Amino Acid Sequence. Amino Acid Substitution. Animal. Binding Sites. Blotting, Western. Carrier Proteins. Cell Line. Chromatography, Affinity. Human. Mice. Molecular Sequence Data. Mutation. PC12 Cells. Phosphopeptides. Phosphorylation. Protein Binding. Proteins. RNA, Messenger. Rats. Sequence Alignment. Signal Transduction. Support, Non-U.S. Gov't. Transfection. Tyrosine
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

214. Title:Tc1, from Tityus cambridgei, is the first member of a new subfamily of scorpion toxin that blocks K(+)-channels
View Article: FEBS Lett 2000 Dec 8;486(2):117-20
CD Volume:329
Print Article: Pages: 117-120
Author(s):Batista CV Gomez Lagunas F Lucas S Possani LD
Author Affiliation:Department of Molecular Recognition and Structural Biology, Institute of Biotechnology, National Autonomous University of Mexico, Cuernavaca, Mexico
Abstract:A new peptide, Tc1, containing only 23 amino acids closely packed by three disulfide bridges was isolated from the Amazonian scorpion Tityus cambridgei. It blocks reversibly the Shaker B K(+)-channels with a K(d) of 65 nM and displaces binding of noxiustoxin to mouse brain synaptosome membranes. It is the shortest known peptide from scorpion venom that recognizes K(+)-channels and constitutes a new structural subfamily of toxin, classified as alphaKTx 13.1
Descriptors:Amino Acid Sequence. Animal. Cell Line. Mice. Molecular Sequence Data. Neurotoxins. Peptides. Potassium Channels. Scorpion Venoms. Scorpions. Spodoptera. Support, Non-U.S. Gov't. Synaptosomes
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

215. Title:Ganoderma extract activates MAP kinases and induces the neuronal differentiation of rat pheochromocytoma PC12 cells
View Article: FEBS Lett 2000 Dec 15;486(3):291-6
CD Volume:329
Print Article: Pages: 291-296
Author(s):Cheung WM Hui WS Chu PW Chiu SW Ip NY
Author Affiliation:Department of Biochemistry and Biotechnology Research Institute, Hong Kong University of Science and Technology, PR China
Abstract:The pharmacology and clinical application of traditional Chinese medicine has been extensively documented. We have used an in vitro model system, PC12 cells, to demonstrate the presence of neuroactive

compounds in Ganoderma lucidum (lingzhi). Ganoderma extract induced the neuronal differentiation of PC12 cells and prevented nerve growth factor-dependent PC12 neurons from apoptosis. Moreover, these effects of ganoderma might be mediated via the ras/extracellular signal-regulated kinase (Erk) and cAMP-response element binding protein (CREB) signaling pathways, as demonstrated by the phosphorylation of Erk1, Erk2 and CREB. Thus, our data not only present the first evidence of the presence of neuroactive compounds that mediate the neuronal differentiation and neuroprotection of the PC12 cells, but also reveal the potential signaling molecules involved in its action
Descriptors:Animal. Apoptosis. Cell Differentiation. Cell Division. DNA-Binding Protein, Cyclic AMP-Responsive. Dose-Response Relationship, Drug. Drugs, Chinese Herbal. In Situ Nick-End Labeling. Mitogen-Activated Protein Kinases. Nerve Growth Factor. Neurofilament Proteins. Neurons. PC12 Cells. Pheochromocytoma. Phosphorylation. Rats. Receptor, trkA. Reishi. Signal Transduction. Support, Non-U.S. Gov't. p42 MAP Kinase
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

216. Title:Regulation of Wee1 kinase in response to protein synthesis inhibition
View Article: FEBS Lett 2000 Dec 15;486(3):305-9
CD Volume:329
Print Article: Pages: 305-309
Author(s):Suda M Yamada S Toda T Miyakawa T Hirata D
Author Affiliation:Department of Molecular Biotechnology, Graduate School of Advanced Sciences of Matter, Hiroshima University, Japan
Abstract:To investigate the mechanism coupling growth (protein synthesis) with cell division, we examined the relationship between the tyrosine kinase Wee1 that inhibits Cdc2-Cdc13 mitosis-inducing kinase by phosphorylating it, and protein synthesis inhibition in fission yeast. The wee1-50 mutant showed supersensitivity to protein synthesis inhibitor, cycloheximide. Wee1 was essential for the G(2) delay upon a partial inhibition of protein synthesis. Indeed, the protein synthesis inhibition caused an increase in the Wee1 protein by the Sty1/Spc1 MAPK-dependent transcriptional and the Sty1/Spc1 MAPK-independent post-transcriptional regulations. Further, the results indicated that the post-transcriptional regulation is important for the G(2) delay
Descriptors:Cell Cycle. Cell Cycle Proteins. Cell Division. Cyclin B. Cycloheximide. G2 Phase. Gene Expression Regulation, Fungal. Mitogen-Activated Protein Kinases. Mitosis. Protein Synthesis Inhibitors. Protein p34cdc2. Protein-Tyrosine Kinase. RNA Processing, Post-Transcriptional. RNA, Messenger. Schizosaccharomyces. Up-Regulation (Physiology)
Geographic Locator:NETHERLANDS
ISSN:0014-5793
Year:2000
Journal Title:FEBS Letters

217. Title:Changes in quality of sugar-cane juice upon delayed extraction and storage
View Article: Food Chemistry. 2000. 68 (4). 395-401
CD Volume:326
Print Article: Pages: 395-401
Author(s):Yusof S Shian L S Osman A
Author Affiliation:Faculty of Food Science and Biotechnology, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia
Language:English

Abstract:The quality of sugarcane juice extracted from stored canes, as well as changes in quality of fresh juice stored at different temperatures, were studied. Cane stems were stored at 10 plus or minus 1 deg C, 85-88% relative humidity (RH) and 27 plus or minus 1 deg C, 55-85% RH, while fresh juice was stored at 5 plus or minus 1 deg C, 61-84% RH and 27 plus or minus 1 deg C, 55-85% RH. The physicochemical parameters evaluated were juice yield, juice colour, total soluble solids, sugar content (sucrose, fructose, glucose), titratable acidity, pH, chlorophyll content and sensory evaluation for colour and flavour. Viscosity and total microbial count on stored cane juice were also determined. Results showed that low temperature storage (10 deg C) of canes was able to maintain the quality of juice for up to 9 days while low temperature storage (5 deg C) of juice could last for only 4 days. During storage, sucrose contents decreased while fructose, glucose and titratable acidity increased in both types of samples. The colour changes in juice extracted from stored canes was inconspicuous until day 9. Deterioration of cane stored at 27 plus or minus 1 deg C occurred faster than that stored at 10 plus or minus 1 deg C. Fresh sugarcane juice became spoiled after 4 days when stored at 5 plus or minus 1 deg C and 1 day when stored at 27 plus or minus 1 deg C. Microbial count, especially lactic acid bacteria count, increased during storage of cane juice
Descriptors:extraction. sugarcane. chlorophyll. deterioration. storage. evaluation. flavour. fructose. humidity. lactic-acid. relative-humidity. sucrose. temperature. storage-decay. sugar-loss. juice-quality. glucose
Organism Descriptors:Saccharum
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:QQ020. QQ050. QQ500
Supplementary Info:11 ref
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry

218. Title:Dietary intake of organophosphate pesticides in Kuwait
View Article: Food Chemistry. 2000. 69 (3). 331-338
CD Volume:326
Print Article: Pages: 331-338
Author(s):Sawaya W N Al Awadhi F A Saeed T Al Omair A Husain A Ahmad N Al Omirah H Al Zenki S Khalafawi S Al Otaibi J Al Amiri H
Author Affiliation:Biotechnology Department, Food Resources Division, Kuwait Institute for Scientific Research, PO Box 24885, 13109 Safat, Kuwait
Language:English
Abstract:The State of Kuwait, in cooperation with the US FDA, conducted a total diet study (TDS) to estimate pesticide intake by the population. The organophosphate (OP) pesticide levels in 139 food items, constituting the TDS core list, are reported here. The TDS core food list was established through a nationwide food consumption survey. All foods were prepared as eaten, and analysed for their organochlorine pesticide, OP, carbamate, benzimidazole and phenyl urea contents. The FDA's Multiresidue Methods, PAM I, were used employing GC, HPLC and GPC. Twenty-five of the foods analysed contained OPs. These included 7 of 12 cereal products (chloropyriphos=0.03-0.21 ppm and fenitrothion=0.016-0.84 ppm), 6 of 16 vegetables (diazinon=0.05-0.2 ppm, and chlorpyrifos, and fenthione sulfone), 1 of 16 fruits (monocrotophos) and 11 of 47 composite dishes (chlorpyrifos methyl=0.011-0.089 ppm and fenitrothion 0.011-0.044 ppm). The higher

levels of fenitrothion in one cereal product exceeded the MRLs, and warrant corrective and preventive measures. The daily intakes of OP pesticide residues are discussed in light of the ADIs of the FAO/WHO (1993)
Descriptors:organophosphorus-compounds. intake. pesticides. cereal-products. diet-studies. food-consumption. foods. fruits. organochlorine-compounds. organochlorine-pesticides. pesticide-residues. residues. standards. urea. vegetables. chlorpyrifos. fenitrothion. diazinon. fenthion. monocrotophos. chlorpyrifos-methyl. insecticide-residues. environment. agricultural-entomology
Geographic Locator:Kuwait
Organism Descriptors:arthropods
Supplemental Descriptors:invertebrates. animals. Persian-Gulf-States. West-Asia. Asia. Middle-East. Developing-Countries
Subject Codes:QQ200
Supplementary Info:13 ref
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry
Copyright:Copyright CAB International

219. Title:The use of gene technology for optimal development of pork meat quality
View Article: Food Chemistry. 2000. 69 (4). 397-405
CD Volume:326
Print Article: Pages: 397-405
Author(s):Vries A G de Faucitano L Sosnicki A Plastow G S
Author Variant:de-Vries-A-G
Author Affiliation:PIC Europe, Fyfield Wick, Abingdon OX13 5NA, UK
Document Editor:Toldra-F. Troy-D-J
Conference Title:Special issue: new developments in guaranteeing the optimal sensory quality of meat
Language:English
Abstract:Opportunities for gene technology in relation to the quality of pork are discussed. After dealing with breed effects and within-breed variation, an overview of major genes and DNA technology is given. It is demonstrated that some of the breed effects can be fully explained from the presence of a single gene with major effect. Within breeds, there is considerable genetic variation in relevant meat quality traits like waterholding capacity and intramuscular fat. Again, part of this variation is due to major genes. As a result, DNA marker technology can play an important role in improving meat quality. Selective breeding based on this technology will also increase the uniformity of the final product. Furthermore, the exploitation of major genes can be highly relevant for differentiation of breeding populations for specific markets
Descriptors:meat-quality. pigmeat. major-genes. marker-genes. reviews. selective-breeding. biotechnology
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. LL120. QQ500
Supplementary Info:80 ref
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry
Copyright:Copyright CAB International

220. Title:Physical properties of lipase-catalyzed transesterified blends of palm stearin and anhydrous milk fat
View Article: Food Chemistry. 2000. 70 (2). 215-219
CD Volume:326
Print Article: Pages: 215-219
Author(s):Lai O M Ghazali H M Cho F Chong C L
Author Affiliation:Department of Biotechnology, Faculty of Food Science and Biotechnology, Universiti Putra Malaysia, UPM 43400 Serdang, Selangor, D.E., Malaysia
Language:English
Abstract:Palm stearin (PS) and anhydrous milk fat (AMF) blends, formulated by mixing 40 to 80% PS in increments of 10% (w/w), were subjected to transesterification catalysed by lipases from Pseudomonas spp. and Rhizomucor miehei (Lipozyme IM60). The physical properties of the transesterified products were evaluated by slip melting point (SMP), differential scanning calorimetry (DSC), solid fat content (SFC) and X-ray diffraction (XRD) analyses. SMP results indicated that the Pseudomonas spp. lipase caused a bigger drop in SMP (15.6%) for a PS:AMF (40:60) blend compared to 12.5% reduction when R. miehei lipase was used. The same blend, when reacted with either of the lipases, had a residual SFC of 7.1% at 40 deg C. Generally, for all other ratios of PS:AMF blends, the percentage of reduction in SMP was higher in the Pseudomonas lipase-catalysed blends compared to the R. miehei lipase-catalysed blends. Pseudomonas lipase also successfully changed the polymorphic form of unreacted PS:AMF blends from a mixture of beta and beta ' crystals to a predominantly beta ' mixture following transesterification. On the other hand, transesterification with R. miehei lipase resulted in a product that was beta ' dominating
Descriptors:milk-fat. properties. physical-properties. polymorphism. ratios. evaluation. X-ray-diffraction. esterification. mixtures. palm-oils
Identifiers:scanning calorimetry
Organism Descriptors:Pseudomonas
Supplemental Descriptors:Pseudomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:QQ010. QQ500
Supplementary Info:13 ref
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry

221. Title:Enzymatic transesterification of palm stearin: anhydrous milk fat mixtures using 1,3-specific and non-specific lipases
View Article: Food Chemistry. 2000. 70 (2). 221-225
CD Volume:326
Print Article: Pages: 221-225
Author(s):Lai O M Ghazali H M Cho F Chong C L
Author Affiliation:Department of Biotechnology, Faculty of Food Science and Biotechnology, Universiti Putra Malaysia, UPM 43400 Serdang, Selangor, D.E., Malaysia
Language:English
Abstract:The physical characteristics of a palm stearin:anhydrous milk fat (40:60) mixture, enzymatically transesterified in a solvent-free system, was investigated by monitoring changes in the slip melting point (SMP), solid fat content (SFC) and melting characteristics. The enzymes used were 1,3-specific lipases from Aspergillus niger, Rhizomucor miehei, Rhizopus javanicus, Rhizopus niveus, Alcaligenes spp. and non-specific lipases from Pseudomonas spp. and Candida rugosa. Results indicated that Pseudomonas lipase-catalysed mixtures produced the highest degree of transesterification (33.9%) and rate of

transesterification (50.0/h), followed by R. miehei lipase at 32.3% and 27.1/h. The highest percentage of free fatty acid (FFA) liberated was also from the reaction mixture catalysed by Pseudomonas (2.61%) lipase followed by Alcaligenes (2.56%) and R. miehei (2.88%) lipases. The SMP of all the transesterified PS:AMF mixtures underwent only slight reductions, ranging from 0.5 to 2.5 deg C with reactions catalysed by Pseudomonas and R. miehei lipases, producing the biggest decrease in SMP values
Descriptors:milk-fat. mixtures. monitoring. enzymes. esterification. fatty-acids. stearin. trans-fatty-acids. palm-oils
Identifiers:Rhizopus javanicus. Rhizopus niveus. lipases
Organism Descriptors:Aspergillus-niger. Rhizomucor-miehei. Alcaligenes. Pseudomonas. Candida-rugosa
Supplemental Descriptors:Aspergillus. Deuteromycotina. Eumycota. fungi. Rhizomucor. Mucorales. Zygomycotina. Gracilicutes. bacteria. prokaryotes. Pseudomonadaceae. Candida
Subject Codes:QQ010. QQ500. ZZ900
Supplementary Info:11 ref
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry
Copyright:Copyright CAB International

222. Title:Characterisation of anthocyanins derived from carrot (Daucus carota) cell culture
View Article: Food Chemistry. 2000. 70 (3). 361-363
CD Volume:326
Print Article: Pages: 361-363
Author(s):Narayan M S Venkataraman L V
Author Affiliation:Plant Cell Biotechnology Department, Central Food Technological Research Institute, Mysore 570 013, India
Language:English
Abstract:Two anthocyanin pigments were isolated from cell cultures of carrot cv. Nentes scarlet-104. Chemical hydrolysis, column and paper chromatography, HPLC, proton and 13C NMR and mass spectroscopic studies indicated the presence of cyanidin-3-lathyroside (90%) and cyanidin-3-beta -D-glucopyranoside (10%) in callus cultures; only cyanidin-3-lathyroside (0.05%) was found in the explant. There was no acylated anthocyanin present in this carrot cultivar as reported in others
Descriptors:anthocyanins. carrots. cell-culture. in-vitro-culture. plant-composition. chemical-composition. callus. cell-suspensions. chromatography. plant-pigments. cultivars. chemical-structure
Identifiers:in vitro production
Organism Descriptors:Daucus-carota
Supplemental Descriptors:Daucus. Apiaceae. Apiales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF170. WW000. FF020. FF040
Supplementary Info:8 ref
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry
Copyright:Copyright CAB International

223. Title:Physical and textural properties of an experimental table margarine prepared from lipase-catalysed transesterified palm stearin: Palm kernel olein mixture during storage
View Article: Food Chemistry. 71 (2). 1 November, 2000. 173-179
CD Volume:326
Print Article: Pages: 173-179

Author(s):Laia O M Ghazalia H M Cho France Chong C L
Author Affiliation:Department of Biotechnology, Faculty of Food Science and Biotechnology, Universiti Putra Malaysia, UPM 43400, Serdang, Selangor Darul Ehsan
Language:English
Language of Summary:English (EN)
Abstract:The storage performances of an experimental table margarine prepared from Rhizomucor miehei-catalysed transesterified palm stearin (PS): palm kernel olein (PKO) (40:60) mixture and a commercial margarine, stored at temperatures of 20 and 30degreeC were evaluated for their slip melting point (SMP), peroxide value (PV), cone penetrometry (CP), storage modulus (G') and solid fat content (SFC). All samples showed acceptable PV levels after three months of storage. Cone penetrometric, SMP and SFC results indicated that generally the experimental samples were firmer than the commercial samples. Significant correlations were observed between SFC and penetration values ($r=0.82$; $P<0.01$). Interestingly, the storage modulus (G') values and yield values of the samples also showed significant correlations ($r=0.89$; $P<0.001$)
Descriptors:palm kernel olein: fats and oils, margarine ingredient; table margarine: fats and oils, physical properties, storage performance, textural properties; transesterified palm stearin: fats and oils, margarine ingredient. Foods. fungal lipase
Organism Descriptors:Rhizomucor miehei (Phycomycetes)
Supplemental Descriptors:Phycomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Foods
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry

224. Title:Purification and characterization of sago starch-degrading glucoamylase from Acremonium sp. endophytic fungus
View Article: Food Chemistry. 71 (2). 1 November, 2000. 221-227
CD Volume:326
Print Article: Pages: 221-227
Author(s):Marlida Yetti Saari Nazamid Hassan Zaiton Radu Son Bakar Jamilah
Author Affiliation:Department of Food Science, Faculty of Food Science and Biotechnology, University Putra Malaysia, 43400 UPM, Serdang, Selangor
Language:English
Language of Summary:English (EN)
Abstract:A novel sago starch degrading glucoamylase which had a strong amylopectin-hydrolyzing-activity was purified to homogeneity from a culture filtrate of Acremonium sp. isolated from forest trees. The purified enzyme was an oligomeric protein of two sub-units with molecular weights of 22 and 39 kDa. Optimum temperature and pH for enzyme activity were around 55degreeC and 5.5, respectively. The enzyme was stable in a pH range of 3.0-7.0 and temperatures up to 60degreeC. The purified enzyme was strongly inhibited by EDTA. The enzyme catalyzed hydrolysis of amylose and amylopectin, showed apparent Km values of 10.0 and 3.8 mg/ml and Vmax of 195 mumol/ml/min and 391 mumol/ml/min, respectively. Glucose was the sole product released by the hydrolysis, indicating that this enzyme displays an exo-action of starch-degrading activity
Descriptors:Enzymology (Biochemistry and Molecular Biophysics); Foods. EDTA: enzyme inhibitor; amylopectin: hydrolysis; amylose: hydrolysis; fungal glucoamylase: characterization, food processing agent, purification; glucose: release; sago starch: degradation
Organism Descriptors:Acremonium sp. (Fungi Imperfecti or Deuteromycetes)

Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Foods
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry

225. Title:Comparison of methods of analysis of time-intensity data: Application to Scotch malt whisky
View Article: Food Chemistry. 71 (3). 15 November, 2000. 319-326
CD Volume:326
Print Article: Pages: 319-326
Author(s):Piggott John R Hunter E Anthony Margomenou Lila
Author Affiliation:Department of Bioscience and Biotechnology, University of Strathclyde, 204 George Street, Glasgow, G1 1XW
Language:English
Language of Summary:English (EN)
Abstract:Time-intensity (TI) data typically consist of assessments at 1 s intervals of a set of samples by a panel of assessors. Some means of summarising the data must be found, and the data must be represented in a way which allows comparisons between samples. Parameters such as maximum intensity, time to maximum, and total duration are typically used and samples compared by analysis of variance. Thirteen assessors scored sweet taste intensity for 60 s, for 20 whisky samples drawn from 5 types of cask after 4 maturation times. Scaling and then averaging of the transformed data provided the best summary, and ante-dependence modelling showed that the intensity value at each time-point of the curve was dependent on the previous five time-points. Small effects of cask type and maturation time were found on sweet taste in whisky samples
Descriptors:Scotch malt whisky: alcoholic beverage; cask type; maturation time; sweet taste intensity. Models and Simulations (Computational Biology); Foods
Subject Codes:Models and Simulations (Computational Biology); Foods
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry

226. Title:Dynamic analyses of sensory and microstructural properties of cream cheese
View Article: Food Chemistry. 71 (3). 15 November, 2000. 363-378
CD Volume:326
Print Article: Pages: 363-378
Author(s):Wendin Karin Langton Maud Caous Lisbeth Hall Gunnar
Author Affiliation:SIK, Swedish Institute for Food and Biotechnology AB, SE-402 29, Goteborg
Language:English
Language of Summary:English (EN)
Abstract:Flavour and texture in cream cheese depend on the microstructure. The objective of this work was to study the influence of fat content, salt content and homogenisation pressure on the microstructure and sensory properties of cream cheese. Twelve types of cream cheese were produced according to a full-factorial design, whereby the fat content was set at three levels, the salt content at two levels and the homogenisation pressure at two levels. The cheeses were analysed by a sensory panel, using both quantitative descriptive profiling and time intensity (TI) evaluation, and by using a confocal laser scanning microscope, CLSM,

whereby the microstructure of the cheeses was analysed. All the design parameters had a significant influence on the flavour and texture, although fat had the largest effect. Interaction effects between the design parameters were also found to influence the character of cream cheese. The results showed that it is possible to create a cream cheese with lower fat content and with sensory attributes similar to the attributes in cream cheese with high fat content, by modification of production parameters
Descriptors:cream cheese: dairy product; fat content; flavor; homogenization pressure; microstructural properties; salt content; sensory properties; texture. Foods
Subject Codes:Foods
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry

227. Title:Evaluation of turbidity: Correlation between Kerstez turbidimeter and nephelometric turbidimeter
View Article: Food Chemistry. 71 (4). December, 2000. 563-566
CD Volume:326
Print Article: Pages: 563-566
Author(s):Collado Fernandez M Gonzalez Sanjose M L Pino Navarro R
Author Affiliation:Department of Biotechnology and Food Science, University of Burgos, Plaza Misael Banuelos s/n, 09001, Burgos
Language:English
Language of Summary:English (EN)
Abstract:Turbidity is a quality parameter that has an important role in food liquid acceptance. Cloudiness of beverages and covering liquid are a consequence of manufacture processes and storage conditions. Spanish legislation defines the covering liquid turbidity in canning by Kerstez turbidimeter units (KTU), which is a sensorial measure. It is necessary to find a correlation between sensorial and instrumental measurements. This work studied the relationship between KTU and nephelometric turbidimeter units (NTU) and established a mathematical model, which allowed the expression of the turbidity of liquid products in KTU from measurements in nephelometric turbidimeter units. This mathematical model corresponds to a non-linear simple correlation model (KTU/NTU). The best adjustment was a Reciprocal-Y model
Descriptors:Kerstez turbidimeter units: mathematical model; Reciprocal Y-model: mathematical model; Spanish legislation; beverages: beverage, cloudiness; food liquid acceptance; nephelometric turbidimeter units: mathematical model; turbidity. Models and Simulations (Computational Biology); Foods; Methods and Techniques
Subject Codes:Models and Simulations (Computational Biology); Foods; Methods and Techniques
ISSN:0308-8146
Year:2000
Journal Title:Food Chemistry

228. Title:Public-private alliances in biotechnology. Can they narrow the knowledge gaps between rich and poor?
View Article: Food Policy. 2000. 25 (4). 499-513
CD Volume:336
Print Article: Pages: 499-513
Author(s):Rausser G Simon L Ameden H

Author Affiliation:Giannini Foundation of Agricultural Economics, 101 Giannini Hall #3100, University of California at Berkeley, Berkeley, CA 94720-3100, USA
Document Editor:Pachico-D. Hertford-R. Janvry-A-de
Conference Title:Special issue: Assessing the impact of agricultural research on poverty alleviation
Language:English
Abstract:In the area of science and technology, the knowledge gap between rich and poor countries is wide and increasing. In the area of biotechnology research, a second gap has recently emerged between private life science companies and public research institutions. As a result, a gap is rapidly widening between cutting-edge research in the developed world and publicly sponsored research being undertaken in the developing world. An obvious strategy for narrowing this gap is to form public-private research alliances. To overcome intervening obstacles, public research institutions in the developing world need to adopt creative new approaches to the process of negotiating with their potential private partners. These approaches must focus on leveraging the complementarities and potential synergies between their knowledge assets and those of the private sector. Concurrently, institutional arrangements must be set in place that are geared toward managing the risks and dangers of greatest concern to their constituencies
Descriptors:biotechnology. research-support. private-sector. public-sector. partnerships. research-institutes
Subject Codes:WW000. AA500. EE110
Supplementary Info:26 ref
ISSN:0306-9192
Year:2000
Journal Title:Food Policy

229. Title:Screening for species-specific DNA families in Musa acuminata
View Article: Fruits (Paris) 2000. 55 (1). 3-15
CD Volume:318
Print Article: Pages: 3-15
Author(s):Baurens F C Noyer J L Lanaud C Lagoda P J L
Author Affiliation:Vitropic SA, ZAE les Avants, 34270 Saint-Mathieu-de-Treviers, France
Language:English
Language of Summary:french. spanish
Abstract:A method of targeting species-specific repetitive elements is proposed for cloning and subsequent development of molecular marker systems based on the polymerase chain reaction. Genomic libraries were constructed and screened by Southern hybridization. Species-specificity was estimated using a specificity index (Si) based on differences in intensities of hybridization signals. Four different M. acuminata subspecies, three different M. balbisiana type and one M. schizocarpa genomic libraries were constructed, characterized and screened for species-specific probes. The Si proved essential for discriminating species-specific from non-specific repetitive DNA fragments. The total repetitive DNA content of the Musa genome could be assessed. Several A genome repetitive elements could be identified and are described. Within the Eumusa section, M. acuminata species-specific DNA elements were identified as either short interspersed elements (SINEs) or copia-like interspersed sequences. The banana genome is composed of 77% repetitive elements and 23% single copy sequences. The strategy presented allows for identification of repetitive elements with copy numbers above 1000. These may be used to study the genomic

composition of complex banana polyploid cultivars by in situ hybridization
Descriptors:DNA. bananas. DNA-cloning. cultivars. genomes. polymerase-chain-reaction. repetitive-DNA. techniques. DNA-libraries. DNA-hybridization. nucleotide-sequences. molecular-genetics. genetic-markers. fruit-crops. biotechnology. plant-genetic-resources
Identifiers:in situ hybridization. Musa schizocarpa
Organism Descriptors:Musa. Musa-acuminata. Musa-balbisiana
Supplemental Descriptors:Musaceae. Zingiberales. monocotyledons. angiosperms. Spermatophyta. plants. Musa
Subject Codes:FF020. FF003. WW000
Supplementary Info:22 ref
ISSN:0248-1294
Year:2000
Journal Title:Fruits
Copyright:Copyright CAB International

230. Title:Molecular cloning and characterization of Japanese eel ovarian P450c17 (CYP17) cDNA
View Article: General and Comparative Endocrinology. 2000. 118 (1). 123-133
CD Volume:326
Print Article: Pages: 123-133
Author(s):Kazeto Y Ijiri S Todo T Adachi S Yamauchi K
Author Affiliation:Department of Biology, Faculty of Fisheries, Hokkaido University, 3-1-1 Minato-cho, Hakodate, Hokkaido 041-8611, Japan
Language:English
Abstract:A cDNA encoding Japanese eel (Anguilla japonica) ovarian cytochrome P-450c17 (steroid 17- alpha -monooxygenase) was isolated and sequenced. The cDNA encoded a protein of 510 amino acids that showed high homology to it's counterparts from rainbow trout (74% homology) and mammals (45-55% homology). The gene was expressed as a single transcript of 2.4 kb. Levels of this transcript increased during ovarian development. It is concluded that the enzyme activity does not correspond to changes in transcription of this gene
Descriptors:complementary-DNA. ovaries. cytochrome-P-450. oxygenases. genes. nucleotide-sequences. biotechnology
Organism Descriptors:Anguilla-japonica
Supplemental Descriptors:Anguilla. Anguillidae. Anguilliformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms
Subject Codes:LL240. LL250. MM300. LL600. WW000
Supplementary Info:37 ref
ISSN:0016-6480
Year:2000
Journal Title:General and Comparative Endocrinology
Copyright:Copyright CAB International

231. Title:Estrogen-induced vitellogenin mRNA and protein in sheepshead minnow (Cyprinodon variegatus)
View Article: Gen Comp Endocrinol 2000 Dec;120(3):300-13
CD Volume:326
Print Article: Pages: 300-313
Author(s):Bowman CJ Kroll KJ Hemmer MJ Folmar LC Denslow ND
Author Affiliation:Interdisciplinary Center for Biotechnology Research, University of Florida, Gainesville, Florida 32610, USA
Abstract:Many environmentally persistent xenobiotic chemicals appear to disrupt normal endocrine function by acting as ligands for endogenous steroid receptors, including the estrogen receptor. Xenobiotics that bind to the estrogen receptor may elicit several effects, one of which is

activating estrogen-responsive genes, such as vitellogenin (Vtg). Primers to vitellogenin mRNA have been used to amplify a portion of the coding sequence in sheepshead minnow (SHM) (Cyprinodon variegatus). Two Vtg cDNA fragments from SHM were isolated exhibiting 72% sequence homology and corresponding to the two Vtg genes identified in the mummichog, Fundulus heteroclitus. Using these Vtg cDNA fragments as sensitive genetic probes, we evaluated the initial estrogenic response of fish exposed to natural or anthropogenic chemicals. These probes were used to study in vivo gene induction in SHM exposed to 17beta-estradiol (E(2)) and ethinylestradiol (EE(2)) under controlled laboratory conditions. Hepatic Vtg mRNA was upregulated and plasma Vtg synthesis in estrogen-induced SHM was assessed. Two in vivo time-course experiments were conducted; a single injection of E(2) followed over 72 h and a double E(2) injection examined for 12 days. These two protocols provided evidence for differential hepatic Vtg mRNA regulation resulting from a single or a double injection. In a separate experiment using an aqueous flowthrough system, constant exposures to low doses of E(2) (200 ng/L) and EE(2) (100 ng/L) induced hepatic Vtg mRNA and plasma Vtg to levels comparable with the E(2) injections. Larger aqueous exposure doses (2000 ng/L E(2) or 1000 ng/L EE(2)) in the flowthrough experiment resulted in greater responses of hepatic Vtg mRNA and plasma Vtg at 7 days. Constant aqueous exposure to E(2) (2000 ng/L) or EE(2) (1000 ng/L) may thus be more effective than a single large-dose injection (5 mg/kg) to stimulate Vtg gene activation and synthesis

Descriptors:Amino Acid Sequence. Animal. Blotting, Northern. Cyprinidae. DNA Probes. DNA, Complementary. Estradiol. Estrogens. Ethinyl Estradiol. Gene Expression Regulation. Kinetics. Liver. Male. Molecular Sequence Data. RNA, Messenger. Support, U.S. Gov't, Non-P.H.S.. Vitellogenin

Geographic Locator:UNITED STATES

ISSN:0016-6480
Year:2000
Journal Title:General and Comparative Endocrinology

232. Title:Molecular cloning and characterization of alternatively spliced transcripts of the turkey pituitary adenylate cyclase-activating polypeptide

View Article: General and Comparative Endocrinology. 2000. 120 (3). 326-335
CD Volume:326
Print Article: Pages: 326-335

Author(s):Yoo SeungJun You SeungKwon Kim HyungGee Kim SungChan Choi YunJaie El Halawani M Farris J Foster D N
Author Variant:Yoo-S-J. You-S-W. Kim-H-G. Kim-S-C. Choi-Y-J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744, South Korea, Korea Republic

Language:English

Abstract:Pituitary adenylate cyclase-activating polypeptide (PACAP) is a neuropeptide that has been shown previously to increase the release of somatotropin and prolactin in mammals. In the present work, reverse-transcription PCR and rapid amplification of cDNA ends was used to isolate a turkey PACAP cDNA and its associated PACAP-related peptide (PRP). In comparison with a range of known homologues the deduced amino acid sequences of turkey PACAP and PRP showed 87-97 and 52-63% similarity respectively. Using northern blotting 2 major transcripts, of 1.3 and 3.0 kb, of PACAP were detected. The highest levels of PACAP mRNA were detected in the hypothalamus, the cerebrum and the cerebellum; most other tissues had relatively low levels of PACAP mRNA. Two isoforms of PACAP were generated by alternative splicing; the

smaller form was expressed in the hypothalamus during early development and decreased significantly during later stages
Descriptors:genes. neuropeptides. nucleotide-sequences. complementary-DNA. messenger-RNA. brain. cerebellum. hypothalamus. poultry
Organism Descriptors:turkeys
Supplemental Descriptors:Meleagris. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry
Subject Codes:LL240. LL600. WW000
Supplementary Info:39 ref
ISSN:0016-6480
Year:2000
Journal Title:General and Comparative Endocrinology
Copyright:Copyright CAB International

233. Title:Extensive genetic interactions between PRP8 and PRP17/CDC40, two yeast genes involved in pre-mRNA splicing and cell cycle progression
View Article: Genetics 2000 Jan;154(1):61-71
CD Volume:302
Print Article: Pages: 61-71
Author(s):Ben Yehuda S Russell CS Dix I Beggs JD Kupiec M
Author Affiliation:Department of Molecular Microbiology and Biotechnology, Tel Aviv University, Ramat Aviv 69978, Israel
Abstract:Biochemical and genetic experiments have shown that the PRP17 gene of the yeast Saccharomyces cerevisiae encodes a protein that plays a role during the second catalytic step of the splicing reaction. It was found recently that PRP17 is identical to the cell division cycle CDC40 gene. cdc40 mutants arrest at the restrictive temperature after the completion of DNA replication. Although the PRP17/CDC40 gene product is essential only at elevated temperatures, splicing intermediates accumulate in prp17 mutants even at the permissive temperature. In this report we describe extensive genetic interactions between PRP17/CDC40 and the PRP8 gene. PRP8 encodes a highly conserved U5 snRNP protein required for spliceosome assembly and for both catalytic steps of the splicing reaction. We show that mutations in the PRP8 gene are able to suppress the temperature-sensitive growth phenotype and the splicing defect conferred by the absence of the Prp17 protein. In addition, these mutations are capable of suppressing certain alterations in the conserved PyAG trinucleotide at the 3' splice junction, as detected by an ACT1-CUP1 splicing reporter system. Moreover, other PRP8 alleles exhibit synthetic lethality with the absence of Prp17p and show a reduced ability to splice an intron bearing an altered 3' splice junction. On the basis of these findings, we propose a model for the mode of interaction between the Prp8 and Prp17 proteins during the second catalytic step of the splicing reaction
Descriptors:Alleles. Base Sequence. Cell Cycle. Cell Cycle Proteins. Dosage Compensation (Genetics). Fungal Proteins. *Genes, Fungal. Mutagenesis. Phenotype. RNA. RNA Precursors. *RNA Splicing. RNA, Messenger. Saccharomyces cerevisiae. Support, Non-U.S. Gov't
Geographic Locator:UNITED STATES
ISSN:0016-6731
Year:2000
Journal Title:Genetics

234. Title:Ancient allelism at the cytosolic chaperonin- alpha -encoding gene of the zebrafish
View Article: Genetics. 2000. 154 (1). 311-322
CD Volume:302
Print Article: Pages: 311-322
Author(s):Takami K Figueroa F Mayer W E Klein J

Author Affiliation:Max-Planck-Institut fur Biologie, Abteilung Immungenetik, D-72076 Tubingen, Germany
Language:English
Abstract:The T-complex protein 1 (TCP1) gene codes for the cytosolic chaperonin CCT- alpha subunit of the group II chaperonins. The gene was first described in house mice, in which it is closely linked to the T locus at a distance of approx equal to 11 cM from the MHC. In the present work, the zebrafish (Danio rerio) TCP1 gene was isolated, sequenced and mapped. In zebrafish the T homologue is linked to the class I Mhc loci, the TCP1 locus segregated independently of both the T and the Mhc loci. Despite its conservation between species, the zebrafish TCP1 locus was highly polymorphic. A sample of 15 individuals and a cDNA library was screened; 12 alleles were found and some of the allelic pairs were found to differ by up to 9 nucleotides in a 275-bp stretch of sequence. The substitutions occurred in translated and untranslated regions but in the former they occurred predominantly at synonymous codon sites. Phylogenetically, the alleles fell into 2 groups distinguished by the presence or absence of a 10-bp insertion/deletion in the 3' untranslated region. It is suggested that the 2 groups diverged as long as 3.5 million years ago, and that the polymorphic differences accumulated by genetic drift in geographically isolated populations
Descriptors:genes. alleles. complementary-DNA. genetic-drift. genetic-polymorphism. gene-mapping. nucleotide-sequences. chaperonins. biotechnology
Organism Descriptors:Danio-rerio
Supplemental Descriptors:Danio. Cyprinidae. Cypriniformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms
Subject Codes:MM120. MM300. LL240. WW000
Supplementary Info:44 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

235. Title:A chromosome-based model for estimating the number of conserved segments between pairs of species from comparative genetic maps
View Article: Genetics. 2000. 154 (1). 323-332
CD Volume:302
Print Article: Pages: 323-332
Author(s):Waddington D Springbett A J Burt D W
Author Affiliation:Roslin Institute (Edinburgh), Roslin, Midlothian EH25 9PS, Scotland, UK
Language:English
Abstract:When the maps produced during comparative genetic mapping of 2 species give the positions of genes (or any set of orthologous DNA sequences) on chromosomes, syntenic blocks of 1 or more genes may be identified and used, with appropriate models, to estimate the number of chromosomal segments conserved between the 2 species. In the present work a model for the distribution of the lengths of unobserved segments on each chromosome is proposed that allows for widely differing chromosome lengths. The model uses as data either the counts of genes in a syntenic block or the distance between extreme members of a block, or both. The parameters of the proposed segment length distribution, estimated by maximum likelihood, give predictions of the number of conserved segments per chromosome. The model is applied to data from 2 comparative maps for fowls, 1 with man and 1 with mice
Descriptors:chromosomes. gene-mapping. genes. genomes. mathematical-models. biotechnology. poultry
Organism Descriptors:fowls

Supplemental Descriptors:Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals
Subject Codes:LL240. ZZ100. WW000
Supplementary Info:31 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

236. Title:A genetic test to determine the origin of maternal transmission ratio distortion: meiotic drive at the mouse Om locus
View Article: Genetics. 2000. 154 (1). 333-342
CD Volume:302
Print Article: Pages: 333-342
Author(s):Villena F P M de Casa Esperon E de la Briscoe T L Sapienza C
Author Variant:de-Villena-F-P-M. de-la-Casa-Esperon-E
Author Affiliation:Fels Institute for Cancer Research and Molecular Biology, Temple University School of Medicine, Philadelphia, Pennsylvania 19140, USA
Language:English
Abstract:It has been shown previously that the progeny of crosses between heterozygous female and C57BL/6 male mice show transmission ratio distortion at the ovum mutant (Om) locus on chromosome 11. In the present work, evidence was obtained that the distortion maps to a single locus on chromosome 11, closely linked to Om, and that gene conversion is not implicated in the origin of this phenomenon. To further investigate the origin of the transmission ratio distortion a test was performed that used the effect of recombination on maternal meiotic drive. The genetic test discriminated between unequal segregation of alleles during meiosis and lethality, based on the analysis of genotype at the distorted locus and the centromere of the same chromosome. This test was used to determine the cause of the transmission ratio distortion observed at the Om locus. It is concluded that transmission ratio distortion at Om is due to unequal segregation of alleles to the polar body at the second meiotic division. Since the presence of segregation distortion at Om also depends on the genotype of the sire, it is concluded that spermatozoa can influence segregation of maternal chromosomes to the second polar body
Descriptors:transmission. alleles. chromosomes. crosses. genotypes. meiosis. gene-mapping. progeny. recombination. spermatozoa. sires. segregation-distortion. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000
Supplementary Info:2 pp. of ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

237. Title:Sex-of-offspring-specific transmission ratio distortion on mouse chromosome X
View Article: Genetics. 2000. 154 (1). 343-350
CD Volume:302
Print Article: Pages: 343-350
Author(s):Casa Esperon E de la Villena F P M de Verner A E Briscoe T L Malette J M Rosa M Jin WenHui Sapienza C
Author Variant:Jin-W-H. de-la-Casa-Esperon-E. de-Villena-F-P-M

Author Affiliation:Fels Institute for Cancer Research and Molecular Biology, Temple University School of Medicine, Philadelphia, Pennsylvania 19140, USA
Language:English
Abstract:During studies of the DDK syndrome, sex ratio distortion in favour of males was observed among the offspring of F1 backcrosses between the C57BL/6 and DDK strains. Significant and reproducible transmission ratio distortion in favour of the inheritance of DDK alleles at loci on the X chromosome among female offspring but not among male offspring in (C57BL/6xDDK)F1xC57BL/6 and (C57BL/6-PgklaxDDK)F1xC57BL/6 backcrosses was also observed. The transmission ratio distortion was maximal at DXMit210 in the central region of the X chromosome and decreased progressively at proximal and distal loci, in a manner consistent with the predictions of a single distorted locus model. DXMit210 is closely linked to 2 distortion-controlling loci (Dcsx1 and Dcsx2) described previously in interspecific backcrosses. It is suggested that the female-offspring-specific transmission ratio distortion is the result of the death of embryos with particular genotypes. The previous suggestion that the transmission ratio distortion observed on the X chromosome in interspecific backcrosses is the result of loss of embryos was confirmed
Descriptors:chromosomes. sex-differences. segregation-distortion. alleles. embryo-mortality. inheritance. sex-ratio. X-chromosome. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000. LL250
Supplementary Info:31 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

238. Title:Male-offspring-specific, haplotype-dependent, nonrandom cosegregation of alleles at loci on two mouse chromosomes
View Article: Genetics. 2000. 154 (1). 351-356
CD Volume:302
Print Article: Pages: 351-356
Author(s):Villena F P M de Casa Esperon E de la Briscoe T L Malette J M Sapienza C
Author Variant:de-Villena-F-P-M. de-la-Casa-Esperon-E
Author Affiliation:Fels Institute for Cancer Research and Molecular Biology, Temple University School of Medicine, Philadelphia, Pennsylvania 19140, USA
Language:English
Abstract:F1 backcrosses involving the DDK and C57BL/6 inbred mouse strains show transmission ratio distortion at loci on 2 chromosomes, 11 and X. Transmission ratio distortion on the X chromosome is restricted to female offspring while that on chromosome 11 is present in offspring of both sexes. In the present work, the effects of inheritance of alleles at loci on 1 chromosome on inheritance of alleles on the other was investigated. A strong non-random association between the inheritance of alleles at loci on both chromosomes was found among male offspring; independent assortment occurred among female offspring. Evidence was obtained that the mechanism by which this phenomenon occurs involves preferential cosegregation of non-parental chromatids of both chromosomes at the second meiotic division, after the ova has been fertilized by a C57BL/6 spermatozoon bearing a Y chromosome. It is concluded that these observations confirm the influence of spermatozoa

on the segregation of chromatids during female meiosis and that a locus or loci on the Y chromosome are involved in this instance of meiotic drive
Descriptors:alleles. chromosomes. inheritance. meiosis. ova. segregation-distortion. spermatozoa. strains. transmission. sex-chromosomes. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. LL250. WW000
Supplementary Info:22 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

239. Title:Cytologically integrated physical restriction fragment length polymorphism maps for the barley genome based on translocation breakpoints
View Article: Genetics. 2000. 154 (1). 397-412
CD Volume:302
Print Article: Pages: 397-412
Author(s):Kunzel G Korzun L Meister A
Author Affiliation:Institut fur Pflanzengenetik und Kulturpflanzenforschung (IPK), 06466 Gatersleben, Germany
Language:English
Abstract:Microdissected translocation chromosomes were used for PCR with sequence-tagged site primers derived from >300 genetically mapped RFLP probes. The positions of 240 translocation breakpoints were integrated as physical landmarks into linkage maps of the 7 barley chromosomes. This strategy proved to be highly efficient in relating physical to genetic distances. A very heterogeneous distribution of recombination rates was found along individual chromosomes. Recombination was mainly confined to a few relatively small areas spaced by large segments in which recombination is severely suppressed. The regions of highest recombination frequency (less than or equal to 1 Mb/cM) correspond to only 4.9% of the total barley genome and harbored 47.3% of the 429 markers of the studied RFLP map. The results for barley correspond well with those obtained by deletion mapping in wheat. This indicates that chromosomal regions characterized by similar recombination frequencies and marker densities are highly conserved between the genomes of barley and wheat
Descriptors:barley. genomes. restriction-fragment-length-polymorphism. chromosome-translocation. linkage. gene-mapping. polymerase-chain-reaction. wheat. cereals. biotechnology
Organism Descriptors:Hordeum-vulgare. Triticum-aestivum. Triticum
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum
Subject Codes:FF020. WW000
Supplementary Info:3 pp. of ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

240. Title:Quantitative trait loci and candidate gene mapping of bud set and bud flush in Populus
View Article: Genetics. 2000. 154 (2). 837-845
CD Volume:303

Print Article: Pages: 837-845
Author(s):Frewen B E Chen T H H Howe G T Davis J Rohde A Boerjan W Bradshaw H D Jr
Author Affiliation:College of Forest Resources, Box 354115, 3501 NE 41st St., University of Washington, Seattle, WA 98195, USA
Language:English
Abstract:The genetic control of bud phenology in hybrid poplar was studied by mapping quantitative trait loci (QTL) affecting the timing of autumn bud set and spring bud flush. The founders of the mapping pedigree were collected from widely separated latitudes to maximize segregating variation for dormancy-related traits in the F2 generation of a cross involving a female Populus trichocarpa [P. balsamifera subsp. trichocarpa] parent from Washington State (48 deg N) and a male P. deltoides parent from Texas (31 deg N). Bud set and bud flush timing were measured on the F2 generation in a replicated clonal field trial conducted at Corvallis, Oregon. Using a linkage map constructed of amplified fragment length polymorphism and microsatellite markers, three QTL controlling bud set and six QTL controlling bud flush were detected. Additionally, five candidate genes believed to be involved in perception of photoperiod (PHYB1 and PHYB2) or transduction of abscisic acid response signals (ABI1B, ABI1D and ABI3) were placed on the QTL map. PHYB2 and ABI1B were coincident with QTL affecting bud set and bud flush
Descriptors:gene-mapping. poplars. abscisic-acid. genes. linkage. phenology. photoperiod. buds. quantitative-trait-loci. microsatellites. plant-growth-regulators. interspecific-hybridization. forest-trees. broadleaves. biotechnology. growth-inhibitors
Geographic Locator:USA. Texas. Washington
Identifiers:Populus balsamifera subsp. trichocarpa. amplified fragment length polymorphism
Organism Descriptors:Populus-deltoides. Populus-interamericana
Supplemental Descriptors:Populus. Salicaceae. Salicales. dicotyledons. angiosperms. Spermatophyta. plants. North-America. America. Developed-Countries. OECD-Countries. Southern-Plains-States-of-USA. West-South-Central-States-of-USA. Southern-States-of-USA. USA. Great-Plains-States-of-USA. Gulf-States-of-USA. Southwestern-States-of-USA. Pacific-Northwest-States-of-USA. Pacific-States-of-USA. Western-States-of-USA
Subject Codes:KK100. FF060. FF020. WW000
Supplementary Info:28 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

241. Title:Estimation of population parameters and recombination rates from single nucleotide polymorphisms
View Article: Genetics. 2000. 154 (2). 931-942
CD Volume:303
Print Article: Pages: 931-942
Author(s):Nielsen R
Author Affiliation:Department of Organismic and Evolutionary Biology, Harvard University, 288 Biology Laboratories, 16 Divinity Avenue, Cambridge, MA 02138, USA
Language:English
Abstract:Some general likelihood and Bayesian methods for analysing single nucleotide polymorphisms (SNPs) are presented. First, an efficient method for estimating demographic parameters from SNPs in linkage equilibrium is derived. The method is applied in the estimation of

growth rates of a human population based on 37 SNP loci. It is demonstrated how ascertainment biases, due to biased sampling of loci, can be avoided, at least in some cases, by appropriate conditioning when calculating the likelihood function. Second, a Markov chain Monte Carlo (MCMC) method for analysing linked SNPs is developed. This method can be used for Bayesian and likelihood inference on linked SNPs. The utility of the method is illustrated by estimating recombination rates in a human data set containing 17 SNPs and 60 individuals. Both methods are based on assumptions of low mutation rates
Descriptors:recombination. population-genetics. mutations. techniques. Bayesian-theory. genetic-polymorphism. linkage. statistical-analysis. biotechnology
Subject Codes:ZZ100. WW000. LL240
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

242. Title:Bipartite structure of the SGS1 DNA helicase in Saccharomyces cerevisiae
View Article: Genetics 2000 Mar;154(3):1101-14
CD Volume:303
Print Article: Pages: 1101-1114
Author(s):Mullen JR Kaliraman V Brill SJ
Author Affiliation:Department of Molecular Biology and Biochemistry, Center for Advanced Biotechnology and Medicine, Rutgers University, Piscataway, New Jersey 08855, USA
Abstract:SGS1 in yeast encodes a DNA helicase with homology to the human BLM and WRN proteins. This group of proteins is characterized by a highly conserved DNA helicase domain homologous to Escherichia coli RecQ and a large N-terminal domain of unknown function. To determine the role of these domains in SGS1 function, we constructed a series of truncation and helicase-defective (-hd) alleles and examined their ability to complement several sgs1 phenotypes. Certain SGS1 alleles showed distinct phenotypes: sgs1-hd failed to complement the MMS hypersensitivity and hyper-recombination phenotypes, but partially complemented the slow-growth suppression of top3 sgs1 strains and the top1 sgs1 growth defect. Unexpectedly, an allele that encodes the amino terminus alone showed essentially complete complementation of the hyper-recombination and top1 sgs1 defects. In contrast, an allele encoding the helicase domain alone was unable to complement any sgs1 phenotype. Small truncations of the N terminus resulted in hyper-recombination and slow-growth phenotypes in excess of the null allele. These hypermorphic phenotypes could be relieved by deleting more of the N terminus, or in some cases, by a point mutation in the helicase domain. Intragenic complementation experiments demonstrate that both the amino terminus and the DNA helicase are required for full SGS1 function. We conclude that the amino terminus of Sgs1 has an essential role in SGS1 function, distinct from that of the DNA helicase, with which it genetically interacts
Descriptors:Binding Sites. DNA Helicases. DNA Topoisomerase. Genetic Complementation Test. Methyl Methanesulfonate. Mutagenesis. Mutagens. Phenotype. *Protein Conformation. Recombination, Genetic. Saccharomyces cerevisiae. Structure-Activity Relationship. Support, Non-U.S. Gov't. Support, U.S. Gov't, P.H.S.
Geographic Locator:UNITED STATES
ISSN:0016-6731
Year:2000
Journal Title:Genetics

243. Title:A detailed linkage map of Medaka, Oryzias latipes: comparative genomics and genome evolution
View Article: Genetics. 2000. 154 (4). 1773-1784
CD Volume:303
Print Article: Pages: 1773-1784
Author(s):Naruse K Fukamachi S Mitani H Kondo M Matsuoka T Kondo S Hanamura N Morita Y Hasegawa K Nishigaki R Shimada A Wada H Kusakabe T Suzuki N Kinoshita M Kanamori A Terado T Kimura H Nonaka M Shima A
Author Affiliation:Department of Biological Sciences, Graduate School of Science, University of Tokyo, Bunkyo-ku 7-3-1, Tokyo 113-0033, Japan
Language:English
Abstract:We mapped 633 markers (488 amplified fragment length polymorphisms (AFLPs), 28 random amplified polymorphic DNA markers (RAPDs), 34 internal repeat sequences (IRSs), 75 expressed sequence tags (ESTs), 4 sequence tagged sites (STSs), and 4 phenotypic markers) for the medaka (Oryzias latipes), a teleost fish of the order Beloniformes. Linkage was determined using a reference typing DNA panel from 39 cell lines derived from backcross progeny. This panel provided unlimited DNA for the accumulation of mapping data. The total map length of Medaka was 1354.5 cM and 24 linkage groups were detected, corresponding to the haploid chromosome number of the organism. 13-49 markers for each linkage group were obtained. Conserved synteny between medaka and zebrafish was observed for 2 independent linkage groups. Unlike zebrafish, however, the medaka linkage map showed obvious restriction of recombination on the linkage group containing the male-determining region (Y) locus compared to the autosomal chromosomes
Descriptors:genomes. gene-mapping. genetic-markers. chromosomes. random-amplified-polymorphic-DNA. linkage. biotechnology
Organism Descriptors:Oryzias-latipes
Supplemental Descriptors:Oryzias. Oryziatidae. Cyprinodontiformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms
Subject Codes:LL240. WW000. MM300
Supplementary Info:43 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

244. Title:The origin of the domestic pig: independent domestication and subsequent introgression
View Article: Genetics. 2000. 154 (4). 1785-1791
CD Volume:303
Print Article: Pages: 1785-1791
Author(s):Giuffra E Kijas J M H Amarger V Carlborg O Jeon J T Andersson L
Author Affiliation:Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala Biomedical Centre, Box 597, S-751 24 Uppsala, Sweden
Language:English
Abstract:The domestic pig originates from the Eurasian wild boar (Sus scrofa). We have sequenced mitochondrial DNA and nuclear genes (melanocortin receptor 1, tyrosinase and glucosephosphate isomerase pseudogene) from wild and domestic pigs from Asia and Europe. Clear evidence was obtained for domestication to have occurred independently from wild boar subspecies in Europe and Asia. The time since divergence of the ancestral forms was estimated at approx equal to 500 000 years, well before domestication approx equal to 9000 years ago. Historical records indicate that Asian pigs were introduced into Europe during the

18th and early 19th centuries. We found molecular evidence for this introgression and the data indicated a hybrid origin of some major "European" pig breeds. The nucleotide sequences reported have been deposited with the GenBank database with the accession numbers AF181958-AF181964
Descriptors:domestication. introgression. nucleotide-sequences. genes. genetic-diversity. genetics. mitochondrial-DNA. pig-breeds. wild-pigs. receptors. pseudogenes. glucose-6-phosphate-isomerase. oxygenases. biotechnology
Identifiers:melanocortin
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. WW000
Supplementary Info:32 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

245. Title:Paramutation alters regulatory control of the maize pl locus
View Article: Genetics. 2000. 154 (4). 1827-1838
CD Volume:303
Print Article: Pages: 1827-1838
Author(s):Hollick J B Patterson G I Asmundsson I M Chandler V L
Author Affiliation:Institute of Molecular Biology, University of Oregon, Eugene, Oregon 97403-1229, USA
Language:English
Abstract:The maize purple plant (pl) locus encodes a transcription factor required for anthocyanin pigment synthesis in vegetative and floral tissues. The strongly expressed Pl-Rhoades (Pl-Rh) allele is unstable, spontaneously changing to weaker expression states (Pl') at low frequencies and exclusively changing to Pl' in Pl'/Pl-Rh heterozygotes. The weakly expressed Pl' state is mitotically and meiotically stable, yet reversible. This type of allele-dependent, heritable alteration of gene control is called paramutation. Expression studies herein demonstrate that visible differences in anthocyanin pigment levels mirror pl RNA abundance and that pl paramutation is associated with reduced transcription of the pl gene. This transcriptional alteration is accompanied by acquisition of light-dependent regulation. Restriction endonuclease mapping indicates that these changes in pl gene regulation are not associated with detectable DNA alterations or with extensive changes in cytosine methylation patterns. Genetic tests show that Pl-Blotched (Pl-Bh), a structurally similar pl allele encoding an identical pl RNA and PL protein, does not participate in pl paramutation. This result suggests that if cis-acting sequences are required for pl paramutation they are distinct from the protein coding and immediately adjacent regions. A model is discussed in which pl paramutation results in heritable changes of chromatin structure that fundamentally alter regulatory interactions occurring during plant development
Descriptors:maize. plant-development. genes. anthocyanins. transcription-factors. gene-expression. plant-pigments. alleles. mutations. genetic-models. cereals. biotechnology
Organism Descriptors:Zea-mays
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060. FF020. WW000
Supplementary Info:47 ref

ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

246. Title:Analysis of chromosomal rearrangements induced by postmeiotic mutagenesis with ethylnitrosourea in zebrafish
View Article: Genetics. 2000. 155 (1). 261-272
CD Volume:303
Print Article: Pages: 261-272
Author(s):Imai Y Feldman B Schier A F Talbot W S
Author Affiliation:Department of Developmental Biology, Beckman Center, Stanford University School of Medicine, Stanford, California 94305-5329, USA
Language:English
Abstract:Here we report the identification and analysis of five mutations induced in zebrafish by postmeiotic N-ethyl-N-nitrosourea ENU treatment. One mutation, snailhouse Stanford 1 (snhst1), is a translocation involving linkage group (LG) 11 and LG 14. The other four mutations, one-eyed pinhead Stanford 2 (oepst2), knypek Stanford 3 (knyst3), Stanford 4 an unnamed deletion on linkage group 13 (Df(LG 13)st4), and cyclops Stanford 5 (cycst5), are deletions on linkage groups 10, 14, 13 and 12 respectively, ranging in size from less than 3 cM to greater than 20 cM. These results show that germ cell stage is an important determinant of the type of mutations induced. The induction of chromosomal rearrangements may account for the elevated frequency of specific-locus mutations observed after treatment of postmeiotic gametes with ENU
Descriptors:mutagenesis. deletions. gametes. gene-mapping. germ-cells. mutations. N-ethyl-N-nitrosourea. chromosome-translocation. biotechnology
Organism Descriptors:Danio-rerio
Supplemental Descriptors:Danio. Cyprinidae. Cypriniformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms
Subject Codes:LL240. WW000
Supplementary Info:60 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

247. Title:Evidence for recent invasion of the medaka fish genome by the Tol2 transposable element
View Article: Genetics. 2000. 155 (1). 273-281
CD Volume:303
Print Article: Pages: 273-281
Author(s):Koga A Shimada A Shima A Sakaizumi M Tachida H Hori H
Author Affiliation:Division of Biological Sciences, Graduate School of Science, Nagoya University, Nagoya 464-8602, Japan
Language:English
Abstract:Transposable element from Oryzias latipes 2 (Tol2) is a transposable element of the terminal-inverted-repeat class, residing in the genome of the medaka fish Oryzias latipes. The genus Oryzias contains more than 10 species for which phylogenetic relationships have previously been estimated. To infer the history of Tol2 in this genus we performed genomic Southern blots and PCR analyses of 10 of the species. It was revealed that Tol2 occurs in 2 of the 10 species (O. curvinotus and O. latipes) and that the length and the restriction map structure of Tol2 are identical in the two cases. Sequencing analysis revealed an extremely low level of divergence compared with that in a nuclear gene.

These results suggest recent incorporation of Tol2 into one or both of the two species, implying horizontal transfer of Tol2 from one species to the other or into them both from a common source
Descriptors:genomes. genes. transposable-elements. nucleotide-sequences. phylogenetics. biotechnology
Organism Descriptors:Oryzias-latipes
Supplemental Descriptors:Oryzias. Oryziatidae. Cyprinodontiformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms
Subject Codes:MM120. MM300. LL240. WW000
Supplementary Info:53 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

248. Title:Heritability of the maternal meiotic drive system linked to Om and high-resolution mapping of the responder locus in mouse
View Article: Genetics. 2000. 155 (1). 283-289
CD Volume:303
Print Article: Pages: 283-289
Author(s):Villena F P M de Casa Esperon E de la Williams J W Malette J M Rosa M Sapienza C
Author Variant:de-Villena-F-P-M. de-la-Casa-Esperon-E
Author Affiliation:Fels Institute for Cancer Research and Molecular Biology, Temple University School of Medicine, Philadelphia, Pennsylvania 19140, USA
Language:English
Abstract:Matings between (C57BL/6xDDK)F1 females and C57BL/6 males result in a significant excess of offspring inheriting maternal DDK alleles in the central region of mouse chromosome 11 due to meiotic drive at the second meiotic division. We have shown previously that the locus subject to selection is in the vicinity of D11Mit66, a marker closely linked to the ovum mutant (Om) locus that controls the preimplantation embryonic lethal phenotype known as the "DDK syndrome." We have also shown that observation of meiotic drive in this system depends upon the genotype of the sire. Here we show that females that are heterozygous at Om retain the meiotic drive phenotype and define a 0.32-cM candidate interval for the Responder locus in this drive system. Analysis of the inheritance of alleles at Om among the offspring of F1 intercrosses indicates that the effect of the sire is determined by the sperm genotype at Om or a locus linked to Om
Descriptors:alleles. chromosomes. genotypes. inheritance. phenotypes. spermatozoa. meiotic-drive. genes. gene-mapping. segregation-distortion. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000
Supplementary Info:38 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

249. Title:Genomic, transcriptional and mutational analysis of the mouse microphthalmia locus
View Article: Genetics. 2000. 155 (1). 291-300
CD Volume:303

Print Article: Pages: 291-300
Author(s):Hallsson J H Favor J Hodgkinson C Glaser T Lamoreux M L Magnusdottir R Gunnarsson G J Sweet H O Copeland N G Jenkins N A Steingrimsson E
Author Affiliation:Department of Biochemistry and Molecular Biology, School of Medicine, University of Iceland, 101 Reykjavik, Iceland
Language:English
Abstract:Mouse microphthalmia transcription factor (Mitf) mutations affect the development of four cell types: melanocytes, mast cells, osteoclasts and pigmented epithelial cells of the eye. The mutations are phenotypically diverse and can be arranged in an allelic series. Here we report the complete exon/intron structure of the mouse Mitf gene and show it to be similar to the human gene. We also found that the mouse gene is transcriptionally complex and is capable of generating at least 13 Mitf isoforms. Some of these isoforms are missing important functional domains of the protein, suggesting that they might play an inhibitory role in Mitf function and signal transduction. We determined the molecular basis for 6 microphthalmia mutations. Two of the mutations are reported for the first time here (Mitfmi-enu198 and Mitfmi-x39), while the others (Mitfmi-ws, Mitfmi-bws, Mitfmi-ew, and Mitfmi-di) have been described but the molecular basis for the mutation not determined. When analyzed in terms of the genomic and transcriptional data presented here, it is apparent that these mutations result from RNA processing or transcriptional defects. Three of the mutations (Mitfmi-x39, Mitfmi-bws, and Mitfmi-ws) produce proteins that are missing important functional domains of the protein identified in in vitro studies, further confirming a biological role for these domains in the whole animal
Descriptors:genes. microphthalmia. mutations. transcription-factors. exons. introns. nucleotide-sequences. biotechnology
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000
Supplementary Info:40 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

250. Title:Complete repopulation of mouse mitochondrial DNA-less cells with rat mitochondrial DNA restores mitochondrial translation but not mitochondrial respiratory function
View Article: Genetics. 2000. 155 (1). 301-307
CD Volume:303
Print Article: Pages: 301-307
Author(s):Yamaoka M Isobe K Shitara H Yonekawa H Miyabayashi S Hayashi J I
Author Affiliation:Institute of Biological Sciences, University of Tsukuba, Ibaraki 305-8572, Japan
Language:English
Abstract:By the fusion of mtDNA-less (rho 0) cells of Mus musculus domesticus with platelets from different species, mtDNA repopulated cell hybrids (cybrids) were obtained for finding the mtDNA species that could induce mitochondrial abnormalities. Expression of mitochondrial dysfunction might be expected in these cybrids due to incompatibility between nuclear and mitochondrial genomes from different species. The results showed that mouse rho 0 cells could receive mtDNA from a different mouse species, M. spretus, or even mtDNA from rats, Rattus norvegicus, and that the introduced rat mtDNA, but not M. spretus mtDNA, caused mitochondrial dysfunction, even though rat mtDNA could restore normal

mitochondrial translation in the cybrids. Considering that mitochondrial respiratory complexes consist of nuclear DNA- and mtDNA-coded polypeptides, these observations suggest that the nuclear and mitochondrial interactions required for replication, transcription and translation of introduced rat mtDNA must be less stringently controlled than those required for formation of normal respiratory complexes. As no procedure for introduction of mutagenized mouse mtDNA into living cells has yet been established, these findings provide important insights into generating mtDNA-knockout mice
Descriptors:mitochondrial-DNA. transgenics. respiration. biotechnology
Organism Descriptors:rats. mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL240. WW000. LL600
Supplementary Info:25 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

251. Title:Comparative genetics of nucleotide binding site-leucine rich repeat resistance gene homologues in the genomes of two dicotyledons: tomato and Arabidopsis
View Article: Genetics. 2000. 155 (1). 309-322
CD Volume:303
Print Article: Pages: 309-322
Author(s):Pan QiLin Liu YongSheng Budai Hadrian O Sela M Carmel Goren L Zamir D Fluhr R
Author Variant:Pan-Q-L. Liu-Y-S
Author Affiliation:Department of Plant Science, Weizmann Institute of Science, Rehovot 76100, Israel
Language:English
Abstract:The presence of a single resistance (R) gene allele can determine plant disease resistance. The protein products of such genes may act as receptors that specifically interact with pathogen-derived factors. Most functionally defined R-genes are of the nucleotide binding site-leucine rich repeat (NBS-LRR) supergene family and are present as large multigene families. The specificity of R-gene interactions together with the robustness of plant-pathogen interactions raises the question of their gene number and diversity in the genome. Genomic sequences from tomato showing significant homology to genes conferring race-specific resistance to pathogens were identified by systematically "scanning" the genome using a variety of primer pairs based on ubiquitous NBS motifs. Over 70 sequences were isolated and 10% are putative pseudogenes. Mapping of the amplified sequences on the tomato genetic map revealed their organization as mixed clusters of R-gene homologues that showed in many cases linkage to genetically characterized tomato resistance loci. Interspecific examination within Lycopersicon showed the existence of a null allele. Consideration of the tomato and potato comparative genetic maps unveiled conserved syntenic positions of R-gene homologues. Phylogenetic clustering of R-gene homologues within tomato and other Solanaceae family members was observed but not with R-gene homologues from Arabidopsis thaliana. Our data indicate remarkably rapid evolution of R-gene homologues during diversification of plant families
Descriptors:molecular-genetics. genomes. disease-resistance. diversification. genes. linkage. gene-mapping. plant-pathogens. phylogenetics. plant-diseases. evolution. biotechnology. plant-pathology
Organism Descriptors:Arabidopsis-thaliana. Lycopersicon. Solanaceae

Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Solanaceae. Solanales
Subject Codes:FF003. FF020. HH600. FF610. WW000
Supplementary Info:88 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

252. Title:The developmental expression of the maize regulatory gene Hopi determines germination-dependent anthocyanin accumulation
View Article: Genetics. 2000. 155 (1). 323-336
CD Volume:303
Print Article: Pages: 323-336
Author(s):Petroni K Cominelli E Consonni G Gusmaroli G Gavazzi G Tonelli C
Author Affiliation:Dipartimento di Genetica e di Biologia dei Microrganismi, Universita degli Studi di Milano, 20133 Milan, Italy
Language:English
Abstract:The Hopi gene is a member of the maize r1 gene family. By genetic and molecular analyses we report that Hopi consists of a single gene residing on chromosome 10 approx equal to 4.5 cM distal to r1. Hopi conditions anthocyanin deposition in aleurone, scutellum, pericarp, root, mesocotyl, leaves, and anthers, thus representing one of the broadest specifications of pigmentation pattern reported to date of all the r1 genes. A unique feature of the Hopi gene is that seeds are completely devoid of pigment at maturity but show a photoinducible germination-dependent anthocyanin accumulation in aleurone and scutellum. Our analysis has shown that the Hopi transcript is not present in scutellum of developing seeds but is induced only upon germination and that the simultaneous presence of both C1 and Hopi mRNAs is necessary to achieve A1 activation in scutella. We conclude that the expression pattern of the Hopi gene accounts for the germination-dependent anthocyanin synthesis in scutella, whereas the developmental competence of germinating seeds to induce anthocyanin production in scutella results from the combination of the light-inducible expression of C1 and the developmentally regulated expression of the Hopi gene
Descriptors:maize. genes. seed-germination. gene-expression. plant-development. anthocyanins. plant-pigments. seeds. plant-tissues. colour. light. aleurone-layer. scutellum. seed-development. cereals. biotechnology
Organism Descriptors:Zea-mays
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060. FF020
Supplementary Info:69 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

253. Title:Whole-genome characterization of embryonic stage inbreeding depression in a selfed loblolly pine family
View Article: Genetics. 2000. 155 (1). 337-348
CD Volume:303
Print Article: Pages: 337-348
Author(s):Remington D L O'Malley D M
Author Affiliation:Department of Forestry, North Carolina State University, Raleigh, NC 27695, USA
Language:English

Abstract:Inbreeding depression is important in the evolution of plant populations and mating systems. Previous studies have suggested that early-acting inbreeding depression in plants is primarily due to lethal alleles and possibly epistatic interactions. Recent advances in molecular markers now make genetic mapping a powerful tool to study the genetic architecture of inbreeding depression. We describe a genome-wide evaluation of embryonic viability loci in a selfed family of loblolly pine (Pinus taeda), using data from AFLP markers from an essentially complete genome map. Locus positions and effects were estimated from segregation ratios using a maximum-likelihood interval mapping procedure. We identified 19 loci showing moderately deleterious to lethal embryonic effects. These loci account for >13 lethal equivalents, greater than the average of 8.5 lethal equivalents reported for loblolly pine. Viability alleles show predominantly recessive action, although potential overdominance occurs at 3 loci. We found no evidence for epistasis in the distribution of pairwise marker correlations or in the regression of fitness on the number of markers linked to deleterious alleles. The predominant role of semilethal alleles in embryonic inbreeding depression has implications for the evolution of isolated populations and for genetic conservation and breeding programmes in conifers
Descriptors:inbreeding-depression. alleles. forest-trees. gene-mapping. genetics. lethals. epistasis. plant-embryos. genetic-markers. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Pinus-taeda. Pinopsida
Supplemental Descriptors:Pinus. Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants
Subject Codes:KK100. FF020. WW000
Supplementary Info:42 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics

254. Title:Highly recombinogenic regions at seed storage protein loci on chromosome 1DS of Aegilops tauschii, the D-genome donor of wheat
View Article: Genetics. 2000. 155 (1). 361-367
CD Volume:303
Print Article: Pages: 361-367
Author(s):Spielmeyer W Moullet O Laroche A Lagudah E S
Author Affiliation:CSIRO Plant Industry, Canberra, ACT 2601, Australia
Language:English
Abstract:A detailed RFLP map was constructed of the distal end of the short arm of chromosome 1D of Aegilops tauschii, the diploid D-genome donor species of hexaploid wheat. Ae. tauschii was used to overcome some of the limitations commonly associated with molecular studies of wheat such as low levels of DNA polymorphism. Detection of multiple loci by most RFLP probes suggests that gene duplication events have occurred throughout this chromosomal region. Large DNA fragments isolated from a BAC library of Ae. tauschii were used to determine the relationship between physical and genetic distance at seed storage protein loci located at the distal end of chromosome 1DS. Highly recombinogenic regions were identified where the ratio of physical to genetic distance was estimated to be <20 kb/cM. These results are discussed in relation to the genome-wide estimate of the relationship between physical and genetic distance

Descriptors:plant-proteins. restriction-fragment-length-polymorphism. wild-relatives. gene-mapping. seeds. recombination. duplication. cereals. wheat. biotechnology. plant-genetic-resources
Organism Descriptors:Aegilops-tauschii. Triticum
Supplemental Descriptors:Aegilops. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. PP720. FF020
Supplementary Info:37 ref
ISSN:0016-6731
Year:2000
Journal Title:Genetics
Copyright:Copyright CAB International

255. Title:courtless, the Drosophila UBC7 homolog, is involved in male courtship behavior and spermatogenesis
View Article: Genetics 2000 Jul;155(3):1267-80
CD Volume:303
Print Article: Pages: 1267-1280
Author(s):Orgad S Rosenfeld G Greenspan RJ Segal D
Author Affiliation:Department of Molecular Microbiology and Biotechnology, Tel-Aviv University, Tel-Aviv 69978, Israel
Abstract:The courtless (col) mutation disrupts early steps of courtship behavior in Drosophila males, as well as the development of their sperm. Most of the homozygous col/col males (78%) do not court at all. Only 5% perform the entire ritual and copulate, yet these matings produce no progeny. The col gene maps to polytene chromosome band 47D. It encodes two proteins that differ in their carboxy termini and are the Drosophila homologs of the yeast ubiquitin-conjugating enzyme UBC7. The col mutation is caused by an insertion of a P element into the 3' UTR of the gene, which probably disrupts translational regulatory elements. As a consequence, the homozygous mutants exhibit a six- to sevenfold increase in the level of the COL protein. The col product is essential, and deletions that remove the col gene are lethal. During embryonic development col is expressed primarily in the CNS. Our results implicate the ubiquitin-mediated system in the development and function of the nervous system and in meiosis during spermatogenesis
Descriptors:Alleles. Animal. Animals, Transgenic. Base Sequence. Cloning, Molecular. *Courtship. Drosophila. Female. Gene Expression. Homozygote. Insect Proteins. Ligases. Male. Meiosis. Molecular Sequence Data. Mutation. Physical Chromosome Mapping. Sequence Homology, Amino Acid. Sex Behavior, Animal. Spermatogenesis. Support, Non-U.S. Gov't. Transfection. Ubiquitin
Geographic Locator:UNITED STATES
ISSN:0016-6731
Year:2000
Journal Title:Genetics

256. Title:Two medfly promoters that have originated by recent gene duplication drive distinct sex, tissue and temporal expression patterns
View Article: Genetics. 2000. 156 (1). 173-182
CD Volume:304
Print Article: Pages: 173-182
Author(s):Christophides G K Livadaras I Savakis C Komitopoulou K
Author Affiliation:Department of Genetics and Biotechnology, School of Biological Sciences, University of Athens, Panepistimiopolis, Athens 15701, Greece
Language:English
Abstract:Genes encoding predominantly male-specific serum polypeptides (MSSPs) in the medfly Ceratitis capitata are members of a multigene family that

are structurally similar to the genes encoding odorant binding proteins of insects. To study the transcriptional regulation of the genes MSSP-alpha 2 and MSSP- beta 2, overlapping fragments of their promoters, containing the 5' UTRs and 5' flanking regions, were fused to the lacZ reporter gene and introduced into the medfly genome via Minos-mediated germline transformation. Transgenic flies were functionally assayed for beta -galactosidase activity. Despite their extensive sequence similarity, the two gene promoters show distinct expression patterns of the reporter gene, consistent with previously reported evidence for analogous transcriptional activity of the corresponding endogenous genes. The MSSP- alpha 2 promoter drives gene expression specifically in the fat body of the adult males, whereas the MSSP- beta 2 promoter directs gene expression in the midgut of both sexes. In contrast, similar transformation experiments in Drosophila melanogaster showed that both promoters drive the expression of the reporter gene in the midgut of adult flies of both sexes. Thus, the very same MSSP- alpha 2 promoter fragment directs expression in the adult male fat body in Ceratitis, but in the midgut of both sexes in Drosophila. Our data suggest that through the evolution of the MSSP gene family a limited number of mutations that occurred within certain cis-acting elements, in combination with new medfly-specific trans-acting factors, endowed these recently duplicated genes with distinct sex-, tissue-, and temporal-specific expression patterns

Descriptors:gene-expression. polypeptides. molecular-genetics. transgenic-animals. transcription-factors

Organism Descriptors:Ceratitis-capitata

Supplemental Descriptors:Ceratitis. Tephritidae. Diptera. insects. arthropods. invertebrates. animals

Subject Codes:FF620. YY300. YY200

Supplementary Info:48 ref

ISSN:0016-6731

Year:2000

Journal Title:Genetics

257. Title:Genetic and physical interactions between factors involved in both cell cycle progression and pre-mRNA splicing in Saccharomyces cerevisiae

View Article: Genetics 2000 Dec;156(4):1503-17

CD Volume:304

Print Article: Pages: 1503-1517

Author(s):Ben Yehuda S Dix I Russell CS McGarvey M Beggs JD Kupiec M

Author Affiliation:Department of Molecular Microbiology and Biotechnology, Tel Aviv University, Ramat Aviv 69978, Israel

Abstract:The PRP17/CDC40 gene of Saccharomyces cerevisiae functions in two different cellular processes: pre-mRNA splicing and cell cycle progression. The Prp17/Cdc40 protein participates in the second step of the splicing reaction and, in addition, prp17/cdc40 mutant cells held at the restrictive temperature arrest in the G2 phase of the cell cycle. Here we describe the identification of nine genes that, when mutated, show synthetic lethality with the prp17/cdc40Delta allele. Six of these encode known splicing factors: Prp8p, Slu7p, Prp16p, Prp22p, Slt11p, and U2 snRNA. The other three, SYF1, SYF2, and SYF3, represent genes also involved in cell cycle progression and in pre-mRNA splicing. Syf1p and Syf3p are highly conserved proteins containing several copies of a repeated motif, which we term RTPR. This newly defined motif is shared by proteins involved in RNA processing and represents a subfamily of the known TPR (tetratricopeptide repeat) motif. Using two-hybrid interaction screens and biochemical analysis, we show that the

SYF gene products interact with each other and with four other proteins: Isy1p, Cef1p, Prp22p, and Ntc20p. We discuss the role played by these proteins in splicing and cell cycle progression
Descriptors:Amino Acid Motifs. Amino Acid Sequence. Animal. Caenorhabditis elegans. Cell Cycle. Cell Cycle Proteins. Comparative Study. Fungal Proteins. G2 Phase. *Genes, Structural, Fungal. Human. Molecular Sequence Data. RNA Precursors. RNA Splicing. RNA, Fungal. RNA, Small Nuclear. RNA-Binding Proteins. Saccharomyces cerevisiae. Sequence Alignment. Sequence Homology, Amino Acid. Spliceosomes. Support, Non-U.S. Gov't
Geographic Locator:UNITED STATES
ISSN:0016-6731
Year:2000
Journal Title:Genetics

258. Title:A simple method for the detection of BHV-1 [bovine herpesvirus 1] from infected MDBK cells by polymerase chain reaction
View Article: Indian Veterinary Journal. 2000. 77 (2). 98-102
CD Volume:317
Print Article: Pages: 98-102
Author(s):Tiwari A K Kataria R S Butchaiah G Prasad N
Author Affiliation:National Biotechnology Centre, Indian Veterinary Research Institute, Izatangar, U.P. - 243 122, India
Language:English
Descriptors:diagnostic-techniques. diagnosis. polymerase-chain-reaction
Organism Descriptors:bovine-herpesvirus-1. cattle
Supplemental Descriptors:bovine-herpesvirus. Herpesviridae. viruses. Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL821. LL886
Supplementary Info:13 ref
ISSN:0019-6479
Year:2000
Journal Title:Indian Veterinary Journal

259. Title:Cloning and expression of cellulase genes from Ruminococcus albus
View Article: Indian Veterinary Journal. 2000. 77 (6). 475-478
CD Volume:317
Print Article: Pages: 475-478
Author(s):Vijayarani K Thirumurugan G Nachimuthu K Padmanaban V D
Author Affiliation:Faculty of Basic Sciences, Department of Animal Biotechnology, Madras Veterinary College, Chennai - 600 007, India
Language:English
Abstract:In the present study, a total of 935 ampicillin resistant colonies were obtained in pBR322 cloning using partially digested genomic DNA fragments of Ruminococcus albus. The presence of cellulase genes and 5 colonies were found to carry the same recombinant plasmid DNA with a 2.1 kb and 2.5 kb Hind lll insert and designated as pRA1 and pRA2. Homology between the cloned DNA fragment and the genomic DNA of Ruminococcus albus was checked by dot-blot hybridization. Results indicate that pRA1 and pRA2 utilized cellobiose more efficiently than carboxy methyl cellulose confirming their cellulolytic activity
Descriptors:ampicillin. cell-cloning. cellulase. DNA-cloning. genes. recombinant-DNA. rumen-bacteria
Organism Descriptors:Ruminococcus-albus
Supplemental Descriptors:Ruminococcus. Lachnospiraceae. Firmicutes. bacteria. prokaryotes
Subject Codes:WW000. ZZ395

Supplementary Info:10 ref
ISSN:0019-6479
Year:2000
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

260. Title:Isolation and characterisation of cellulolytic bacteria from bovine rumen
View Article: Indian Veterinary Journal. 2000. 77 (8). 652-654
CD Volume:317
Print Article: Pages: 652-654
Author(s):Vijayarani K Nachimuthu K Padmanaban V D
Author Affiliation:Department of Animal Biotechnology, Madras Veterinary College, Tamil Nadu Veterinary and Animal Sciences University, Chennai - 600 007, India
Language:English
Abstract:Six anaerobic bacteria were isolated from rumen samples collected from fistulated Jersey crossbred cattle. All isolates were observed to be non-motile Gram positive cocci. Four were classified as Ruminococcus albus and 2 were classified as R. flavefaciens. R. albus produced white colonies with their cells single or in pairs while R. flavefaciens produced yellow colonies with their cells single, in pairs or in short chains. All the isolates wre cellulolytic and fermented cellobiose, cellulose, lactose and xylan. R. albus isolates produced acetate, formate and lactate whereas R. flavefaciens produced acetate, formate, lactate and succinate as fermentation end products
Descriptors:acetates. carbohydrate-metabolism. cellobiose. cellulolytic-microorganisms. cellulose. cellulose-digestion. fermentation. formates. lactose. rumen. xylan
Identifiers:Ruminococcus flavefaciens
Organism Descriptors:cattle. Ruminococcus. Ruminococcus-albus
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Lachnospiraceae. Firmicutes. bacteria. prokaryotes. Ruminococcus. Peptococcaceae
Subject Codes:LL510. ZZ394
Supplementary Info:10 ref
ISSN:0019-6479
Year:2000
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

261. Title:Molecular cloning and partial sequencing of a cellulase gene from a rumen anaerobic bacterium
View Article: Indian Veterinary Journal. 2000. 77 (8). 659-661
CD Volume:317
Print Article: Pages: 659-661
Author(s):Vijayarani K Nachimuthu K Padmanaban V D
Author Affiliation:Faculty of Basic Sciences, Department of Animal Biotechnology, Madras Veterinary College, Chennai - 00 007, India
Language:English
Abstract:The genes responsible for cellulase activity from Ruminococcus albus were sequenced and cloned. One recombinant colony with a 1.4 kb Hind III insert resembling an endogluconase gene was cloned and partially sequenced. The partial nucleotide sequence of the cloned gene and its deducted amino acid sequence obtained revealed an open reading frame of 318 bp encoding a polypeptide of 106 amino acids
Descriptors:cellulase. clones. genes. nucleotide-sequences. open-reading-frames. polypeptides. rumen-bacteria
Organism Descriptors:Ruminococcus-albus

Supplemental Descriptors:Ruminococcus. Lachnospiraceae. Firmicutes. bacteria. prokaryotes
Subject Codes:HH600. LL510. LL650. LL821
Supplementary Info:9 ref
ISSN:0019-6479
Year:2000
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

262. Title:Isolation and characterisation of streptococcus bovis from bovine rumen
View Article: Indian Veterinary Journal. 2000. 77 (9). 745-747
CD Volume:317
Print Article: Pages: 745-747
Author(s):Vijayarani K Rao R G Nachimuthu K Padmanaban V D
Author Affiliation:Dept. of Animal Biotechnology, Madras Veterinary College, Tamil Nadu Veterinary and Animal Sciences University, Chennai - 600 007, India
Language:English
Descriptors:characterization. rumen-bacteria. strains. taxonomy
Organism Descriptors:cattle. Streptococcus-bovis
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Streptococcus. Streptococcaceae. Firmicutes. bacteria. prokaryotes
Subject Codes:LL821. ZZ380
Supplementary Info:7 ref
ISSN:0019-6479
Year:2000
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

263. Title:Studies on multiple arbitrary amplicon profiling in cattle using a single, virus-specific, 22-mer oligonucleotide primer
View Article: Indian Veterinary Journal. 2000. 77 (11). 941-943
CD Volume:318
Print Article: Pages: 941-943
Author(s):Mukhopadhyaya P N Mehta H H Rathod R N
Author Affiliation:Biotechnology Laboratory, National Dairy Development Board, Anand - 388 001, Gujarat, India
Language:English
Abstract:A 22-mer oligonucleotide primer, specific for a promoter region of the bacteriophage T7, belonging to the family Podoviridae, was used for PCR to generate multiple amplicons in cattle. No sequence information of the template DNA was required to demonstrate the phenomenon. The methodology involved a primary amplification at low stringency followed by a final amplification at a higher stringency of annealing temperature. The generality of the technique was tested by application to non descript breeds of buffalo, sheep and goat
Descriptors:DNA. genomes. nucleotide-sequences. oligonucleotides
Identifiers:amplicons
Organism Descriptors:cattle. ruminants
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. WW000
Supplementary Info:5 ref
ISSN:0019-6479
Year:2000
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

264. Title:Enantiomeric synthesis of (S)-2-methylbutanoic acid methyl ester, apple flavor, using lipases in organic solvent
View Article: Journal of Agricultural and Food Chemistry. 48 (2). Feb., 2000. 524- 530
CD Volume:301
Print Article: Pages: 524-530
Author(s):Kwon Dae Young Hong Yun Jeong Yoon Suk Hoo
Author Affiliation:Food Science and Biotechnology Division, Korea Food Research Institute, San 46-1, Paekhyondong, Poondang, Songnam, Kyongki-do, 463-420
Language:English
Language of Summary:English (EN)
Abstract:Enantiomeric selective synthesis of (S)-2-methylbutanoic acid methyl ester, which is known as a major apple and strawberry flavor, was performed from racemic 2-methylbutanoic acid using lipases in organic solvent. Among 20 lipases, lipase IM 20 (immobilized lipase of Rhizomucor miehei), lipase AP (Aspergillus niger), and lipase FAP-15 (Aspergillus javanicus) exhibited higher enzymatic activities and enantioselectivities and were selected for the synthesis of (S)-2-methylbutanoic acid methyl ester. Using these enzymes, the reaction conditions such as temperature and lyophilizing pH were optimized, and kinetic parameters were determined. All of the reactions were performed in isooctane, which was identified as the best reaction media for nonaqueous systems. At 20 degreeC maximum enantiomeric excess was observed, while synthetic activity increased as the temperature increased. Only lipases lyophilized at pH 5.5, 6.0, 6.5, and 7.0 showed synthetic activity. In this pH range, enantioselectivities were not influenced by the lyophilizing pH. The KM,S and KM,R values for ester synthetic activity of lipase were 1120 and 1240 mM, respectively. Enzyme activity was inhibited by (S)-2-methylbutanoic amide, and its Ki was calculated as 84 mM. (S)-2-Methylbutanoic amide acted as a competitive inhibitor
Descriptors:Biochemistry and Molecular Biophysics; Bioprocess Engineering; Foods. (S)-2-methylbutanoic acid methyl ester: apple flavor compound, enantiomeric synthesis; lipases: FAP-15, IM 20
Organism Descriptors:Aspergillus javanicus (Fungi Imperfecti or Deuteromycetes); Aspergillus niger (Fungi Imperfecti or Deuteromycetes); Rhizomucor miehei (Phycomycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae; Phycomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering; Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

265. Title:Delignified cellulosic material supported biocatalyst as freeze-dried product in alcoholic fermentation
View Article: Journal of Agricultural and Food Chemistry. 48 (3). March, 2000. 958-961
CD Volume:301
Print Article: Pages: 958-961
Author(s):Iconomopoulou M Kanellaki M Psarianos K Koutinas A A
Author Affiliation:Food Biotechnology Group, Department of Chemistry, University of Patras, 26500, Patras
Language:English

Language of Summary:English (EN)
Abstract:Freeze-dried delignified cellulosic (DC) material supported biocatalyst is proposed as a suitable form of biocatalyst to be preserved. The alcoholic fermentation of glucose using freeze-dried immobilized cells is reported. Freeze-dried immobilized baker's yeast cells on DC material do not need any protective medium during freeze-drying. The effect of initial glucose concentration and temperature on the alcoholic fermentation kinetic parameters is reported in the present study. It was found that the freeze-dried immobilized cells ferment more quickly than free freeze-dried cells and have a lower fermentation rate as compared with wet immobilized cells. However, repeated batch fermentations showed freeze-dried immobilized cells to ferment at about the same fermentation rate as wet immobilized cells. The results indicate that the freeze-dried immobilized cells must be further studied to establish a process for the preservation of immobilized cells
Descriptors:alcoholic fermentation; immobilized, freeze-dried cell uses; industrial applications. Bioprocess Engineering. Delignified cellulosic material supported biocatalyst
Organism Descriptors:baker's yeast (Ascomycetes)
Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

266. Title:Analysis of metal cations and inorganic anions in olive oil mill waste waters by atomic absorption spectroscopy and ion chromatography. Detection of metals bound mainly to the organic polymeric fraction
View Article: Journal of Agricultural and Food Chemistry. 48 (4). April, 2000. 1405-1410
CD Volume:301
Print Article: Pages: 1405-1410
Author(s):Arienzo Michele Capasso Renato
Author Affiliation:Dipartimento di Scienze Chimico-Agrarie, Universita di Napoli "Federico II", Via Universita 100, 80055, Portici, Napoli
Language:English
Language of Summary:English (EN)
Abstract:Metal cations were quantitatively detected by atomic absorption spectrometry in samples of olive oil mill waste waters obtained by a pressure process (omww1) (K, 17.1; Mg, 2.72; Ca, 2.24; Na, 0.40; Fe, 0.123; Zn, 0.0630; Mn, 0.0147; Cu, 0.00860 g L-1) and a centrifugation process (omww2) (K, 9.80; Mg, 1.65; Ca, 1.35; Na, 0.162; Fe, 0.0330; Zn, 0.0301; Mn, 0.00910; Cu, 0.00980 g L-1). The inorganic anions, determined in the same samples by ion chromatography, proved to be Cl-, H2PO4-, F-, SO42-, and NO3- (1.61, 1.05, 0.66, 0.52, and 0.023 g L-1, respectively, in omww1 and 0.61, 0.40, 0.25, 0.20, and 0.0090 g L-1, respectively, in omww2). Most of the metal cations were revealed to be bound to the omww organic polymeric fraction (opf), composed of polysaccharides, phenol polymers, and proteins. Opf relative molecular weight was substantially estimated in the range between 1000 and 30000 Da for apprx75% and in the range from 30000 to 100000 Da for apprx25%. The free residual cations pool proved to be neutralized by the inorganic counteranions. Finally, the possible exploitation of this material in agriculture and in environmental biotechnology processes is also discussed in the light of its chemical and biochemical oxygen demand parameters

Descriptors:olive mill wastewater. Foods; Methods and Techniques. inorganic anions; metal cations
Organism Descriptors:Olea europea [olive] (Oleaceae)
Supplemental Descriptors:Oleaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods; Methods and Techniques
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

267. Title:Formation of the mutagen IFP in model systems and detection in restaurant meats
View Article: Journal of Agricultural and Food Chemistry. 48 (5). May, 2000. 1721- 1726
CD Volume:301
Print Article: Pages: 1721-1726
Author(s):Pais Pilar Tanga Mary J Salmon Cynthia P Knize Mark G
Author Affiliation:Biology and Biotechnology Research Program, Lawrence Livermore National Laboratory, University of California, Livermore, CA, 94551- 9900
Language:English
Language of Summary:English (EN)
Abstract:Mixtures of the free amino acids, creatine and glucose, were dry-heated to model the potential formation of heterocyclic amines in meats. The formation of the mutagenic amine IFP (determined to be 2-amino-(1,6-dimethylfuro(3,2-e)imidazo(4,5-b))pyridine) was investigated by varying heating time, heating temperature, and precursors. With an optimized mixture of glutamine, creatine, and glucose, heated at 200 degreeC for 60 min, 2 mg of IFP was purified for studies to define its structure. Trideuteriomethyl-IFP was made from trideuteriomethylcreatinine in the model system for use in LC- MS detection of IFP in foods. Analysis of well-done meats purchased from restaurants showed about half to contain IFP at levels from 1.4 to 46 ng/g of cooked meat, demonstrating human exposure to this mutagen
Descriptors:cooked meat; model system; restaurant meat. Foods; Toxicology. IFP: amine, formation, mutagen; heterocyclic amines
Subject Codes:Foods; Toxicology
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

268. Title:Effect of storage temperature and pyruvate on kinetics of anthocyanin degradation, vitisin A derivative formation, and color characteristics of model solutions
View Article: Journal of Agricultural and Food Chemistry. 48 (6). June, 2000. 2135-2141
CD Volume:301
Print Article: Pages: 2135-2141
Author(s):Romero Concepcion Bakker Johanna
Author Affiliation:Department of Food Biotechnology, Instituto de la Grasa (CSIC), Avda. Padre Garcia Tejero 4, 41012, Sevilla
Language:English
Language of Summary:English (EN)
Abstract:The formation of vitisin A, an anthocyanin formed naturally in small quantities in maturing port wines, was studied in model wine solutions at several storage temperatures (10, 15, 20, and 32 degreeC). Vitisin A was formed through the interaction between malvidin 3-glucoside and

pyruvic acid, Acylated forms of vitisin A, having the 6-position of the sugar acylated with acetic acid (3- acetylvitisin A) and p-coumaric acid (3-p-coumarylvitisin A), were also formed through the interaction between pyruvic acid and malvidin 3-acetylglucoside and malvidin 3-p-coumarylglucoside, respectively. A maximum degradation of the anthocyanins was obtained at higher temperatures, and it followed a first-order kinetics both with and without pyruvic acid in the solution. Whereas at low temperatures (10 and 15 degreeC) the presence of pyruvic acid accelerated the kinetic reaction, at higher temperatures (20 and 32 degreeC) it decreased it. The activation energy values for the degradation of the three anthocyanins in model solutions without and with pyruvic acid were not significantly different from each other. At low temperatures the highest concentrations of vitisin A compounds were obtained. All solutions showed a decrease in L* value, indicating that all solutions became darker. This change increased with increasing temperature. All model solutions increased in the hue angle, indicating that the solutions changed from a bluish-red to an orange-red or even brownish-red color. Samples without pyruvic acid remained lighter and became browner than those with pyruvic acid. A good correlation between the amount of vitisin A in the solution and hue angle was found, indicating that vitisin A may contribute the orange-red of solutions, compared to the browner control

Descriptors:color characteristics; model wine solution: wine; storage temperature effect. Foods. anthocyanin: degradation kinetics; pyruvate; pyruvic acid; vitisin A

Subject Codes:Foods

ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

269. Title:Insecticidal and fumigant activities of Cinnamomum cassia bark-derived materials against Mechoris ursulus (Coleoptera: Attelabidae)

View Article: Journal of Agricultural and Food Chemistry. 48 (6). June, 2000. 2528-2531
CD Volume:301
Print Article: Pages: 2528-2531

Author(s):Park Il Kwon Lee Hoi Seon Lee Sang Gil Park Ji Doo Ahn Young Joon
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744

Language:English
Language of Summary:English (EN)

Abstract:The insecticidal and fumigant activities of Cinnamomum cassia (Blume) bark-derived materials against the oak nut weevil (Mechoris ursulus Roelofs) were examined using filter paper diffusion and fumigation methods and compared to those of the commercially available Cinnamomum bark-derived compounds (eugenol, salicylaldehyde, trans-cinnamic acid, and cinnamyl alcohol). The biologically active constituent of the Cinnamomum bark was characterized as trans-cinnamaldehyde by spectroscopic analysis. In a test with the filter paper diffusion method, trans-cinnamaldehyde showed 100 and 83.3% mortality at rates of 2.5 and 1.0 mg/filter paper, respectively. At 2.5 mg/paper, strong insecticidal activity was produced from eugenol (90.0% mortality) and salicylaldehyde (88.9%), whereas trans-cinnamic acid revealed moderate activity (73.3%). At 5 mg/paper, weak insecticidal activity (50.0%) was produced from cinnamyl alcohol. In a fumigation test, the Cinnamomum bark-derived compounds were much more effective against M. ursulus larvae in closed cups than in open ones. These results indicate that the insecticidal activity of test compounds was attributable to

fumigant action, although there is also significant contact toxicity. As a naturally occurring insect-control agent, the Cinnamomum bark-derived materials described could be useful as a new preventive agent against damage caused by M. ursulus
Descriptors:Cinnamomum cassia bark-derived materials: fumigant, insecticide. Economic Entomology; Pest Assessment Control and Management; Pesticides
Organism Descriptors:Cinnamomum cassia (Lauraceae); Mechoris ursulus [oak nut weevil] (Coleoptera): pest
Supplemental Descriptors:Coleoptera: Insecta, Arthropoda, Invertebrata, Animalia; Lauraceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Arthropods; Dicots; Insects; Invertebrates; Plants; Spermatophytes; Vascular Plants
Subject Codes:Economic Entomology; Pest Assessment Control and Management; Pesticides
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

270. Title:Cordycepin: Selective growth inhibitor derived from liquid culture of Cordyceps militaris against Clostridium spp
View Article: Journal of Agricultural and Food Chemistry. 48 (7). July, 2000. 2744-2748
CD Volume:301
Print Article: Pages: 2744-2748
Author(s):Ahn Young Joon Park Suck Joon Lee Sang Gil Shin Sang Cheol Choi Don Ha
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744
Language:English
Language of Summary:English (EN)
Abstract:The growth responses of nine human intestinal bacteria to liquid culture of Cordyceps militaris Link. Pt. (Ascomycotina: Clavicipitaceae) collected from a pupa of Bombyx mori L. (Lepidoptera: Bombycidae) were examined using spectrophotometric and impregnated paper disk methods and compared to those of tetracycline and chloramphenicol, as well as those of Coptis japonica root-derived berberine chloride. The biologically active constituent of the cultures was characterized as cordycepin (3'- deoxyadenosine) by spectroscopic analysis. This compound revealed potent growth-inhibiting activity toward Clostridium paraputrificum and Clostridium perfringens at 10 mug/disk without adverse effects on the growth of Bifidobacterium bifidum, Bifidobacterium breve, Bifidobacterium longum, Bifidobacterium adolescentis, Lactobacillus acidophilus, and Lactobacillus casei, whereas tetracycline and chloramphenicol inhibited the growth of these lactic acid-producing bacteria, clostridia and Escherichia coli. However, C. militaris- derived materials revealed no growth stimulation on the bifidobacteria and lactobacilli. These results may be an indication of at least one of the pharmacological actions of C. militaris. As a naturally occurring antibacterial agent, cordycepin could be useful as a new preventive agent against various diseases caused by clostridia
Descriptors:bacterial growth. Infection; Pharmacognosy (Pharmacology). Coptis maponica root-derived berberine chloride; cordycepin: antibacterial agent, antibacterial-drug, selective bacterial growth inhibitor
Organism Descriptors:Bifidobacterium adolescentis (Irregular Nonsporing Gram-Positive Rods): human intestinal bacteria; Bifidobacterium bifidum (Irregular Nonsporing Gram-Positive Rods): human intestinal bacteria; Bifidobacterium breve (Irregular Nonsporing Gram-Positive Rods): human

intestinal bacteria; Bifidobacterium longum (Irregular Nonsporing Gram-Positive Rods): human intestinal bacteria; Bombyx mori (Lepidoptera): host, pupa; Clostridium paraputrificum (Endospore-forming Gram-Positives): human intestinal bacteria; Clostridium perfringens (Endospore-forming Gram-Positives): human intestinal bacteria; Clostridium spp. (Endospore-forming Gram- Positives): harmful organism; Coptis maponica (Ranunculaceae); Cordyceps militaris (Ascomycetes): beneficial organism, possible antineoplastic association; Escherichia coli (Enterobacteriaceae): human intestinal bacteria; Lactobacillus acidophilus (Regular Nonsporing Gram-Positive Rods): human intestinal bacteria; Lactobacillus casei (Regular Nonsporing Gram-Positive Rods): human intestinal bacteria

Supplemental Descriptors:Ascomycetes: Fungi, Plantae; Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Irregular Nonsporing Gram-Positive Rods: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms; Lepidoptera: Insecta, Arthropoda, Invertebrata, Animalia; Ranunculaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Regular Nonsporing Gram-Positive Rods: Eubacteria, Bacteria, Microorganisms. Angiosperms; Animals; Arthropods; Bacteria; Dicots; Eubacteria; Fungi; Insects; Invertebrates; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants

Subject Codes:Infection; Pharmacognosy (Pharmacology)

ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

271. Title:Sensitive spectrophotometric assay for 3-hydroxy-substituted flavonoids, based on their binding with molybdenum, antimony, or bismuth

View Article: Journal of Agricultural and Food Chemistry. 48 (7). July, 2000. 2802-2806
CD Volume:301
Print Article: Pages: 2802-2806

Author(s):Viswanathan Palaniswamy Sriram Venkataraman Yogeeswaran Ganesa
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Language:English
Language of Summary:English (EN)

Abstract:A sensitive spectrophotometric assay has been developed for flavonoids based on their binding with molybdenum, antimony, or bismuth. Acetylation of the hydroxy group of flavonoids abolished metal binding, thus suggesting a direct role of the hydroxyl groups. From a comparison of several related flavonoids differing in the position of hydroxyl substitutions, the hydroxyl group at position 3 was found to be an important requirement for the formation of a yellow complex. This flavonoid metal complex showed that a specific and significant bathochromic shift in the visible spectrum of the native flavonoid and the corresponding lambdamax value was used for the colorimetric assays with different metal salts. The molybdenum complex was found to yield higher absorbance compared to antimony and bismuth complexes of various flavonoids. The present method offers a sensitive assay in the 5-25 nM range for these flavonoids and gave comparable results with HPLC quantitative determination

Descriptors:bathochromicity. Biochemistry and Molecular Biophysics; Methods and Techniques. 3-hydroxy-substituted flavonoid: binding; antimony; bismuth; fisetin; metal complex; molybdenum; quercetin
Subject Codes:Biochemistry and Molecular Biophysics; Methods and Techniques
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

272. Title:Development of a sensitive ELISA for the determination of fumonisin B1 in cereals
View Article: Journal of Agricultural and Food Chemistry. 48 (7). July, 2000. 2821-2825
CD Volume:301
Print Article: Pages: 2821-2825
Author(s):Barna Vetro Ildiko Szabo Erzsebet Fazekas Bela Solti Laszlo
Author Affiliation:Agricultural Biotechnology Center, H-2101, Godollo
Language:English
Language of Summary:English (EN)
Abstract:Monoclonal fumonisin B1 antibodies with high titer were raised by using FB1-glutaraldehyde-keyhole limpet hemocyanin immunogen prepared by a short cross-linker reagent (glutaraldehyde). Mean cross-reactivities of the selected monoclonal antibody for FB1, FB2 and FB3 were 100, 91.8, and 209%, respectively; no reactivity was found with hydrolyzed fumonisin. A direct, competitive enzyme- linked immunosorbent assay for the quantitative determination of FB1 in cereals has been developed with this antibody. Fifty percent acetonitrile-based solvent with some additives was used for extraction of cereals, and the diluted extracts were used without cleanup in the test. The mean within-assay and interassay coefficients of variation for the standard curve were <10%. The measuring range of this test is 10-500 ng/g, with a detection limit of 7.6 ng/g FB1. The toxin recovery from cereals infected with 50- 200 ng/g of FB1 varied between 61 and 84%. According to the comparable results of naturally infected maize samples, this test proved to be suitable for the rapid screening of food and feed samples for the presence of FBs
Descriptors:cereal: grain product; food chemistry. Foods; Methods and Techniques; Toxicology. fumonisin B-1: mycotoxin
Organism Descriptors:cereal (Angiospermae): grain crop
Supplemental Descriptors:Angiospermae: Spermatophyta, Plantae. Angiosperms; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods; Methods and Techniques; Toxicology
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

273. Title:Degradation behavior of soy protein-wheat gluten films in simulated soil conditions
View Article: Journal of Agricultural and Food Chemistry. 48 (7). July, 2000. 3027-3031
CD Volume:301
Print Article: Pages: 3027-3031
Author(s):Park S K Hettiarachchy N S Were L
Author Affiliation:Center for Biomaterials and Biotechnology, Department of Materials Science and Engineering, Kwangju Institute of Science and Technology, Kwangju, 500-712
Language:English
Language of Summary:English (EN)

Abstract:Films containing soy protein and wheat gluten were exposed to simulated farmland soil mix over a period of 30 days and monitored for degradation. The simulated farmland soil mix (topsoil/sand/Sunshine compost/vermiculite, 59:6:25:10, wt %) was mixed and stored at ambient humidity (48-55%) and temperature (20- 24 degreeC); the soil mix was constantly maintained at 15% moisture by weight. Research focused on evaluating the effectiveness of gluten and cysteine additions on biodegradable behavior in the simulated farmland soil conditions. The four types of films, soy protein (S:G 1:0); soy protein with cysteine addition
Descriptors:packaging biodegradability; simulated soil conditions; soy protein-wheat gluten film: degradation behavior. Biochemistry and Molecular Biophysics; Pollution Assessment Control and Management; Waste Management (Sanitation). cysteine; gluten; protein
Subject Codes:Biochemistry and Molecular Biophysics; Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

274. Title:Cloning and expression of an acidic pectin methylesterase from jelly fig (Ficus awkeotsang)
View Article: Journal of Agricultural and Food Chemistry. 48 (7). July, 2000. 3052-3057
CD Volume:301
Print Article: Pages: 3052-3057
Author(s):Ding Joe L C Lee Tiger T T Wang Miki M C Tai Sorgan S K Tzen Jason T C
Author Affiliation:Graduate Institute of Agricultural Biotechnology, National Chung-Hsing University, Taichung, 40227
Language:English
Language of Summary:English (EN)
Abstract:Pectin methylesterase (PME) is the key enzyme responsible for the gelation of jelly curd in the water extract of jelly fig (Ficus awkeotasang) achenes. The jelly fig PME extracted from achenes was isoelectrofocused at pH 2.5 and subjected to N-terminal amino acid sequencing. A cDNA fragment encoding the mature protein of this acidic PME was obtained by PCR cloning using a poly(T) primer and a degenerate primer designed according to the N-terminal sequence of the purified PME. The complete cDNA sequence of its precursor protein was further obtained by PCR using the same strategy. The PME clone was overexpressed in Escherichia coli, and its expressed protein was immunologically recognized as strongly as the original antigen using antibodies against purified PME. Fractionation analysis revealed that the overexpressed PME was predominantly present in the pellet and thus presumably formed insoluble inclusion bodies in E. coli cells
Descriptors:food chemistry; jelly curd: Taiwanese drink component. Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics); Foods. acidic pectin methylesterase [EC 3.1.1.11]: cloning, expression; cDNA [complementary DNA]; jelly fig achene water extract: gelation
Organism Descriptors:Ficus awkeotsang [jelly fig] (Moraceae)
Supplemental Descriptors:Moraceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics); Foods
ISSN:0021-8561
Year:2000

Journal Title:Journal of Agricultural and Food Chemistry

275. Title:Mechanical and structural properties of milk protein edible films cross-linked by heating and gamma-irradiation
View Article: Journal of Agricultural and Food Chemistry. 48 (8). August, 2000. 3202-3209
CD Volume:302
Print Article: Pages: 3202-3209
Author(s):Vachon C Yu H L Yefsah R Alain R St Gelais D Lacroix M
Author Affiliation:Microbiology and Biotechnology Research Center, Canadian Irradiation Center, INRS-Institut Armand-Frappier, 531 Boulevard des Prairies, Laval, PQ, H7V 1B7
Language:English
Language of Summary:English (EN)
Abstract:The mechanical properties of cross-linked edible films based on calcium caseinate and two type of whey proteins (commercial and isolate) were investigated. Cross-linking of the proteins was carried out using thermal and radiative treatments. Size-exclusion chromatography performed on the cross-linked proteins showed that gamma-irradiation increased the molecular weight of calcium caseinate, while it changed little for the whey proteins. However, heating of the whey protein solution induced cross-linking. For both cross-linked proteins, the molecular weight distribution was gtoreq2 X 103 kDa. Combined thermal and radiative treatments were applied to protein formulations with various ratios of calcium caseinate and whey proteins. Whey protein isolate could replace up to 50% of calcium caseinate without decreasing the puncture strength of the films. Films based on commercial whey protein and calcium caseinate were weaker than those containing whey protein isolate. Electron microscopy showed that the mechanical characteristics of these films are closely related to their microstructures
Descriptors:food chemistry; milk protein edible film: cross-linking, dairy product, gamma-irradiation effect, heating effect, mechanical properties, structural properties. Biochemistry and Molecular Biophysics; Foods. milk protein
Subject Codes:Biochemistry and Molecular Biophysics; Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

276. Title:Free polyunsaturated fatty acids cause taste deterioration of salmon during frozen storage
View Article: Journal of Agricultural and Food Chemistry. 48 (8). August, 2000. 3280-3285
CD Volume:302
Print Article: Pages: 3280-3285
Author(s):Refsgaard Hanne H F Brockhoff Per M B Jensen Benny
Author Affiliation:Department of Biotechnology, Technical University of Denmark, Building 221, DK-2800, Lyngby
Language:English
Language of Summary:English (EN)
Abstract:Increased intensity of train oil taste, bitterness, and metal taste are the most pronounced sensory changes during frozen storage of salmon (Refsgaard, H. H. F.; Brockhoff, P. B.; Jensen, B. Sensory and Chemical Changes in Farmed Atlantic Salmon (Salmo salar) during Frozen Storage. J. Agric. Food Chem. 1998a, 46, 3473-3479). Addition of each of the unsaturated fatty acids: palmitoleic acid (16:1, n - 7), linoleic acid

(C18:2, n - 6), eicosapentaenoic acid (EPA; C20:5, n - 3) and docosahexaenoic acid (DHA; C22:6, n - 3) to fresh minced salmon changed the sensory perception and increased the intensity of train oil taste, bitterness, and metal taste. The added level of each fatty acid (apprx1 mg/g salmon meat) was equivalent to the concentration of the fatty acids determined in salmon stored as fillet at -10 degreeC for 6 months. The effect of addition of the fatty acids on the intensity of train oil taste, bitterness and metal taste was in the order: DHA > palmitoleic acid > linoleic acid > EPA. Formation of free fatty acids was inhibited by cooking the salmon meat before storage. Furthermore, no changes in phospholipid level were observed during frozen storage. The results suggest that enzymatic hydrolysis of neutral lipids plays a major role in the sensory deterioration of salmon during frozen storage

Descriptors:farmed fish flavor change; food chemistry; salmon: fish, flavor deterioration, taste; storage effect. Foods. free polyunsaturated fatty acid

Organism Descriptors:Salmo salar [salmon] (Osteichthyes)

Supplemental Descriptors:Osteichthyes: Pisces, Vertebrata, Chordata, Animalia. Animals; Chordates; Fish; Nonhuman Vertebrates; Vertebrates

Subject Codes:Foods

ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

277. Title:A group-specific microbiological test for the detection of tetracycline residues in raw milk

View Article: Journal of Agricultural and Food Chemistry. 48 (8). August, 2000. 3372-3377
CD Volume:302
Print Article: Pages: 3372-3377

Author(s):Kurittu Jussi Lonnberg Stefan Virta Marko Karp Matti
Author Affiliation:Department of Biotechnology, University of Turku, Tykistokatu 6A, FIN-20520, Turku

Language:English

Language of Summary:English (EN)

Abstract:The potentiality of using a luminescent Escherichia coli strain for the specific detection of tetracycline residues in raw bovine milk was investigated. The sensor cells contain a reporter plasmid carrying the bacterial luciferase operon of Photorhabdus luminescens under the control of the tetracycline responsive control region from transposon Tn10. Incubation of the cells with the sample containing tetracyclines increases the light emission of the sensor cells. The most sensitive tetracycline detection was achieved in 120 min and by using CDTA as a chelating agent in the assay. Heat-treatment of milk before the assay decreased the variations in background luminescence signals and in tetracycline- induced luminescence between different milk samples. The detection limits for tetracycline, oxytetracycline, chlortetracycline, doxycycline, methacycline, demeclocycline, and minocycline were between 2 and 35 ng/mL. Nontetracycline antibiotics did not significantly interfere with the detection of tetracyclines

Descriptors:food chemistry; food contamination; raw milk: dairy product. Foods; Methods and Techniques; Toxicology. antibiotics: residue; luciferase; tetracycline: antibiotic, residue

Organism Descriptors:Escherichia coli (Enterobacteriaceae); Photorhabdus luminescens (Enterobacteriaceae)

Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms

Subject Codes:Foods; Methods and Techniques; Toxicology
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

278. Title:Extraction of natural complex phenols and tannins from grape seeds by using supercritical mixtures of carbon dioxide and alcohol
View Article: Journal of Agricultural and Food Chemistry. 48 (8). August, 2000. 3408-3412
CD Volume:302
Print Article: Pages: 3408-3412
Author(s):Murga Ruth Ruiz Rocio Beltran Sagrario Cabezas Jose L
Author Affiliation:Department of Biotechnology and Food Science, University of Burgos, Plaza Misael Banuelos s/n, 09071, Burgos
Language:English
Language of Summary:English (EN)
Abstract:Proanthocyanidins are supposed to have some therapeutical properties as antioxidants and antineoplasics. Most of the proanthocyanidins, however, are not commercialized since their separation from natural sources is either very expensive or not well-known. In this work, the feasibility of application of mixtures of carbon dioxide and alcohol under supercritical conditions for selective extraction of some phenolic compounds from grape seeds has been studied, among them some low polymerized proanthocyanidins, their main monomer units, (+)-catechin and (-)- epicatechin, and some low molecular weight phenolic compounds, like gallic acid. An analytical-scale supercritical fluid extractor, whose operation was previously optimized, was used to carry out the experiments. A commercial concentrate of complex phenols and tannins from grape seeds was subjected to supercritical extraction in order to find the best operation conditions before directly extracting defatted milled grape seeds. The solvent capacity was found to increase with pressure and with the amount of alcohol used as cosolvent as expected. Such variation in solvent capacity could be used for design of a selective separation process where individual phenolic compounds or groups of them could be obtained. HPLC coupled with two types of detectors, diode array and mass spectrometry, was used for tentative identification and quantification of complex phenols and tannins in the extracts and in the raw materials used for extraction
Descriptors:food chemistry. Foods; Methods and Techniques. natural complex phenols; tannins
Organism Descriptors:grape (Vitaceae): seed
Supplemental Descriptors:Vitaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods; Methods and Techniques
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

279. Title:Relationship between the microstructure and the mechanical and barrier properties of whey protein films
View Article: Journal of Agricultural and Food Chemistry. 48 (9). September, 2000. 3806-3816
CD Volume:302
Print Article: Pages: 3806-3816
Author(s):Anker Martin Stading Mats Hermansson Anne Marie
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Language:English
Language of Summary:English (EN)
Abstract:This work was focused on the relationship between the microstructure and the mechanical and barrier properties of whey protein isolate (WPI) films. Sorbitol (S) and glycerol (G) were used as plasticizers and the pH was varied between 7 and 9. The films were cast from heated aqueous solutions and dried in a climate room at 23 degreeC and 50% relative humidity for 16 h. The microstructure of the films was found to be dependent on the concentration, the plasticizers, and the pH. When the concentration increased, a more aggregated structure was formed, with a denser protein network and larger pores. This resulted in increased water vapor permeability (WVP) and decreased oxygen permeability (OP). When G was used as a plasticizer instead of S, the microstructure was different, and the moisture content and WVP approximately doubled. When the pH increased from 7 to 9, a denser protein structure was formed, the strain at break increased, and the OP decreased
Descriptors:Biochemistry and Molecular Biophysics; Foods. glycerol; oxygen; sorbitol; water vapor; whey protein film: barrier properties, mechanical properties, microstructure, permeability
Subject Codes:Biochemistry and Molecular Biophysics; Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

280. Title:Desorption behavior of sorbed flavor compounds from packaging films with ethanol solution
View Article: Journal of Agricultural and Food Chemistry. 48 (9). September, 2000. 4310-4313
CD Volume:302
Print Article: Pages: 4310-4313
Author(s):Hwang Yoon Hee Matsui Toshiro Hanada Tamaki Shimoda Mitsuya Matsumoto Kiyoshi Osajima Yutaka
Author Affiliation:Bioscience and Biotechnology, Division of Bioresource and Bioenvironmental Sciences, Graduate School, Kyushu University, 6-10- 1, Hakozaki, Higashi-ku, Fukuoka, 812-8581
Language:English
Language of Summary:English (EN)
Abstract:Desorption behavior of sorbed flavor compounds such as ethyl esters, n-aldehydes, and n-alcohols from LDPE and PET films was investigated in 0 to 100% (v/v) ethanol solutions at 20 degreeC, 50 degreeC, and 60 degreeC. In both films, the desorption apparently increased with increasing ethanol concentration and treatment temperature, depending on the compatibility of the flavor compound with the solvent. Namely, the partition coefficient of ethyl esters, n-aldehydes, and n-alcohols in the LDPE film turned out to be approximately zero at gtoreq60%, gtoreq80%, and gtoreq40% (v/v) ethanol, respectively (for PET film, gtoreq80%, gtoreq80%, and gtoreq40% (v/v) ethanol concentrations were required for complete desorption, respectively). As for physical properties (heat of fusion, melting point, and tensile strength and elongation at break) of LDPE and PET films, there were no significant differences between intact film and the treated film with 60% (v/v) ethanol for 30 min at 60 degreeC. These results suggest that it is possible to apply a desorption solvent such as ethanol solution for desorption of sorbed flavor compounds from packaging films with no physical change in the film properties by this desorption treatment
Descriptors:packaging film; recycling. Biochemistry and Molecular Biophysics; Foods; Waste Management (Sanitation). ethanol solution; flavor compounds: desorption behavior, sorbed status

Subject Codes:Biochemistry and Molecular Biophysics; Foods; Waste Management (Sanitation)
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

281. Title:Growth and anthraquinone production of Morinda elliptica cell suspension cultures in a stirred-tank bioreactor
View Article: Journal of Agricultural and Food Chemistry. 48 (9). September, 2000. 4432-4438
CD Volume:302
Print Article: Pages: 4432-4438
Author(s):Abdullah Mohd A Ariff Arbakariya B Marziah Mahmood Ali Abdul M Lajis Nordin H
Author Affiliation:Department of Biotechnology, Universiti Putra Malaysia, 43400 UPM, Serdang, Selangor: arbarif@fsb.upm.edu.my
Language:English
Language of Summary:English (EN)
Abstract:The effects of medium strategy, number of impellers, aeration mode, and mode of operation on Morinda elliptica cell suspension cultures in a stirred-tank bioreactor are described. A lower number of impellers and continuous aeration contributed toward high cell growth rate, whereas a higher number of impellers reduced cell growth rate, although not anthraquinone yield. The semicontinuous mode could indirectly imitate the larger scale version of production medium strategy and improved anthraquinone production even with 0.012% (v/v) antifoam addition. Production medium promoted both growth (maximum dry cell weight of 24.6 g/L) and anthraquinone formation (maximum content of 19.5 mg/g of dry cell weight), without any necessity for antifoam addition. Cultures in production medium or with higher growth rate and anthraquinone production were less acidic than cultures in growth medium or with lower growth rate and anthraquinone production. Using the best operating variables, growth of M. elliptica cells (24.6 g/L) and anthraquinone yield (0.25 g/L) were 45% and 140%, respectively, lower than those using a shake flask culture after 12 days of cultivation
Descriptors:growth. Bioprocess Engineering; Development; Metabolism. anthraquinone: production
Organism Descriptors:Morinda elliptica (Rubiaceae)
Supplemental Descriptors:Rubiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Bioprocess Engineering; Development; Metabolism
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

282. Title:Molecular cloning, characterization, and expression of a cDNA coding copper/zinc superoxide dismutase from black porgy
View Article: Journal of Agricultural and Food Chemistry. 48 (9). September, 2000. 4444-4447
CD Volume:302
Print Article: Pages: 4444-4447
Author(s):Lin Chi Tsai Lee Tung Liang Duan Kow Jen Ken Chuian Fu
Author Affiliation:Institute of Marine Biotechnology, National Taiwan Ocean University, 2 Pei-Ning Road, Keelung, 2024: ctlin@ntou66.ntou.edu.tw
Language:English
Language of Summary:English (EN)

Abstract:A full-length complementary DNA (cDNA) clone encoding a putative copper/zinc superoxide dismutase (Cu/Zn-SOD) was amplified by a Polymerase Chain Reaction (PCR) based technique from cDNA synthesized from black porgy, Acanthopagrus schlegeli, mRNA. Nucleotide sequence analysis of this cDNA clone revealed that it comprised a complete open reading frame coding for 154 amino acid residues. The deduced amino acid sequence showed slightly higher identity (72.8-78.1%) with shark and swordfish Cu/Zn-SOD than with Cu/Zn-SOD from mammalian (68.1-70.7%) and plant (55.5-56.5%) sources. The residues required for coordinating copper and zinc are conserved as they are among all reported Cu/Zn-SOD sequences. The deduced amino acid sequence lacks mitochondria targeting sequence, which suggests that the black porgy cDNA clone encodes a cytosolic Cu/Zn-SOD. The coding region of Cu/Zn-SOD from black porgy was introduced into an expression vector, pET-20b(+), and transformed into Escherichia coli AD494(DE3)pLysS. A predominant achromatic zone was detected by activity staining of native PAGE. This indicates that the Cu/Zn-SOD cDNA clone can express active Cu/Zn- SOD enzyme in E. coli
Descriptors:Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics). copper/zinc superoxide dismutase; copper/zinc superoxide dismutase- encoding complementary DNA: characterization, expression, molecular cloning
Organism Descriptors:Acanthopagrus schlegeli [black porgy] (Osteichthyes)
Supplemental Descriptors:Osteichthyes: Pisces, Vertebrata, Chordata, Animalia. Animals; Chordates; Fish; Nonhuman Vertebrates; Vertebrates
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

283. Title:Irreversible unfolding of myoglobin in an aqueous solution by supercritical carbon dioxide
View Article: Journal of Agricultural and Food Chemistry. 48 (10). October, 2000. 4535-4539
CD Volume:302
Print Article: Pages: 4535-4539
Author(s):Ishikawa Hiroya Shimoda Mitsuya Yonekura Akiyoshi Mishima Keiko Matsumoto Kiyoshi Osajima Yutaka
Author Affiliation:Laboratory of Food Biotechnology, Department of Bioscience and Biotechnology, Division of Bioresource and Bioenvironmental Science, Graduate School of Kyushu University, Fukuoka, 812-8581: ishikawa@agr.kyushu-u.ac.jp
Language:English
Language of Summary:English (EN)
Abstract:The conformational changes in myoglobin, treated by microbubbling of supercritical carbon dioxide (SC-CO2), were investigated by measuring the circular dichroism spectra in the ultraviolet range and compared with those in other proteins (ovoalbumin, bovine serum albumin, and beta-lactoglobulin). Irreversible unfoldings were observed after the microbubbling of SC-CO2 at 35 degreeC and 30 MPa for 30 min. The degree of unfolding depended on the number of intramolecular S-S bonds. alpha-Helix contents of myoglobin decreased with increasing density of SC-CO2. Unfolding of myoglobin induced by heating, pH-lowering, and the addition of a denaturant were reversible. The irreversible unfolding of myoglobin was also observed by the bubbling of gaseous CO2 under atmospheric pressure, but heating was required

Descriptors:Biochemistry and Molecular Biophysics. aqueous solution; mycoglobin: irreversible unfolding; supercritical carbon dioxide: mcirobubbling
Subject Codes:Biochemistry and Molecular Biophysics
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

284. Title:Fining treatments of white wines by means of polymeric adjuvants for their stabilization against browning
View Article: Journal of Agricultural and Food Chemistry. 48 (10). October, 2000. 4619-4627
CD Volume:302
Print Article: Pages: 4619-4627
Author(s):Spagna Giovanni Barbagallo Riccardo N Pifferi Pier Giorgio
Author Affiliation:Food Biotechnology Group, Department of Horticolture, Floricolture, Arboricolture and Agroindustrial Technology (DOFATA), University of Catania, Via Santa Sofia 98, 95123, Catania: spggnn@iol.it
Language:English
Language of Summary:English (EN)
Abstract:Browning and maderization represent important problems for white wine stability. Essentially, this is due to polyphenol oxidation in the wine. The problem has been remedied by adsorption of polyphenol compounds with polymeric adjuvants (chitosans, scleroprotein, and polylactic acid) not used traditionally in wine-making. In particular, some chitosans reduced the polyphenol content and stabilized two Italian white wines (Trebbiano and Albana) to the same extent as did potassium caseinate, an adjuvant normally used in enology. Moreover, chitosans could be reused after a simple regeneration process
Descriptors:browning; maderization; white wine: alcoholic beverage. Foods. chitosan; polymeric adjuvants; polyphenols
Subject Codes:Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

285. Title:Development and characterization of a flavoring agent from oyster cooker effluent
View Article: Journal of Agricultural and Food Chemistry. 48 (10). October, 2000. 4839-4843
CD Volume:302
Print Article: Pages: 4839-4843
Author(s):Kim D S Baek H H Ahn C B Byun D S Jung K J Lee H G Cadwallader K R Kim H R
Author Affiliation:Faculty of Food Science and Biotechnology, Pukyong National University, Pusan, 608-737: hrkim@pknu.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:The general composition of concentrated oyster cooker effluent (OCE) was 80% moisture, 6.7% total nitrogen, 2.4% glycogen, and 8.5% ash. Optimum conditions for enzymatic hydrolysis of OCE were 50 degreeC, 2 h of reaction time, 0.1% amylase mixture (alpha- amylase plus glucoamylase), and 0.2% protease NP. Hydrolysis of OCE led to an increase in free amino acids, with taurine comprising apprx20% of the total. Inosine monophosphate was predominant (456 mg/100 g) among nucleotides and related compounds. Enzyme hydrolysis increased

extractable nitrogen by apprx2-fold. Trimethylamine, trimethylamine oxide, and total creatinine levels were not affected by enzyme treatment. Predominant aroma-active components of enzyme-hydrolyzed OCE included 2-acetyl-1-pyrroline and 3-(methylthio)propanal. Results of this study may help alleviate the wastewater disposal problem currently caused by OCE
Descriptors:aroma; flavor; flavoring potential; oyster byproducts; oyster cooker effluent: composition; oysters: seafood. Foods. oyster cooker effluent-derived flavoring agent: characterization, development
Subject Codes:Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

286. Title:Volatile compounds in the production of liquid beet sugar
View Article: Journal of Agricultural and Food Chemistry. 48 (10). October, 2000. 4844-4850
CD Volume:302
Print Article: Pages: 4844-4850
Author(s):Pihlsgard Per Larsson Mats Leufven Anders Lingnert Hans
Author Affiliation:Swedish Institute for Food and Biotechnology (SIK), SE-402 29, Goteborg: per.pihlsgard@sik.se
Language:English
Language of Summary:English (EN)
Abstract:Samples from different parts of a beet sugar factory and refinery were analyzed with respect to volatile compounds by means of liquid- liquid extraction followed by gas chromatography-mass spectrometry (GC-MS). A limited number of the samples were analyzed by means of gas phase extraction (headspace) followed by GC-MS. Selected compounds were followed through the sugar manufacturing process. The behavior of different compounds varied greatly throughout the process, with some compounds such as geosmin (trans-1,10-dimethyl- trans-9-decalol), dimethyl disulfide, and propionic and hexanoic acid present at the beginning of the process but disappearing rapidly after further processing. Other compounds, such as indole, dihydrobenzofuran, and 2-phenylethanol, were not detected at the start of the process but were formed later on and removed in the final product. In the final product, three pyrazines remained at fairly low concentrations, together with 3-methylcyclopentadione, ethylhexanol, and methyl pyrrole ketone
Descriptors:liquid beet sugar: production, sugar product. Biochemistry and Molecular Biophysics; Foods. 2-phenylethanol; 3-methylcyclopentadione; dihydrobenzofuran; dimethyl disulfide; ethylhexanol; geosmin; hexanoic acid; indole; methyl pyrrole ketone; propionic acid; volatile compounds: flavor
Subject Codes:Biochemistry and Molecular Biophysics; Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

287. Title:Latent polyphenol oxidases from sago log (Metroxylon sagu): Partial purification, activation, and some properties
View Article: Journal of Agricultural and Food Chemistry. 48 (10). October, 2000. 5041-5045
CD Volume:302
Print Article: Pages: 5041-5045
Author(s):Onsa Galila Hassan bin Saari Nazamid Selamat Jinap Bakar Jamilah

Author Affiliation:Department of Food Science, Faculty of Food Science and Biotechnology, University Putra Malaysia, 43400, Serdang, Selangor: nazamid@fsb.upm.edu.my
Language:English
Language of Summary:English (EN)
Abstract:Latent polyphenol oxidase (LPPO), an enzyme responsible for the browning reaction of sago starches during processing and storage, was investigated. The enzyme was effectively extracted and partially purified from the pith using combinations of nonionic detergents. With Triton X-114 and a temperature-induced phase partitioning method, the enzyme showed a recovery of 70% and purification of 4.1-fold. Native PAGE analysis of the partially purified LPPO revealed three activity bands when stained with catechol and two bands with pyrogallol. The molecular masses of the enzymes were estimated by SDS-PAGE to be 37, 45, and 53 kDa. The enzyme showed optimum pH values of 4.5 with 4-methylcatechol as a substrate and 7.5 with pyrogallol. The LPPO was highly reactive toward diphenols and triphenols. The activity of the enzyme was greatly enhanced in the presence of trypsin, SDS, ethanol, and linoleic acid
Descriptors:log. Enzymology (Biochemistry and Molecular Biophysics); Foods. latent polyphenol oxidase: activation, characterization, partial purification, properties
Organism Descriptors:Metroxylon sagu [sago palm] (Palmae). pith
Supplemental Descriptors:Palmae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

288. Title:Development of surface plasmon resonance-based immunoassay for aflatoxin B1
View Article: Journal of Agricultural and Food Chemistry. 48 (11). November, 2000. 5097-5104
CD Volume:302
Print Article: Pages: 5097-5104
Author(s):Daly Stephen J Keating Gary J Dillon Paul P Manning Bernadette M O'Kennedy Richard Lee Heather A Morgan Michael R A
Author Affiliation:School of Biotechnology, Dublin City University, Dublin 9: okennedr@ccmail.dcu.ie
Language:English
Language of Summary:English (EN)
Abstract:Aflatoxins are a group of highly toxic fungal secondary metabolites that occur in Aspergillus species and may contaminate foodstuffs and feeds. Two different anti-aflatoxin B1 antibodies were examined to develop a surface plasmon resonance (SPR)-based immunoassay to aflatoxin B1. A conjugate consisting of aflatoxin B1-bovine serum albumin (BSA) was immobilized on the dextran gel surface. Competition between immobilized aflatoxin B1 conjugate and free aflatoxin B1 in solution for binding to antibody injected over the surface formed the basis for the assay. Regeneration of the antibody from the immobilized conjugate surface is essential for the development of such an inhibitive immunoassay. Problems were encountered with the regeneration of the sensor surface, due to the high-affinity binding of the antibodies. Conventional regeneration solutions consisting of low concentrations of NaOH and HCl worked to a degree, but regeneration was at the expense of the integrity of the immobilized conjugate. A

polyclonal anti-aflatoxin B1 antibody was produced and was found to be regenerable using an organic solution consisting of 1 M ethanolamine with 20% (v/v) acetonitrile, pH 12.0. This combined high ionic strength and extreme pH, as well as chaotrophic properties and allowed the development of an inhibitive immunoassay. The assay had a linear range of 3.0-98.0 ng mL-1 with good reproducibility
Descriptors:antibody regeneration. Biochemistry and Molecular Biophysics; Methods and Techniques. aflatoxin B-1
Organism Descriptors:Aspergillus (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Biochemistry and Molecular Biophysics; Methods and Techniques
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

289. Title:Rapid and complete extraction of phenols from olive oil and determination by means of a coulometric electrode array system
View Article: Journal of Agricultural and Food Chemistry. 48 (11). November, 2000. 5178-5183
CD Volume:302
Print Article: Pages: 5178-5183
Author(s):Brenes Manuel Garcia Aranzazu Garcia Pedro Garrido Antonio
Author Affiliation:Food Biotechnology Department, Instituto de la Grasa, CSIC, Avenida Padre Garcia Tejero 4, 41012, Sevilla: brenes@cica.es
Language:English
Language of Summary:English (EN)
Abstract:Extraction methods to determine olive oil phenols are not exhaustive. A procedure to test their effectiveness, based on the treatment of the extracted oil with 2 N HCl followed by analysis of phenols in the aqueous phase, has been developed. It was concluded, using this test, that 15-40% of phenols remained unextracted when the liquid/liquid extraction method with 80% methanol was applied. Solid phase extraction (C18 cartridge) succeeded in retaining most of the phenols in the cartridge, but the recovery yield from the sorbent material was low. However, a new extraction method, based on the use of N,N-dimethylformamide (DMF) as an extraction solvent, achieved a complete extraction of phenols from oils. The proposed method requires a lower amount of oil, solvents, energy, and labor than the traditional ones. Because of the low concentration of phenols in the DMF extract, the highly sensitive electrochemical detector (EC) technique was studied. All of the phenols detected by the traditional UV detectors were also detected by EC using a coulometric array system. A rapid and complete analytical methodology of phenols in olive oil has been proposed based on coupling DMF extraction and EC detection
Descriptors:electrochemical methods; olive oil: fats and oils. Biochemistry and Molecular Biophysics; Foods; Methods and Techniques. N,N-dimethylformamide; methanol; phenol: extraction
Subject Codes:Biochemistry and Molecular Biophysics; Foods; Methods and Techniques
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

290. Title:Development of biodegradable films from whey proteins by cross-linking and entrapment in cellulose

View Article: Journal of Agricultural and Food Chemistry. 48 (11). November, 2000. 5566-5575
CD Volume:302
Print Article: Pages: 5566-5575
Author(s):Le Tien C Letendre M Ispas Szabo P Mateescu M A Delmas Patterson G Yu H L Lacroix M
Author Affiliation:Research Center in Microbiology and Biotechnology, Canadian Irradiation Center, INRS-Institut Armand-Frappier, 531 Boulevard Des Prairies, Laval, PQ, H7V 1B7: monique_lacroix@inrs- iaf.uquebec.ca
Language:English
Language of Summary:English (EN)
Abstract:When cross-linked by heating or by gamma-irradiation and entrapped in cellulose, whey proteins can generate insoluble biofilms with good mechanical properties and high resistance to attack by proteolytic enzymes. Interchain cross-linking of proteins generated an increase in the puncture strength, and a decrease in water vapor permeability. Gelatin was added in film formulation as a stabilizer to improve the puncture strength and film appearance. The structure of the biofilms was also analyzed. SDS-PAGE revealed that heating and gamma-irradiation produce an increase of the molecular weight of the cross-linked protein. Size exclusion chromatography showed a molecular mass of 40 kDa for un-cross-linked whey proteins, whereas for the soluble fractions of the cross-linked proteins, molecular distributions were between 600 and 3800 kDa for the heated proteins and between 1000 and 2000 kDa for gamma-irradiated proteins. No major alteration of the structural conformation of the proteins was observed by FTIR for biofilms obtained after heat treatment, whereas gamma-irradiation induced some modifications in the protein structure. X-ray diffraction analysis suggests that cross-linking by gamma-irradiation seems to modify the conformation of proteins, which became more ordered and more stable
Descriptors:film development; heating effects; proteolysis; rheological properties. Biochemistry and Molecular Biophysics. biodegradable films; cellulose: cross-linking, entrapment; whey proteins
Subject Codes:Biochemistry and Molecular Biophysics
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

291. Title:Development of a dual-label time-resolved fluorometric immunoassay for the simultaneous detection of two recombinant proteins in potato
View Article: Journal of Agricultural and Food Chemistry. 48 (12). December, 2000. 5868-5873
CD Volume:302
Print Article: Pages: 5868-5873
Author(s):Bookout Jeffrey T Joaquim Tony R Magin Kimberly M Rogan Glennon J Lirette Ronald P
Author Affiliation:Regulatory Sciences, Product Characterization Group, Monsanto Company, 700 Chesterfield Parkway North, St. Louis, MO, 63198: jeffrey.t.bookout@monsanto.com
Language:English
Language of Summary:English (EN)
Abstract:Immunological methods such as ELISA have been traditionally employed to quantify protein levels in plants improved through modern biotechnology. Combined trait products (i.e., plants producing multiple recombinant proteins) created by introducing multiple genetic traits by transformation or traditional breeding methods have prompted the need for the development of analytical assay technologies capable of

detecting and quantifying multiple proteins in a single assay. The development of a two-site, sandwich, dual-label, time-resolved fluorometry-based immunoassay (TRFIA) capable of simultaneously quantitating two recombinant proteins (CP4 EPSPS and Cry3A) in plant sample extracts of genetically improved potato cultivars is reported here. The performance characteristics of TRFIA were similar to or exceeded those of current ELISA methods used to detect and quantitate these proteins. TRFIA is a practical and reliable assay for the quantitation of proteins in genetically improved potato plants and offers an alternative approach to conventional ELISA methods with the added benefit of multiple analyte detection

Descriptors:Biochemistry and Molecular Biophysics; Methods and Techniques. 5-enol-pyruvylshikimate-3-phosphate synthase: recombinant protein; Cry3A protein: recombinant protein

Organism Descriptors:potato (Solanaceae): genetically improved

Supplemental Descriptors:Solanaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Biochemistry and Molecular Biophysics; Methods and Techniques

ISSN:0021-8561

Year:2000

Journal Title:Journal of Agricultural and Food Chemistry

292. Title:Compositional analysis of tubers from insect and virus resistant potato plants

View Article: Journal of Agricultural and Food Chemistry. 48 (12). December, 2000. 5936-5945

CD Volume:302

Print Article: Pages: 5936-5945

Author(s):Rogan Glennon J Bookout Jeff T Duncan David R Fuchs Roy L Lavrik Paul B Love Stephen L Mueth Mike Olson Tammy Owens Elizabeth D Raymond Peter J Zalewski James

Author Affiliation:Monsanto Agricultural Co., 700 Chesterfield Village Parkway, St. Louis, MO, 63198: glennon.j.rogan@monsanto.com

Language:English

Language of Summary:English (EN)

Abstract:Genetically modified potato plants that are resistant to the Colorado potato beetle, plus either the potato leaf roll virus or potato virus Y, have recently been commercialized. As part of the safety assessment for plants produced by modern biotechnology, the composition of the food/feed must be compared to that of the food/feed produced by an equivalent plant variety from a conventional source. The composition of important nutritional and antinutritional factors in tubers produced by virus-and insect- resistant potato plants were compared to tubers produced by conventional potato plants. Key nutritional, quality, and antinutritional components measured were total solids, vitamin C, dextrose, sucrose, soluble protein, and glycoalkaloids. Proximate analyses included fat, ash, calories, total protein, and crude fiber. Minor nutrients measured were vitamin B6, niacin, copper, magnesium, potassium, and amino acids. The results from these analyses confirm that tubers produced by insect-and virus-protected varieties are substantially equivalent to tubers produced by conventional potato varieties

Descriptors:ash content; potato tubers: nutritional composition, vegetable. Foods. amino acids; antinutritional components; copper; crude fiber; dextrose; fat; glycoalkaloids; magnesium; niacin; potassium; soluble protein; sucrose; total protein; total solids; vitamin B-6; vitamin C

Organism Descriptors:potato (Solanaceae): genetically modified, insect resistant, virus resistant

Supplemental Descriptors:Solanaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

293. Title:Comparative evaluation of antioxidant potential of alaternin (2-hydroxyemodin) and emodin
View Article: Journal of Agricultural and Food Chemistry. 48 (12). December, 2000. 6347-6351
CD Volume:302
Print Article: Pages: 6347-6351
Author(s):Choi Jae Sue Chung Hae Young Jung Hyun Ah Park Hye Jin Yokozawa Takako
Author Affiliation:Faculty of Food Science and Biotechnology, Pukyong National University, Pusan, 608-737: choijs@pknu.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:The antioxidant activities of alaternin (2-hydroxyemodin) and emodin were compared for their respective potentials to inhibit lipid peroxidation in the linoleic acid system by the thiocyanate method, to inhibit total reactive oxygen species generation in kidney homogenates using 2',7'-dichlorodihydrofluorescein diacetate, to inhibit peroxynitrite formation by the 3- morpholinosydnonimine system, which generates superoxide radical and nitrogen monooxide, and to scavenge authentic peroxynitrites. Both alaternin and emodin were found to inhibit the peroxidation of linoleic acid by the thiocyanate method in a dose-dependent manner. Whereas the former shows inhibitory activities in reactive oxygen- and nitogen-mediated reactions, the latter does not. These results indicate that alaternin is a potentially effective and versatile antioxidant and can be used to protect biological systems and functions against various oxidative stresses
Descriptors:lipid peroxidation. Biochemistry and Molecular Biophysics. alaternin: antioxidant; emodin: antioxidant; linoleic acid; nitrogen monooxide: generation; peroxynitrite: formation; reactive oxygen species: generation; superoxide radical: generation
Organism Descriptors:rat (Muridae): animal model. kidney: excretory system
Supplemental Descriptors:Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia. Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
Subject Codes:Biochemistry and Molecular Biophysics
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

294. Title:Effect of dietary conjugated linoleic acid on lipid peroxidation and histological change in rat liver tissues
View Article: Journal of Agricultural and Food Chemistry. 48 (12). December, 2000. 6367-6371
CD Volume:302
Print Article: Pages: 6367-6371
Author(s):Yamasaki Masao Mansho Keiko Mishima Hiroko Kimura Genki Sasaki Masafumi Kasai Masaaki Tachibana Hirofumi Yamada Koji
Author Affiliation:Laboratory of Food Chemistry, Department of Bioscience and Biotechnology, Division of Bioresource and Bioenvironmental Sciences,

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Language:English
Language of Summary:English (EN)
Abstract:The effect of dietary conjugated linoleic acid (CLA) on hepatic lipid parameters in Sprague-Dawley rats was examined. When rats were fed a diet containing CLA at 0 (control), 1, or 2% of the weight of the amount of food given of 3 weeks, the liver weight exhibited a slight increase in the CLA-fed groups, although the difference was not significant. Lipid accumulation in the hepatocytes of CLA-fed rats was also demonstrated by electron microscopic observation. In addition, the liver thiobarbituric acid reactive substances levels were significantly higher in the 2 wt % CLA group than in the other two dietary groups, and the levels of phosphatidylcholine hydroperoxide were higher in CLA-fed group when compared to that of the control group. On the other hand, the serum lipid peroxide levels were comparable among all three dietary groups. Levels of triglycerides in the white adipose tissue (WAT) and serum nonesterified fatty acid (NEFA) were reduced in a CLA-dose-dependent manner. CLA was shown to accumulate in the WAT much more than in the serum or liver. These results suggest that CLA accelerates the decomposition of storage lipids in WAT and the clearance of serum NEFA levels, resulting in lipid peroxidation and a morphological change in the liver
Descriptors:Digestive System (Ingestion and Assimilation); Nutrition. conjugated linoleic acid: dietary intake; lipid: accumulation; lipid peroxide; nonesterified fatty acid; phosphatidylcholine hydroperoxide; thiobarbituric acid reactive substances; triglycerides
Organism Descriptors:Sprague-Dawley rat (Muridae): animal model. hepatocytes: digestive system; liver: digestive system; serum: blood and lymphatics; white adipose tissue
Supplemental Descriptors:Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia. Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
Subject Codes:Digestive System (Ingestion and Assimilation); Nutrition
ISSN:0021-8561
Year:2000
Journal Title:Journal of Agricultural and Food Chemistry

295. Title:Reduced oxygen tension and EDTA improve bovine zygote development in a chemically defined medium
View Article: Journal of Animal Science. 78 (1). Jan., 2000. 152-157
CD Volume:318
Print Article: Pages: 152-157
Author(s):Olson S E Seidel G E Jr
Author Affiliation:Animal Reproduction and Biotechnology Laboratory, Colorado State University, Fort Collins, CO, 80523
Language:English
Language of Summary:English (EN)
Abstract:Bovine zygotes produced by in vitro oocyte maturation and fertilization were cultured for 7.5 d in a chemically defined medium without serum or proteins, except .12IU/mL of insulin. In Exp. 1, embryos were cultured in approximately 20% oxygen (i.e., 5% CO2 in air) or 5% CO2; 5% O2; 90% N2, with the metal chelators EDTA or diethylenetetraaminopentaacetic acid (DTPA) at 0, 5, 25, or 125 muM. More (P < .01) embryos developed to blastocysts at 5% O2 (17%) than at apprx20% O2 (7%). Also, embryos grown at 5% O2 averaged more cells than embryos cultured at apprx20% O2 (38 vs 29 cells for morulae and blastocysts and 15 vs 12 cells including all embryos; P < .05). There were interactions (P < .01)

among chelator, concentration of chelator, and oxygen tension. The most efficacious treatments were 5muM EDTA at 5 or apprx20% O2 (24 and 20% blastocysts), 5 muM DTPA at 5% O2 (28% blastocysts), and 25 muM EDTA at 5% O2 (25% blastocysts). High concentrations of either chelator were detrimental, especially at apprx20% O2. In Exp. 2, a smaller range of chelator concentrations was compared (EDTA: 3, 9, 27, or 81 muM, DTPA: 3 or 15 muM) in 5% O2. More embryos developed to blastocysts and expanded blastocysts with 3 muM EDTA than the control without a chelator (20 and 16% vs 7 and 3%, respectively; P < .05). However, in Exp. 3, which concerned embryo development in .33, 1, 3, or 27 muM EDTA and .33, 1, or 3 muM DTPA, no concentration of either chelator was better (P > .1) than the control

Descriptors:zygote development: improved. Animal Husbandry (Agriculture); Development; Methods and Techniques; Reproductive System (Reproduction). EDTA; oxygen: tension reduction

Organism Descriptors:bovine (Bovidae): blastocyst, embryo, zygote. oocytes: reproductive system

Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates

Subject Codes:Animal Husbandry (Agriculture); Development; Methods and Techniques; Reproductive System (Reproduction)

ISSN:0021-8812
Year:2000
Journal Title:Journal of Animal Science

296. Title:Localization of POU1F1 to bovine, ovine, and caprine 1q21-22
View Article: Journal of Animal Science. 2000. 78 (1). 242-243
CD Volume:318
Print Article: Pages: 242-243
Author(s):Woollard J Tuggle C K Ponce de Leon F A
Author Variant:de-Leon-F-A-Ponce
Author Affiliation:Department of Animal Science, Iowa State University, Ames 50011, USA
Language:English
Abstract:A cattle lambda genomic library (Clontech, Inc., Palo Alto, CA) was screened by using the bovine POU1F1 cDNA. Positive recombinant phage were characterized by restriction digestion and Southern blotting analysis. Further analysis of an approximate 12 000-bp DNA fragment containing exons 3 through 6 and flanking genomic regions of the cattle POU1F1 gene included subcloning and sequencing of the exon 4 and exon 6 regions. Metaphase spreads were prepared from lymphoid cells obtained from cattle, sheep and goats (2 males and 2 females for each species). Standard cell culture procedures were used. To generate R-banded metaphases (RBP), cells were synchronized with methotrexate (10-6 M) for 17 h followed by addition of 20 micro g/ml of bromodeoxyuridine (BrdU) during the late synthesis phase. Standard cell harvesting and slide preparation procedures were used. Fluorescent in situ hybridization (FISH) was also carried out. The 12 000-bp genomic DNA fragment of the bovine POU1F1 gene was labelled with biotin-16-dATP by nick translation. Probe was detected with FITC-conjugated avidin DCS. After propidium iodide staining, slides were mounted with an alkaline antifade p-phenylenediamine, pH 11 (PPD-11). At least 20 metaphases from each of the animals were analysed. Cattle 1q21-22, sheep 1q21-22 and goat 1q21-22 genes were located. It is concluded that the current mapping of POU1F1 to identical locations in cattle, sheep and goat further extends this large region of homology. The nucleotide sequences

reported in this paper have been submitted to GenBank with accession numbers I38350 and I38351
Descriptors:localization. complementary-DNA. chromosomes. chromosome-banding. clones. DNA. nucleotide-sequences. exons. molecular-genetics. transcription-factors. translation. vectors. gene-mapping. biotechnology
Organism Descriptors:goats. sheep. cattle
Supplemental Descriptors:Capra. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Ovis. Bos
Subject Codes:LL240. WW000
Supplementary Info:9 ref
ISSN:0021-8812
Year:2000
Journal Title:Journal of Animal Science
Copyright:Copyright CAB International

297. Title:Two highly polymorphic dinucleotide microsatellites in rainbow trout (Oncorhynchus mykiss): OmyRGT18TUF and OmyRGT23TUF
View Article: Journal of Animal Science. 2000. 78 (2). 490-491
CD Volume:318
Print Article: Pages: 490-491
Author(s):Khoo S K Ozaki A Sakamoto T Okamoto N
Author Affiliation:Department of Aquatic Biosciences, Tokyo University of Fisheries, Minato, Tokyo 108-8477, Japan
Language:English
Abstract:Two multiallelic dinucleotide repeat (CA-microsatellite) polymorphisms in genomic DNA of rainbow trout (Oncorhynchus mykiss) were detected by PCR and designated as OmyRGT18TUF and OmyRGT23TUF. 17 unrelated rainbow trout obtained from 5 Japanese hatcheries were used. 11 and 10 alleles were detected in OmyRGT18TUF and OmyRGT23TUF respectively. The corresponding heterozygosities were 81 and 83%. The size and frequency of the alleles are presented
Descriptors:microsatellites. genetic-polymorphism. alleles. biotechnology
Organism Descriptors:Oncorhynchus. rainbow-trout. fishes
Supplemental Descriptors:Salmonidae. Salmoniformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms. Salmo
Subject Codes:LL240. WW000. MM300
ISSN:0021-8812
Year:2000
Journal Title:Journal of Animal Science
Copyright:Copyright CAB International

298. Title:Rapid communication: Cloning of bovine serum amyloid A3 cDNA
View Article: Journal of Animal Science. 78 (10). October, 2000. 2756-2757
CD Volume:319
Print Article: Pages: 2756-2757
Author(s):Kho Y J Cho K K Kim S C Kim S H Chung M I Baik M G Choi Y J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon, 441-744: cyjcow@snu.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:No Abstract available
Descriptors:lactation. Molecular Genetics (Biochemistry and Molecular Biophysics). bovine serum amyloid A3 cDNA: cloning; mRNA [messenger RNA]
Organism Descriptors:Bos taurus (Bovidae): breed-Holstein. mammary tissue

Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0021-8812
Year:2000
Journal Title:Journal of Animal Science

299. Title:Rigor temperature and meat quality characteristics of lamb longissimus muscle
View Article: Journal of Animal Science. 78 (11). November, 2000. 2842-2848
CD Volume:319
Print Article: Pages: 2842-2848
Author(s):Geesink G H Bekhit A D Bickerstaffe R
Author Affiliation:Molecular Biotechnology Group, Animal and Food Sciences Division, Lincoln University, Canterbury: geesinkg@whio.lincoln.ac.nz
Language:English
Language of Summary:English (EN)
Abstract:The present experiment was conducted to determine the effect of muscle temperature during the prerigor and early postrigor period on meat tenderness, postmortem proteolysis, calpain system activity, water-holding capacity, and color. Lamb longissimus muscle (n = 14) from the right and left carcass sides was excised immediately after dressing, divided into an anterior and posterior sample, vacuum-packaged, and stored overnight at 5 to 35degreeC. Further storage, up to 14 d postmortem, was at 2degreeC. Tenderness at 1 d postmortem, tenderization during further storage, and postmortem proteolysis were negatively affected by overnight incubation above 25degreeC. This effect could be explained by an effect of temperature on muscle contraction and activity of the calpain system. Muscle contraction was at a minimum after incubation at 15degreeC. Water-holding capacity was negatively affected by incubation above 25degreeC. Color scores improved with increasing incubation temperature at 1 d postmortem. However, after 14 d of postmortem storage, no differences in color scores were observed. Based on the present results and results of other groups, a temperature around 15degreeC at the onset of rigor seems optimal to maximize tenderness without having detrimental effects on water- holding capacity or color
Descriptors:calpain system; lamb: meat, tenderness; muscle temperature; postmortem proteolysis; rigor temperature. Foods; Muscular System (Movement and Support)
Organism Descriptors:sheep (Bovidae): breed-Romney x Coopworth, lamb. longissimus muscle: color, muscular system, water-holding capacity
Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Foods; Muscular System (Movement and Support)
ISSN:0021-8812
Year:2000
Journal Title:Journal of Animal Science

300. Title:A three-cascaded-enzymes biosensor to determine lactose concentration in raw milk
View Article: Journal of Dairy Science. 83 (9). September, 2000. 1939-1945
CD Volume:319
Print Article: Pages: 1939-1945
Author(s):Eshkenazi I Maltz E Zion B Rishpon J

Author Affiliation:Department of Molecular Microbiology and Biotechnology, Tel-Aviv University, Ramat-Aviv, 69978: rishpon@post.tau.ac.il
Language:English
Language of Summary:English (EN)
Abstract:The increasing demand for on-line measurement of milk composition directs science and industry to search for practical solutions, and biosensors may be a possibility. The specific objective of this work was to develop an electrochemical biosensor to determine lactose concentration in fresh raw milk. The sensor is based on serial reactions of three enzymes-beta-galactosidase, glucose oxidase, and horseradish peroxidase-immobilized on a glassy carbon electrode. The sequential enzymatic reactions increase the selectivity and sensitivity of the sensor. The sensor requires dilution of the raw milk and the addition of 5-aminosalicylic acid. Lactose concentrations in raw milk measured by the sensor were in good agreement with those measured by a reference laboratory using infrared technology. The results were obtained in milk samples that varied in fat and protein composition. From the results, we conclude that an electrochemical biosensor for determination of lactose concentration in fresh raw milk can be developed, and that the biosensor presented in this study maintained the qualities required for further development into an online sensor in the milking parlor
Descriptors:biotechnology; dairy science; food chemistry; milking parlors; raw milk: chemical analysis, dairy product. Enzymology (Biochemistry and Molecular Biophysics); Equipment, Apparatus, Devices and Instrumentation; Foods. immobilized enzymes: applications; lactose: concentration analysis
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Equipment, Apparatus, Devices and Instrumentation; Foods
ISSN:0022-0302
Year:2000
Journal Title:Journal of Dairy Science

301. Title:Induced lactation in prepubertal Holstein heifers
View Article: Journal of Dairy Science. 83 (11). November, 2000. 2459-2463
CD Volume:319
Print Article: Pages: 2459-2463
Author(s):Ball S Polson K Emeny J Eyestone W Akerst R M
Author Affiliation:Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, VA, 24061: rma@vt.edu
Language:English
Language of Summary:English (EN)
Abstract:Lactation was hormonally induced in six prepuberal Holstein heifers by seven daily injections of estrogen and progesterone and three injections of dexamethasone on d 18, 19, and 20, followed by twice daily hand milking beginning on d 21. Heifers were about 6 mo old and weighed 162 kg at the beginning of the experiment. Secretions were obtained from five of six of heifers, and twice daily milking continued for 75 d in three of five heifers. The volume of milk obtained on d 7 ranged from 32 to 500 ml and averaged 4.7, 4.1, and 3.7% lactose, protein, and fat, respectively. In the first natural lactation, milk yield and composition were nearly identical for controls and induced heifers. Serum alpha-lactalbumin was increased in induced heifers after treatment with dexamethasone and was highest on d 10 after onset of milking. Our data suggest that sufficient secretions for extensive biochemical testing can be obtained following hormonal induction of lactation in a majority of prepubertal heifers. Moreover, hormonal induction of lactation had no apparent effect on reproduction or first

natural lactation. While it is unlikely that hormonal induction of lactation in prepubertal heifers is practical from a dairy production viewpoint, the advent of biotechnology for production of therapeutic recombinant proteins in the mammary gland of transgenic livestock has made early detection of these transgenic proteins very desirable. We conclude that induction of lactation in prepubertal heifers is a viable technique for testing the expression of mammary- linked gene constructs in transgenic cattle
Descriptors:lactation: hormonal induction; milk: composition, dairy product, yield. Animal Husbandry (Agriculture); Foods. alpha-lactalbumin; dexamethasone; estrogen; fat; lactose; progesterone; protein
Organism Descriptors:cattle (Bovidae): breed-Holstein, dairy animal, female, heifer. serum: blood and lymphatics
Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Animal Husbandry (Agriculture); Foods
ISSN:0022-0302
Year:2000
Journal Title:Journal of Dairy Science

302. Title:Plant-bacterial combinations to phytoremediate soil contaminated with high concentrations of 2,4,6-trinitrotoluene
View Article: Journal of Environmental Quality. 2000. 29 (1). 311-316
CD Volume:320
Print Article: Pages: 311-316
Author(s):Siciliano S D Greer C W
Author Affiliation:Biotechnology Research Institute, 6100 Royalmount, Montreal, QC, H4P 2R2 Canada
Language:English
Abstract:The explosive 2,4,6-trinitrotoluene (TNT) is a contaminant of concern at abandoned manufacturing and military sites because of its mobility and toxicity. Phytoremediation may be important in natural attenuation scenarios by reducing TNT levels at point sources. A phytoremediation system suitable for use in soils contaminated with high TNT levels was developed. Sixteen grasses were screened for their tolerance to 41 g TNT kg-1 soil. Meadow bromegrass (Bromus erectus), perennial ryegrass (Lolium perenne) and sweet vernalgrass (Anthoxanthum odoratum) grew in this soil. Inoculating these grasses with Pseudomonas sp. Strain I4, capable of transforming TNT into mono- and di-amino metabolites, increased the growth of meadow bromegrass but was lethal to perennial ryegrass and sweet vernalgrass. Meadow bromegrass inoculated with Strain I4 reduced TNT levels by 30% compared with the control soil and had 50% more plant biomass than non-inoculated plants. Meadow bromegrass, combined with Strain I4, increased the percentage of the culturable soil heterotrophic population containing the genes involved in 2-nitrotoluene (ntdAa) metabolism 3-fold, as well as the population containing the genes involved in 4-nitrotoluene (ntnM) metabolism 14-fold. Strain I4 inoculation of meadow brome-grass altered the portion of the rhizosphere community involved in nitroaromatic metabolism and led to a reduction in soil TNT levels
Descriptors:reclamation. soil-types. polluted-soils. contamination. explosives. point-sources. rhizosphere. soil-toxicity
Organism Descriptors:Anthoxanthum-odoratum. Bromus-erectus. Poaceae. grasses. Lolium-perenne
Supplemental Descriptors:Anthoxanthum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Bromus. Lolium
Subject Codes:PP600. XX400. PP720

Supplementary Info:47 ref
ISSN:0047-2425
Year:2000
Journal Title:Journal of Environmental Quality

303. Title:Content of biogenic amines in table olives
View Article: Journal of Food Protection. 63 (1). Jan., 2000. 111-116
CD Volume:320
Print Article: Pages: 111-116
Author(s):Garcia Garcia P Brenes Balbuena M Hornero Mendez D Garcia Borrego A Garrido Fernandez A
Author Affiliation:Food Biotechnology Department, Instituto de la Grasa (C.S.I.C.), Avda. Padre Garcia Tejero, 4, 41012, Seville
Language:English
Language of Summary:English (EN)
Abstract:Content of biogenic amines in flesh and brines of table olives was determined by high-pressure liquid chromatography analysis of their benzoyl derivatives. No biogenic amines were found in the flesh of fresh fruits at any stage of ripeness. Contents of biogenic amines in Spanish-style green or stored olives increased throughout the brining period but were always higher in the former. Putrescine was the amine found in the highest concentration. Small quantities of cadaverine were found in the samples taken after 3 months of brining. This compound and histamine, tyramine, and tryptamine were also found in samples taken after 12 months. Gordal cultivar showed the highest contents, followed by Manzanilla and Hojiblanca. No relationship was found between contents of biogenic amines and lactic acid production or table olive spoilages, although zapatera olives had considerably higher amounts than those brines that had undergone a normal process. Concentrations in directly brined olives were markedly lower than contents in Spanish-style olives. With respect to partition between flesh and brine, there was equilibrium between both media in the case of Spanish-style olives, whereas the contents in directly brined olives were higher in flesh than brine
Descriptors:Spanish-style green olives: biogenic amine content, vegetable; table olives: biogenic amine content, vegetable. Foods. cadaverine; histamine; putrescine; tryptamine; tyramine
Organism Descriptors:Olea europaea [table olive] (Oleaceae): cultivar-Gordal, cultivar- Hojiblanca, cultivar-Manzanilla
Supplemental Descriptors:Oleaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods
ISSN:0362-028X
Year:2000
Journal Title:Journal of Food Protection

304. Title:Microbial testing methods for detection of residual cleaning agents and disinfectants: Prevention of ATP bioluminescence measurement errors in the food industry
View Article: Journal of Food Protection. 63 (2). Feb., 2000. 210-215
CD Volume:320
Print Article: Pages: 210-215
Author(s):Lappalainen Juha Loikkanen Satu Havana Marika Karp Matti Sjoberg Anna Maija Wirtanen Gun
Author Affiliation:Department of Biotechnology, University of Turku, Turku
Language:English
Language of Summary:English (EN)

Abstract:The ATP luminescence measurement is based on the presence of an enzymatic reaction and may significantly be affected by cleaning agents and disinfectants. In addition, disinfectants can also reduce the activity of the luciferase enzyme and also act as ATP- releasing agents. The agents disrupt the cell walls but preserve ATP in measurable form, and therefore correlation with culture methods can be poor. Therefore, if a rapid method is used to detect ATP, a control must be used for reliable results. The possible effect of disinfectants can be eliminated with a rapid test to minimize sources of error. In the present study a microbiological residue testing method that is nonspecific for residues was developed. The effects of a total of 38 commercial cleaning agents and disinfectants of various types were assessed using two microbiological methods, the Vibrio fischeri photobacteria test and Micrococcus luteus inhibition zone technique. The results show that the V. fischeri photobacteria test is very sensitive. This test can therefore be used for testing cleaning agent residues on surfaces in very small amounts. A small study was also carried out in a food factory to show applicability in processing facilities. The study showed, that a need for this type of method exists in food processing
Descriptors:Foods; Methods and Techniques. ATP; cleaning agents; disinfectants
Organism Descriptors:Micrococcus luteus (Micrococcaceae); Vibrio fischeri (Vibrionaceae)
Supplemental Descriptors:Micrococcaceae: Gram-Positive Cocci, Eubacteria, Bacteria, Microorganisms; Vibrionaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Foods; Methods and Techniques
ISSN:0362-028X
Year:2000
Journal Title:Journal of Food Protection

305. Title:Continuous source outbreak of campylobacteriosis traced to chicken
View Article: Journal of Food Protection.. 63 (3). March, 2000. 309-314
CD Volume:320
Print Article: Pages: 309-314
Author(s):Pearson Andrew D Greenwood Melody H Donaldson Jackie Healing Timothy D Jones Dennis M Shahamat Manouchehr Feltham R Kevin A Colwell Rita R
Author Affiliation:Center of Marine Biotechnology, University of Maryland, Biotechnology Institute, 701 E. Pratt Street, Baltimore, MD, 21202
Language:English
Language of Summary:English (EN)
Abstract:Poultry is a source of human campylobacteriosis, but a large continuous source outbreak, heretofore, has not been attributed to both a single source of poultry and single serotype of Campylobacter. Here we report an outbreak of C. jejuni affecting 6 catering college trainees and 13 patrons of a restaurant in southern England. An epidemiological investigation successfully tracked the outbreak source to the farm of origin. Frequency of occurrence of campylobacters and outbreak serotype distribution were determined in index cases, the local population, and local chicken suppliers. The source farm was investigated and the effect of interventions assessed. A single outbreak serotype of C. jejuni was isolated from trainee chefs, patrons, and chicken supplied to the college by Wholesaler A. The Campylobacter isolation rate for Wholesaler A was 89% (98% outbreak serotype), compared to 40% for non-Wholesaler A (10% outbreak serotype). The isolation rate for 14 months averaged 85% (99% outbreak serotype) in chickens grown on two farms (X and Y) supplying Wholesaler A, contributing apprx40% to all local

cases. In the research reported here, a specific strain and hygiene practice were found to be important for understanding transmission of Campylobacter from poultry to humans in this outbreak
Descriptors:chicken: poultry product. Foods; Infection; Epidemiology (Population Studies). campylobacteriosis: bacterial disease, outbreak
Geographic Locator:southern England (UK, Europe, Palearctic region)
Organism Descriptors:Campylobacter jejuni (Aerobic Helical or Vibrioid Gram-Negatives): food contaminant, pathogen; human (Hominidae): host
Supplemental Descriptors:Aerobic Helical or Vibrioid Gram-Negatives: Eubacteria, Bacteria, Microorganisms; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia. Animals; Bacteria; Chordates; Eubacteria; Humans; Mammals; Microorganisms; Primates; Vertebrates
Subject Codes:Foods; Infection; Epidemiology (Population Studies)
ISSN:0362-028X
Year:2000
Journal Title:Journal of Food Protection

306. Title:Effects of gamma radiation on sensory qualities, microbiological and chemical properties of salted and fermented squid
View Article: Journal of Food Protection. 63 (7). July, 2000. 934-939
CD Volume:320
Print Article: Pages: 934-939
Author(s):Byun Myung Woo Lee Kyong Haeng Kim Dong Ho Kim Jae Hun Yook Hong Sun Ahn Hyun Joo
Author Affiliation:Team for Radiation Food Science and Biotechnology, Korea Atomic Energy Research Institute, Yusong, Taejon, 305-353
Language:English
Language of Summary:English (EN)
Abstract:The effects of gamma radiation on sensory quality, microbial population, and chemical properties of salted and fermented squid were investigated. Squid (Todarodes pacificus) was sliced, washed, and then salted with 5, 10, and 20% (wt/wt) sodium chloride. Salted squid was irradiated with dosages of 0, 2.5, 5.0, and 10 kGy of gamma radiation and fermented at 15degreeC for 50 days. Proximate composition, salinity, water activity, sensory evaluation, and total microbiological populations were examined. Chemical analyses providing information on degree of fermentation, such as amino nitrogen (AN), volatile basic nitrogen (VBN), trimethylamine (TMA), and hypoxanthine (Hx) were also conducted. Irradiated squid was not different in proximate composition, salinity, and water activity from nonirradiated squid. Sensory evaluation scores, total bacteria populations, and pH values were variable depending on salt concentration and irradiation dose. During fermentation, AN, VBN, TMA, and Hx contents increased rapidly as the salt concentration and irradiation dose decreased. Specifically, these chemical compounds of salted and fermented squid prepared with 10% salt and 10 kGy of gamma radiation maintained the appropriate level of fermentation. The present results showed that the combination of low salt concentration (10%) and gamma radiation was effective in processing salted and fermented squid and extending its shelf life compared to control (20% of salt) without adding any food additives
Descriptors:squid: chemical properties, microbiological properties, seafood, sensory quality, shelf life. Foods. amino nitrogen; hypoxanthine; sodium chloride; trimethylamine; volatile basic nitrogen
Organism Descriptors:Todarodes pacificus [squid] (Cephalopoda)
Supplemental Descriptors:Cephalopoda: Mollusca, Invertebrata, Animalia. Animals; Invertebrates; Mollusks
Subject Codes:Foods
ISSN:0362-028X

Year:2000
Journal Title:Journal of Food Protection

307. Title:Effects of gamma radiation on the conformational and antigenic properties of a heat-stable major allergen in brown shrimp
View Article: Journal of Food Protection. 63 (7). July, 2000. 940-944
CD Volume:320
Print Article: Pages: 940-944
Author(s):Byun Myung Woo Kim Jae Hun Lee Ju Woon Park Jung Won Hong Chein Soo Kang Il Jun
Author Affiliation:The Team for Radiation Food Science and Biotechnology, Korea Atomic Energy Research Institute, Yusong, Taejon, 305-600
Language:English
Language of Summary:English (EN)
Abstract:This study was performed to evaluate the application of food irradiation technology as a method for reducing shrimp allergy without adverse effects. Shrimp heat-stable protein (HSP) was isolated and gamma irradiated at 0, 1, 3, 5, 7, or 10 kGy in the condition of solution (1 mg/ml), and fresh shrimp was also irradiated. Conformational change of irradiated HSP was monitored by means of spectrometric measures, enzyme-linked immunosorbent assay with mouse monoclonal antibody, or human patients' sera and sodium dodecyl sulfate-polyacrylamide gel electrophoresis. The ability of the immunoglobulin E of patients allergic to shrimp to bind to irradiated HSP was dose dependently reduced. The amount of intact HSP in an irradiated solution was reduced by gamma irradiation, depending on the dose. Sodium dodecyl sulfate- polyacrylamide gel electrophoresis showed that the main band disappeared and the traces induced from coagulation appeared at a higher molecular weight zone. The binding ability of immunoglobulin E to allergens in the extracts from irradiated shrimp decreased, depending on the dose. The results provide a new method so that food irradiation technology can be applied to reduce allergenicity of shrimp
Descriptors:brown shrimp: seafood. Biochemistry and Molecular Biophysics; Immune System (Chemical Coordination and Homeostasis); Foods. shrimp allergy: immune system disease. immunoglobulin E; shrimp heat-stable protein: allergen, antigenic properties, conformational properties
Organism Descriptors:human (Hominidae)
Supplemental Descriptors:Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia. Animals; Chordates; Humans; Mammals; Primates; Vertebrates
Subject Codes:Biochemistry and Molecular Biophysics; Immune System (Chemical Coordination and Homeostasis); Foods
ISSN:0362-028X
Year:2000
Journal Title:Journal of Food Protection

308. Title:Qualitative detection of tetracycline residues in milk with a luminescence-based microbial method: The effect of milk composition and assay performance in relation to an immunoassay and a microbial inhibition assay
View Article: Journal of Food Protection. 63 (7). July, 2000. 953-957
CD Volume:320
Print Article: Pages: 953-957
Author(s):Kurittu Jussi Lonnberg Stefan Virta Marko Karp Matti
Author Affiliation:Department of Biotechnology, University of Turku, Tykistokatu 6A, FIN-20520, Turku
Language:English

Language of Summary:English (EN)
Abstract:Performance of Tet-Lux, a newly developed microbiological test for the detection of tetracycline residues in raw milk, based on tetracycline-controlled luminescence activation of the test bacteria, was evaluated in bovine milks with variable amounts of somatic cells, bacteria, fat, protein, and natural inhibitory compounds. The sensitivity of Tet-Lux was also compared to a commercially available tetracycline immunoassay (Snap, Idexx Laboratories Inc.) and to a microbial inhibition test (Delvotest SP, Gist-Brogades). There were slight differences in the luminescence signals between different milk samples, but no single factor could be pointed out to be responsible for them. There appeared to be a modest inverse relationship between luminescence and increasing fat and protein content. The amount of somatic cells, bacteria, and the natural inhibitors lysozyme and lactoferrin did not affect the luminescence response. The test fulfilled the sensitivity requirement specified by the European Union (maximum residue limit 100 ng/ml for tetracyclines). The Tet- Lux test was clearly more sensitive to all tetracyclines tested (oxytetracycline, tetracycline, chlortetracycline, doxycycline, demeclocycline, methacycline, minocycline) than Delvotest SP, and for five tetracyclines out of seven more sensitive than Snap. The test provides a fast, simple, and robust microbial method for the qualitative detection of tetracycline residues in milk
Descriptors:bovine milk: composition, dairy product. Foods; Methods and Techniques. chlortetracycline: food contaminant; demeclocycline: food contaminant; doxycycline: food contaminant; fat; methacycline: food contaminant; minocycline: food contaminant; oxytetracycline: food contaminant; protein; tetracycline: food contaminant
Subject Codes:Foods; Methods and Techniques
ISSN:0362-028X
Year:2000
Journal Title:Journal of Food Protection

309. Title:Transformation of Korean chrysanthemum (Dendranthema zawadskii x D. x grandiflorum) and insertion of the maize autonomous element Ac using Agrobacterium tumefaciens
View Article: Journal of Genetics & Breeding. 2000. 54 (1). 19-24
CD Volume:321
Print Article: Pages: 19-24
Author(s):Tosca A Delledonne M Furini A Belenghi B Fogher C Frangi P
Author Affiliation:Centro Lombardo per l'Incremento della Floro Orto Frutticoltura, Fondazione Minoprio, Viale Raimondi 54, 22070 Vertemate con Minoprio (CO), Italy
Language:English
Abstract:Genetic transformation of Korean chrysanthemum (Dendranthema zawadskii x D. x grandiflorum [D. morifolium]) has been successfully achieved by co-cultivation with Agrobacterium tumefaciens strain EHA101 carrying the plasmid pIGP3 containing the maize transposable element Ac and the nptII gene as selectable marker. Selection with 100 mg l-1 kanamycin led to a transformation frequency of 7.8% with respect to co-cultivated explants. The nptII gene was detected by PCR analysis in transgenic regenerants and in the 4 progenies achieved. Southern blot analysis confirmed the presence of Ac in both the primary transformants and in their progeny. The restriction analysis of DNA with the methylation sensitive enzyme PvuII showed that the transposon was in a non-methylated status at the PvuII sites. We hypothesize that the Ac element is inserted in an active form and Ac might be successfully employed as gene tagging system in Korean chrysanthemum and related diploid species

Descriptors:chrysanthemums. genetic-transformation. transgenic-plants. transposable-elements. gene-tagging. ornamental-plants. biotechnology
Identifiers:Dendranthema zawadskii x Dendranthema morifolium. Dendranthema zawadskii
Organism Descriptors:Agrobacterium-tumefaciens. Dendranthema-morifolium
Supplemental Descriptors:Agrobacterium. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Dendranthema. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:20 ref
ISSN:0394-9257
Year:2000
Journal Title:Journal of Genetics & Breeding
Copyright:Copyright CAB International

310. Title:Use of molecular markers for studying genetic diversity in durum wheat (Triticum durum Desf.)
View Article: Journal of Genetics & Breeding. 2000. 54 (1). 25-33
CD Volume:321
Print Article: Pages: 25-33
Author(s):Szucs P Juhasz A Karsai I Lang L Veisz O Bedo Z
Author Affiliation:Agricultural Research Institute of the Hungarian Academy of Sciences, H-2462 Martonvasar, PO Box 19, Hungary
Language:English
Abstract:Diversity analysis was carried out using RFLP and RAPD markers to reveal differences between T. durum genotypes. In the RAPD analyses, 23 winter T. durum genotypes of different origins were examined (using three T. aestivum and three T. monococcum varieties as reference genotypes). Five of these were also tested using the RFLP method. Polymorphism was demonstrated between the 5 winter T. durum genotypes by 13 of the 47 RFLP probe x restriction endonuclease combinations (28%) and by 8 of the 16 RAPD primers (50%). Similarity values ranging from 0.04 to 0.14 were obtained with RFLP and 0.03 to 0.18 with RAPD. The correlation between the JD values obtained using the two methods was moderate, but not significant (r2 = 0.42). In the course of divergence analysis of the 23 T. durum genotypes using the RAPD method, 87.5% of the 16 primers revealed polymorphism. In this case, the value of the JD coefficient was between 0.03 and 0.74. The JD coefficients closely correlated to the groupings suggested by the pedigrees. In the present experiments, polymorphism was successfully demonstrated between T. durum genotypes with a relatively narrow genetic basis using RFLP probes and RAPD primers. These results can be utilised in the design of breeding programmes and could help in the development of T. durum crosses aimed at mapping DNA markers linked to various agronomic traits. They also draw attention to the restricted genetic basis of the cultivated T. durum genotypes
Descriptors:genetic-diversity. genetic-markers. restriction-fragment-length-polymorphism. random-amplified-polymorphic-DNA. cereals. wheat. biotechnology
Organism Descriptors:Triticum-durum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:44 ref
ISSN:0394-9257
Year:2000
Journal Title:Journal of Genetics & Breeding
Copyright:Copyright CAB International

311. Title:Role of growth regulators and glutamine for enhancing regeneration response in wheat (Triticum aestivum L.)
View Article: Journal of Genetics & Breeding. 2000. 54 (1). 71-75
CD Volume:321
Print Article: Pages: 71-75
Author(s):Shrivastava S Singh N Chawla H S
Author Affiliation:Genetics & Plant Breeding Dept., G. B. Pant Univ. of Agric. & Tech., Pantnagar, U.P. 263 145, India
Language:English
Abstract:The applicability of cereal tissue depends on reliable plant regeneration procedures. The objective of the investigation was to study the role of growth regulators and glutamine amino acid on regenerative ability from young and old callus cultures of high yielding genotypes of wheat. Callus was induced from immature embryo explants of 1-1.5 mm diameter on Murashige and Skoog (MS) basal medium supplemented with 2 mg/l 2, 4-D. Shoot formation was obtained from young calli (10- to 12-week-old) on MS medium without growth regulators. From young calli increase in regeneration frequency was obtained when cytokinin concentration increased from 1 to 2 mg/l. The addition of auxin to cytokinin containing media increased the regeneration frequency. When the medium contained 2 mg/l cytokinin and 0.5 mg/l NAA an average regeneration frequency of 91% was obtained. There was little increase in regeneration frequency when cytokinin and auxin medium was further supplemented with glutamine (150 mg/l). Regeneration from old calli (28- to 30-week-old) was obtained only when the medium contained growth regulators. There was progressive increase in regeneration frequency with the increase in cytokinin concentration from 1 to 3 mg/l. The same cytokinin medium when supplemented with low levels of auxin showed 3-6% increase in regeneration frequency. There was pronounced effect of glutamine on old callus cultures in increasing the regenerative ability by 6 to 10% when cytokinin or cytokinin-auxin containing media were supplemented with glutamine. Shoot induction frequency of 55% could be obtained from old callus cultures in a medium containing 3 mg/l cytokinin, 0.5 mg/l auxin and 150 mg/l glutamine
Descriptors:glutamine. plant-growth-regulators. regeneration. wheat. embryo-culture. 2,4-D. cytokinins. auxins. NAA. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. FF170
Supplementary Info:10 ref
ISSN:0394-9257
Year:2000
Journal Title:Journal of Genetics & Breeding

312. Title:Two soybean mutants with increased total and sulphur amino acid content induced by sodium azide
View Article: Journal of Genetics & Breeding. 2000. 54 (2). 83-87
CD Volume:321
Print Article: Pages: 83-87
Author(s):Hajduch M Debre F Bohmova B Dolesova P Pret'ova A
Author Affiliation:Institute of Plant Genetics and Biotechnology, Slovak Academy of Sciences, Akademicka 2, P.O. Box 39A, SK-950 07 Nitra, Slovakia
Language:English
Abstract:Soyabean (Glycine max var. Tolena) seeds were treated with 1 mM solution of sodium azide and the M3 generation was examined for variation in seed protein composition and in amino acid content. The genetic variability of seed protein composition and content of total

and sulphur amino acids were significantly increased by mutagenic treatment, when compared with Tolena control. Two mutants, designated as 236/6 and 240/8, were identified among 165 M3 plants to have significantly increased total amino acid and/or sulphur amino acid content. Total amino acids content of mutant 236/6 showed a 29% increase in comparison with Tolena control. Mutant 240/8 contained 31% more total amino acids and 36% more sulphur amino acids when compared to Tolena. This mutant showed also 46% increase in content of glutamic acid compared with control. The two mutants improved or retained investigated agronomical characters of Tolena

Descriptors:mutants. soyabeans. sulfur-amino-acids. glutamic-acid. mutagens. amino-acids. seed-treatment. sodium-azide. induced-mutations. seeds. chemical-composition. plant-proteins

Organism Descriptors:Glycine-max. Glycine-(Fabaceae)

Supplemental Descriptors:Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF020. FF040. QQ050. QQ500

Supplementary Info:17 ref

ISSN:0394-9257

Year:2000

Journal Title:Journal of Genetics & Breeding

313. Title:Yield potential and stability behaviour of in vitro derived somaclones of Japanese mint (Mentha arvensis L.) under different environments

View Article: Journal of Genetics & Breeding. 2000. 54 (2). 109-115

CD Volume:321

Print Article: Pages: 109-115

Author(s):Kukreja A K Dhawan O P Ahuja P S Sharma S Sushil Kumar

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Author Affiliation:Genetic Resources and Biotechnology Division, Central Institute of Medicinal and Aromatic Plants, P.O. CIMAP, Lucknow-226016, India

Language:English

Abstract:Performance and stability behaviour of six in vitro derived somaclones (Sc 59, Sc 93, Sc 114, Sc 121, Sc 124, Sc 179) of Japanese mint (Mentha arvensis) were estimated for herb and oil yield and some yield attributes at two widely different environments (Lucknow and Pantnagar) over a period of three years. Amongst the six somaclones evaluated, only Sc 93 and Sc 179 maintained their significant superiority over the parent for herb and oil yield trait at both locations (Lucknow and Pantnagar) every year. However, oil quality of both the clones in terms of menthol content was comparable to control. Significant genotype x environment (G x E) interactions were observed for all the agronomic traits (plant height, leaf-stem weight ratio, oil yield, oil content, herb yield and menthol content), suggesting that all traits were highly affected by environmental changes. Stability parameter, deviation from regression (s2d) of each in vitro developed somaclone for all characters, was highly significant as against the non-significant deviations in the control, suggesting that although somaclones Sc 93 and Sc 179 may exhibit better herb and oil yield traits, the genotypic stability was highly affected. Importance of G x E interactions and stability parameters as a prerequisite in breeding strategies for improvement of Japanese mint through somaclonal breeding approach is discussed

Descriptors:essential-oil-plants. essential-oils. yields. genotype-environment-interaction. stability. somaclonal-variation

Geographic Locator:India. Uttar-Pradesh

Organism Descriptors:Mentha-arvensis
Supplemental Descriptors:Mentha. Lamiaceae. Lamiales. dicotyledons. angiosperms. Spermatophyta. plants. South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations. India
Subject Codes:FF003. FF020. FF100
Supplementary Info:17 ref
ISSN:0394-9257
Year:2000
Journal Title:Journal of Genetics & Breeding
Copyright:Copyright CAB International

314. Title:Species relationship and hybrid identification in sorghum using RAPD, protein and isozyme techniques
View Article: Journal of Genetics & Breeding. 2000. 54 (2). 117-124
CD Volume:321
Print Article: Pages: 117-124
Author(s):Renganayaki K Amirthadevaranthinam A Sadasivam S
Author Affiliation:Crop Biotechnology Center, Texas A&M university, College Station, TX 77840-2123, USA
Language:English
Abstract:Randomly amplified polymorphic DNA (RAPD), protein and isoenzyme markers were used to study the variation among five Sorghum spp. and hybrids. Polymorphisms were observed among the species. The primer OPG 17 resulted in the highest number of clear markers and several polymorphic fragments. A genetic similarity study indicated that S. sudanense and S. propinquum possessed greater similarity (0.60), suggesting significant cross breeding between them. Cultivated sorghum, S. bicolor, exhibited the highest genetic similarity with S. halepense (2n = 40) followed by S. propinquum and S. sudanense. RAPD pattern in hybrids implied that they shared markers from their parents and possessed some unique markers, which could be helpful to study the introgression pattern. Seed protein and isozyme studies revealed that wild species and hybrids had some distinctive polypeptides that could help in species and hybrid cataloguing
Descriptors:identification. crossbreeding. hybrids. interspecific-hybridization. introgression. isoenzymes. random-amplified-polymorphic-DNA. polymorphism. plant-proteins. genetic-markers. genetic-distance. wild-relatives
Identifiers:Sorghum propinquum
Organism Descriptors:Sorghum-bicolor. Sorghum-halepense. Sorghum-sudanense
Supplemental Descriptors:Sorghum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. PP720. FF005. WW000. FF060
Supplementary Info:38 ref
ISSN:0394-9257
Year:2000
Journal Title:Journal of Genetics & Breeding
Copyright:Copyright CAB International

315. Title:Wild relatives of chickpea: multiple disease resistance and problems to introgression in the cultigen
View Article: Journal of Genetics & Breeding. 2000. 54 (3). 213-219
CD Volume:321
Print Article: Pages: 213-219
Author(s):Stamigna C Crino P Saccardo F
Author Affiliation:ENEA C.R. Casaccia, Biotechnology & Agriculture Division, Via Anguillarese 301, 00060 Rome, Italy
Language:English

Abstract:A large number of accessions of Cicer species have been tested for resistance to aggressive isolates of the third Italian pathogenic group of Ascochyta rabiei. Interesting levels of resistance were found in accessions of C. judaicum, C. bijugum and C. pinnatifidum; three of them (ILWC 76, ILWC 150, ILWC 186) showed double resistance to both Ascochyta blight and Fusarium wilt. Interspecific hybridizations C. arietinum x C. judaicum, C. arietinum x C. bijugum, C. arietinum x C. pinnatifidum were unsuccessfully tried. Foreign pollen germinated on the stigma and grew down through the style of flowers of C. arietinum 24 h after pollination. This suggested absence of interspecific incompatibility barriers at both the stigmatic and the stylar levels. Zygote formation was clearly observed 48 h later. Embryo growth, evident until to the third day after pollination, continued up to the sixth day, when a globular embryo was noted, but then the endosperm started to collapse. Occurrence of post-zygotic incompatibility barriers was demonstrated in all crosses
Descriptors:chickpeas. plant-genetic-resources. interspecific-hybridization. plant-pathogens. plant-pathogenic-fungi. plant-diseases. disease-resistance. varietal-reactions. fungal-diseases. pollination. endosperm. wild-relatives
Geographic Locator:Italy
Identifiers:Cicer judaicum. Cicer bijugum. Cicer pinnatifidum
Organism Descriptors:Cicer. Ascochyta-rabiei. Fusarium. Cicer-arietinum
Supplemental Descriptors:Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Southern-Europe. Europe. Mediterranean-Region. Developed-Countries. European-Union-Countries. OECD-Countries. Ascochyta. Deuteromycotina. Eumycota. fungi. Cicer
Subject Codes:FF020. FF005. PP720. FF060. FF610. HH600
Supplementary Info:32 ref
ISSN:0394-9257
Year:2000
Journal Title:Journal of Genetics & Breeding

316. Title:Inheritance of organogenesis parameters in cotyledons of sunflower (Helianthuus annuus L.)
View Article: Journal of Genetics & Breeding. 2000. 54 (3). 227-231
CD Volume:321
Print Article: Pages: 227-231
Author(s):Sarrafi A Kayyal H Al Chaarani G R Cantin F Chaline A S Durielle E
Author Affiliation:Department of Biotechnology and Plant Breeding, BAP, INP-ENSAT 18 Chemin de Borde Rouge B.P. 107, 31326 Castanet, France
Language:English
Abstract:Crosses were made between five cytoplasmic male sterile and five restorer sunflower inbred lines. Twenty five F1 hybrids and their parents were studied for their organogenesis ability in a randomized lock design with three replications. Each replication per genotype consisted of ten Petri dishes with four explants. Seeds were surface sterilized and subsequently germinated on hormone-free half strength MS medium. Regeneration medium consisted of full MS medium modified by the addition of hormones and solidified with 7 g agar/litre. Statistical analysis showed a high genetic variability for organogenesis parameters studied. Both general and specific combining abilities were significant for all of the organogenesis parameters, with either positive or negative values. Most of general combining ability values were less important than those of specific combining ability, indicating the importance of dominant gene effects controlling the organogenesis responses in the material studied

Descriptors:general-combining-ability. specific-combining-ability. combining-ability. inbred-lines. sunflowers. regenerative-ability. in-vitro-regeneration. culture-media. organogenesis. cytoplasmic-male-sterility. cotyledons
Organism Descriptors:Helianthus-annuus
Supplemental Descriptors:Helianthus. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. FF170. WW000
Supplementary Info:27 ref
ISSN:0394-9257
Year:2000
Journal Title:Journal of Genetics & Breeding

317. Title:Hydrophobic properties and chemical characterization of natural water repellent materials in Australian sands
View Article: Journal of Hydrology (Amsterdam) 2000. 231/232. 47-58
CD Volume:331
Print Article: Pages: 47-58
Author(s):Franco C M M Clarke P J Tate M E Oades J M
Author Affiliation:Biotechnology, School of Medicine, Flinders University of South Australia, GPO Box 2100, Adelaide, SA 5001, Australia
Conference Title:Water repellency in soils. Selected papers from an International Workshop held at the DLO Winand Staring Centre for Integrated Land, Soil and Water Research, Netherlands, 2-4 September 1998
Language:English
Abstract:Water-repellency in non-wetting sands is due to hydrophobic waxes present on the surface of sand grains and contained in particulate organic matter present in these sands. This study investigates the physicochemical characteristics of these natural waxes and compares them to waxes extracted from potential original source materials. Non-polar and polar hydrophobic wax extracts were obtained from whole non-wetting sand, and its individual constituents, and associated organic matter. These included the sand fraction, the intrinsic particulate organic matter, tree litter, eucalyptus leaves, bark, lucerne and lupin plants, and fungi and actinomycetes isolated from these sands. Waxes were characterized for their hydrophobic properties and composition of their chemical constituents. The hydrophobicities of the waxes were assessed by measuring the water-repellency induced after treating acid washed sand with wax extracts. Non-polar and polar wax extracts of the tree litter displayed hydrophobic properties that were similar to the corresponding waxes isolated from non-wetting sand and intrinsic particulate organic matter. Unlike these plant-derived waxes, the microbial wax extracts possessed different hydrophobic properties. Characterization of the components of the extracted waxes by GC-MS analysis showed a strong similarity in the composition of waxes isolated from non-wetting sand, tree litter and other plant material. The major components found were unbranched and branched C16 to C36 fatty acids and their esters, alkanes, phytanols, phytanes, and sterols. Some of these components were not detected in the microbial waxes. Unextracted samples, as well as wax extracts of non-wetting sand, intrinsic particulate organic matter, tree litter and fresh plant material were further analysed by solution and solid state NMR spectroscopy which indicated the relative content of the different chemical species present
Descriptors:characterization. properties. repellents. acids. alkanes. analysis. bark. characteristics. composition. extracts. fatty-acids. litter. lucerne. lupins. nuclear-magnetic-resonance. nuclear-magnetic-

resonance-spectroscopy. organic-matter. sand. sand-fraction. spectroscopy. sterols. waxes. hydrophobicity. water-repellent-soils
Geographic Locator:Australia
Organism Descriptors:Eucalyptus. Medicago-sativa. Medicago. Lupinus
Supplemental Descriptors:Myrtaceae. Myrtales. dicotyledons. angiosperms. Spermatophyta. plants. Medicago. Papilionoideae. Fabaceae. Fabales. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries
Subject Codes:JJ200. JJ400. JJ300
Supplementary Info:21 ref
ISSN:0022-1694
Year:2000
Journal Title:Journal of Hydrology

318. Title:Amelioration of water repellency: application of slow-release fertilisers to stimulate microbial breakdown of waxes
View Article: Journal of Hydrology (Amsterdam) 2000. 231/232. 342-351
CD Volume:331
Print Article: Pages: 342-351
Author(s):Franco C M M Michelsen P P Oades J M
Author Affiliation:Biotechnology, School of Medicine, Flinders University of South Australia, GPO Box 2100, Adelaide, South Australia 5001, Australia
Conference Title:Water repellency in soils. Selected papers from an International Workshop held at the DLO Winand Staring Centre for Integrated Land, Soil and Water Research, Netherlands, 2-4 September 1998
Language:English
Abstract:The use of slow-release fertilizers to stimulate indigenous wax-degrading microorganisms to reduce repellency on water repellent sands and to boost agricultural production was investigated . Laboratory and glasshouse experiments conducted with two slow-release sources of nitrogen and phosphorus (MaxBac(R) (N: P: K: S 22:5.7:0:0.6) and MagAMP(R)(N: P: K: Mg 7:20:5:9)) added to water repellent sand, in the absence of plant growth, resulted in a significant drop in hydrophobicity values apparently due to stimulation of wax-degrading microorganisms already present in the soil. Accordingly, two field experiments were set up in the south east of South Australia in which three different rates of the slow-release fertilizers were applied together with a low rate of kaolinitic, Mundulla clay. Subterranean clover was sown, but weeds were not controlled due to the unknown effect of herbicides on the soil microbial population. There was a significant decrease in water repellency at one site in the spring of the second year for the highest rates of MaxBac(R) compared to the unfertilized control at a depth of 0-5 cm. At the end of the summer, however, the water repellency had risen to the same value as the untreated controls at both sites. The following winter and spring, there was a decrease in water repellency at both sites, though there was no clear trend between treatments. The presence of plant growth was a key factor in the lack of a sustained effect of the fertilizers. The reduction in hydrophobicity, either due to degradation of waxes or the movement of dissolved organic matter, was reversed when temperatures were elevated in summer. Dissolved organic matter was decreased the severity of water repellency and may be an important factor in developing an amelioration strategy
Descriptors:breakdown. fertilizers. controlled-release. waxes. degradation. greenhouses. herbicides. hydrophobicity. microorganisms. nitrogen. organic-matter. phosphorus. repellents. research. sand. summer.

temperature. treatment. weeds. winter. bioremediation. soil-organic-matter
Geographic Locator:Australia. South-Australia
Organism Descriptors:Trifolium. Trifolium-subterraneum
Supplemental Descriptors:Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Trifolium. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Australia
Subject Codes:JJ300. WW000. JJ700
Supplementary Info:16 ref
ISSN:0022-1694
Year:2000
Journal Title:Journal of Hydrology
Copyright:Copyright CAB International

319. Title:Pathogenicity, development, and reproduction of Heterorhabditis bacteriophora and Steinernema carpocapsae under axenic in vivo conditions
View Article: Journal of Invertebrate Pathology. 2000. 75 (1). 55-58
CD Volume:329
Print Article: Pages: 55-58
Author(s):Han RiChou Ehlers R U
Author Variant:Han-R-C
Author Affiliation:Institute for Phytopathology, Department for Biotechnology and Biological Control, Christian-Albrechts-University Kiel, Klausdorfer Strasse 28-36, 24223 Raisdorf, Germany
Language:English
Abstract:The development and pathogenicity of bacteria-free Heterorhabditis bacteriophora and Steinernema carpocapsae dauer juveniles were studied in axenic Galleria mellonella. Dauer juveniles of H. bacteriophora invaded axenic larvae of G. mellonella, but these nematodes had no pathogenic effect. When treated with axenic juveniles of S. carpocapsae, all larvae died after 3 days. H. bacteriophora developed into hermaphrodites containing eggs and J1, but development beyond the J1 stage was not observed. Injection of bacterial supernatant into larvae at nematode inoculation or 5 days after nematode inoculation did not induce further development but resulted in insect death. Axenic juveniles of S. carpocapsae developed into adults and produced offspring. After 3 weeks, there were 5275 nematodes/larva, with 6.7, 39.2, 11.9 and 42.2% were dauer juveniles, other juvenile stages, males and females, respectively
Descriptors:entomopathogens. pathogenicity. biological-development. entomophilic-nematodes. insect-pests. nematology. natural-enemies. pathogens. agricultural-entomology
Identifiers:Rhabditida
Organism Descriptors:Heterorhabditis. Heterorhabditis-bacteriophora. Steinernema. Steinernema-carpocapsae. Galleria-mellonella. arthropods
Supplemental Descriptors:Heterorhabditidae. Nematoda. invertebrates. animals. Heterorhabditis. Steinernematidae. Steinernema. Galleria. Pyralidae. Lepidoptera. insects. arthropods
Subject Codes:YY700. FF620
Supplementary Info:24 ref
ISSN:0022-2011
Year:2000
Journal Title:Journal of Invertebrate Pathology
Copyright:Copyright CAB International

320. Title:Crystal structure of human procathepsin X: a cysteine protease with the proregion covalently linked to the active site cysteine

View Article: J Mol Biol 2000 Jan 28;295(4):939-51
CD Volume:304
Print Article: Pages: 939-951
Author(s):Sivaraman J Nagler DK Zhang R Menard R Cygler M
Author Affiliation:Biotechnology Research Institute, National Research Council of Canada, 6100 Royalmount Avenue, Montreal, Quebec, H4P 2R2, Canada
Abstract:Human cathepsin X is one of many proteins discovered in recent years through the mining of sequence databases. Its sequence shows clear homology to cysteine proteases from the papain family, containing the characteristic residue patterns, including the active site. However, the proregion of cathepsin X is only 38 residues long, the shortest among papain-like enzymes, and the cathepsin X sequence has an atypical insertion in the regions proximal to the active site. This protein was recently expressed and partially characterized biochemically. Unlike most other cysteine proteases from the papain family, procathepsin X is incapable of autoprocessing in vitro but can be processed under reducing conditions by exogenous cathepsin L. Atypically, the mature enzyme is primarily a carboxypeptidase and has extremely poor endopeptidase activity. We have determined the three-dimensional structure of the procathepsin X at 1.7 A resolution. The overall structure of the mature enzyme is characteristic for enzymes of the papain superfamily, but contains several novel features. Most interestingly, the short proregion binds to the enzyme with the aid of a covalent bond between the cysteine residue in the proregion (Cys10p) and the active site cysteine residue (Cys31). This is the first example of a zymogen in which the inhibition of enzyme's proteolytic activity by the proregion is achieved through a reversible covalent modification of the active site nucleophile. Such mode of binding requires less contact area between the proregion and the enzyme than observed in other procathepsins, and no auxiliary binding site on the enzyme surface is used. A three-residue insertion in a highly conserved region, just prior to the active site cysteine residue, confers a significantly different shape on the S' subsites, compared to other proteases from papain family. The 3D structure provides an explanation for the rather unusual carboxypeptidase activity of this enzyme and confirms the predictions based on homology modeling. Another long insertion in the cathepsin X amino acid sequence forms a beta-hairpin pointing away from the active site. This insertion, thought to be an equivalent of cathepsin B occluding loop, is located on the side of the protein, distant from the substrate binding site
Descriptors:Amino Acid Sequence. Binding Sites. Cathepsins. Crystallography, X-Ray. *Cysteine. Enzyme Precursors. Human. Molecular Sequence Data. Protein Structure, Secondary. Recombinant Proteins. Sequence Alignment. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't
Geographic Locator:ENGLAND
ISSN:0022-2836
Year:2000
Journal Title:Journal of Molecular Biology

321. Title:The solution structure of ribosomal protein L36 from Thermus thermophilus reveals a zinc-ribbon-like fold
View Article: J Mol Biol 2000 Feb 11;296(1):169-80
CD Volume:306
Print Article: Pages: 169-180
Author(s):Hard T Rak A Allard P Kloo L Garber M
Author Affiliation:Department of Biotechnology, Center for Structural Biochemistry, Novum, Huddinge, S-141 57, Sweden. Torleif.Hard@biochem.kth.se

Abstract:We have determined the solution NMR structure of the ribosomal protein L36 from Thermus thermophilus. L36 is the smallest protein in the large subunit of the prokaryotic ribosome. The sequence contains three completely conserved cysteine residues and one conserved histidine residue in a C-X(2)-C-X(12)-C-X(4)-H motif. Extended X-ray absorption fine structure spectroscopy was used to confirm that a purified L36 sample contains an equimolar amount of zinc. The structure of L36 was determined using simulated annealing based on NOE distance restraints, dihedral angle restraints and hydrogen bond distance restraints derived from NMR spectra of (15)N-labeled and non-labeled L36 samples at pH 7 and 12 degrees C, and by imposing tetrahedral zinc ion coordination geometry. The L36 fold is characterized by a triple-stranded antiparallel beta-sheet with the zinc-binding site at one end. The structure of the zinc site is well-determined and shows that the three cysteine sulphur atoms are supported by hydrogen bonds to backbone amide protons. The conserved histidine residue is located in a short 3(10)-helix and coordinates zinc by the N(delta1) atom. The electrostatic surface potential and location of conserved Arg, Lys and His side-chains suggest a large continuous L36-rRNA interaction interface. The folding topology as well as position and conformation of many conserved side-chains in L36 are very similar to those of zinc-ribbon domains found in the archaeal transcription factor TFIIB N terminus and the eukaryal transcription elongation factor hTFIIS C terminus. Given the relative antiquity of the ribosome it is possible that L36 reflects the parent of transcription-related zinc ribbons

Descriptors:Amino Acid Motifs. Amino Acid Sequence. Binding Sites. Conserved Sequence. Cysteine. Electrostatics. Histidine. Hydrogen Bonding. Models, Molecular. Molecular Sequence Data. *Nuclear Magnetic Resonance, Biomolecular. Protein Structure, Secondary. Protein Structure, Tertiary. RNA, Ribosomal. Ribosomal Proteins. Sequence Alignment. Solutions. Support, Non-U.S. Gov't. Thermus thermophilus. Zinc

Geographic Locator:ENGLAND

ISSN:0022-2836
Year:2000
Journal Title:Journal of Molecular Biology

322. Title:Stator structure and subunit composition of the V(1)/V(0) Na(+)-ATPase of the thermophilic bacterium Caloramator fervidus

View Article: J Mol Biol 2000 Feb 11;296(1):311-21
CD Volume:306
Print Article: Pages: 311-321

Author(s):Ubbink Kok T Boekema EJ van Breemen JF Brisson A Konings WN Lolkema JS

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Abstract:The V-type Na(+)-ATPase of the thermophilic, anaerobic bacterium Caloramator fervidus was purified to homogeneity. The subunit compositions of the catalytic V(1) and membrane-embedded V(0) parts were determined and the structure of the enzyme complex was studied by electron microscopy. The V(1) headpiece consists of seven subunits present in one to three copies, and the V(0) part of two subunits in a ratio of 5:2. An analysis of over 7500 single particle images obtained by electron microscopy of the purified V(1)V(0) enzyme complex revealed that the stalk region, connecting the V(1) and V(0) parts, contains two peripheral stalks in addition to a central stalk. One of the two is connected to the V(0) part, while the other is connected to the first via a bar-like structure that is positioned just above V(0), parallel with the plane of the membrane. In projection, this bar seems to

contact the central stalk. The data show that the stator structure that prevents rotation of the static part of V(0) relative to V(1) in the rotary catalysis mechanism of energy coupling in ATPases/ATPsynthases is more complex than previously thought
Descriptors:Adenosine Triphosphate. Adenosinetriphosphatase. Bacillaceae. Catalytic Domain. Enzyme Stability. Membrane Proteins. Microscopy, Electron. Models, Molecular. Molecular Weight. Protein Denaturation. *Protein Structure, Quaternary. Rotation. Sodium. Temperature
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323. Title:Rational design of cyclodextrin glycosyltransferase from Bacillus circulans strain 251 to increase alpha -cyclodextrin production
View Article: Journal of Molecular Biology. 2000. 296 (4). 1027-1038
CD Volume:306
Print Article: Pages: 1027-1038
Author(s):Veen B A van der Uitdehaag J C M Penninga D Alebeek G J W M van Smith L M Dijkstra B W Dijkhuizen L
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Language:English
Identifiers:cyclodextrin glycosyltransferase
Organism Descriptors:Bacillus. Bacillus-circulans
Supplemental Descriptors:Bacillaceae. Firmicutes. bacteria. prokaryotes. Bacillus
Subject Codes:QQ020. WW000. ZZ500
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324. Title:Combination of threading potentials and sequence profiles improves fold recognition
View Article: J Mol Biol 2000 Mar 10;296(5):1319-31
CD Volume:307
Print Article: Pages: 1319-1331
Author(s):Panchenko AR Marchler Bauer A Bryant SH
Author Affiliation:National Center for Biotechnology Information, National Institutes of Health, Building 38A, Room 8N805, Bethesda, MD 20894, USA
Abstract:Using a benchmark set of structurally similar proteins, we conduct a series of threading experiments intended to identify a scoring function with an optimal combination of contact-potential and sequence-profile terms. The benchmark set is selected to include many medium-difficulty fold recognition targets, where sequence similarity is undetectable by BLAST but structural similarity is extensive. The contact potential is based on the log-odds of non-local contacts involving different amino acid pairs, in native as opposed to randomly compacted structures. The sequence profile term is that used in PSI-BLAST. We find that combination of these terms significantly improves the success rate of fold recognition over use of either term alone, with respect to both recognition sensitivity and the accuracy of threading models. Improvement is greatest for targets between 10 % and 20 % sequence identity and 60 % to 80 % superimposable residues, where the number of models crossing critical accuracy and significance thresholds more than

doubles. We suggest that these improvements account for the successful performance of the combined scoring function at CASP3. We discuss possible explanations as to why sequence-profile and contact-potential terms appear complementary
Descriptors:*Algorithms. Computational Biology. Conserved Sequence. Evolution, Molecular. *Protein Folding. Proteins. Sensitivity and Specificity. Sequence Alignment. *Sequence Homology, Amino Acid. Software. Support, U.S. Gov't, P.H.S.. Templates. Thermodynamics
Geographic Locator:ENGLAND
ISSN:0022-2836
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325. Title:Experimental analysis and computer prediction of CTF/NFI transcription factor DNA binding sites
View Article: J Mol Biol 2000 Apr 7;297(4):833-48
CD Volume:307
Print Article: Pages: 833-848
Author(s):Roulet E Bucher P Schneider R Wingender E Dusserre Y Werner T Mermod N
Author Affiliation:Laboratory of Molecular Biotechnology, Centre for Biotechnology UNIL-EPFL and Institute of Animal Biology University of Lausanne, Lausanne, CH-1015, Switzerland
Abstract:Accurate prediction of transcription factor binding sites is needed to unravel the function and regulation of genes discovered in genome sequencing projects. To evaluate current computer prediction tools, we have begun a systematic study of the sequence-specific DNA-binding of a transcription factor belonging to the CTF/NFI family. Using a systematic collection of rationally designed oligonucleotides combined with an in vitro DNA binding assay, we found that the sequence specificity of this protein cannot be represented by a simple consensus sequence or weight matrix. For instance, CTF/NFI uses a flexible DNA binding mode that allows for variations of the binding site length. From the experimental data, we derived a novel prediction method using a generalised profile as a binding site predictor. Experimental evaluation of the generalised profile indicated that it accurately predicts the binding affinity of the transcription factor to natural or synthetic DNA sequences. Furthermore, the in vitro measured binding affinities of a subset of oligonucleotides were found to correlate with their transcriptional activities in transfected cells. The combined computational-experimental approach exemplified in this work thus resulted in an accurate prediction method for CTF/NFI binding sites potentially functioning as regulatory regions in vivo
Descriptors:Adenoviruses, Human. Algorithms. Base Sequence. Binding Sites. Cell Line. *Computer Simulation. Consensus Sequence. DNA. DNA-Binding Proteins. Dimerization. Human. Mutation. Oligodeoxyribonucleotides. Promoter Regions (Genetics). Replication Origin. Reproducibility of Results. Response Elements. Substrate Specificity. Support, Non-U.S. Gov't. Thermodynamics. Trans-Activation (Genetics). Transcription Factors. Transfection
Geographic Locator:ENGLAND
ISSN:0022-2836
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Journal Title:Journal of Molecular Biology

326. Title:The solution structure of Rhodobacter sphaeroides LH1beta reveals two helical domains separated by a more flexible region: structural consequences for the LH1 complex
View Article: J Mol Biol 2000 Apr 21;298(1):83-94
CD Volume:304

Print Article: Pages: 83-94
Author(s):Conroy MJ Westerhuis WH Parkes Loach PS Loach PA Hunter CN Williamson MP
Author Affiliation:Krebs Institute, Department of Molecular Biology and Biotechnology, University of Sheffield, UK
Abstract:Here, the solution structure of the Rhodobacter sphaeroides core light-harvesting complex beta polypeptide solubilised in chloroform:methanol is presented. The structure, determined by homonuclear NMR spectroscopy and distance geometry, comprises two alpha helical regions (residue -34 to -15 and -11 to +6, using the numbering system in which the conserved histidine residue is numbered zero) joined by a more flexible four amino acid residue linker. The C-terminal helix forms the membrane spanning region in the intact LH1 complex, whilst the N-terminal helix must lie in the lipid head groups or in the cytoplasm, and form the basis of interaction with the alpha polypeptide. The structure of a mutant beta polypeptide W(+9)F was also determined. This mutant, which is deficient in a hydrogen bond donor to the bacteriochlorophyll, showed an identical structure to the wild-type, implying that observed differences in interaction with other LH1 polypeptides must arise from cofactor binding. Using these structures we propose a modification to existing models of the intact LH1 complex by replacing the continuous helix of the beta polypeptide with two helices, one of which lies at an acute angle to the membrane plane. We suggest that a key difference between LH1 and LH2 is that the beta subunit is more bent in LH1. This modification puts the N terminus of LH1beta close to the reaction centre H subunit, and provides a rationale for the different ring sizes of LH1 and LH2 complexes
Descriptors:Amino Acid Sequence. Amino Acid Substitution. Bacteriochlorophylls. Binding Sites. Hydrogen Bonding. Models, Molecular. Molecular Sequence Data. Mutation. Nuclear Magnetic Resonance, Biomolecular. Photosynthetic Reaction Center, Bacterial. Pliability. Protein Structure, Secondary. Reproducibility of Results. Rhodobacter sphaeroides. Rhodospirillum. Solutions. Solvents. Structure-Activity Relationship. Support, Non-U.S. Gov't
Geographic Locator:ENGLAND
ISSN:0022-2836
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Journal Title:Journal of Molecular Biology

327. Title:The crystal structure of a sulfurtransferase from Azotobacter vinelandii highlights the evolutionary relationship between the rhodanese [thiosulfate sulfurtransferase] and phosphatase enzyme families
View Article: Journal of Molecular Biology. 2000. 298 (4). 691-704
CD Volume:305
Print Article: Pages: 691-704
Author(s):Bordo D Deriu D Colnaghi R Carpen A Pagani S Bolognesi M
Author Affiliation:Advanced Biotechnology Center, IST and Department of Physics, University of Genova INFM, Largo R. Benzi, 10 I-16132 Genova, Italy
Language:English
Descriptors:phosphoric-monoester-hydrolases. structure. thiosulfate-sulfurtransferase. enzymes. crystals. genes
Identifiers:sulfurtransferase
Organism Descriptors:Azotobacter. Azotobacter-vinelandii
Supplemental Descriptors:Pseudomonadaceae. Gracilicutes. bacteria. prokaryotes. Azotobacter
Subject Codes:JJ100. ZZ395
Supplementary Info:71 ref
ISSN:0022-2836

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328. Title:Phylogenetic analysis of the cadherin superfamily allows identification of six major subfamilies besides several solitary members
View Article: J Mol Biol 2000 Jun 9;299(3):551-72
CD Volume:307
Print Article: Pages: 551-572
Author(s):Nollet F Kools P van Roy F
Author Affiliation:Molecular Cell Biology Unit, Department of Molecular Biology, Flanders Interuniversity Institute for Biotechnology, Ledeganckstraat 35, Ghent, B-9000, Belgium
Abstract:Cadherins play an important role in specific cell-cell adhesion events. Their expression appears to be tightly regulated during development and each tissue or cell type shows a characteristic pattern of cadherin molecules. Inappropriate regulation of their expression levels or functionality has been observed in human malignancies, in many cases leading to aggravated cancer cell invasion and metastasis. The cadherins form a superfamily with at least six subfamilies, which can be distinguished on the basis of protein domain composition, genomic structure, and phylogenetic analysis of the protein sequences. These subfamilies comprise classical or type-I cadherins, atypical or type-II cadherins, desmocollins, desmogleins, protocadherins and Flamingo cadherins. In addition, several cadherins clearly occupy isolated positions in the cadherin superfamily (cadherin-13, -15, -16, -17, Dachsous, RET, FAT, MEGF1 and most invertebrate cadherins). We suggest a different evolutionary origin of the protocadherin and Flamingo cadherin genes versus the genes encoding desmogleins, desmocollins, classical cadherins, and atypical cadherins. The present phylogenetic analysis may accelerate the functional investigation of the whole cadherin superfamily by allowing focused research of prototype cadherins within each subfamily
Descriptors:Amino Acid Sequence. Animal. Cadherins. Gene Expression. Human. Molecular Sequence Data. Multigene Family. *Phylogeny. Protein Structure, Tertiary. Sequence Alignment. Structure-Activity Relationship. Support, Non-U.S. Gov't
Geographic Locator:ENGLAND
ISSN:0022-2836
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Journal Title:Journal of Molecular Biology

329. Title:Estimating the number of protein folds and families from complete genome data
View Article: J Mol Biol 2000 Jun 16;299(4):897-905
CD Volume:307
Print Article: Pages: 897-905
Author(s):Wolf YI Grishin NV Koonin EV
Author Affiliation:National Center for Biotechnology Information National Library of Medicine, National Institutes of Health, Bethesda, MD, 20894, USA
Abstract:Using the data on proteins encoded in complete genomes, combined with a rigorous theory of the sampling process, we estimate the total number of protein folds and families, as well as the number of folds and families in each genome. The total number of folds in globular, water-soluble proteins is estimated at about 1000, with structural information currently available for about one-third of the number. The sequenced genomes of unicellular organisms encode from approximately

25%, for the minimal genomes of the Mycoplasmas, to 70-80% for larger genomes, such as Escherichia coli and yeast, of the total number of folds. The number of protein families with significant sequence conservation was estimated to be between 4000 and 7000, with structures available for about 20% of these

Descriptors:*Conserved Sequence. Databases, Factual. *Genome. Genome, Archaeal. Genome, Bacterial. Genome, Fungal. *Protein Folding. Protein Structure, Tertiary. Proteins. Sampling Studies. Solubility. Statistical Distributions. Water

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Journal Title:Journal of Molecular Biology

330. Title:A DNA structural atlas for Escherichia coli

View Article: J Mol Biol 2000 Jun 16;299(4):907-30
CD Volume:307
Print Article: Pages: 907-930

Author(s):Pedersen AG Jensen LJ Brunak S Staerfeldt HH Ussery DW
Author Affiliation:Center for Biological Sequence Analysis, Department of Biotechnology, The Technical University of Denmark, Building 208, DK-2800 Lyngby, Denmark

Abstract:We have performed a computational analysis of DNA structural features in 18 fully sequenced prokaryotic genomes using models for DNA curvature, DNA flexibility, and DNA stability. The structural values that are computed for the Escherichia coli chromosome are significantly different from (and generally more extreme than) that expected from the nucleotide composition. To aid this analysis, we have constructed tools that plot structural measures for all positions in a long DNA sequence (e.g. an entire chromosome) in the form of color-coded wheels (http://www.cbs.dtu. dk/services/GenomeAtlas/). We find that these "structural atlases" are useful for the discovery of interesting features that may then be investigated in more depth using statistical methods. From investigation of the E. coli structural atlas, we discovered a genome-wide trend, where an extended region encompassing the terminus displays a high of level curvature, a low level of flexibility, and a low degree of helix stability. The same situation is found in the distantly related Gram-positive bacterium Bacillus subtilis, suggesting that the phenomenon is biologically relevant. Based on a search for long DNA segments where all the independent structural measures agree, we have found a set of 20 regions with identical and very extreme structural properties. Due to their strong inherent curvature, we suggest that these may function as topological domain boundaries by efficiently organizing plectonemically supercoiled DNA. Interestingly, we find that in practically all the investigated eubacterial and archaeal genomes, there is a trend for promoter DNA being more curved, less flexible, and less stable than DNA in coding regions and in intergenic DNA without promoters. This trend is present regardless of the absolute levels of the structural parameters, and we suggest that this may be related to the requirement for helix unwinding during initiation of transcription, or perhaps to the previously observed location of promoters at the apex of plectonemically supercoiled DNA. We have also analyzed the structural similarities between groups of genes by clustering all RNA and protein-encoding genes in E. coli, based on the average structural parameters. We find that most ribosomal genes (protein-encoding as well as rRNA genes) cluster together, and we suggest that DNA structure may play a role in the transcription of these highly expressed genes

Descriptors:Bacterial Proteins. Base Pairing. Color. Computational Biology. Computer Simulation. Crystallography, X-Ray. DNA, Bacterial. DNA, Superhelical. Deoxyribonuclease I. Escherichia coli. Genes, Bacterial. *Genome, Bacterial. Models, Molecular. *Nucleic Acid Conformation. Nucleosomes. Pattern Recognition. Phylogeny. Pliability. Promoter Regions (Genetics). RNA, Bacterial. Software. Statistics. Support, Non-U.S. Gov't. Thermodynamics
Geographic Locator:ENGLAND
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331. Title:Characterization of a conserved alpha-helical, coiled-coil motif at the C-terminal domain of the ATP-dependent FtsH (HflB) protease of Escherichia coli
View Article: J Mol Biol 2000 Jun 16;299(4):953-64
CD Volume:307
Print Article: Pages: 953-964
Author(s):Shotland Y Teff D Koby S Kobiler O Oppenheim AB
Author Affiliation:Department of Molecular Genetics and Biotechnology, The Hebrew University-Hadassah Medical School, Jerusalem, P.O. Box 12272, Israel
Abstract:FtsH (HflB) is an ATP-dependent protease found in prokaryotic cells, mitochondria and chloroplasts. Here, we have identified, in the carboxy-terminal region of FtsH (HfIB), a short alpha helix predicted of forming a coiled-coil, leucine zipper, structure. This region appears to be structurally conserved. The presence of the coiled-coil motif in the Escherichia coli FtsH (HflB) was demonstrated by circular dichroism and cross-linking experiments. Mutational analysis showed that three highly conserved leucine residues are essential for FtsH (HfIB) activity in vivo and in vitro. Purified proteins mutated in the conserved leucine residues, were found to be defective in the degradation of E. coli sigma(32) and the bacteriophage lambda CII proteins. In addition, the mutant proteins were defective in the binding of CII The mutations did not interfere with the ATPase activity of FtsH (HflB). Finally, the mutant proteins were found to be more sensitive to trypsin degradation than the wild-type enzyme suggesting that the alpha helical region is an important structural element of FtsH (HflB)
Descriptors:Adenosinetriphosphatase. Amino Acid Motifs. Amino Acid Sequence. Bacterial Proteins. Circular Dichroism. Conserved Sequence. Cross-Linking Reagents. Escherichia coli. Heat-Shock Proteins. Membrane Proteins. Models, Molecular. Molecular Sequence Data. Molecular Weight. Mutation. Peptide Fragments. Protein Binding. Protein Structure, Secondary. Protein Structure, Tertiary. Recombinant Fusion Proteins. Sequence Alignment. Support, Non-U.S. Gov't. Transcription Factors. Trypsin
Geographic Locator:ENGLAND
ISSN:0022-2836
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Journal Title:Journal of Molecular Biology

332. Title:Crystal structure of Streptomyces olivaceoviridis E-86 beta -xylanase containing xylan-binding domain
View Article: Journal of Molecular Biology. 2000. 300 (3). 575-585
CD Volume:308
Print Article: Pages: 575-585
Author(s):Fujimoto Z Kuno A Kaneko S Yoshida S Kobayashi H Kusakabe I Mizuno H

Author Affiliation:Department of Biotechnology, National Institute of Agrobiological Resources, Tsukuba, Ibaraki 305-8602, Japan
Language:English
Identifiers:crystal structure. Streptomyces olivaceoviridis. beta -xylanase
Organism Descriptors:Streptomyces
Supplemental Descriptors:Streptomycetaceae. Actinomycetales. Firmicutes. bacteria. prokaryotes
Subject Codes:QQ020. ZZ500
Supplementary Info:2 pp. of ref
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333. Title:Structures of chitobiase mutants complexed with the substrate Di-N-acetyl-d-glucosamine: the catalytic role of the conserved acidic pair, aspartate 539 and glutamate 540
View Article: J Mol Biol 2000 Jul 14;300(3):611-7
CD Volume:308
Print Article: Pages: 611-617
Author(s):Prag G Papanikolau Y Tavlas G Vorgias CE Petratos K Oppenheim AB
Author Affiliation:The Department of Molecular Genetics and Biotechnology, The Hebrew University-Hadassah Medical School, Jerusalem, 91120, Israel
Abstract:The catalytic domain of chitobiase (beta-N-1-4 acetylhexosaminidase) from Serratia marcescens, is an alpha/beta TIM-barrel. This enzyme belongs to family 20 of glycosyl hydrolases in which a conserved amino acid pair, aspartate-glutamate, is present (Asp539-Glu540). It was proposed that catalysis by this enzyme family is carried out by glutamate 540 acting as a proton donor and by the acetamido group of the substrate as a nucleophile. We investigated the role of Asp539 and Glu540 by site-directed mutagenesis, biochemical characterization and by structural analyses of chitobiase -substrate co-crystals. We found that both residues are essential for chitobiase activity. The mutations, however, led to subtle changes in the catalytic site. Our results support the model that Glu540 acts as the proton donor and that Asp539 acts in several different ways. Asp539 restrains the acetamido group of the substrate in a specific orientation by forming a hydrogen bond with N2 of the non-reduced (-1) sugar. In addition, this residue participates in substrate binding. It is also required for the correct positioning of Glu540 and may provide additional negative charge at the active site. Thus, these biochemical and structural studies provide a molecular explanation for the functional importance and conservation of these residues
Descriptors:Acetylglucosamine. Acetylglucosaminidase. Amino Acid Substitution. Aspartic Acid. Binding Sites. Catalysis. Conserved Sequence. Crystallization. Crystallography, X-Ray. Glutamic Acid. Hydrogen Bonding. Kinetics. Models, Molecular. Molecular Sequence Data. Mutation. Protein Binding. Protein Conformation. Serratia marcescens. Structure-Activity Relationship. Support, Non-U.S. Gov't. Thermodynamics
Geographic Locator:ENGLAND
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Journal Title:Journal of Molecular Biology

334. Title:Multiple regulators and their interactions in vivo and in vitro with the cbb regulons of Rhodobacter capsulatus
View Article: J Mol Biol 2000 Jul 28;300(5):1079-99
CD Volume:308

Print Article: Pages: 1079-1099
Author(s):Vichivanives P Bird TH Bauer CE Robert Tabita F
Author Affiliation:Department of Microbiology and Plant Biotechnology Center, The Ohio State University, 484 West 12th Avenue, Columbus, OH 43210-1292, USA
Abstract:The cbb(I) and cbb(II) operons encode structural genes which are important for carbon dioxide fixation via the Calvin-Benson-Bassham reductive pentose phosphate pathway in Rhodobacter capsulatus. Each operon is regulated by cognate LysR-type transcriptional activators, CbbR(I) and CbbR(II), with the product of the cbbR(I) gene, CbbR(I), able to control its own transcription under some growth conditions. Furthermore, CbbR(I) may at least partially regulate the cbb(II) operon, with significant, yet regulated transcription of the cbb(II) operon occurring in the absence of any CbbR. These results suggested the importance of additional regulators. Thus, in addition to the rather specific control exerted by CbbR, a more globally significant regulatory system, the RegA-RegB (PrrA-PrrB) two-component system, was found to contribute to transcriptional regulation of each cbb operon. The regA and regB mutant strains were found to contain constitutive levels of form I and form II RubisCO, the major proteins encoded by the cbb(I) and cbb(II) operons, respectively. In addition, DNaseI footprint analyses indicated that RegA*, a constitutively active mutant form of RegA, binds specifically to cbb(I) and cbb(II) promoter-operator regions. CbbR(I), CbbR(II), and RegA binding loci were localized relative to transcription start sites, leading to a coherent picture of how each of these regulators interacts with specific promoter-operator sequences of the cbb operons
Descriptors:Bacterial Proteins. Base Sequence. DNA Footprinting. DNA, Bacterial. DNA-Binding Proteins. Deoxyribonuclease I. Gene Expression Regulation, Bacterial. Models, Genetic. Molecular Sequence Data. Mutation. Operator Regions (Genetics). Promoter Regions (Genetics). Protein Binding. Protein Kinases. RNA, Messenger. Regulon. Rhodobacter capsulatus. Ribulose-Bisphosphate Carboxylase. Sequence Alignment. Support, U.S. Gov't, P.H.S.. Transcription Factors. Transcription, Genetic
Geographic Locator:ENGLAND
ISSN:0022-2836
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Journal Title:Journal of Molecular Biology

335. Title:fhlA repression by OxyS RNA: kissing complex formation at two sites results in a stable antisense-target RNA complex
View Article: J Mol Biol 2000 Jul 28;300(5):1101-12
CD Volume:308
Print Article: Pages: 1101-1112
Author(s):Argaman L Altuvia S
Author Affiliation:Department of Molecular Genetics and Biotechnology, The Hebrew University- Hadassah Medical School, Jerusalem, 91120, Israel
Abstract:OxyS is a small untranslated RNA that is induced in response to oxidative stress in Escherichia coli. This small RNA acts as a global regulator affecting the expression of multiple genes. OxyS represses the translation of fhlA, a transcriptional activator for formate metabolism. Previously, we have shown that fhlA repression by OxyS is mediated through base-pairing with a short sequence overlapping the ribosome binding site. Here we show that the OxyS-fhlA interaction involves a second site residing further downstream, within the coding region of fhlA. Mutations that disrupt pairing at this site affect the ability of OxyS to prevent 30 S ribosomes from binding to fhlA mRNA. Structure probing of fhlA mRNA demonstrates that both sites reside in

the loops of two stem-loop structures. OxyS-fhlA pairing analysis shows that OxyS binds wild-type fhlA with an apparent dissociation constant of 25 nM, indicating that kissing complex formation between OxyS and fhlA results in a stable antisense-target complex. Mutations at either site, which disrupt pairing of OxyS to fhlA, decrease the stability of this complex. Our results indicate that kissing complex formation is sufficient to repress fhlA translation by OxyS

Descriptors:Base Sequence. Binding Sites. Escherichia coli. Gene Expression Regulation, Bacterial. Genes, Reporter. Models, Molecular. Molecular Sequence Data. Mutagenesis, Site-Directed. Nucleic Acid Conformation. Nucleic Acid Hybridization. Oxidative Stress. RNA Stability. RNA, Antisense. RNA, Bacterial. RNA, Messenger. Regulatory Sequences, Nucleic Acid. Ribosomes. Sulfuric Acid Esters. Support, Non-U.S. Gov't. Thermodynamics. Trans-Activators. Translation, Genetic

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336. Title:Crystal structure of human grancalcin, a member of the penta-EF-hand protein family

View Article: J Mol Biol 2000 Jul 28;300(5):1271-81
CD Volume:308
Print Article: Pages: 1271-1281

Author(s):Jia J Han Q Borregaard N Lollike K Cygler M
Author Affiliation:Biotechnology Research Institute, National Research Council of Canada, 6100 Royalmount Avenue, Montreal, Quebec, H4P 2R2, Canada

Abstract:Grancalcin is a Ca(2+)-binding protein expressed at high level in neutrophils. It belongs to the PEF family, proteins containing five EF-hand motifs and which are known to associate with membranes in Ca(2+)-dependent manner. Prototypic members of this family are Ca(2+)-binding domains of calpain. Our recent finding that grancalcin interacts with L-plastin, a protein known to have actin bundling activity, suggests that grancalcin may play a role in regulation of adherence and migration of neutrophils. The structure of human grancalcin has been determined at 1.9 A resolution in the absence of calcium (R-factor of 0.212 and R-free of 0.249) and at 2. 5 A resolution in the presence of calcium (R-factor of 0.226 and R-free of 0.281). The molecule is predominantly alpha-helical: it contains eight alpha-helices and only two short stretches of two-stranded beta-sheets between the loops of paired EF-hands. Grancalcin forms dimers through the association of the unpaired EF5 hands in a manner similar to that observed in calpain, confirming this mode of association as a paradigm for the PEF family. Only one Ca(2+) was found per dimer under crystallization conditions that included CaCl(2). This cation binds to EF3 in one molecule, while this site in the second molecule of the dimer is unoccupied. This unoccupied site shows higher mobility. The structure determined in the presence of calcium, although does not represent a fully Ca(2+)-loaded form, suggests that calcium induces rather small conformational rearrangements. Comparison with calpain suggests further that the relatively small magnitude of conformational changes invoked by calcium alone may be a characteristic feature of the PEF family. Moreover, the largest differences are localized to the EF1, thus supporting the notion that calcium signaling occurs through this portion of the molecule and that it may involve the N-terminal Gly/Pro rich segment. Electrostatic potential distribution shows significant differences between grancalcin and calpain domain VI demonstrating their distinct character

Descriptors:Amino Acid Sequence. Animal. Binding Sites. Calcium. Calcium-Binding Proteins. Calpain. Crystallography, X-Ray. Dimerization. *EF Hand Motifs. Electrostatics. Human. Models, Molecular. Molecular Sequence Data. Neutrophils. Phosphoproteins. Protein Binding. Protein Structure, Secondary. Protein Structure, Tertiary. Rats. Recombinant Proteins. Sequence Alignment
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337. Title:Highly efficient selection of phage antibodies mediated by display of antigen as Lpp-OmpA' fusions on live bacteria
View Article: J Mol Biol 2000 Aug 25;301(4):893-904
CD Volume:305
Print Article: Pages: 893-904
Author(s):Benhar I Azriel R Nahary L Shaky S Berdichevsky Y Tamarkin A Wels W
Author Affiliation:Department of Molecular Microbiology and Biotechnology, The George S. Wise Faculty of Life Sciences, Green Building, Room 202, Ramat Aviv 69978, Israel. benhar@post.tau.ac.il
Abstract:Delayed infectivity panning (DIP) is a novel approach for the in vivo isolation of interacting protein pairs. DIP combines phage display and cell surface display of polypeptides as follows: an antigen is displayed in many copies on the surface of F(+) Escherichia coli cells by fusing it to a Lpp-OmpA' hybrid. To prevent premature, non-specific infection by phage, the cells are rendered functionally F(-) by growth at 16 degrees C. The antigen-displaying cells are used to capture antibody-displaying phage by virtue of the antibody-antigen interaction. Following removal of unbound phage, infection of the cells by bound phage is initiated by raising the temperature to 37 degrees C that facilitates F pilus expression. The phage then dissociate from the antigen and infect the bacteria through the F pilus. Using specific scFv antibodies and the human ErbB2 proto-oncogene and IL2-Ralpha chain as model antibody-antigen pairs, we demonstrate enrichment of those phage that display a specific antibody over phage that display an irrelevant antibody of over 1,000,000 in a single DIP cycle. We further show the successful isolation of anti-toxin, anti-receptor, anti-enzyme and anti-peptide antibodies from several immune phage libraries, a shuffled library and a large synthetic human library. The effectiveness of DIP makes it suitable for the isolation of rare clones present in large libraries.Since DIP can be applied for most of the phage libraries already existing, it could be a powerful tool for the rapid isolation and characterization of binders in numerous protein-protein interactions
Descriptors:Antibodies. Antibody Specificity. Antigen-Antibody Reactions. Antigens. Bacterial Outer Membrane Proteins. Bacteriophages. Carrier Proteins. Cloning, Molecular. Escherichia coli. Fimbriae, Bacterial. Human. Immunoglobulin Variable Region. *Peptide Library. Protein Binding. Receptor, erbB-2. Receptors, Interleukin-2. Recombinant Fusion Proteins. Sensitivity and Specificity. Support, Non-U.S. Gov't. Temperature
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Journal Title:Journal of Molecular Biology

338. Title:Arrangement of photosystem II supercomplexes in crystalline macrodomains within the thylakoid membrane of green plant chloroplasts
View Article: J Mol Biol 2000 Sep 1;301(5):1123-33

CD Volume:305
Print Article: Pages: 1123-1133
Author(s):Boekema EJ van Breemen JF van Roon H Dekker JP
Author Affiliation:Department of Biophysical Chemistry, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Nijenborgh 4, Groningen, 9747 AG, The Netherlands. boekema@chem.rug.nl
Abstract:The chloroplast thylakoid membrane of green plants is organized in stacked grana membranes and unstacked stroma membranes. We investigated the structural organization of Photosystem II (PSII) in paired grana membrane fragments by transmission electron microscopy. The membrane fragments were obtained by a short treatment of thylakoid membranes with the mild detergent n-dodecyl-alpha, d-maltoside and are thought to reflect the grana membranes in a native state. The membranes frequently show crystalline macrodomains in which PSII is organized in rows spaced by either 26.3 nm (large-spaced crystals) or 23 nm (small-spaced crystals). The small-spaced crystals are less common but better ordered. Image analysis of the crystals by an aperiodic approach revealed the precise positions of the core parts of PSII in the lattices, as well as features of the peripheral light-harvesting antenna. Together, they indicate that the so-called C(2)S(2) and C(2)S(2)M supercomplexes form the basic motifs of the small-spaced and large-spaced crystals, respectively. An analysis of a pair of membranes with a well-ordered large-spaced crystal reveals that many PSII complexes in one layer face only light-harvesting complexes (LHCII) in the other layer. The implications of this type of organization for the efficient transfer of excitation energy from LHCII to PSII and for the stacking of grana membranes are discussed
Descriptors:Crystallization. Macromolecular Systems. Microscopy, Electron. Photosynthetic Reaction Center, Plant. Spinach. Support, Non-U.S. Gov't. Thylakoids
Geographic Locator:ENGLAND
ISSN:0022-2836
Year:2000
Journal Title:Journal of Molecular Biology

339. Title:Mutational analysis of Escherichia coli PepA, a multifunctional DNA-binding aminopeptidase
View Article: J Mol Biol 2000 Sep 15;302(2):411-26
CD Volume:305
Print Article: Pages: 411-426
Author(s):Charlier D Kholti A Huysveld N Gigot D Maes D Thia Toong TL Glansdorff N
Author Affiliation:Microbiologie en Erfelijkheidsleer, Vrije Universiteit Brussel and Microbiology Department of the Flanders Interuniversity Institute for Biotechnology, 1-av. E. Gryson, Brussels, B-1070, Belgium. dcharlie@vub.ac.be
Abstract:Escherichia coli PepA is a hexameric aminopeptidase that is also endowed with a DNA-binding activity that functions in transcription control and plasmid dimer resolution. To gain further insight into the functioning of PepA, mutants were selected on the basis of reduced repressibility of a genomic carA-lacZ fusion and studied for the various cellular processes requiring PepA, i.e. repression of the carAB operon, autoregulation, resolution of ColE1 multimers, and peptide proteolysis. The methylation status of the carAB control region was analysed in several pepA mutants and purified proteins were assayed in vitro for car operator DNA binding. This study provides a critical test of predictions advanced on the basis of the structural analysis of PepA and demonstrates the importance for DNA binding of several secondary structural elements in the N-terminal domain and near the

very C terminus. By analysis of single amino acid substitutions, we could distinguish the mode of PepA action in car regulation from its action in plasmid resolution. We demonstrate that mere binding of PepA to the car control region is not sufficient to explain its role in pyrimidine-specific regulation; protein-protein interactions appear to play an important role in transcriptional repression. The multifunctional character of PepA and of an increasing number of transcriptional regulators that combine catalytic and regulatory properties, of which several participate in the metabolism of arginine and of the pyrimidines, suggests that enzymes and DNA (RNA) binding proteins fulfilling an essential primeval function may have been recruited in evolution to fulfil an additional regulatory task

Descriptors:Adenine. Aminopeptidases. Catalysis. Chromosomes, Bacterial. DNA Methylation. DNA, Bacterial. DNA-Binding Proteins. Escherichia coli. Feedback. Gene Expression Regulation, Bacterial. Genes, Reporter. Leucine. Models, Molecular. Multienzyme Complexes. Mutation. Nucleic Acid Conformation. Operator Regions (Genetics). Oxygenases. Plasmids. Promoter Regions (Genetics). Protein Binding. Protein Structure, Secondary. Repressor Proteins. Structure-Activity Relationship. Support, Non-U.S. Gov't

Geographic Locator:ENGLAND

ISSN:0022-2836
Year:2000
Journal Title:Journal of Molecular Biology

340. Title:Functional and crystallographic characterization of Salmonella typhimurium Cu,Zn superoxide dismutase coded by the sodCI virulence gene

View Article: J Mol Biol 2000 Sep 15;302(2):465-78
CD Volume:305
Print Article: Pages: 465-478

Author(s):Pesce A Battistoni A Stroppolo ME Polizio F Nardini M Kroll JS Langford PR O'Neill P Sette M Desideri A Bolognesi M

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Abstract:The functional and three-dimensional structural features of Cu,Zn superoxide dismutase coded by the Salmonella typhimurium sodCI gene, have been characterized. Measurements of the catalytic rate indicate that this enzyme is the most efficient superoxide dismutase analyzed so far, a feature that may be related to the exclusive association of the sodCI gene with the most pathogenic Salmonella serotypes. The enzyme active-site copper ion is highly accessible to external probes, as indicated by quenching of the water proton relaxation rate upon addition of iodide. The shape of the electron paramagnetic resonance spectrum is dependent on the frozen or liquid state of the enzyme solution, suggesting relative flexibility of the copper ion environment. The crystal structure (R-factor 22.6%, at 2.3 A resolution) indicates that the dimeric enzyme adopts the quaternary assembly typical of prokaryotic Cu,Zn superoxide dismutases. However, when compared to the structures of the homologous enzymes from Photobacterium leiognathi and Actinobacillus pleuropneumoniae, the subunit interface of Salmonella Cu,Zn superoxide dismutase shows substitution of 11 out of 19 interface residues. As a consequence, the network of structural water molecules that fill the dimer interface cavity is structured differently from the other dimeric bacterial enzymes. The crystallographic and functional characterization of this Salmonella Cu,Zn superoxide dismutase indicates that structural

variability and catalytic efficiency are higher in prokaryotic than in the eukaryotic homologous enzymes
Descriptors:Amino Acid Sequence. Binding Sites. Catalysis. Copper. Crystallization. Crystallography, X-Ray. Dimerization. Electromagnetic Fields. Electron Spin Resonance Spectroscopy. Freezing. Genes, Bacterial. Hydrogen-Ion Concentration. Iodides. Kinetics. Models, Molecular. Nuclear Magnetic Resonance, Biomolecular. Protein Structure, Quaternary. Protein Structure, Secondary. Protons. Salmonella typhimurium. Sequence Alignment. Solutions. Superoxide Dismutase. Support, Non-U.S. Gov't. Temperature. Virulence. Water
Geographic Locator:ENGLAND
ISSN:0022-2836
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Journal Title:Journal of Molecular Biology

341. Title:Probing the catalytic mechanism of GDP-4-keto-6-deoxy-d-mannose Epimerase/Reductase by kinetic and crystallographic characterization of site-specific mutants
View Article: J Mol Biol 2000 Oct 13;303(1):77-91
CD Volume:306
Print Article: Pages: 77-91
Author(s):Rosano C Bisso A Izzo G Tonetti M Sturla L De Flora A Bolognesi M
Author Affiliation:Department of Physics-INFM and Advanced Biotechnology Center-IST, University of Genova, Largo Rosanna Benzi 10, Genova, I-16132, Italy
Abstract:GDP-4-keto-6-deoxy-d-mannose epimerase/reductase is a bifunctional enzyme responsible for the last step in the biosynthesis of GDP-l-fucose, the substrate of fucosyl transferases. Several cell-surface antigens, including the leukocyte Lewis system and cell-surface antigens in pathogenic bacteria, depend on the availability of GDP-l-fucose for their expression. Therefore, the enzyme is a potential target for therapy in pathological states depending on selectin-mediated cell-to-cell interactions. Previous crystallographic investigations have shown that GDP-4-keto-6-deoxy-d-mannose epimerase/reductase belongs to the short-chain dehydrogenase/reductase protein homology family. The enzyme active-site region is at the interface of an N-terminal NADPH-binding domain and a C-terminal domain, held to bind the substrate. The design, expression and functional characterization of seven site-specific mutant forms of GDP-4-keto-6-deoxy-d-mannose epimerase/reductase are reported here. In parallel, the crystal structures of the native holoenzyme and of three mutants (Ser107Ala, Tyr136Glu and Lys140Arg) have been investigated and refined at 1. 45-1.60 A resolution, based on synchrotron data (R-factors range between 12.6 % and 13.9 %). The refined protein models show that besides the active-site residues Ser107, Tyr136 and Lys140, whose mutations impair the overall enzymatic activity and may affect the coenzyme binding mode, side-chains capable of proton exchange, located around the expected substrate (GDP-4-keto-6-deoxy-d-mannose) binding pocket, are selectively required during the epimerization and reduction steps. Among these, Cys109 and His179 may play a primary role in proton exchange between the enzyme and the epimerization catalytic intermediates. Finally, the additional role of mutated active-site residues involved in substrate recognition and in enzyme stability has been analyzed
Descriptors:Amino Acid Substitution. Binding Sites. Carbohydrate Epimerases. Catalysis. Chromatography, Thin Layer. Crystallography, X-Ray. Deoxy Sugars. Enzyme Stability. Escherichia coli. Fucose. Guanosine Diphosphate Mannose. Holoenzymes. Hydrogen Bonding. Kinetics. Models, Molecular. Multienzyme Complexes. Mutagenesis, Site-Directed.

Mutation. NADP. Protein Conformation. Protons. Structure-Activity Relationship. Substrate Specificity. Sugar Alcohol Dehydrogenases. Support, Non-U.S. Gov't
Geographic Locator:ENGLAND
ISSN:0022-2836
Year:2000
Journal Title:Journal of Molecular Biology

342. Title:Structural basis for the binding of an immunodominant peptide from myelin basic protein in different registers by two HLA-DR2 proteins
View Article: J Mol Biol 2000 Nov 24;304(2):177-88
CD Volume:306
Print Article: Pages: 177-188
Author(s):Li Y Li H Martin R Mariuzza RA
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Abstract:Susceptibility to multiple sclerosis (MS) is associated with certain MHC class II haplotypes, in particular HLA-DR2. Two DR beta chains, DRB1*1501 and DRB5*0101, are co-expressed in the HLA-DR2 haplotype, resulting in the formation of two functional cell surface heterodimers, HLA-DR2a (DRA*0101, DRB5*0101) and HLA-DR2b (DRA*0101, DRB1*1501). Both isotypes can present an immunodominant peptide of myelin basic protein (MBP 84-102) to MBP-specific T cells from MS patients. We have determined the crystal structure of HLA-DR2a complexed with MBP 86-105 to 1.9 A resolution. A comparison of this structure with that of HLA-DR2b complexed with MBP 85-99, reported previously, reveals that the peptide register is shifted by three residues, such that the MBP peptide is bound in strikingly different conformations by the two MHC molecules. This shift in binding register is attributable to a large P1 pocket in DR2a, which accommodates Phe92, in conjunction with a relatively shallow P4 pocket, which is occupied by Ile95. In DR2b, by contrast, the small P1 pocket accommodates Val89, while the deep P4 pocket is filled by Phe92. In both complexes, however, the C-terminal half of the peptide is positioned higher in the binding groove than in other MHC class II/peptide structures. As a result of the register shift, different side-chains of the MBP peptide are displayed for interaction with T cell receptors in the DR2a and DR2b complexes. These results demonstrate that MHC molecules can impose different alignments and conformations on the same bound peptide as a consequence of topological differences in their peptide-binding sites, thereby creating distinct T cell epitopes
Descriptors:Alleles. Amino Acid Sequence. Binding Sites. Comparative Study. Crystallography, X-Ray. HLA-DR2 Antigen. Human. Immunodominant Epitopes. Models, Molecular. Molecular Sequence Data. Multiple Sclerosis. Myelin Basic Proteins. Peptide Fragments. Protein Conformation. Protein Subunits. Receptors, Antigen, T-Cell. Sequence Alignment. Support, Non-U.S. Gov't. Support, U.S. Gov't, P.H.S.
Geographic Locator:ENGLAND
ISSN:0022-2836
Year:2000
Journal Title:Journal of Molecular Biology

343. Title:Achievements in management and utilization of southern grasslands
View Article: Journal of Range Management. 2000. 53 (1). 17-22
CD Volume:321
Print Article: Pages: 17-22
Author(s):Hoveland C S
Author Affiliation:Department of Crop & Soil Sciences, University of Georgia, Athens, Georgia 30602, USA

Language:English
Language of Summary:spanish
Abstract:Grasslands in the humid southern USA are utilized primarily for grazing on improved pastures, most of which were developed since the 1930s and 1940s. Virtually all of these grasslands were developed from species introduced from other areas of the world. Major achievements in successfully developing these grasslands, often on eroded cropland, were: (a) introduction of Kentucky 31 tall fescue (Festuca arundinacea); (b) introduction of Pensacola bahiagrass (Paspalum notatum); (c) breeding of Coastal bermudagrass (Cynodon dactylon); (d) fertilizer and lime use along with availability of low-cost N; (e) no-till planting of winter annual grasses; (f) pasture renovation with legumes; (g) herbicides for weed control; (h) recycling of agricultural wastes in forage production; (i) development of round hay baler; (j) controlled grazing; (k) discovery of the tall fescue fungal endophyte and its effect on livestock and the grass plant; (l) development of grazing-tolerant alfalfa (Medicago sativa); (m) improved cool season annual grasses and legumes for winter grazing; and (n) near infrared reflectance spectroscopy for rapid and low-cost forage analysis. Future areas of emphasis in improvement of these grasslands may include: (a) greater use of grazing-tolerant grasses and legumes; (b) stress-tolerant tall fescue with "friendly" non-toxic endophytes; (c) feed antidotes to the toxins of endophyte-infected tall fescue; (d) use of herbicide-and pest-resistant biotechnology genes in forage plants; (e) use of gypsum to alleviate subsoil acidity and improve rooting depth of aluminum-sensitive forage cultivars; (f) greater use of computers in information access and decision making by livestock producers; (g) greater use of forages for wildlife food; (h) breeding of pasture plants with greater winter productivity; (i) development of a perennial grass biomass energy industry for electrical generation and liquid fuel production
Descriptors:grasslands. decision-making. endophytes. forage. grazing. gypsum. hay. herbicides. legumes. livestock. pastures. pasture-plants. productivity. recycling. reflectance. rooting. rooting-depth. toxins. weeds. weed-control. wildlife. grassland-improvement. sward-renovation. reclamation. reviews. lucerne
Geographic Locator:Kentucky. USA. Southern-States-of-USA
Organism Descriptors:Medicago-sativa. Paspalum-notatum. Cynodon-dactylon. Festuca. Festuca-arundinacea. grasses. Poaceae. Paspalum
Supplemental Descriptors:Medicago. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Paspalum. Poaceae. Cyperales. monocotyledons. Cynodon. Festuca. Appalachian-States-of-USA. Southern-States-of-USA. USA. North-America. America. Developed-Countries. OECD-Countries. East-South-Central-States-of-USA
Subject Codes:FF007. PP350
Supplementary Info:34 ref
ISSN:0022-409X
Year:2000
Journal Title:Journal of Range Management

344. Title:Induction of superovulation by inhibin vaccine in cyclic guinea-pigs
View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 1-7
CD Volume:321
Print Article: Pages: 1-7
Author(s):Shi F Ozawa M Komura H Watanabe G Tsonis C G Suzuki A K Taya K
Author Affiliation:Laboratory of Veterinary Physiology, Tokyo University of Agriculture and Technology, Tokyo 183-8509, Japan
Language:English

Abstract:At 3 months of age, 18 female guineapigs were each given a subcutaneous progesterone implant for 4 weeks. A week after removal of the implants, the animals (in equal numbers) were given a subcutaneous injection of 1 ml placebo (saline in oil emulsion; control), 25 or 50 micro g inhibin vaccine 3 times at 4-week intervals. Blood samples were collected weekly throughout the experiment for measuring inhibin antibody titres. After the 3rd injection of inhibin vaccine, blood samples and ovaries were collected on the morning of day 8 after oestrus. Inhibin vaccine increased the ovulation rate in a dose-dependent manner (placebo, 4.2 plus or minus 0.4; 25 micro g inhibin vaccine, 6.2 plus or minus 0.9; 50 micro g inhibin vaccine, 9.8 plus or minus 0.9) without any effects on the duration of the oestrous cycle. Active immunization against inhibin increased the number of atretic follicles of 300-399 micro m in diameter on day 8 after ovulation. This is thought to be the first study to show that active immunization against inhibin may be a useful method for inducing multiple ovulation in guineapigs
Descriptors:inhibin. superovulation. vaccines. immunization. ovarian-follicles. oestrous-cycle. oestrus. ovaries. ovulation-rate. placebos. progesterone. biotechnology
Organism Descriptors:guineapigs
Supplemental Descriptors:Cavia. Caviidae. rodents. mammals. vertebrates. Chordata. animals
Subject Codes:LL250. LL600. WW000
Supplementary Info:55 ref
ISSN:0022-4251
Year:2000
Journal Title:Journal of Reproduction and Fertility

345. Title:Effect of exogenous LH pulses on the fate of the first dominant follicle in postpartum beef cows nursing calves
View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 9-17
CD Volume:321
Print Article: Pages: 9-17
Author(s):Duffy P Crowe M A Boland M P Roche J F
Author Affiliation:Faculty of Agriculture, University College Dublin, Lyons Research Farm, Newcastle, Co. Dublin, Irish Republic
Language:English
Abstract:In the first of 2 experiments, 8 Limousin x Friesian cows received 0.84 ml saline and 8 received 50 micro g porcine LH (pLH; Lutropin) as hourly pulses for 3-5 days from the 2nd day of dominance of the first dominant follicle (day 0). In experiment 2, 21 cows in equal numbers received 0.84 ml saline, 50 micro g pLH or 100 micro g pLH as hourly pulses for 3 days. Appropriate ovarian scanning and assays of blood samples were carried out. In experiment 1, the number of dominant follicles that underwent atresia was not affected by increasing the number of LH pulses, but the duration of dominance (days) of the first and second dominant follicles and maximum size (mm) of the second dominant follicle was increased ($P<0.05$). Oestradiol concentrations were higher ($P<0.05$) in cows given hourly pLH pulses (3.1 plus or minus 1.2 pg/ml) than in controls (1.2 plus or minus 0.2 pg/ml). Four of 8 treated cows had an anovulatory LH surge. The number of follicle waves to first ovulation was similar in control (4.6 plus or minus 0.9) and pLH treated cows (3.9 plus or minus 0.5). In experiment 2, 4 of 7 cows given pulses of 100 micro g pLH ovulated the first dominant follicle, and the interval from calving to first ovulation was decreased ($P<0.05$). In the remaining 3 cows, the duration of dominance of the first dominant follicle was increased ($P<0.005$), the maximum size of the first dominant follicle was greater ($P<0.05$), and the interval

(days) from the start of infusion to new wave emergence was longer (P<0.05) compared with cows that failed to ovulate in the 50 micro g pLH or control groups. It is concluded that hourly pulses of pLH from day 1 after dominance of the first dominant follicle in postpartum beef cows prolongs dominance or induces it to ovulate. The results support the hypothesis that LH pulse frequency is a key determinant of the fate of the dominant follicle in the early postpartum period
Descriptors:cows. atresia. LH. ovarian-follicles. estradiol. ovaries. ovulation. postpartum-period. biotechnology
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. WW000
Supplementary Info:29 ref
ISSN:0022-4251
Year:2000
Journal Title:Journal of Reproduction and Fertility
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346. Title:Effect of inhibitors and uncouplers of oxidative phosphorylation during compaction and blastulation of bovine embryos cultured in vitro
View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 47-55
CD Volume:321
Print Article: Pages: 47-55
Author(s):Thompson J G McNaughton C Gasparrini B McGowan L T Tervit H R
Author Affiliation:AgResearch Ruakura Research Centre, Private Bag 3123, Hamilton, New Zealand
Language:English
Abstract:The effect of inhibiting ATP production via oxidative phosphorylation during peri-compaction of in vitro produced bovine embryos was investigated. This was achieved by: (i) varying the atmospheric O2 concentration (0, 1, 2, 4 and 7%); (ii) addition of oxidative phosphorylation inhibitors, NaN3 and antimycin A; and (iii) addition of 2,4-dinitrophenol, an uncoupler of oxidative phosphorylation from electron transport. The development of embryos under various O2 concentrations from day 5 to day 7 of development indicated that an optimal concentration occurred at approximately 2%. Addition of >100 micro mol/litre NaN3 was toxic to embryo development, but 5-10 micro mol/litre NaN3 stimulated embryo development by 10-25%. A similar result was observed after addition of 2,4-dinitrophenol, whereas antimycin A was inhibitory at 1 micro mol/litre. At concentrations of NaN3 or 2,4-dinitrophenol that stimulated embryo development, the number of cells of the resulting blastocysts was also significantly increased. Addition of NaN3 from day 1 of development inhibited subsequent development. Metabolic data of NaN3-treated embryos revealed that O2 uptake was significantly lower at 100 micro mol/litre. There was a log linear increase (P<0.05) in glucose uptake between 0, 10 and 100 micro mol/litre NaN3. It is concluded that ATP production via oxidative phosphorylation is essential for bovine embryo development in vitro. However, transient (subacute) inhibition appears to be beneficial to embryo development and the number of cells, perhaps by creating a more favourable intracellular environment
Descriptors:embryos. in-vitro. inhibitors. ATP. electron-transfer. embryonic-development. glucose. uptake. inhibition. oxidative-phosphorylation. antimycin-A. culture-media. oxygen. sodium-nitrite. biotechnology
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. LL700. WW000

Supplementary Info:34 ref
ISSN:0022-4251
Year:2000
Journal Title:Journal of Reproduction and Fertility

347. Title:Effects of superovulated heifer diet type and quantity on relative mRNA abundances and pyruvate metabolism in recovered embryos
View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 69-78
CD Volume:321
Print Article: Pages: 69-78
Author(s):Wrenzycki C Sousa P de Overstrom E W Duby R T Herrmann D Watson A J Niemann H O'Callaghan D Boland M P
Author Variant:de-Sousa-P
Author Affiliation:Department of Biotechnology, Institut fur Tierzucht und Tierverhalten (FAL), Mariensee, 31535 Neustadt, Germany
Language:English
Abstract:Crossbred heifers were fed a daily ration of grass silage supplemented with a citrus-beet pulp-based concentrate at 3 kg/day (n = 18) or ad lib. (n = 19), or a barley-based concentrate at 3 kg/day (n = 20) or ad lib. (n = 19) for 116 days. In embryos derived from heifers fed the pulp-based diets, the relative abundances of mRNA for the alpha 1 subunit of Na/K-ATPase and the antioxidant enzyme Cu/Zn-SOD were not affected by day of collection or quantity of diet. In embryos derived from heifers fed the barley-based diets, the relative abundances of the Na/K-ATPase transcripts were also not changed by these main effects, while the relative abundances of the Cu/Zn-SOD transcripts were affected by day of collection and by the quantity of diet. Pyruvate metabolism was affected by day of collection, and was significantly increased in day-8 embryos compared with day-7 and day-6 embryos. Diet quantity did not affect pyruvate utilization, whereas diet type did increase pyruvate metabolism in the barley group compared with the pulp group. This is thought to be the first study to show that molecular and metabolic variations may exist in embryos derived in vivo and developed in donor heifers on nutritional regimens differing in type and quantity. Differences in embryos collected on different developmental days may be attributed to varying cell numbers. Alterations in the relative abundances of the Cu/Zn-SOD transcripts and pyruvate metabolism caused by the quantity of diet fed to the donor animals were attributed to alterations in metabolic end-products that accumulated in reproductive tract fluids, whereas differences in embryonic metabolism caused by type of diet were related to the composition of the diet. It is concluded that the results characterize embryos produced in vivo at the molecular level, and that the molecular markers used in the study can differentiate between populations of embryos produced under different nutritional regimens and determine conditions conducive to the production of good quality embryos
Descriptors:embryos. metabolism. messenger-RNA. pyruvic-acid. barley. diets. embryonic-development. heifers. feeding. nutrition. gene-expression. grass-silage. concentrates. superovulation. biotechnology
Organism Descriptors:cattle. Hordeum-vulgare
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:LL520. LL250. LL240. WW000
Supplementary Info:69 ref
ISSN:0022-4251
Year:2000
Journal Title:Journal of Reproduction and Fertility

348. Title:Effects of the Booroola Fec gene on ovarian follicular populations in superovulated Romanov ewes pretreated with a GnRH antagonist
View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 85-94
CD Volume:321
Print Article: Pages: 85-94
Author(s):Dufour J J Cognie Y Mermillod P Mariana J C Romain R F
Author Affiliation:Departement des sciences animales, Faculte des sciences de l'agriculture et de l'alimentation, Cite Universitaire, Sainte-Foy, Quebec, G1K 7P4, Canada
Language:English
Abstract:Endocrine control of follicular growth was studied in mature Romanov ewes carrying (RF+) or not carrying (R++) the Booroola Fec gene during an oestrous cycle after gonadotropin-dependent follicles were suppressed by treatment with GnRH antagonist (Antarelix, 0.5 mg per day) for 10 days or ewes were treated with saline (control). Purified pig FSH (pFSH, containing <1 micro g LH per 150 micro g FSH) was injected i.m. twice daily (08.00 and 17.00 h) in decreasing doses over 3 days in saline-treated (20 mg pFSH from day 12 to day 14) or 4 days for Antarelix-treated (36 mg pFSH from day 11 to day 14) ewes. The left ovary was removed after saline or Antarelix treatment and the right ovary was removed at the end of the superovulatory treatment. Ewes of both genotypes treated with Antarelix had lower plasma LH concentrations than did controls from day 0 to day 10. This inhibitory effect increased with day of treatment. The variability in FSH concentrations during the initial 10 days was reduced by Antarelix treatment in both genotypes. Plasma FSH concentrations were higher in RF+ than in R++ ewes. In both genotypes, FSH concentrations varied significantly with day of treatment, with the lowest concentrations on day 8 and the highest on day 5. RF+ ewes had a greater total and atretic number of antral follicles 0.62-1.12, 1.12-2.00 and 2.00-3.00 mm in diameter (for classes 2, 3 and 4 respectively) than did R++ ewes before and after superovulatory treatment. After superovulatory treatment, the total number of atretic and non-atretic follicles >3.00 mm in diameter (class 5) increased in both genotypes. Superovulatory treatment also increased the number of total and atretic class 4 follicles in RF+ ewes only. Conversely, superovulatory treatment decreased the mean number of class 3 follicles in both genotypes, while the number of atretic follicles was decreased only in R++ ewes. Antarelix significantly reduced the percentage of follicles >2.00 mm in diameter in RF+ but not in R++ ewes. Antarelix treatment before superovulation increased the total number of class 4 follicles in both genotypes but the increase was significantly greater in RF+ than in R++ ewes. It is concluded that Antarelix pretreatment favours a greater superovulatory response in Romanov ewes carrying the Fec gene because ovulatory follicles are recruited from a wider range of follicular size classes
Descriptors:ewes. GnRH. ovaries. Romanov. genes. ovarian-follicles. FSH. genotypes. inhibition. oestrous-cycle. LH. antagonists. biotechnology
Geographic Locator:Canada
Identifiers:Booroola
Organism Descriptors:sheep
Supplemental Descriptors:Ovis. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. North-America. America. Developed-Countries. Commonwealth-of-Nations. OECD-Countries
Subject Codes:LL250. LL240. WW000
Supplementary Info:22 ref
ISSN:0022-4251

Year:2000
Journal Title:Journal of Reproduction and Fertility
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349. Title:Hysteroscopic insemination of small numbers of spermatozoa at the uterotubal junction of preovulatory mares
View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 95-100
CD Volume:321
Print Article: Pages: 95-100
Author(s):Morris L H A Hunter R H F Allen W R
Author Affiliation:University of Cambridge, Department of Clinical Veterinary Medicine Equine Fertility Unit, Mertoun Paddocks, Woodditton Road, Newmarket, Suffolk CB8 9BH, UK
Language:English
Abstract:Mares were inseminated with motile spermatozoa suspended in 30-150 micro l Tyrode's medium directly onto the uterotubal papilla at the anterior tip of the uterine horn, ipsilateral to the ovary containing a dominant preovulatory follicle of more than or equal to 35 mm in diameter, by means of a fine gamete intrafallopian transfer (GIFT) catheter passed through the working channel of a strobed light videoendoscope. Insemination of 10, 8, 25, 14, 11 and 10 mares with, respectively, 10.0, 5.0, 1.0, 0.5, 0.1 or 0.001 x 106 motile spermatozoa resulted in conception rates of, respectively, 60, 75, 64, 29, 22 and 10%. Deposition of 1.0 x 106 motile spermatozoa onto the uterotubal papilla began to approach the limit of successful fertilization. These doses were much lower than the 3-15 x 109 spermatozoa normally ejaculated by fertile stallions during mating, and the accepted minimum dose of 500 x 106 spermatozoa used for conventional uterine body insemination in mares. It is concluded that the simplicity of the technique offers a practical means of exploiting new breeding technologies that require very small numbers of spermatozoa in horse breeding
Descriptors:artificial-insemination. mares. spermatozoa. conception-rate. fertilization. ovaries. stallions. uterus. techniques. biotechnology
Geographic Locator:UK
Organism Descriptors:horses
Supplemental Descriptors:Equus. Equidae. Perissodactyla. mammals. vertebrates. Chordata. animals. ungulates. British-Isles. Western-Europe. Europe. Developed-Countries. Commonwealth-of-Nations. European-Union-Countries. OECD-Countries
Subject Codes:LL250. WW000. LL240. ZZ900
Supplementary Info:30 ref
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Journal Title:Journal of Reproduction and Fertility
Copyright:Copyright CAB International

350. Title:Effects of activin A and follistatin on developmental kinetics of bovine embryos: cinematographic analysis in a chemically defined medium
View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 119-125
CD Volume:321
Print Article: Pages: 119-125
Author(s):Yoshioka K Suzuki C Iwamura S
Author Affiliation:Laboratory of Theriogenology, National Institute of Animal Health, Tsukuba 305-0856, Japan
Language:English
Abstract:The effects of recombinant human activin A and follistatin on the developmental kinetics of bovine presumptive zygotes matured and fertilized in vitro using time-lapse cinematography were investigated.

The presumptive zygotes were cultured for 9 days in a chemically defined medium (modified synthetic oviduct fluid, control) or modified synthetic oviduct fluid supplemented with activin A or follistatin. Development under cine-recording conditions was similar to that in an incubator. Addition of activin A to modified synthetic oviduct fluid increased, while addition of follistatin decreased, the percentage of zygotes that developed to morulae and blastocysts. Follistatin significantly prolonged the timing of development to the 9-16-cell stage compared with the control and activin A media. Activin A significantly shortened the duration of the 3rd cell cycle compared with the control, but follistatin significantly prolonged the 4th cell cycle compared with the control and activin A. Developmental arrest (lag-phase) during the 4-8-cell stage was observed in 95% of embryos that developed to >9-16-cell stage in all treatments. The greater the number of cells at the onset of the lag-phase, the earlier the onset and the shorter the duration of the phase, the further embryos were able to develop by day 9 in all treatments. The number of cells at the onset of the lag-phase in the medium containing activin A was significantly higher than it was in control or follistatin-containing media. Activin A significantly shortened the duration of the lag-phase compared with follistatin. It is concluded that activin A enhances in vitro development of bovine embryos by improving developmental kinetics

Descriptors:activins. embryos. culture-media. follistatin. kinetics. cell-cycle. in-vitro. embryonic-development. zygotes. in-vitro-fertilization. maturation. biotechnology

Organism Descriptors:cattle

Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates

Subject Codes:LL250. WW000. LL600

Supplementary Info:27 ref

ISSN:0022-4251

Year:2000

Journal Title:Journal of Reproduction and Fertility

351. Title:Effect of GnRH antagonist-induced prolonged follicular phase on follicular atresia and oocyte developmental competence in vitro in superovulated heifers

View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 137-144

CD Volume:321

Print Article: Pages: 137-144

Author(s):Oussaid B Lonergan P Khatir H Guler A Monniaux D Touze J L Beckers J F Cognie Y Mermillod P

Author Affiliation:INRA, Unite Physiologie de la Reproduction des Mammiferes Domestiques, 37380 Nouzilly, France

Language:English

Abstract:Oestrous cycles were synchronized in 12 heifers with progestogen (norgestomet) implants for 10 days. On day 4 (oestrus = day 0), heifers were stimulated with 24 mg pFSH for 4 days and luteolysis was induced on day 6 with 2 ml PG (Estrumate). Animals in the control group (n = 4) were killed 24 h after the last FSH injection. At this time, heifers in groups A36h (n = 4) and A60h (n = 4) were treated with 1.6 mg GnRH antagonist (Antarelix) at 12-h intervals for 36 and 60 h respectively, and then killed. After dissection of ovarian follicles, oocytes were collected for individual in vitro maturation, fertilization and culture; follicular fluid was collected for determination of steroid concentrations, and granulosa cells were smeared, fixed and stained for evaluation of pycnosis rates. Granulosa cell smears showed that 90% of follicles were healthy in the control group. 36 and 58% of the

follicles in group A36h showed signs of early or advanced atresia respectively, while 90% of the follicles in group A60h showed signs of late atresia. Intrafollicular concentrations of oestradiol decreased (P<0.0001) from healthy follicles (799.14 plus or minus 40.65 ng/ml) to late atretic follicles (3.96 plus or minus 0.59 ng/ml). Progesterone concentrations were higher (P<0.0001) in healthy follicles compared with atretic follicles, irrespective of degree of atresia. Oestradiol:progesterone ratios decreased (P<0.0001) from healthy (4.58 plus or minus 0.25) to late atretic follicles (0.07 plus or minus 0.009). The intrafollicular concentrations of oestradiol and progesterone were higher (P<0.0001) in the control than in the treated groups. The oestradiol:progesterone ratio was higher (P<0.0001) in the control (4.55 plus or minus 0.25) than in the A36h (0.40 plus or minus 0.05) and A60h (0.07 plus or minus 0.009) groups. The cleavage rate of fertilized oocytes, blastocyst rate and number of cells per blastocyst were not significantly different among control (85%, 41% and 95 plus or minus 8), A36h (86%, 56% and 93 plus or minus 5) and A60h (88%, 58% and 79 plus or minus 4) groups. There were no significant differences in the blastocyst rates from oocytes derived from healthy (45%), early atretic (54%), advanced atretic (57%) and late atretic (53%) follicles. It is concluded that the maintenance of the preovulatory follicles in superovulated heifers with a GnRH antagonist induced more atresia and a decrease in oestradiol and progesterone concentrations. However, the developmental potential in vitro to day 8 of the oocytes recovered from these atretic follicles was not affected

Descriptors:atresia. GnRH. heifers. in-vitro. blastocyst. antagonists. in-vitro-fertilization. ovarian-follicles. follicular-fluid. FSH. progestogens. granulosa-cells. maturation. luteolysis. estradiol. oestrus. oocytes. ovaries. progesterone. superovulation. development. LH. biotechnology

Geographic Locator:France

Supplemental Descriptors:Western-Europe. Europe. Mediterranean-Region. Developed-Countries. European-Union-Countries. OECD-Countries

Subject Codes:LL250. LL600. WW000. LL700

Supplementary Info:60 ref

ISSN:0022-4251

Year:2000

Journal Title:Journal of Reproduction and Fertility

352. Title:Effect of long-term selection for early postnatal growth rate on survival and prenatal development of transferred mouse embryos

View Article: Journal of Reproduction and Fertility. 2000. 118 (1). 205-210

CD Volume:321

Print Article: Pages: 205-210

Author(s):Ernst C A Rhees B K Miao C H Atchley W R

Author Affiliation:Department of Genetics, North Carolina State University, Raleigh, NC 27695-7614, USA

Language:English

Abstract:Reciprocal embryo transfer procedures were performed among mouse selection lines to examine prenatal maternal effects on survival and development of transferred embryos. Mice were from generations 28 and 29 of an experiment to select for (i) increased body weight gain from 0 to 10 days (E+); (ii) decreased body weight gain from 0 to 10 days (E-); or (iii) a randomly bred control line (C). A total of 118 embryo transfer procedures performed 12 h after conception resulted in 983 progeny born to 89 litters. There was a 39% overall embryo survival rate and 75% overall pregnancy success rate. Response to superovulation and oestrous synchronization was lower (P<0.01) in the E+ line. E+

individuals that did superovulate produced an average of 37 oocytes per flush, which was higher (P<0.01) than in the control line (29 oocytes per flush). The ability to complete pregnancy successfully was not affected by uterine environment or embryo-uterine interaction. In contrast, embryo survival in successful pregnancies was significantly affected by uterine environment. There were large maternal effects for body weight and tail length at birth; E+ recipients produced pups that were larger (P<0.01) than those of E- recipients, which in turn were larger (P<0.01) than pups produced by control recipients

Descriptors:embryos. growth-rate. survival. conception. embryo-transfer. selection. lines. oestrus. maternal-effects. oocytes. pregnancy. progeny. superovulation. synchronization. weight-gain. embryonic-development. biotechnology

Organism Descriptors:mice

Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals

Subject Codes:LL240. LL250. WW000. LL600

Supplementary Info:19 ref

ISSN:0022-4251

Year:2000

Journal Title:Journal of Reproduction and Fertility

353. Title:Effect of nutrition and superovulation on oocyte morphology, follicular fluid composition and systemic hormone concentrations in ewes

View Article: Journal of Reproduction and Fertility. 2000. 118 (2). 303-313

CD Volume:321

Print Article: Pages: 303-313

Author(s):O'Callaghan D Yaakub H Hyttel P Spicer L J Boland M P

Author Affiliation:Faculty of Veterinary Medicine, University College, Dublin, Irish Republic

Language:English

Abstract:The effect of dietary intake on follicle and oocyte morphology in unstimulated and superovulated ewes was investigated. 54 ewes were fed grass meal at 0.5, 1.0 or 2.0 times maintenance energy requirements (M) for 32 days. Oestrous cycles were synchronized using progestogen pessaries and unstimulated or superovulated with 200 mg pig FSH. The ewes were killed and ovaries were collected 36 or 12 h before the anticipated LH surge. Serum progesterone concentrations in ewes on day 10 after withdrawal of the pessary were lower (P<0.05) in ewes fed 2.0M than in those fed 0.5M or 1.0M. LH pulse frequency tended to be higher in ewes fed 2.0M than 1.0M (1.0 plus or minus 0.3 vs. 0.3 plus or minus 0.2 pulses per 8 h) on day 6 after removal of the pessary but the effect was not significant. In unstimulated ewes, more (P<0.05) follicles (more than or equal to 3 mm in diameter) were observed in ewes fed 2.0M (3.5 plus or minus 0.3) than in those fed 0.5M (2.4 plus or minus 0.3) or 1.0M (2.4 plus or minus 0.5). Fewer (P<0.05) follicles were observed in superovulated ewes on 0.5M (7.5 plus or minus 1.2) than in those on 1.0M (12.0 plus or minus 0.5) or 2.0M (12.3 plus or minus 1.4). Follicular fluid progesterone concentrations were higher (P<0.05) in ewes fed 0.5M than in those fed 1.0M or 2.0M. Insulin-like growth factor (IGF)-I concentrations were higher (P<0.05) in follicular fluid from ewes on 1.0M than from those on 0.5M or 2.0M, whereas IGF-II concentrations were lower (P<0.05) in follicular fluid from ewes on 2.0M than from those on 1.0M or 0.5M. Superovulation increased (P<0.01) follicular fluid progesterone, oestradiol, IGF-I and IGF-II concentrations. Concentrations of the 34, 22 and 20 kDa IGF binding proteins were lower (P<0.05) in follicles from superovulated than in

those from unstimulated ewes. Oocytes from superovulated ewes showed abnormalities such as premature activation of cumulus expansion and vacuolation of the nucleolus and increased frequency of detachment of interchromatin-like granules from the nucleolar remnant. It is concluded that both high and low dietary intakes can alter systemic and follicular fluid hormone concentrations. Relative to dietary effects, the effects of superovulation were greater and involved substantial increases in follicular fluid hormone concentrations and abnormal oocyte morphology

Descriptors:ewes. hormones. follicular-fluid. nutrition. superovulation. abnormalities. binding-proteins. energy-requirements. ovarian-follicles. FSH. growth-factors. insulin-like-growth-factor. estradiol. oocytes. ovaries. progesterone. feed-intake. reproduction. biotechnology

Organism Descriptors:sheep

Supplemental Descriptors:Ovis. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates

Subject Codes:LL250. LL600. WW000. LL510

Supplementary Info:73 ref

ISSN:0022-4251

Year:2000

Journal Title:Journal of Reproduction and Fertility

354. Title:Meiotic competence of in vitro grown goat oocytes

View Article: Journal of Reproduction and Fertility. 2000. 118 (2). 367-373

CD Volume:321

Print Article: Pages: 367-373

Author(s):Crozet N Dahirel M Gall L

Author Affiliation:Institut National de la Recherche Agronomique, Unite de Physiologie animale, 78352 Jouy-en-Josas Cedex, France

Language:English

Abstract:The objective of this study was to grow meiotically incompetent goat oocytes from early antral follicles in vitro and to render them competent to undergo germinal vesicle breakdown. Cumulus-oocyte complexes with pieces of parietal granulosa cells were isolated from follicles 0.35-0.45 mm in diameter using both mechanical and enzymatic methods. The cumulus-oocyte complexes were divided into 2 groups according to oocyte diameter (group A; <95 micro m, group B; >95 micro m) and cultured for 8 or 9 days on granulosa cell monolayers. Within 8 days of culture, the mean oocyte diameter increased from 86 plus or minus 0.4 to 95 plus or minus 0.7 micro m in group A and from 106 plus or minus 0.2 to 109 plus or minus 0.5 micro m in group B. After 9 days of culture, the mean diameter of oocytes from groups A and B were 99 plus or minus 0.5 and 112 plus or minus 0.4 micro m respectively. The meiotic competence of oocytes grown in vitro was evaluated by in vitro maturation. Within 8 days of culture, only 3% of oocytes from group A and 6% of oocytes from group B acquired the ability to undergo germinal vesicle breakdown. After 9 days of culture, 7% of group A and 42% of group B oocytes were competent to resume meiosis. The expression of p34cdc2 in oocytes grown in vitro was analysed by the western blot technique. During 9 days of culture, p34cdc2 accumulated in both groups of growing oocytes, but its concentration was lower than in fully grown oocytes used as controls. It is concluded that goat oocytes from early antral follicles can grow, accumulate p34cdc2 and acquire the ability to resume meiosis, when cultured for 9 days on granulosa cell monolayers

Descriptors:in-vitro. oocytes. ovarian-follicles. granulosa-cells. maturation. meiosis. culture-media. biotechnology

Organism Descriptors:goats
Supplemental Descriptors:Capra. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. LL700. WW000. LL600
Supplementary Info:21 ref
ISSN:0022-4251
Year:2000
Journal Title:Journal of Reproduction and Fertility
Copyright:Copyright CAB International

355. Title:Production of interferon by red deer (Cervus elaphus) conceptuses and the effects of roIFN- tau on the timing of luteolysis and the success of asynchronous embryo transfer
View Article: Journal of Reproduction and Fertility. 2000. 118 (2). 387-395
CD Volume:321
Print Article: Pages: 387-395
Author(s):Demmers K J Jabbour H N Deakin D W Flint A P F
Author Affiliation:Division of Animal Physiology, School of Biological Sciences, University of Nottingham, Sutton Bonington Campus, Loughborough, LE12 5RD, UK
Language:English
Abstract:The role of interferon in early pregnancy in red deer was investigated by (1) measuring production of interferon by the conceptus, (2) testing the anti-luteolytic effect of recombinant interferon- tau in non-pregnant hinds, and (3) treatment of hinds with interferon after asynchronous embryo transfer. Blastocysts were collected from 34 hinds by uterine flushing 14 (n = 2), 16 (n = 2), 18 (n = 8), 20 (n = 13) or 22 (n = 9) days after synchronization of oestrus with progesterone withdrawal. Interferon anti-viral activity was detectable in uterine flushings from day 16 to day 22, and increased (P<0.01) with duration of gestation and developmental stage. When interferon- tau was administered daily between day 14 and day 20 to non-pregnant hinds to mimic natural blastocyst production, luteolysis was delayed by a dose of 0.2 mg/day (27.3 plus or minus 1.3 days after synchronization, n = 4 vs. 21 plus or minus 0 days in control hinds, n = 3; P<0.05). Interferon- tau was administered to hinds after asynchronous embryo transfer to determine whether it protects the conceptus against early pregnancy loss. Embryos (n = 24) collected on day 6 from naturally mated, superovulated donors (n = 15) were transferred into synchronized recipients on day 10 or day 11. Interferon- tau treatment (0.2 mg daily from days 14 to 20) increased calving rate from 0 to 64% in all recipients (0/11 vs. 7/11, P<0.005), and from 0 to 67% in day 10 recipients (0/8 vs. 6/9, P<0.01). It is concluded that increased success rate of asynchronous embryo transfer after interferon- tau treatment in cervids may be of benefit where mismatched embryo-maternal signalling leads to failure in the establishment of pregnancy
Descriptors:embryos. embryo-transfer. interferon. luteolysis. blastocyst. maternal-recognition. calving-rate. conceptus. pregnancy. oestrus. progesterone. synchronization. biotechnology
Organism Descriptors:Cervus-elaphus. red-deer
Supplemental Descriptors:Cervus. Cervidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Cervus-elaphus
Subject Codes:LL250. WW000. LL600. LL050
Supplementary Info:46 ref
ISSN:0022-4251
Year:2000
Journal Title:Journal of Reproduction and Fertility
Copyright:Copyright CAB International

356. Title:Volatiles as an indicator of fungal activity and differentiation between species, and the potential use of electronic nose technology for early detection of grain spoilage
View Article: Journal of Stored Products Research. 2000. 36 (4). 319-340
CD Volume:337
Print Article: Pages: 319-340
Author(s):Magan N Evans P
Author Affiliation:Applied Mycology Group, Cranfield Biotechnology Centre, Cranfield University, Cranfield, Bedford M K43 0AL, UK
Language:English
Abstract:There is significant interest in methods for the early detection of quality changes in cereal grains. The development of electronic nose technology in recent years has stimulated interest in the use of characteristic volatiles and odours as a rapid, early indication of deterioration in grain quality. This review details the current status of this area of research. The range of volatiles produced by spoilage fungi in vitro and on grain are described, and the key volatile groups indicative of spoilage are identified. The relationship between current grain quality descriptors and the general classes of off-odours as defined in the literature, e.g. sour, musty, are not very accurate and the possible correlation between these for wheat, maize and other cereals, and volatiles are detailed. Examples of differentiation of spoilage moulds and between grain types using an electronic nose instrument are described. The potential for rapid and remote grain classification and future prospects for the use of such technology as a major descriptor of quality are discussed
Descriptors:grain. cereal-grains. cereals. classification. maize. volatile-compounds. wheat. plant-diseases. plant-pathogens. moulds. detection. techniques. plant-pathology
Organism Descriptors:Zea-mays. Triticum-aestivum. Triticum
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum
Subject Codes:FF610
Supplementary Info:2 pp. of ref
ISSN:0022-474X
Year:2000
Journal Title:Journal of Stored Products Research

357. Title:Effect of asynchronous non-surgical transfer of porcine embryos on pregnancy rate and embryonic survival
View Article: Livestock Production Science. 2000. 64 (2/3). 281-284
CD Volume:331
Print Article: Pages: 281-284
Author(s):Hazeleger W Noordhuizen J P T M Kemp B
Author Affiliation:Wageningen Institute of Animal Sciences, Department of Animal Husbandry, Wageningen Agricultural University, P.O. Box 338, 6700 AH Wageningen, Netherlands
Language:English
Abstract:Embryo survival was determined after non-surgical transfer to recipients with a variable synchrony of ovulation. Groups of 10 to 15 freshly weaned multiparous sows (donors and recipients) were checked and paired for time of ovulation, resulting in recipients ovulating from 24 h before to 36 h after the donors ('asynchrony' of -24 to +36 h). Embryos were collected from 34 donors at 120 h (range 108-132 h) after ovulation and 16.6 plus or minus 2.4 morulae and blastocysts were transferred to 31 recipients. Pregnant recipients were slaughtered on day 35 (day 0 = ovulation) to evaluate embryonic survival. 12 recipients were pregnant at day 21 and 5 were still pregnant at day 35.

One recipient was excluded due to cystic ovaries. An asynchrony of +18 to +36 h resulted in 1/12 recipients pregnant at day 21 and no pregnancies at day 35, while an asynchrony of -24 to +12 h resulted in 11/18 recipients pregnant at day 21 and 5 still pregnant at day 35 ($P<0.05$). The presence of more than or equal to 6 morulae within a litter never resulted in pregnancies at day 21 (0/9), while with <6 morulae, 12/21 recipients were pregnant at day 21 ($P<0.05$), irrespective of the degree of asynchrony. It is concluded that only blastocysts should be transferred successfully by a non-surgical procedure at 108-132 h after ovulation. Recipients should ovulate between 24 h before to 12 h after the donors. Transfers to recipients ovulating 18-36 h after the donors appear to lead to very low pregnancy rates

Descriptors:embryos. sows. morula. blastocyst. pregnancy-rate. survival. ovaries. ovulation. recipients. embryo-transfer. biotechnology
Geographic Locator:Netherlands
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Western-Europe. Europe. Developed-Countries. Benelux. European-Union-Countries. OECD-Countries
Subject Codes:LL240. LL250. WW000
Supplementary Info:11 ref
ISSN:0301-6226
Year:2000
Journal Title:Livestock Production Science

358. Title:Impact of biotechnology on (cross)breeding programmes in pigs
View Article: Livestock Production Science. 2000. 65 (1/2). 57-70
CD Volume:331
Print Article: Pages: 57-70
Author(s):Visscher P Pong Wong R Whittemore C Haley C
Author Affiliation:University of Edinburgh, West Mains Road, Edinburgh EH9 3JG, Scotland, UK
Language:English
Abstract:A review. Crossbreeding programmes in pigs exploit between breed complementarity of additive genetic effects and heterosis generated by non-additive genetic effects. Within breed, improvement programmes may focus on additive effects and hence the enhancement of complementarity, but non-additive variation is not generally used in within line selection or for mate selection at the multiplier or commercial level. In this paper, we discuss the impact of new biotechnological tools, particularly molecular markers, multiple ovulation and embryo transfer (MOET), and cloning, on structures and methods in crossbreeding. At the between line level, genetic marker information could allow better prediction of heterosis in novel crosses from information on genetic distances. Within the crossbreeding structure, the same technique might be applied at the multiplier and commercial level to exploit specific combining abilities of particular animals. Combining simple MOET and cloning protocols could radically alter the dissemination of crossbreeding benefits and their delivery to the farmer. The combination of MOET, cloning and genomic tools could result in speed genetics programmes, i.e. fast introgression and recurrent selection methods. Thus, the ultimate impact of biotechnology will be increased rates of progress, efficient use of variation, reduced genetic lag, and the removal of one or two tiers in the breeding pyramid. The costs of new technologies are discussed briefly

Descriptors:biotechnology. animal-cloning. crossbreeding. crosses. embryos. embryo-transfer. genetic-effects. breeding-programmes. genetic-markers. genetics. heterosis. introgression. MOET. ovulation. reviews
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. LL250. WW000. LL120
Supplementary Info:31 ref
ISSN:0301-6226
Year:2000
Journal Title:Livestock Production Science
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359. Title:The influence of Debaryomyces hansenii and Candida utilis on the aroma formation in garlic spiced fermented sausages and model minces
View Article: Meat Science. 56 (4). December, 2000. 357-368
CD Volume:335
Print Article: Pages: 357-368
Author(s):Olesen Pelle Thonning Stahnke Louise Heller
Author Affiliation:Department of Biotechnology, Technical University of Denmark, Building 221, DK-2800, Lyngby
Language:English
Language of Summary:English (EN)
Abstract:The influence of the yeast starter cultures Debaryomyces hansenii and Candida utilis on fermented meat aroma was studied in model minces and in commercial-type fermented sausages. Volatile compounds from model minces and sausages were collected using diffusive and dynamic headspace sampling respectively and were identified by gas chromatography/mass spectrometry (GC/MS). A triangle test was carried out on the sausages to detect whether the yeast influenced the sausage odour. C. utilis demonstrated high metabolic activity in the model minces, producing several volatile compounds, in particularly esters. C. utilis also seemed to ferment the amino acids valine, isoleucine and leucine into compounds important for the aroma of sausages. D. hansenii on the contrary, had very little effect on the production of volatile compounds in the model minces. In the sausage experiment both yeast cultures died out before the ripening process ended and the sensory analysis showed only a slight difference between the sausages. A fungistatic test of the garlic powder added to the sausages indicated that garlic inhibits the growth of the yeast starter cultures
Descriptors:garlic: fungistatic effect, herbs and spices; garlic spiced fermented sausages: aroma, meat product; model minces. Foods. esters; isoleucine; leucine; valine; volatile compounds
Organism Descriptors:Candida utilis (Fungi Imperfecti or Deuteromycetes): fermentation agent; Debaryomyces hansenii (Ascomycetes): fermentation agent
Supplemental Descriptors:Ascomycetes: Fungi, Plantae; Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Foods
ISSN:0309-1740
Year:2000
Journal Title:Meat Science

360. Title:Fipronil-related heterocyclic compounds: Structure-activity relationships for interaction with gamma-aminobutyric acid- and voltage-gated ion channels and insecticidal action
View Article: Pesticide Biochemistry and Physiology.. 66 (2). Feb., 2000. 92-104

CD Volume:332
Print Article: Pages: 92-104
Author(s):Ozoe Yoshihisa Yagi Kazuo Nakamura Masafumi Akamatsu Miki Miyake Takashi Matsumura Fumio
Author Affiliation:Department of Life Science and Biotechnology, Shimane University, Matsue, Shimane, 690-8504
Language:English
Language of Summary:English (EN)
Abstract:To investigate the role of the heterocyclic moieties of nitrogen-containing phenyl heterocyclic compounds (PHCs) in interaction with gamma-aminobutyric acid (GABA)-gated chloride channels, diverse classes of PHCs were examined for their ability to inhibit the specific binding of (3H)4'-ethynyl-4-n-propylbicycloorthobenzoate (EBOB), a noncompetitive GABA antagonist, to housefly head and rat brain membranes. PHCs that inhibited (3H)EBOB binding include pyrazoles; 1H-1,2,3-triazoles; a 1H-1,2,4-triazole; 1,3,4-oxadiazol- 2(3H)-ones; a 1,3,4-oxadiazole-2(3H)-thione; 1,2,4-oxadiazoles; a 1,2,4-thiadiazole; thiazoles; a 4(3H)-pyrimidinone; and a 2,4(1H,3H)-pyrimidinedione. An analogue (1) of the pyrazole insecticide fipronil, bearing an SCF3 group in place of the S(O)CF3, was found to be the most potent inhibitor with IC50s of 7.55 and 177 nM in housefly head and rat brain membranes, respectively. 3-(2,6-Dichloro-4-trifluoromethylphenyl)-5-t-butyl- 1,3,4-oxadiazol-2(3H)-one exhibited the highest selectivity for housefly GABA receptors versus rat receptors (IC50 rat/IC50 fly >204). PHCs that exhibited a comparable selectivity include a pyrazole and a 1H-1,2,3-triazole. Interaction of 16 selected PHCs with rat brain GABA-gated channels was also examined using (35S)t-butylbicyclophosphorothionate (TBPS), a radioligand for the mammalian noncompetitive antagonist site. A plot of pIC50s of 12 PHCs revealed a close correlation (r = 0.93) between their potency in inhibiting (3H)EBOB and (35S)TBPS binding. Scatchard analyses of the inhibition of (35S)TBPS binding by 1 suggested a competitive- type inhibition. A plot of the potency of 14 PHCs in inhibiting (3H)EBOB binding to housefly head membranes against their piperonyl butoxide-synergized insecticidal effect on German cockroaches yielded a close correlation (r = 0.89), with the exception of five triazoles and a 2.4(1H,3H)-pyrimidinedione. Although several selected PHCs also inhibited the specific binding of (3H)batrachotoxinin A 20-alpha-benzoate, a tritiated analogue of the sodium channel activator batrachotoxinin, to synaptosomes and membranes prepared from mouse brains, housefly heads, and American cockroach nerve cords, the concentrations required were higher than those of standard compounds producing significant effects on this system. The results demonstrate that a variety of five- and six- membered, nitrogen-containing heterocyclic compounds, bearing a 2,6- dichloro-4-trifluoromethyphenyl or 2,4,6-trichlorophenyl group, interact with ionotropic GABA receptors. Several PHCs display higher affinities for housefly GABA receptors and high selectivity as compared to rat GABA receptors. PHCs' insecticidal activity is mediated by their interaction with GABA-gated chloride channels
Descriptors:competitive inhibition; heterocyclic moieties; insecticidal action. Membranes (Cell Biology); Pesticides. fipronil: insecticide; gamma-aminobutyric acid [GABA]; hydrogen -3- 4'-n-propylbicycloorthobenzoate [EBOB]: GABA antagonist; phenyl heterocyclic compounds [PHCs]: insecticide, potency
Organism Descriptors:American cockroach (Orthoptera); German cockroach (Orthoptera); housefly (Diptera); rat (Muridae). GABA-gated ion channels; brain membrane: nervous system; head; nerve cord: nervous system; voltage-gated ion channels

Supplemental Descriptors:Diptera: Insecta, Arthropoda, Invertebrata, Animalia; Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia; Orthoptera: Insecta, Arthropoda, Invertebrata, Animalia. Animals; Arthropods; Chordates; Insects; Invertebrates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
Subject Codes:Membranes (Cell Biology); Pesticides
ISSN:0048-3575
Year:2000
Journal Title:Pesticide Biochemistry and Physiology

361. Title:Pepper gene encoding thionin is differentially induced by pathogens, ethylene and methyl jasmonate
View Article: Physiological and Molecular Plant Pathology. 2000. 56 (5). 207-216
CD Volume:321
Print Article: Pages: 207-216
Author(s):Lee SungChul Hong JeumKyu Kim YoungJin Hwang ByungKook
Author Variant:Lee-S-C. Hong-J-K. Kim-Y-J. Hwang-B-K
Author Affiliation:Department of Agricultural Biology, Korea University, Seoul 136-701, Korea Republic
Language:English
Abstract:A novel thionin cDNA (CATHION1, GenBank accession no. AF112869) was cloned from leaves of Capsicum annuum cv. Hanbyul infected with Xanthomonas campestris pv. vesicatoria [Xanthomonas vesicatoria]. Expression of the thionin gene in response to pathogens and stress-inducing compounds was also examined using northern blot analysis
Descriptors:plant-pathogens. plant-diseases. plant-pathogenic-bacteria. disease-resistance. nucleotide-sequences. gene-expression. stress. elicitors. ethylene. jasmonic-acid. vegetables. biotechnology. fruit-vegetables. plant-pathology
Identifiers:thionins
Organism Descriptors:Capsicum-annuum. Xanthomonas-vesicatoria
Supplemental Descriptors:Capsicum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF020. FF003. WW000. FF610. HH600
Supplementary Info:48 ref
ISSN:0885-5765
Year:2000
Journal Title:Physiological and Molecular Plant Pathology

362. Title:Bean polygalacturonase inhibitor protein-1 (PGIP-1) inhibits polygalacturonases from Stenocarpella maydis
View Article: Physiological and Molecular Plant Pathology. 2000. 57 (1). 5-14
CD Volume:321
Print Article: Pages: 5-14
Author(s):Berger D K Oelofse D Arendse M S Plessis E du Dubery I A
Author Variant:du-Plessis-E
Author Affiliation:Biotechnology Division, ARC-Roodeplaal Vegetable and Ornamental Plant Institute, Private Bag X293, Pretoria, 0001, South Africa
Language:English
Abstract:Polygalacturonase production and inhibition by Phaseolus vulgaris polygalacturonase inhibitor protein was investigated in the maize pathogen Stenocarpella maydis. S. maydis produced polygalacturonase activity when grown in liquid culture with pectin as a sole carbon source. Growth on maize cell wall extract resulted in a 2-fold greater mycelial dry mass. An extract of polygalacturonase inhibiting protein

from P. vulgaris hypocotyls inhibited 66% of S. maydis polygalacturonase activity in the fungal culture supernatant when tested in reducing sugar assay. Inhibition by purified extract was also observed. Overlay activity gels were used to study inhibition of S. maydis polygalacturonase isoenzymes. A bean pgip gene was cloned and used to produce transgenic tomatoes. Extracts from transgenic plants contained a polygalacturonase inhibitor protein which inhibited the polygalacturonase activity of Aspergillus niger by 72%. The bean polygalacturonase inhibitor protein-1 extract from transgenic tomato also inhibited 80% of S. maydis polygalacturonase activity

Descriptors:polygalacturonase. enzymes. plant-pathogens. plant-pathogenic-fungi

Organism Descriptors:Stenocarpella. Stenocarpella-maydis. Phaseolus-vulgaris. Aspergillus-niger

Supplemental Descriptors:Deuteromycotina. Eumycota. fungi. Stenocarpella. Phaseolus. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Aspergillus

Subject Codes:FF005. FF610

Supplementary Info:48 ref

ISSN:0885-5765

Year:2000

Journal Title:Physiological and Molecular Plant Pathology

363. Title:Anthracenone ABA analogue as a potential photoaffinity reagent for ABA-binding proteins

View Article: Phytochemistry (Oxford). 53 (3). Feb., 2000. 349-355

CD Volume:330

Print Article: Pages: 349-355

Author(s):Irvine Nicholas M Rose Patricia A Cutler Adrian J Squires Tim M Abrams Suzanne R

Author Affiliation:Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9

Language:English

Language of Summary:English (EN)

Abstract:An anthracenone analogue of abscisic acid (ABA) was synthesized as a potential photoaffinity reagent and tested for biological activity. Reaction between 10,10'-dimethoxy-9-anthrone with two equivalents of the lithiated dianion of cis-3-methylpent-2-en-4-yn- 1-ol afforded an acetylenic alcohol key intermediate. Subsequent reduction of the triple bond, functional group manipulation of the side chain alcohol and deprotection of the dimethoxy protected anthrone provided anthracenone ABA analogue 7 as a potential photoaffinity reagent for ABA-binding proteins. The effect of natural ABA and the potential photoaffinity anthracenone ABA 7 on corn cell growth was determined at various concentrations. The results show that anthracenone ABA 7 is perceived as ABA-like, although producing less inhibition than ABA itself. For example, 7 at 33 muM produces approximately the same inhibition as ABA at 10 muM

Descriptors:growth inhibition; phytochemistry. Biochemistry and Molecular Biophysics; Chemical Coordination and Homeostasis. ABA [abscisic acid]: plant growth regulator, plant hormone; ABA- binding protein [abscisic acid-binding protein]; anthracenone ABA analogue [anthracenone abscisic acid analogue]: potential photoaffinity reagent; benzophenone

Organism Descriptors:maize (Gramineae)

Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Biochemistry and Molecular Biophysics; Chemical Coordination and Homeostasis
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

364. Title:Distribution of morphinan and benzo[c]phenanthridine alkaloid gene transcript accumulation in Papaver somniferum
View Article: Phytochemistry. 2000. 53 (5). 555-564
CD Volume:330
Print Article: Pages: 555-564
Author(s):Huang FongChin Kutchan T M
Author Variant:Huang-F-C
Author Affiliation:Leibniz-Institut fur Pflanzenbiochemie, Weinberg 3, 06120 Halle/Saale, Germany
Language:English
Abstract:The opium poppy Papaver somniferum produces the antimicrobial benzo[c]phenanthridine alkaloid sanguinarine and the narcotic analgesic morphinan alkaloid morphine. Transcripts of three genes of alkaloid biosynthesis in P. somniferum in developing seedlings, mature plants and plant cell suspension culture were monitored for temporal/spatial or for methyl jasmonate-induced accumulation by RNA gel blot analysis. These genes encoded (S)-N-methylcoclaurine 3'-hydroxylase (CYP80B1) that is common to morphine and sanguinarine biosynthesis, the berberine bridge enzyme (BBE) that lies on the pathway to sanguinarine, and codeinone reductase (COR) the penultimate enzyme of morphine biosynthesis. In developing P. somniferum seedlings, the morphine precursor thebaine was present throughout the first twenty days of germination. In contrast, sanguinarine was present in detectable quantities only after day five after germination and continued to increase at least until day twenty. Accumulation of cyp80b1, bbe1 and cor1 gene transcripts paralleled these differences. In the mature poppy plant, cyp80b1, bbe1 and cor1 gene transcripts were detected in the root, the stem, the leaf lamina and the leaf mid rib. Only cyp80b1 and cor1, however, were found in the flower bud and the capsule. Consistent with the fact that sanguinarine accumulation, but not that of morphine, can be induced in opium poppy cell suspension culture by addition of methyl jasmonate to the culture medium, cyp80b1 and bbe1, but not cor1 transcript accumulated in response to elicitor treatment
Descriptors:biosynthesis. flowers. genes. seed-germination. methyl-jasmonate. RNA. seedlings. gene-expression. antimicrobial-properties. alkaloids. medicinal-plants. biotechnology
Identifiers:sanguinarine
Organism Descriptors:Papaver. Papaver-somniferum
Supplemental Descriptors:Papaveraceae. Papaverales. dicotyledons. angiosperms. Spermatophyta. plants. Papaver
Subject Codes:FF020. FF003. WW000. FF040
Supplementary Info:32 ref
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

365. Title:Differential expression of four sweet potato peroxidase genes in response to abscisic acid and ethephon
View Article: Phytochemistry (Oxford). 54 (1). May, 2000. 19-22
CD Volume:330
Print Article: Pages: 19-22

Author(s):Kim Kee Yeun Kwon Hye Kyoung Kwon Suk Yoon Lee Haeng Soon Hur Yoonkang Bang Jae Wook Choi Kwan Sam Kwak Sang Soo
Author Affiliation:Plant Cell Biotechnology Laboratory, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Yusong, Taejon, 305-600
Language:English
Language of Summary:English (EN)
Abstract:Expression of four peroxidase (POD) genes, three anionic PODs (swpa1, swpa2 and swpa3), and one neutral POD (swpn1) isolated from suspension cultures of sweet potato (Ipomoea batatas) were analyzed by measuring the accumulation of transcripts in suspension cultured cells and leaves of sweet potato in response to the stress-related plant hormones abscisic acid (ABA) and ethephon (an ethylene generating chemical). The four genes responded differently to ABA (0.1 mM) and ethephon (0.1 mM) in cultured cells and leaves. In suspension cultures, ABA reduced the expression levels of swpa1, swpa2, and swpn1, but did not affect the level of swpa3. Ethephon strongly increased expression levels of swpa3 and swpn1, and slightly increased the level of swpa1. The expression level of swpa2 was reduced. Expression levels in intact leaves, however, were significantly changed by this treatment. Expression of the swpa1 and swpa2 genes was induced 15 min after ABA treatment, followed by a decrease to a basal level after 3 h. A strong re-expression occurred after 12 h. Expression of the swpa3 and swpn1 genes occurred from 3 to 24 h after treatment. All four genes were differentially expressed 12 h after ethephon treatment. The swpa2 gene was strongly expressed immediately after ethephon treatment. The results indicate that each POD gene is differentially regulated by ABA and ethylene in whole plants and in cultured cells in vitro
Descriptors:Molecular Genetics (Biochemistry and Molecular Biophysics); Chemical Coordination and Homeostasis. abscisic acid; ethephon; peroxidase; Ipomoea batatas peroxidase gene (Convolvulaceae)
Organism Descriptors:Ipomoea batatas [sweetpotato] (Convolvulaceae)
Supplemental Descriptors:Convolvulaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Chemical Coordination and Homeostasis
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

366. Title:Two antifeedant lignans from the freshwater macrophyte Saururus cernuus
View Article: Phytochemistry (Oxford). 54 (3). June, 2000. 281-287
CD Volume:330
Print Article: Pages: 281-287
Author(s):Kubanek Julia Fenical William Hay Mark E Brown Pam J Lindquist Niels
Author Affiliation:Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, University of California - San Diego, La Jolla, CA, 92093-0204
Language:English
Language of Summary:English (EN)
Abstract:Two diarylbutane derivatives of dihydroguaiaretic acid have been isolated from emergent portions of the southeastern United States freshwater angiosperm Saururus cernuus L. (Saururaceae). Bioassay-guided fractionation of organic extracts of S. cernuus led to the compounds, sauriols A and B, in addition to five previously known lignoids. These metabolites deter feeding by the omnivorous crayfish Procambarus clarkii. The two lignans were identified by analysis of

nuclear magnetic resonance and mass spectral data, and by comparison with spectral data of dihydroguaiaretic acid
Descriptors:Biochemistry and Molecular Biophysics; Freshwater Ecology (Ecology, Environmental Sciences). sauriol A: antifeedant activity, chemical defense, lignan; sauriol B: antifeedant activity, chemical defense, lignan
Organism Descriptors:Procambarus clarkii [crayfish] (Malacostraca); Saururus cernuus (Saururaceae): freshwater macrophyte
Supplemental Descriptors:Malacostraca: Crustacea, Arthropoda, Invertebrata, Animalia; Saururaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Arthropods; Crustaceans; Dicots; Invertebrates; Plants; Spermatophytes; Vascular Plants
Subject Codes:Biochemistry and Molecular Biophysics; Freshwater Ecology (Ecology, Environmental Sciences)
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

367. Title:Species identification of Radix Astragali (Huangqi) by DNA sequence of its 5S-rRNA spacer domain
View Article: Phytochemistry (Oxford). 54 (4). June, 2000. 363-368
CD Volume:330
Print Article: Pages: 363-368
Author(s):Ma X Q Duan J A Zhu D Y Dong T T X Tsim K W K
Author Affiliation:Department of Biology, Biotechnology Research Institute, Hong Kong University of Science and Technology, Clear Water Bay Road, Hong Kong
Language:English
Language of Summary:English (EN)
Abstract:About 300 species and varieties of Astragalus are identified in China, making the identification of the origin of a particular Astragalus species on the consumer market difficult. A molecular genetic approach was developed to identify various species of Astragalus. Although the 5S-rRNA coding sequence is conserved in higher eukaryotes, the spacer domain of the 5S-rRNA gene has great diversity among different species. The 5S-rRNA spacer domain was amplified by polymerase chain reaction (PCR) from the isolated genomic DNA, and the PCR products (apprx300 bp) covering the 5S- rRNA spacer domain were sequenced. The nucleotide sequences of Astragalus membranaceus, A. membranaceus var. mongholicus, A. lehmannianus, A. hoantchy, and of one closely related species Hedysarum polybotrys (Hongqi), were determined. Diversity in DNA sequence and restriction enzyme mapping among various species was found in their 5S-rRNA spacer domains. This is the first report on the detection of 5S-rRNA spacer region sequence of Astragalus, and the results could be used for genetic identification of Huangqi
Descriptors:Molecular Genetics (Biochemistry and Molecular Biophysics); Pharmacognosy (Pharmacology). 5S-rRNA [5S-ribosomal RNA]: spacer domain; DNA
Organism Descriptors:Astragalus hoantchy (Leguminosae): medicinal plant; Astragalus lehmannianus (Leguminosae): medicinal plant; Astragalus membranaceou var. mongholicus (Leguminosae): medicinal plant; Astragalus membranaceus (Leguminosae): medicinal plant; Hedysarum polybotrys (Leguminosae): medicinal plant. Radix Astragali [Huangqi]: crude drug
Supplemental Descriptors:Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Pharmacognosy (Pharmacology)
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

368. Title:N-methylsansalvamide, a cytotoxic cyclic depsipeptide from a marine fungus of the genus Fusarium
View Article: Phytochemistry (Oxford). 55 (3). October, 2000. 223-226
CD Volume:330
Print Article: Pages: 223-226
Author(s):Cueto Mercedes Jensen Paul R Fenical William
Author Affiliation:Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, University of California, San Diego, La Jolla, CA, 92093-0204: wfenical@ucsd.edu
Language:English
Language of Summary:English (EN)
Abstract:N-Methylsansalvamide (1), a new cyclic depsipeptide, was isolated from extracts of a cultured marine fungus, strain CNL-619, identified as a member of the genus Fusarium. N-Methylsansalvamide exhibits weak in vitro cytotoxicity in the NCI human tumor cell line screen (GI50 8.3 muM). The structure of 1 was determined by combined spectral and chemical methods
Descriptors:Biochemistry and Molecular Biophysics; Pharmacognosy (Pharmacology). N-methylsansalvamide: cytotoxic cyclic depsipeptide, structure
Organism Descriptors:Fusarium (Fungi Imperfecti or Deuteromycetes): marine fungus, strain-CNL-619
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Biochemistry and Molecular Biophysics; Pharmacognosy (Pharmacology)
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

369. Title:Antimalarial preracemosols A and B, possible biogenetic precursors of racemosol from Bauhinia malabarica Roxb
View Article: Phytochemistry (Oxford). 55 (4). October, 2000. 349-352
CD Volume:330
Print Article: Pages: 349-352
Author(s):Kittakoop Prasat Kirtikara Kanyawim Tanticharoen Morakot Thebtaranonth Yodhathai
Author Affiliation:National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), 73/1, Rama VI Road, Rajdhevee, Bangkok, 10400: prasat@biotec.or.th
Language:English
Language of Summary:English (EN)
Abstract:Racemosol and demethylracemosol, together with their possible biogenetic precursors, preracemosol A and preracemosol B, were isolated from the roots of Bauhinia malabarica Roxb. While only racemosol and demethylracemosol exhibited cytotoxicity against KB and BC cell lines, all four compounds exhibited moderate antimalarial activity
Descriptors:antimalarial activity; cytotoxicity. Biochemistry and Molecular Biophysics; Pharmacognosy (Pharmacology). bibenzyls; demethylracemosol; preracemosol A: antimalarial activity; preracemosol B: antimalarial activity; racemosol: biosynthesis

Organism Descriptors:BC cell line (Hominidae); Bauhinia malabarica (Leguminosae); KB cell line (Hominidae); Paramecium falciparum (Ciliata): parasite. roots
Supplemental Descriptors:Ciliata: Protozoa, Invertebrata, Animalia; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Chordates; Dicots; Humans; Invertebrates; Mammals; Microorganisms; Plants; Primates; Protozoans; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Biochemistry and Molecular Biophysics; Pharmacognosy (Pharmacology)
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

370. Title:Light activation of vindoline biosynthesis does not require cytomorphogenesis in Catharanthus roseus seedlings
View Article: Phytochemistry (Oxford). 55 (6). November, 2000. 531-536
CD Volume:330
Print Article: Pages: 531-536
Author(s):Vazquez Flota Felipe A St Pierre Benoit De Luca Vincenzo
Author Affiliation:Novartis Agribusiness Biotechnology Research Inc., 3054 Cornwallis Road, Research Triangle Park, NC, 27709-2257: vince.deluca@nabri.novartis.com
Language:English
Language of Summary:English (EN)
Abstract:Upon illumination, the cotyledons of Catharanthus roseus seedlings readily synthesise vindoline from late biosynthetic intermediates, which accumulate in etiolated seedlings. The cellular localisation of tryptophan decarboxylase (TDC) and desacetoxyvindoline 4- hydroxylase (D4H), which catalyse the first and penultimate reactions of vindoline biosynthesis, was identified by immunocytochemistry in developing seedlings. The expression of TDC was restricted to the upper epidermis of cotyledons, whereas that of D4H was confined to laticifer cells. Light exposure of etiolated seedlings significantly induced D4H enzyme activity without changing the steady-state levels of D4H immunoreactive protein or modifying the cellular distribution of D4H expression in dark-grown seedlings. These results suggest that the early and late stages of vindoline biosynthesis occupy different cellular compartments, even in the early phases of etiolated seedling development. The role of light in activating the late stages of vindoline biosynthesis does not, therefore, seem to be related to the formation of the laticifer and idioblast cell types. It is concluded that light is not required for formation of these cell types, whereas regulatory factors, restricted to idioblasts and laticifers, may respond to light to activate localised expression of the late stages of vindoline biosynthesis
Descriptors:cytomorphogenesis; light; light exposure. Development; Metabolism. desacetoxyvindoline 4-hydroxylase: cellular localization, expression; desacetoxyvindoline 4-hydroxylase immunoreactive protein; tryptophan decarboxylase: cellular localization; vindoline: biosynthesis light activation
Organism Descriptors:Catharanthus roseus (Apocynaceae): cultivar-Little Delicata, dark- grown, etiolated, seedling. cotyledon: upper epidermis; idioblast cell; laticifer cell
Supplemental Descriptors:Apocynaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Development; Metabolism
ISSN:0031-9422
Year:2000
Journal Title:Phytochemistry

371. Title:Differences in nitrate and ammonium uptake between Scots pine and European larch
View Article: Plant and Soil. 2000. 221 (1). 1-3
CD Volume:309
Print Article: Pages: 1-3
Author(s):Malagoli M Canal A D Quaggiotti S Pegoraro P Bottacin A
Author Affiliation:Department of Agricultural Biotechnology, University of Padova, Agripolis, 35020 Legnaro, Italy
Conference Title:5th International Symposium on Inorganic Nitrogen Assimilation, Luso, Portugal, 1998
Language:English
Abstract:In forest soils, ammonium is usually the predominant form of inorganic nitrogen. However, the capacity of trees to utilize both NO3- and NH4+ may provide greater flexibility in responding to changes of nitrogen supply from the environment. Such capacity has been studied in seedlings of Scots pine (Pinus sylvestris) and European larch (Larix decidua) grown in the presence or absence of either nitrate or ammonium. Nitrate-induced plants showed a higher nitrate uptake rate than non-induced plants; this difference was almost negligible after 24 h of exposure to NO3-. Ammonium uptake in both species was consistently higher than that of nitrate, regardless of prior nitrogen provision. In both nutrient conditions, larch showed a more efficient transport system in comparison with Scots pine, with higher ammonium and nitrate uptake rates in both induced and non-induced plants. This was consistent also with the activity of nitrate reductase, measured in vivo in roots and leaves
Descriptors:nitrate. uptake. capacity. exposure. forests. forest-soils. nitrate-reductase. nitrogen. roots. seedlings. soil. trees. ammonium. pines
Organism Descriptors:Larix. Pinus-sylvestris. Larix-decidua. Pinus
Supplemental Descriptors:Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants. Pinus. Larix
Subject Codes:FF061. KK100. JJ700
Supplementary Info:12 ref
ISSN:0032-079X
Year:2000
Journal Title:Plant and Soil

372. Title:Estimating crop N uptake from organic residues using a new approach to the 15N isotope dilution technique
View Article: Plant and Soil. 2000. 223 (1/2). 33-44
CD Volume:309
Print Article: Pages: 33-44
Author(s):Hood R Merckx R Jensen E S Powlson D Matijevic M Hardarson G
Author Affiliation:Soil Science Unit, FAO/IAEA Agriculture and Biotechnology Laboratory, A-2444 Seibersdorf, Austria
Language:English
Abstract:Greenhouse experiments were conducted to test a new approach to the 15N isotope dilution technique for estimating crop N uptake from organic inputs. Soils were pre-labelled with 15N fertiliser and a carbon source. These were then incubated until there was stabilization of the 15N abundance of the inorganic N pool and resumption of inorganic N

concentrations. Residues were then applied to the soils and planted with ryegrass (Lolium perenne) to determine the nitrogen derived from the residue (Ndfr) using the isotope dilution equations. This method was compared with the direct method where 15N-labelled residues were added to the soil and Ndfr in the ryegrass calculated directly. Estimates of percentage nitrogen derived from the residue (%Ndfr) alfalfa (Medicago sativa) in the ryegrass, were similar, 22 and 23% for the direct and soil pre-labelling methods, respectively, in the Wechsel sandy loam. Estimates of the %Ndfr from soyabean residues in the Krumbach sandy loam were similar 34% (direct) and 36% (soil pre-labelling approach). However, in the Seibersdorf clay loam, the %Ndfr from soyabean was 49% using the direct method and 61% using the soil pre-labelling method; yet Ndfr from common bean residue was 46% using the direct approach and 40% using the pre-labelling, not significantly different (P>0.05). The soil pre-labelling approach appears to give realistic values for Ndfr. It was not possible to obtain an estimate of Ndfr using the soil pre-labelling method from the maize residues in two of the soils, as there was no increase in the total N of the ryegrass over the growing period. This was probably due to microbial immobilization of inorganic N, as a result of the wide C:N ratio of the residue added. The results suggest that the new soil pre-labelling method is feasible and that it is a potentially useful technique for measuring N release from a wide range or organic residues, but it requires further field-testing

Descriptors:nitrogen. uptake. crops. estimation. crop-residues. methodology. soyabeans. maize. immobilization. sandy-loam-soils. clay-loam-soils. lucerne

Organism Descriptors:Lolium-perenne. Glycine-max. Zea-mays. Medicago-sativa. Glycine-(Fabaceae)

Supplemental Descriptors:Lolium. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales. dicotyledons. Zea. Medicago

Subject Codes:FF061. FF100. JJ700. XX200. ZZ900

Supplementary Info:25 ref

ISSN:0032-079X

Year:2000

Journal Title:Plant and Soil

373. Title:Mycelium of arbuscular mycorrhizal fungi (AMF) from different genera: Form, function and detection

View Article: Plant and Soil. 226 (2). 2000. 131-151

CD Volume:309

Print Article: Pages: 131-151

Author(s):Dodd John C Boddington Claire L Rodriguez Alia Gonzalez Chavez Carmen Mansur Irdika

Author Affiliation:Department of Biosciences, International Institute of Biotechnology - Biotechnology MIRCEN, University of Kent Campus, Canterbury, Kent, CT2 7YW: J.C.Dodd@ukc.ac.uk

Language:English

Language of Summary:English (EN)

Abstract:It is often assumed that all species of arbuscular mycorrhizal fungi (AMF) have the same function because of the ubiquity of the arbuscular mycorrhizal symbiosis and the fact that all AMF occupy the same plant/soil niche. Despite apparent differences in the timing of evolutionary divergence and the morphological characteristics of AMF from the different genera, the majority of studies on these fungi use only species of Glomus. There is increasing evidence, however, that the mechanisms involved in the establishment of a mycorrhiza may differ for

species and genera of AMF and influence their subsequent function. The aim of this paper is to highlight the diversity in the form and function of AMF from different genera, knowledge of which is vital in understanding their ecological roles. Potential use of biochemical and molecular approaches to detect AMF in planta and ex planta is also discussed
Descriptors:Infection; Morphology. isozymes
Organism Descriptors:Gigaspora (Phycomycetes): arbuscular mycorrhizal fung; Glomus (Phycomycetes): arbuscular mycorrhizal fung; Scutellospora (Phycomycetes): arbuscular mycorrhizal fung. hyphae; mycelium: architecture
Supplemental Descriptors:Phycomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Infection; Morphology
ISSN:0032-079X
Year:2000
Journal Title:Plant and Soil

374. Title:A sensitive method for detecting bamboo mosaic virus (BaMV) and establishment of BaMV-free meristem-tip cultures
View Article: Plant Pathology. 2000. 49 (1). 101-107
CD Volume:331
Print Article: Pages: 101-107
Author(s):Hsu Y H Annamalai P Lin C S Chen Y Y Chang W C Lin N S
Author Affiliation:Graduate Institute of Agricultural Biotechnology, National Chung Hsing University, Taichung, 402, Taiwan
Language:English
Abstract:A sensitive method was used to detect bamboo mosaic virus (BaMV) and its associated satellite RNA (satBaMV) by 32P- and digoxigenin (Dig)-labelled probes synthesized from cDNA clones of BaMV genomic (L probe) and satBaMV (S probe) RNA. Both the 32P- and Dig-labelled L and S probes could detect as little as 490 pg of BaMV viral RNA by slot- and dot-blot hybridization. In infected leaf extracts, 32P-labelled L and S probes detected virus at 25-fold higher dilutions than Dig-labelled probes, which were also successfully used to detect BaMV infection in plants derived from meristem-tip culture. However, immunoassays failed to detect BaMV in meristem culture. By dot-blot hybridization assays, 25% of the seedlings were shown to be virus-free. These results suggest that a highly sensitive method for the detection of BaMV infection is required for the establishment of BaMV-free cultures. Meristem-tip culture also provides an efficient method for obtaining virus-free bamboo plants
Descriptors:immunoassay. complementary-DNA. RNA. satellite-RNA. plant-diseases. plant-pathogens. viral-diseases. bamboos. detection. molecular-genetics. shoot-tip-culture. plant-pathology
Identifiers:bamboo mosaic virus. Potexvirus
Organism Descriptors:plant-viruses. Bambusa
Supplemental Descriptors:viruses. plant-pathogens. pathogens. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. potexvirus-group. plant-viruses
Subject Codes:FF610. WW000. ZZ390. ZZ900
Supplementary Info:38 ref
ISSN:0032-0862
Year:2000
Journal Title:Plant Pathology

375. Title:Suppression of clubroot and Verticillium yellows in Chinese cabbage in the field by the root endophytic fungus, Heteroconium chaetospira
View Article: Plant Pathology. 2000. 49 (1). 141-146
CD Volume:331
Print Article: Pages: 141-146
Author(s):Narisawa K Ohki K T Hashiba T
Author Affiliation:Plant Biotechnology Institute, Ibaraki Agricultural Center, Ago, Iwama, Nishi Ibaraki 319-0292, Japan
Language:English
Abstract:Chinese cabbage seedlings inoculated with an isolate of the hyphomycete, Heteroconium chaetospira, were transplanted to the field in Japan. After 3 months, they showed a 52-97% reduction in clubroot (Plasmodiophora brassicae) and a 49-67% reduction in Verticillium (V. dahliae) yellows compared with noninoculated controls. H. chaetospira colonized the cortical cells, especially in the root tip region. Infected plants showed no disease symptoms. The infection process involves the formation of appressoria on the cell surface and the subsequent growth of hyphae within cells. H. chaetospira colonized 18 plant species, indicating a wide range of hosts. It is concluded that it may have potential as a biocontrol agent for clubroot and Verticillium yellows
Descriptors:Chinese-cabbages. plant-diseases. plant-pathogens. plant-pathogenic-fungi. fungal-diseases. biological-control. plant-disease-control. biological-control-agents. vegetables. control. plant-pathology
Geographic Locator:Japan
Identifiers:Heteroconium chaetospira. Heteroconium. Hyphomycetes. mitosporic fungi
Organism Descriptors:Brassica-pekinensis. Verticillium-dahliae. Plasmodiophora-brassicae. Brassica
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Verticillium. Deuteromycotina. Eumycota. fungi. Plasmodiophora. Plasmodiophorales. Myxomycota. East-Asia. Asia. Developed-Countries. OECD-Countries
Subject Codes:FF610. HH100. FF003. FF005. ZZ390
Supplementary Info:18 ref
ISSN:0032-0862
Year:2000
Journal Title:Plant Pathology

376. Title:Characterization of pathotypes among isolates of Xanthomonas axonopodis pv. manihotis in Colombia
View Article: Plant Pathology. 2000. 49 (6). 680-687
CD Volume:331
Print Article: Pages: 680-687
Author(s):Restrepo S Duque M C Verdier V
Author Affiliation:Biotechnology Research Unit, Centro Internacional de Agricultura Tropical (CIAT), Colombia
Language:English
Abstract:Cassava bacterial blight, caused by Xanthomonas axonopodis pv. manihotis (Xam) is a destructive disease occurring in most cassava growing-areas. Although Colombian isolates of Xam differ in DNA polymorphism and pathogenicity, no suitable host differentials have been identified to demonstrate physiological specialization. A set of 26 Xam isolates from three edaphoclimatic zones (ECZs) in Colombia was selected for inoculation on a set of 17 potential cassava differentials. Leaf inoculation and stem puncture were used in order to detect possible specific interactions between cultivars and isolates.

Cultivar x isolate interaction was highly significant (P<0.001) after stem inoculation, but not after leaf inoculation. The stem inoculation technique was used for resistance screening of cassava cultivars for bacterial blight resistance. A highly significant interaction was also detected when cultivar behaviour was rated as area under the disease progress curve (AUDPC) after stem inoculation. Different pathotypes were defined among the 26 isolates and differential cultivars were proposed to define the pathotypic composition of Xam populations in three ECZs in Colombia. The results should help to improve selection of sources of resistance to cassava bacterial blight

Descriptors:cassava. cultivars. pathotypes. plant-diseases. plant-pathogenic-bacteria. plant-pathogens. virulence. screening

Geographic Locator:Colombia

Identifiers:disease resistanceManihot esculenta

Organism Descriptors:Xanthomonas-axonopodis-pv.-manihotis. Manihot-esculenta

Supplemental Descriptors:Xanthomonas-axonopodis. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes. South-America. America. Developing-Countries. Andean-Group. Latin-America. Manihot. Euphorbiaceae. Euphorbiales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF610. HH600. FF020

Supplementary Info:34 ref

ISSN:0032-0862

Year:2000

Journal Title:Plant Pathology

377. Title:Characterization of two cDNA clones encoding isozymes of the F1F0-ATPase inhibitor protein of rice mitochondria

View Article: Planta. 2000. 210 (2). 188-194

CD Volume:334

Print Article: Pages: 188-194

Author(s):Nakazono M Imamura T Tsutsumi N Sasaki T Hirai A

Author Affiliation:Laboratory of Plant Molecular Genetics, Graduate School of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan

Language:English

Abstract:Two cDNA clones encoding F1F0-ATPase [adenosinetriphosphatase] inhibitor proteins, which are loosely associated with the F1 part of the mitochondrial F1F0-ATPase, were characterized from rice (Oryza sativa cv. Nipponbare). A Northern hybridization showed that the two genes (designated as IF1-1 and IF1-2) are transcribed in all the organs examined. However, the steady-state mRNA levels varied among organs. A comparison of the deduced amino acid sequences of the two IF1 genes and the amino acid sequence of the mature IF1 protein from potato revealed that IF1-1 and IF1-2 have N-terminal extensions with features that are characteristic of a mitochondrial targeting signal. To determine the subcellular localization of the gene products, the IF1-1 or IF1-2 proteins were fused in frame to the green fluorescent protein (GFP) or the fused GFP- beta -glucuronidase, and expressed transiently in onion or dayflower epidermal cells. Localized fluorescence was detected in mitochondria, confirming that the two IF1 proteins are targeted to mitochondria

Descriptors:complementary-DNA. clones. isoenzymes. adenosinetriphosphatase. inhibitors. mitochondria. rice. genes. northern-blotting. localization. messenger-RNA. amino-acid-sequences. nucleotide-sequences. gene-expression. cereals. biotechnology

Organism Descriptors:Oryza-sativa. Oryza

Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. WW000
Supplementary Info:28 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

378. Title:High-efficiency induction of soybean hairy roots and propagation of the soybean cyst nematode
View Article: Planta. 2000. 210 (2). 195-204
CD Volume:334
Print Article: Pages: 195-204
Author(s):Cho HyeonJe Farrand S K Noel G R Widholm J M
Author Variant:Cho-H-J
Author Affiliation:Department of Crop Sciences, University of Illinois, 1201 W. Gregory Dr, Urbana, IL 61801, USA
Language:English
Abstract:Cotyledon explants of 10 soyabean (Glycine max) cultivars were inoculated with Agrobacterium rhizogenes strain K599 with and without binary vectors pBI121 or pBINm-gfp5-ER possessing both neomycin phosphotransferase II (nptII) and beta -glucuronidase (gus) or nptII and green fluorescent protein (gfp) genes, respectively. Hairy roots were produced from the wounded surface of 54-95% of the cotyledon explants on MXB selective medium containing 200 micro g ml-1 kanamycin and 500 micro g ml-1 carbenicillin. Putative individual transformed hairy roots were identified by cucumopine analysis and were screened for transgene incorporation using polymerase chain reaction. All of the roots tested were found to be co-transformed with T-DNA from the Ri-plasmid and the transgene from the binary vectors. Southern blot analysis confirmed the presence of the 35S-gfp5 gene in the plant genomes. Transgene expression was also confirmed by histochemical GUS assay and Western blot analysis for the GFP. Attempts to induce shoot formation from the hairy roots failed. Infection of hairy roots of the soyabean cyst nematode (Heterodera glycines)-susceptible cultivar Williams 82, with eggs of H. glycines race 1, resulted in the development of mature cysts about 4-5 weeks after inoculation. Thus, the soyabean cyst nematode could complete its entire life cycle in transformed soyabean hairy-root cultures expressing GFP. This system should be ideal for testing genes that might impart resistance to soyabean cyst nematode
Descriptors:soyabeans. beta-glucuronidase. reporter-genes. assays. cotyledons. explants. genes. inoculation. life-cycle. polymerase-chain-reaction. Southern-blotting. genetic-transformation. grain-legumes. biotechnology. nematology. control. plant-parasitic-nematodes. pest-resistance. plant-nematology
Organism Descriptors:Glycine-max. Glycine-(Fabaceae). Agrobacterium. Agrobacterium-rhizogenes. Heterodera-glycines. Heterodera. Fabaceae
Supplemental Descriptors:Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Agrobacterium. Heterodera. Heteroderidae. Nematoda. invertebrates. animals
Subject Codes:FF020. FF005. HH600. FF620. WW000. FF610
Supplementary Info:38 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

379. Title:Transgene expression driven by heterologous ribulose-1,5-bisphosphate carboxylase/oxygenase small-subunit gene promoters in the vegetative tissues of apple (Malus pumila Mill.)
View Article: Planta. 2000. 210 (2). 232-240
CD Volume:334
Print Article: Pages: 232-240
Author(s):Gittins J R Pellny T K Hiles E R Rosa C Biricolti S James D J
Author Affiliation:Plant Breeding and Biotechnology, Horticulture Research International, East Malling, West Malling, Kent, ME19 6BJ, UK
Language:English
Abstract:It is desirable that the expression of transgenes in genetically modified crops is restricted to the tissues requiring the encoded activity. To this end, studies were conducted to investigate the ability of heterologous ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) small-subunit (SSU) gene promoters, RBCS3CP (0.8 kb) from tomato (Lycopersicon esculentum) and SRS1P (1.5 kb) from soyabean (Glycine max), to drive expression of the beta -glucuronidase (gusA) marker gene in apple (Malus pumila). Transgenic lines of apple cultivar Greensleeves were produced by Agrobacterium-mediated transformation and the level of gusA expression in the vegetative tissues of young plants was compared with that produced using the cauliflower mosaic virus (CaMV) 35S promoter. These quantitative GUS data were assessed for their relationship to the copy number of transgene loci. The precise location of GUS activity in leaves was identified histochemically. The heterologous SSU promoters were active primarily in the green vegetative tissues of apple, although activity in the roots was noticeably higher with the RBCS3C promoter than with the SRS1 promoter. The mean GUS activity in leaf tissue of the SSU promoter transgenics was approximately half that of plants containing the CaMV 35S promoter. Histochemical analysis demonstrated that GUS activity was localised to the mesophyll and palisade cells of the leaf. The influence of light on expression was also determined. The activity of the SRS1 promoter was strictly dependent on light, whereas that of the RBCS3C promoter appeared not to be. Both SSU promoters would be suitable for the expression of transgenes in green photosynthetic tissues of apple
Descriptors:beta-glucuronidase. reporter-genes. marker-genes. mesophyll. soyabeans. genetic-transformation. transgenic-plants. gene-expression. promoters. ribulose-bisphosphate-carboxylase. apples. fruit-crops. fruits. biotechnology
Organism Descriptors:Malus. Malus-pumila. Glycine-max. Glycine-(Fabaceae)
Supplemental Descriptors:Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants. Malus. Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales
Subject Codes:FF020. FF003. WW000
Supplementary Info:39 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

380. Title:The Rhodococcus fascians-plant interaction: morphological traits and biotechnological applications
View Article: Planta. 2000. 210 (2). 241-251
CD Volume:334
Print Article: Pages: 241-251
Author(s):Vereecke D Burssens S Simon Mateo C Inze D Montagu M van Goethals K Jaziri M
Author Variant:van-Montagu-M

Author Affiliation:Laboratorium voor Genetica, Departement Plantengenetica, Vlaams Interuniversitair Instituut voor Biotechnologie, Universiteit Gent, K.L. Ledeganckstraat 35, 9000 Gent, Belgium
Language:English
Abstract:Rhodococcus fascians is a Gram-positive bacterium that infects dicotyledonous and monocotyledonous plants, leading to an alteration in the normal growth process of the host. The disease results from the modulation of the plant hormone balances, and cytokinins are thought to play an important role in the induction of symptoms. The disease effects were investigated in a wide range of plant species. Generally, on the aerial parts of the plants, existing meristems were found to be most sensitive to the action of R. fascians, but, depending on the infection procedure, differentiated tissues as well gave rise to shoots. Similarly, in roots not only actively dividing cells, but also cells with a high competence to divide were strongly affected by R. fascians. The observed symptoms, together with the determined hormone levels in infected plant tissue, suggest that auxins and molecules of bacterial origin are also involved in leafy gall formation. The complexity of symptom development is furthermore illustrated by the necessary and continuous presence of the bacteria for symptom persistence. Indeed, elimination of the bacteria from a leafy gall results in the further development of the multiple embryonic buds of which it consists. This interesting characteristic offers novel biotechnological applications: a leafy gall can be used for germplasm storage and for plant propagation. The presented procedure proves to be routinely applicable to a very wide range of plants, encompassing several recalcitrant species
Descriptors:morphology. auxins. cytokinins. germplasm. induction. meristems. persistence. symptoms. plant-diseases. plant-growth-regulators. plant-pathogenic-bacteria. propagation. biotechnology
Organism Descriptors:Rhodococcus-(bacteria). bacteria. monocotyledons. dicotyledons. Rhodococcus-fascians
Supplemental Descriptors:Nocardiaceae. Actinomycetales. Firmicutes. bacteria. prokaryotes. angiosperms. Spermatophyta. plants. Rhodococcus-(bacteria)
Subject Codes:FF060. FF610. WW000. FF160
Supplementary Info:37 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

381. Title:Leaf-specific overexpression of plastidic glutamine synthetase stimulates the growth of transgenic tobacco seedlings
View Article: Planta. 2000. 210 (2). 252-260
CD Volume:334
Print Article: Pages: 252-260
Author(s):Migge A Carrayol E Hirel B Becker T W
Author Affiliation:Lehrstuhl fur Genetik, Fakultat fur Biologie, Universitat Bielefeld, Postfach 10 01 31, D-33501 Bielefeld, Germany
Language:English
Abstract:The impact of increased plastidic glutamine synthetase [glutamate-ammonia ligase] (GS-2; EC 6.1.3.2) activity on foliar amino acid levels and on biomass production was examined in transgenic tobacco. Tobacco (Nicotiana tabacum cv. Petite Havana SR1) was transformed via Agrobacterium tumefaciens with a binary vector containing a tobacco GS-2 cDNA downstream of the leaf-specific soyabean ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit gene promoter. Two transgenic tobacco lines with 15-18-fold higher foliar GS-2 transcript

levels than the wild type were obtained. The GS-2 protein pools and the specific GS-2 activities were, however, only 2-2.3-fold higher in the leaves of the transgenic plants than in the leaves of the wild type. This discrepancy may reflect a post-transcriptional control of GS-2 protein accumulation. The increased GS-2 activity was correlated with a decrease in the leaf ammonium pool (3.7-fold) and an increase in the levels of some free amino acids, including glutamate (2.5-fold) and glutamine (2.3-fold). The accumulation of soluble protein per unit fresh weight, however, remained unchanged. This result indicates that a process downstream of the synthesis of the primary organic products of N-assimilation is limiting leaf protein accumulation. Nevertheless, the overexpression of GS-2 stimulated the growth rate of the transgenic tobacco seedlings which, consequently, were larger (20-30% on a fresh-weight basis) than wild-type seedlings grown under identical conditions. This result suggests that GS-2 is the rate-limiting enzyme during biomass production in tobacco seedlings. The requirement for glutamate as the ammonium acceptor in the reaction catalysed by GS-2 may imply that there is co-regulation of GS-2 and ferredoxin dependent glutamate synthase (Fd-GOGAT; EC 1.4.7.1) gene expression. Increased leaf GS-2 activity had, however, no influence on the foliar Fd-GOGAT protein abundance. This result suggests that in tobacco leaves, more Fd-GOGAT is present than is required to meet the demands of primary ammonium assimilation and that there is no strong interdependence between GS-2 and Fd-GOGAT protein expression

Descriptors:glutamine. glutamate-ammonia-ligase. seedlings. tobacco. transgenic-plants. amino-acids. assimilation. biomass. biomass-production. complementary-DNA. gene-expression. growth-rate. genetic-transformation. stimulant-plants. biotechnology

Identifiers:glutamate

Organism Descriptors:Nicotiana-tabacum. Agrobacterium. Agrobacterium-tumefaciens. Nicotiana

Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Agrobacterium

Subject Codes:FF020. FF005. WW000. FF060

Supplementary Info:49 ref

ISSN:0032-0935

Year:2000

Journal Title:Planta

382. Title:Control of carbon partitioning and photosynthesis by the triose phosphate/phosphate translocator in transgenic tobacco plants (Nicotiana tabacum L.). I. Comparative physiological analysis of tobacco plants with antisense repression and overexpression of the triose phosphate/phosphate translocator

View Article: Planta. 2000. 210 (3). 371-382

CD Volume:334

Print Article: Pages: 371-382

Author(s):Hausler R E Schlieben N H Nicolay P Fischer K Fischer K L Flugge U I

Author Affiliation:Botanisches Institut der Universitat zu Koln, Gyrhofstrasse 15, D-50931 Koln, Germany

Language:English

Abstract:The physiological properties of transgenic tobacco plants (Nicotiana tabacum) with decreased or increased transport capacities of the chloroplast triose phosphate/phosphate translocator (TPT) were compared in order to investigate the extent to which the TPT controls metabolic fluxes in wild-type tobacco. For this purpose, tobacco lines with an antisense repression of the endogenous TPT (alpha TPT) and tobacco

lines overexpressing the TPT gene isolated from the C4 plant Flaveria trinervia (FtTPT) were used. The F. trinervia TPT expressed in yeast cells exhibited transport characteristics identical to the TPT from C3 plants. Neither antisense TPT plants nor FtTPT overexpressors showed a phenotype when grown in a greenhouse in air. Contents of starch and soluble sugars in upper source leaves were similar in TPT underexpressors and FtTPT overexpressors compared to the wild type at the end of the photoperiod. The FtTPT overexpressors incorporated more 14CO2 in sucrose than the wild type, indicating that the TPT limits sucrose biosynthesis in the wild type. There were only small effects on labelling of amino acids and organic acids. The mobilisation of starch was enhanced in alpha TPT lines but decreased in FtTPT overexpressors compared to the wild type. Enzymes involved in starch mobilisation or utilisation, such as alpha -amylase or hexokinase were increased in alpha TPT plants and, in the case of amylases, decreased in FtTPT overexpressors. Moreover, alpha -amylase activity exhibited a pronounced diurnal variation in alpha TPT lines with a maximum activity after 8 h in the light. These changes in starch hydrolytic activities were confirmed by activity staining of native gels. Activities of glucan phosphorylases were unaffected by either a decrease or an increase in TPT activity. There were also effects of TPT activities on steady-state levels of phosphorylated intermediates as well as total amino acids and malate. In air, there was no or little effect of altered TPT transport activity on either rates of photosynthetic electron transport and/or CO2 assimilation. However, in elevated CO2 (1500 micro l litre-1) and low O2 (2%) the rate of CO2 assimilation was decreased in the alpha TPT lines and was slightly higher in FtTPT lines. This shows that the TPT limits maximum rates of photosynthesis in the wild type

Descriptors:photosynthesis. tobacco. transgenic-plants. amino-acids. amylases. assimilation. biosynthesis. chloroplasts. diurnal-variation. electron-transfer. hexokinase. mobilization. organic-acids. photoperiod. staining. starch. sucrose. sugars. genetic-transformation. gene-expression. antisense-DNA. source-sink-relations. stimulant-plants. biotechnology

Identifiers:alpha -amylase. Flaveria trinervia

Organism Descriptors:Nicotiana. Nicotiana-tabacum. Flaveria. yeasts

Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Nicotiana. Asteraceae. Asterales. Eumycota. fungi. Flaveria

Subject Codes:FF020. FF005. FF060. WW000

Supplementary Info:36 ref

ISSN:0032-0935

Year:2000

Journal Title:Planta

383. Title:Control of carbon partitioning and photosynthesis by the triose phosphate/phosphate translocator in transgenic tobacco plants (Nicotiana tabacum). II. Assessment of control coefficients of the triose phosphate/phosphate translocator

View Article: Planta. 2000. 210 (3). 383-390

CD Volume:334

Print Article: Pages: 383-390

Author(s):Hausler R E Schlieben N H Flugge U I

Author Affiliation:Botanisches Institut der Universitat zu Koln, Gyrhofstrasse 15, D-50931 Koln, Germany

Language:English

Abstract:Transgenic tobacco (Nicotiana tabacum) plants with decreased and increased transport capacities of the chloroplast triose phosphate/phosphate translocator (TPT) were used to study the control the TPT exerts on the flux of starch and sucrose biosynthesis, as well as CO2 assimilation, respiration and photosynthetic electron transport. For this purpose, tobacco lines with an antisense repression of the endogenous TPT (alpha TPT) and tobacco lines overexpressing a TPT gene from Flaveria trinervia (FtTPT) were used. In ambient CO2, there was no or little effect of altered TPT transport activities on either rates of photosynthetic electron transport and/or CO2 assimilation. However, in elevated CO2 (1500 micro l litre-1) and low O2 (2%) the TPT exerted strong control on the rate of CO2 assimilation (control coefficient for the wild type: CJATPT = 0.30) in saturating light. Similarly, the incorporation of 14C into starch in high CO2 was increased in tobacco plants with decreased TPT activity, but was reduced in plants overexpressing the TPT from F. trinervia. Thus, the TPT exerted negative control on the rate of starch biosynthesis with a CJStarchTPT = -0.19 in the wild type estimated from a hyperbolic curve fitted to the data points. This was less than the positive control strength on the rate of sucrose biosynthesis (CJSucTPT = 0.35 in the wild type). Theoretically, the positive control exerted on sucrose biosynthesis should be numerically identical to the negative control on starch biosynthesis unless additional metabolic pathways are affected. The rate of dark respiration showed some correlation with the TPT activity in that it increased in FtTPT overexpressors, but decreased in alpha TPT plants with an apparent control coefficient of CJResTPT = 0.24. If the control on sucrose biosynthesis is referred to as "gain of carbon" (positive control) and the control on starch biosynthesis as well as dark respiration as a "loss of carbon" (negative control) for sucrose biosynthesis and subsequent export, the sum of the control coefficients on dark respiration and starch biosynthesis would be numerically similar to the control coefficient on the rate of sucrose biosynthesis. There was also some control on the rate of photosynthetic electron transport, but only at high light and in elevated CO2 combined with low O2. The control coefficient for the rate of photosynthetic electron transport was CJETRTPT = 0.16 in the wild type. Control coefficients were also calculated for plants with elevated and lowered TPT activity. Furthermore, the extent to which starch degradation/glucose utilisation compensates for the lack of triose phosphate export was assessed. The TPT also exerted control on metabolite contents in air
Descriptors:photosynthesis. tobacco. transgenic-plants. assimilation. biosynthesis. chloroplasts. electron-transfer. respiration. starch. sucrose. source-sink-relations. genetic-transformation. gene-expression. genetic-engineering. biotechnology. stimulant-plants
Identifiers:Flaveria trinervia
Organism Descriptors:Nicotiana-tabacum. Flaveria. Nicotiana
Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Asteraceae. Asterales. Flaveria
Subject Codes:FF020. FF005. FF060. WW000
Supplementary Info:14 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

384. Title:Expression of a Petunia inflata pectin methyl esterase in Solanum tuberosum L. enhances stem elongation and modifies cation distribution
View Article: Planta. 2000. 210 (3). 391-399
CD Volume:334

Print Article: Pages: 391-399
Author(s):Pilling J Willmitzer L Fisahn J
Author Affiliation:Max-Planck-Institut fur Molekulare Pflanzenphysiologie, Am Muhlenberg 1, 14476 Golm, Germany
Language:English
Abstract:Transgenic potato (Solanum tuberosum) plants were constructed with a Petunia inflata-derived cDNA encoding a pectin methyl esterase (PME; EC 3.1.1.11) in sense orientation under the control of the cauliflower mosaic virus 35S promoter. The PME activity was elevated in leaves and tubers of the transgenic lines but slightly reduced in apical segments of stems from mature plants. Stem segments from the base of juvenile PME-overexpressing plants did not differ in PME activity from the control, whereas in apical parts PME was less active than in the wild-type. During the early stages of development stems of these transgenic plants elongated more rapidly than those of the wild-type. Further evidence that overexpression of a plant-derived PME has an impact on plant development is based on modifications of tuber yield, which was reduced in the transgenic lines. Cell walls from transgenic tubers showed significant differences in their cation-binding properties in comparison with the wild-type. In particular, cell walls displayed increased affinity for sodium and calcium, while potassium binding was constant. Furthermore, the total ion content of transgenic potatoes was modified. Indications of PME-mediated differences in the distribution of ions in transgenic plants were also obtained by monitoring relaxations of the membrane potential of roots subsequent to changes in the ionic composition of the bathing solution. However, no effects on the chemical structure of pectin from tuber cell walls could be detected
Descriptors:esterases. complementary-DNA. cell-walls. chemical-structure. ions. development. potassium. potatoes. transgenic-plants. genetic-transformation. gene-expression. genetic-engineering. ornamental-plants. biotechnology
Identifiers:pectin methyl esterase
Organism Descriptors:Petunia. Petunia-inflata. Solanum. Solanum-tuberosum
Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Petunia. Solanum
Subject Codes:FF020. FF005. FF003. WW000. FF060
Supplementary Info:55 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

385. Title:Developmental regulation of the maize Zm-p60.1 gene encoding a beta -glucosidase located to plastids
View Article: Planta. 2000. 210 (3). 407-415
CD Volume:334
Print Article: Pages: 407-415
Author(s):Kristoffersen P Brzobohaty B Hohfeld I Bako L Melkonian M Palme K
Author Affiliation:Max-Delbruck-Laboratorium in der Max-Planck-Gesellschaft, Carl-von-Linne-Weg 10, D-50829 Koln, Germany
Language:English
Abstract:A beta -glucosidase that cleaves the biologically inactive hormone conjugates cytokinin-O- and kinetin-N3-glucosides is encoded by the maize Zm-p60.1 gene. The expression of the Zm-p60.1 gene was analyzed by northern blot analysis and in-situ hybridization. It was found that the expression levels of the Zm-p60.1-specific mRNA changed after pollination of carpellate inflorescences. The Zm-p60.1 cDNA was expressed in Escherichia coli and antibodies were raised against this

protein. An antibody was used to determine the tissue-specific localization of this protein. By in situ immunolocalization experiments, this protein was found to be located in cell layers below the epidermis and around the vascular bundles of the coleoptile. In the primary leaf, the Zm-p60.1 protein was detected in cells of the outermost cell layer and around the vascular tissue. In floral tissue, Zm-p60.1 was present in the glumes, the carpels and in the outer cell layer of the style. In coleoptiles, as determined by immuno-electron microscopy, the Zm-p60.1 protein was located exclusively in the plastids

Descriptors:maize. plastids. antibodies. complementary-DNA. coleoptiles. epidermis. DNA-hybridization. inflorescences. messenger-RNA. pollination. vascular-bundles. vascular-system. gene-expression. kinetin. cereals. biotechnology. plant-growth-regulators. cytokinins

Identifiers:beta -glucosidase

Organism Descriptors:Zea-mays. Escherichia-coli

Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes

Subject Codes:FF020. WW000. FF005. FF060

Supplementary Info:26 ref

ISSN:0032-0935

Year:2000

Journal Title:Planta

386. Title:Alfin1 transcription factor overexpression enhances plant root growth under normal and saline conditions and improves salt tolerance in alfalfa

View Article: Planta. 2000. 210 (3). 416-422

CD Volume:334

Print Article: Pages: 416-422

Author(s):Winicov I

Author Affiliation:Department of Plant Biology, Arizona State University, Main Campus, PO Box 871601, Tempe, AZ 85287-1601, USA

Language:English

Abstract:Plant root development is an essential determinant of plant growth and crop yield that could be enhanced by induced changes in the expression of root-specific regulatory factors. It was reported previously that Alfin1 binds DNA in a sequence-specific manner and that Alfin1 overexpression in transgenic alfalfa (Medicago sativa) enhances expression of the salt-inducible MsPRP2 gene in roots, suggesting that Alfin1 functions to regulate gene expression in roots. Here, it is shown that Alfin1 is an essential gene for root growth and that its overexpression in transgenic plants confers a many-fold increase in root growth under normal and saline conditions. Alfin1-binding sites occur in promoters of genes expressed in roots of a wide variety of plant species and we propose that it is a general root growth regulator. Even though Alfin1 overexpression was under the control of the CaMV 35S promoter, plant shoot growth was not adversely affected. It was further shown that introduction of the Alfin1 transgene in plants confers a dominant characteristic that significantly increases plant growth and salt tolerance

Descriptors:salt-tolerance. transcription. gene-expression. genes. growth-regulators. shoots. growth. transgenic-plants. promoters. genetic-transformation. genetic-engineering. transcription-factors. salinity. fodder-plants. fodder-legumes. biotechnology. lucerne

Organism Descriptors:Medicago-sativa. Medicago. Fabaceae

Supplemental Descriptors:Medicago. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF007. FF900. WW000. FF060
Supplementary Info:27 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
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387. Title:The targeting and accumulation of ectopically expressed oleosin in non-seed tissues of Arabidopsis thaliana
View Article: Planta. 2000. 210 (3). 439-445
CD Volume:334
Print Article: Pages: 439-445
Author(s):Beaudoin F Napier J A
Author Affiliation:IACR-Long Ashton Research Station, Department of Agricultural Sciences, University of Bristol, Long Ashton, Bristol BS41 9AF, UK
Language:English
Abstract:Full-length and N-terminal deletions of a sunflower (Helianthus annuus) oleosin protein were expressed ectopically in transgenic Arabidopsis thaliana. Immunological detection of the sunflower protein revealed that it accumulated in a range of non-oil-storing tissues, including leaves, roots and petals. This accumulation was shown to result from deposition in the microsomal membrane fraction. Expression in oil-storing tissues (such as seeds) of oleosin N-terminal deletions revealed impaired transfer from the endoplasmic reticulum to the oil body. In non-oil-storing tissues, accumulation in the microsomal membrane fraction was progressively reduced by N-terminal deletion. These data confirm the role of the endomembrane system in the targeting of the oleosin and its intimate relationship with oil-body biogenesis
Descriptors:endoplasmic-reticulum. immunology. corolla. seeds. sunflowers. transgenic-plants. genetic-transformation. gene-expression. genetic-engineering. fatty-oil-plants. oil-plants. biotechnology
Identifiers:oleosins
Organism Descriptors:Arabidopsis. Arabidopsis-thaliana. Helianthus. Helianthus-annuus
Supplemental Descriptors:Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Arabidopsis. Asteraceae. Asterales. Helianthus
Subject Codes:FF020. FF060. WW000. FF005
Supplementary Info:29 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

388. Title:Microtubule reorganization in tobacco BY-2 cells stably expressing GFP-MBD
View Article: Planta. 2000. 210 (3). 502-509
CD Volume:334
Print Article: Pages: 502-509
Author(s):Granger C L Cyr R J
Author Affiliation:Biology Department, Pennsylvania State University, University Park, PA 16802, USA
Language:English
Abstract:Microtubule organization plays an important role in plant morphogenesis; however, little is known about how microtubule arrays transit from one organized state to another. The use of a genetically incorporated fluorescent marker would allow long-term observation of microtubule behaviour in living cells. Here, a Nicotiana tabacum cv.

Bright Yellow 2 (BY-2) cell line was characterized that had been stably transformed with a gfp-mbd construct previously demonstrated to label microtubules. Fluorescence levels were low, but interphase and mitotic microtubule arrays, as well as the transitions between these arrays, could be observed in individual gfp-mbd-transformed cells. By comparing several attributes of transformed and untransformed cells it was concluded that the transgenic cells are not adversely affected by low-level expression of the transgene and that these cells will serve as a useful and accurate model system for observing microtubule reorganization in vivo. Indeed, some initial observations were made that are consistent with the involvement of motor proteins in the transition between the spindle and phragmoplast arrays. These observations also support the role of the perinuclear region in nucleating microtubules at the end of cell division with a progressive shift of these microtubules and/or nucleating activity to the cortex to form the interphase cortical array

Descriptors:tobacco. cell-division. cell-lines. fluorescence. microtubules. morphogenesis. transgenic-plants. genetic-transformation. gene-expression. genetic-engineering. stimulant-plants. biotechnology

Organism Descriptors:Nicotiana-tabacum. Nicotiana

Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. WW000. FF005. FF060

Supplementary Info:23 ref

ISSN:0032-0935

Year:2000

Journal Title:Planta

390. Title:Developmentally regulated expression of two MADS-box genes, MdMADS3 and MdMADS4, in the morphogenesis of flower buds and fruits in apple

View Article: Planta. 2000. 210 (4). 519-528

CD Volume:334

Print Article: Pages: 519-528

Author(s):Sung SoonKee Yu GyungHee Nam JongMin Jeong DongHoon An GynHeung

Author Variant:Sung-S-K. Yu-G-H. Nam-J-M. Jeong-D-H. An-G-H

Author Affiliation:Department of Life Science, Pohang University of Science and Technology, Pohang 790-784, Korea Republic

Language:English

Abstract:Two MADS-box genes, MdMADS3 and MdMADS4, were isolated from the apple (Malus xdomestica [Malus pumila]) cultivar Fuji, and their spatial and temporal expression patterns were studied during morphological differentiation of the flower buds and the fruits. Both MdMADS3 and MdMADS4 showed high sequence similarities to FBP2 from petunia, TM5 from tomato, and AGL2 and AGL4 from Arabidopsis. Although MdMADS3 was expressed in the inner three whorls of the floral primordium, its expression was hardly detectable in developing fruit. The second gene, MdMADS4, was ubiquitously expressed in the inflorescence meristem, floral meristem, all four floral organs, and fruit. Moreover, MdMADS4 expression was high in the vascular bundles assigned to the floral tube and the carpellary vascular bundles in fruit at early developmental stages. The MdMADS4 transcript also accumulated in embryos of the developing seeds. These results suggest that MdMADS3 and MdMADS4 are involved in different functions, and that MdMADS4 may function in the important events controlling flower and fruit development. Nucleotide sequence data MdMADS3 and MdMADS4 have been submitted to the EMBL/DDBJ/GenBank databases under the accession numbers U78949 and U78950

Descriptors:flowers. fruits. genes. morphogenesis. developmental-stages. differentiation. plant-embryos. inflorescences. plant-morphology. vascular-bundles. nucleotide-sequences. gene-expression. apples. plant-development. development. fruit-crops. biotechnology
Organism Descriptors:Malus-pumila. Malus
Supplemental Descriptors:Malus. Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF003. WW000. FF060
Supplementary Info:37 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
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391. Title:The Lupinus albus class-III chitinase gene, IF3, is constitutively expressed in vegetative organs and developing seeds
View Article: Planta. 2000. 210 (4). 543-550
CD Volume:334
Print Article: Pages: 543-550
Author(s):Regalado A P Pinheiro C Vidal S Chaves I Ricardo C P P Rodrigues Pousada C
Author Affiliation:Instituto de Tecnologia Quimica e Biologica, Quinta do Marques, Apt. 127, 2781-901 Oeiras, Portugal
Language:English
Abstract:A cDNA fragment encoding a Lupinus albus class-III chitinase, IF3, was isolated, using a cDNA probe from Cucumis sativus, by in-situ plaque hybridization from a cDNA library constructed in the Uni-ZAP XR vector, with mRNAs isolated from mature lupin leaves. The cDNA had a coding sequence of 293 amino acids including a 27-residue N-terminal signal peptide. A class-III chitinase gene was detected by Southern analysis in the L. albus genome. Western blotting experiments showed that the IF3 protein was constitutively present during seed development and in all the studied vegetative lupin organs (i.e., roots, hypocotyls and leaves) at two growth stages (7- and 20-d-old plants). Accumulation of both the IF3 mRNA and IF3 protein was triggered by salicylic acid treatment as well as by abiotic (UV-C light and wounding) and biotic stress conditions (Colletotrichum gloeosporioides [Glomerella cingulata] infection). In necrotic leaves, IF3 chitinase mRNA was present at a higher level than that of another mRNA encoding a pathogenesis-related (PR) protein from L. albus (a PR-10) and that of the rRNAs. We suggest that one role of the IF3 chitinase could be in the defence of the plant against fungal infection, though our results do not exclude other functions for this protein. Nucleotide sequence data have been submitted to the GenBank databases under the accession number Y16415
Descriptors:chitinase. seeds. amino-acid-sequences. complementary-DNA. hypocotyls. lupins. messenger-RNA. salicylic-acid. seed-development. pathogenesis-related-proteins. injuries. plant-pathogens. plant-diseases. disease-resistance. plant-pathogenic-fungi. nucleotide-sequences. gene-expression. fodder-plants. fodder-legumes. biotechnology. plant-growth-regulators. growth-stimulators
Organism Descriptors:Lupinus. Lupinus-albus. Colletotrichum. Glomerella-cingulata. Fabaceae
Supplemental Descriptors:Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Lupinus. Deuteromycotina. Eumycota. fungi. Glomerella. Polystigmatales. Ascomycotina
Subject Codes:FF020. FF007. WW000. HH600. FF610
Supplementary Info:48 ref
ISSN:0032-0935

Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

392. Title:Leucine aminopeptidases: the ubiquity of LAP-N and the specificity of LAP-A
View Article: Planta. 2000. 210 (4). 563-573
CD Volume:334
Print Article: Pages: 563-573
Author(s):Chao W S Pautot V Holzer F M Walling L L
Author Affiliation:Department of Botany and Plant Sciences and Interdepartmental Program in Genetics, University of California, Riverside, CA 92521-0124, USA
Language:English
Abstract:The wound-induced leucine aminopeptidase [cytosol aminopeptidase] (EC 3.4.11.1) genes, LapA1 and LapA2, from tomato (Lycopersicon esculentum) were isolated and characterized. The genes were organized in a tandem array with approximately 6 kb separating their coding regions. Quantitation of LapA mRNA levels in conjunction with nuclear run-on experiments indicated that the LapA genes were primarily under transcriptional control after wounding and infection with Pseudomonas syringae pv. tomato. In contrast, actin genes were down-regulated after pathogen infection. The sequences of the LapA1 and LapA2 5'-flanking regions were determined and several potential regulatory motifs were identified. Ribonuclease protection studies revealed that LapA1 and LapA2 had short 18-bp 5'-untranslated regions (UTR), both genes were expressed after wounding, and LapA1 mRNAs were 3.3-fold more abundant than LapA2 transcripts. While the region surrounding LapA1 was conserved, the 3'-UTRs and 3'-flanking regions of LapA2 had diverged in two inbred tomato lines. The accumulation of LapA mRNAs and of LAP-A (acidic pI), LAP-N (neutral pI) and LAP-related proteins were examined in two monocot and five dicot species. The LAP-N and 66- and 77-kDa LAP-related proteins were detected in healthy and wounded leaves of all plants examined. The LAP-A proteins were only detected in nightshade and their accumulation was distinct from that observed in tomato
Descriptors:aminopeptidases. cytosol-aminopeptidase. genes. messenger-RNA. gene-expression. nucleotide-sequences. enzymes. injuries. tomatoes. vegetables. biotechnology
Organism Descriptors:Lycopersicon. Lycopersicon-esculentum
Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Lycopersicon
Subject Codes:FF020. FF060. FF003
Supplementary Info:50 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

393. Title:A barley gene (rsh1) encoding a ribonuclease S-like homologue specifically expressed in young light-grown leaves
View Article: Planta. 2000. 210 (4). 574-579
CD Volume:334
Print Article: Pages: 574-579
Author(s):Gausing K
Author Affiliation:Department of Molecular and Structural Biology, University of Aarhus, C.F. Mollers Alle 130, 8000 Arhus C, Denmark
Language:English
Abstract:A group of frequent cDNA clones from a young-leaf cDNA library was found to code for a homologue of S-ribonucleases (S-RNases) involved in

gametophytic incompatibility and the so-called S-like RNases active in flowers and in vegetative tissues. The derived amino acid sequence starts with a signal peptide and has a 27-amino-acid C-terminal extension of unknown function. The barley (Hordeum vulgare) gene rsh1 (for RNase S-like homologue) corresponding to the cDNA clones was isolated. The gene has three introns and the position of one intron corresponds to the site of the single, small intron in the S-RNase genes. The deduced amino acid sequence of mature RSH1 shares 35% identical and 58% similar amino acid residues with an S-like RNase from tomato, RNase LE. However, two active-site histidine residues, conserved between all S and S-like RNases are replaced by serine residues in RSH1. The new barley RNase S-like homologue is clearly related to the family of active RNases but is probably not active as an RNase. Sequences from the same class of presumably inactive RNases have been recorded in maize, rice and sorghum. The barley gene is exclusively expressed in young leaf tissue and is substantially induced by light. Nucleotide sequence data for rsh1 have been submitted to the EMBL/DDBJ/GenBank databases under the accession number AF182197
Descriptors:barley. complementary-DNA. genes. histidine. introns. ribonucleases. nucleotide-sequences. gene-expression. light. amino-acid-sequences. self-incompatibility. cereals. biotechnology
Organism Descriptors:Hordeum-vulgare. Hordeum
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. FF005. FF060
Supplementary Info:20 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

394. Title:Salicylic acid-independent induction of pathogenesis-related gene expression by fusicoccin
View Article: Planta. 2000. 210 (4). 599-606
CD Volume:334
Print Article: Pages: 599-606
Author(s):Schaller A Roy P Amrhein N
Author Affiliation:Institute of Plant Sciences, ETH-Zurich, Universitatstrasse 2, 8092 Zurich, Switzerland
Language:English
Abstract:Treatment of tomato plants (Lycopersicon esculentum) with fusicoccin (FC), an activator of the plasma-membrane H+-ATPase [adenosinetriphosphatase] which maintains an electrochemical gradient across the plasma membrane, resulted in a dose-dependent accumulation of transcripts for intra- and extracellular pathogenesis-related (PR) proteins. The accumulation of PR protein transcripts was paralleled by an increase in leaf salicylic acid (SA) content. Transcripts of PR proteins and SA started to accumulate 3 h after FC treatment. 2-Aminoindan-2-phosphonic acid, an inhibitor of SA synthesis, was used to assess the role of SA in FC-mediated induction of PR gene expression. 2-Aminoindan-2-phosphonic acid was found to suppress the accumulation of SA but not the induction of PR gene expression in response to FC treatment. Furthermore, in transgenic tobacco plants overexpressing a bacterial salicylate hydroxylase gene (nahG-tobacco), PR transcripts accumulated after FC treatment to levels similar to those observed in control tobacco plants. The data indicate a role for the proton gradient across the plasma membrane in the SA-independent induction of PR gene expression

Descriptors:fusicoccin. gene-expression. induction. salicylic-acid. tomatoes. plasma-membranes. adenosinetriphosphatase. plant-growth-regulators. pathogenesis-related-proteins. vegetables. biotechnology
Organism Descriptors:Lycopersicon. Lycopersicon-esculentum
Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Lycopersicon
Subject Codes:FF020. FF003. HH600. WW000
Supplementary Info:48 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

395. Title:In vitro biosynthesis of 1,4- beta -galactan attached to rhamnogalacturonan I
View Article: Planta. 2000. 210 (4). 622-629
CD Volume:334
Print Article: Pages: 622-629
Author(s):Geshi N Jorgensen B Scheller H V Ulvskov P
Author Affiliation:Biotechnology Group, Danish Institute of Agricultural Sciences, Thorvaldsensvej 40, 1871 Frederiksberg C, Denmark
Language:English
Abstract:Incubation in the presence of UDP-[14C]galactose of microsomal membranes isolated from suspension-cultured cells of potatoes cv. AZY resulted in a radioactive product insoluble in 70% methanol. The product released only [14C]galactose upon acid hydrolysis. Treatment of the product with Aspergillus niger endo-1,4- beta -galactanase released 65-70% of the radioactivity to a 70% methanol-soluble fraction. To a minor extent, [14C]galactose was also incorporated into proteins; however, these galactoproteins were not a substrate for A. niger endo-1,4- beta -galactanase. Thus, the majority of the 14C-labelled product was 1,4- beta -galactan. Compounds released by the endo-1,4- beta -galactanase treatment were mainly [14C]galactose and [14C]galactobiose, indicating that the synthesized 1,4- beta -galactan was longer than a trimer. In vitro synthesis of 1,4- beta -galactan was most active in 6-day-old cells in the middle of the linear growth phase. The optimal synthesis occurred at pH 6.0 in the presence of 7.5 mM Mn2+. A. aculeatus rhamnogalacturonase A digested at least 50% of the labelled product to smaller fragments of about 14 kDa, suggesting that the synthesized [14C]galactan was attached to the endogenous rhamnogalacturonan I. When rhamnogalacturonase A digests of the labelled product were subsequently treated with endo-1,4- beta -galactanase, radioactivity was not only found as [14C]galactose or [14C]galactobiose but also as larger fragments. The larger fragments were suggested to be the [14C]galactose or [14C]galactobiose still attached to the rhamnogalacturonan backbone, since treatment with beta -galactosidase together with endo-1,4- beta -galactanase digested all radioactivity to the fraction eluting as [14C]galactose. These data indicate that the majority of the [14C]galactan was attached directly to the rhamnose residues in rhamnogalacturonan I
Descriptors:biosynthesis. potatoes. metabolism. galactans. microsomes. plasma-membranes
Identifiers:beta -galactosidase. endo-1,4- beta -galactanase
Organism Descriptors:Aspergillus-aculeatus. Aspergillus-niger. Solanum-tuberosum
Supplemental Descriptors:Aspergillus. Deuteromycotina. Eumycota. fungi. Solanum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060
Supplementary Info:27 ref

ISSN:0032-0935
Year:2000
Journal Title:Planta

396. Title:Expression pattern of (+)- delta -cadinene synthase genes and biosynthesis of sesquiterpene aldehydes in plants of Gossypium arboreum L
View Article: Planta. 2000. 210 (4). 644-651
CD Volume:334
Print Article: Pages: 644-651
Author(s):Tan XiaoPing Liang WanQi Liu ChangJun Luo Ping Heinstein P Chen XiaoYa
Author Variant:Tan-X-P. Liang-W-Q. Liu-C-J. Luo-P. Chen-X-Y
Author Affiliation:National Laboratory of Plant Molecular Genetics, Institute of Plant Physiology of Shanghai Institutes for Biological Science, The Chinese Academy of Sciences, 300 Fenglin Road, Shanghai 200032, China
Language:English
Abstract:The cotton (+)- delta -cadinene synthase, a sesquiterpene cyclase, is encoded by a complex gene family which, based on homology, can be divided into two subfamilies: cad1-A and cad1-C. Southern blots revealed several members of the cad1-C subfamily, and a single member of the cad1-A subfamily, in the diploid Gossypium arboreum genome. One of the cad1-C genes, cad1-C3, was isolated from this species. According to reverse transcriptase-polymerase chain reaction, transcripts of both cad1-C and cad1-A genes appeared in roots from the second day post germination and in 1-d-old cotyledons, whereas the transcription levels were too low to be detected in the hypocotyls. Initially, sesquiterpene cyclase activities were found to be high in the seedlings, then dropped in aerial organs but increased in roots during development. Sesquiterpene aldehyde contents followed the same pattern. In fully developed plants, the transcripts of cad1-C were detected in stems, leaves and pericarps, as well as in the sepals and petals 3 d before anthesis, but not at the day of anthesis. In contrast, cad1-A transcripts were not detected in any of these aerial organs. The sesquiterpene aldehyde contents increased in petals but decreased in sepals after anthesis. Treatment of G. arboreum stems with a Verticillium dahliae elicitor-preparation activated cad1-A transcription, but a significant level of cad1-C transcripts was detected both before and after elicitation. In G. hirsutum cv. GL-5, a glandless cultivar, the cad1-C gene was activated by the same fungal elicitor, followed by the synthesis of the sesquiterpene cyclase, and accumulation of sesquiterpene aldehydes. The cad1 gene expression during development and in response to elicitation, as well as the spatial and temporal pattern of sesquiterpene biosynthesis, constitute a chemical defence machinery in cotton plants
Descriptors:aldehydes. biosynthesis. genes. flowering. cotton. cotyledons. gene-expression. germination. hypocotyls. corolla. seedlings. transcription. sesquiterpenes. enzymes. pathogenesis-related-proteins. plant-pathogens. plant-diseases. disease-resistance. plant-pathogenic-fungi. fibre-plants. biotechnology
Organism Descriptors:Gossypium. Gossypium-arboreum. Verticillium. Verticillium-dahliae
Supplemental Descriptors:Malvaceae. Malvales. dicotyledons. angiosperms. Spermatophyta. plants. Gossypium. Deuteromycotina. Eumycota. fungi. Verticillium
Subject Codes:FF060. FF020. WW000. FF005
Supplementary Info:48 ref
ISSN:0032-0935
Year:2000

Journal Title:Planta
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397. Title:Purification and cloning of an arabinogalactan-protein from xylem of loblolly pine
View Article: Planta. 2000. 210 (4). 686-689
CD Volume:334
Print Article: Pages: 686-689
Author(s):Loopstra C A Puryear J D No EunGyu
Author Variant:No-E-G
Author Affiliation:Department of Forest Science and Crop Biotechnology Center, Texas A&M University, MS 2123, College Station, TX 77843, USA
Language:English
Abstract:An arabinogalactan protein (AGP) was purified from differentiating xylem of loblolly pine (Pinus taeda) and the N-terminal sequence used to identify a cDNA clone. The protein, PtaAGP3, was not coded for by any previously identified AGP-like genes. Moreover, PtaAGP3 was abundantly and preferentially expressed in differentiating xylem. The encoded protein contains four domains, a signal peptide, a cleaved hydrophilic region, a region rich in serine (Ser), alanine (Ala) and proline/hydroxyproline (Pro/Hyp), and a hydrophobic C-terminus. It is postulated to contain a glycosylphosphatidylinositol (GPI) anchor site. If the protein is cleaved at the putative GPI anchor site, as has been observed in other classical AGPs, all but the Ser-Ala-Pro/Hyp-rich domain may be missing from the mature protein. Xylem-specific AGPs are hypothesized to be involved in xylem development
Descriptors:xylem. alanine. serine. proline. hydroxyproline. complementary-DNA. gene-expression. genes. proteins. purification. galactans. plant-development. forest-trees
Organism Descriptors:Pinus-taeda. Pinopsida
Supplemental Descriptors:Pinus. Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants
Subject Codes:KK100. FF040. FF020. FF060
Supplementary Info:29 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
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398. Title:Expression of cucumber lipid-body lipoxygenase in transgenic tobacco: lipid-body lipoxygenase is correctly targeted to seed lipid bodies
View Article: Planta. 2000. 210 (5). 708-714
CD Volume:334
Print Article: Pages: 708-714
Author(s):Hause B Weichert H Hohne M Kindl H Feussner I
Author Affiliation:Institut fur Pflanzenbiochemie, Weinberg 3, D-06120 Halle, Germany
Language:English
Abstract:A particular isoform of lipoxygenase (LOX, EC 1.13.11.12) localized on lipid bodies has been shown by earlier investigations to play a role during seed germination in initiating the mobilization of triacylglycerols. On lipid bodies of germinating cucumber (Cucumis sativus) seedlings, the modification of linoleoyl moieties by this LOX precedes the hydrolysis of the ester bonds. The expression and intracellular location of this particular LOX form was analyzed in leaves and seeds of tobacco (Nicotiana tabacum) transformed with one construct coding for cucumber lipid-body LOX and one construct coding for cucumber LOX fused with a haemagglutinin epitope. In both tissues, the amount of lipid-body LOX was clearly detectable. Biochemical

analysis revealed that in mature seeds the foreign LOX was targeted to lipid bodies, and the preferred location of the LOX on lipid bodies was verified by immunofluorescence microscopy. Cells of the endosperm and of the embryo exhibited fluorescence based on the immunodecoration of LOX protein whereas very weak fluorescent label was visible in seeds of untransformed control plants. Further cytochemical analysis of transformed plants showed that the LOX protein accumulated in the cytoplasm when green leaves lacking lipid bodies were analyzed. Increased LOX activity was shown in young leaves of transformed plants by an increase in the amounts of endogenous (2E)-hexenal and jasmonic acid

Descriptors:lipoxygenase. tobacco. transgenic-plants. plant-embryos. endosperm. fluorescence. jasmonic-acid. seed-germination. seedlings. seeds. triacylglycerols. genetic-transformation. gene-expression. genetic-engineering. vegetables. biotechnology. cucumbers

Organism Descriptors:Nicotiana. Cucumis. Cucumis-sativus. Nicotiana-tabacum

Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Cucurbitaceae. Violales. Cucumis. Nicotiana

Subject Codes:FF020. FF003. FF005. WW000. FF060

Supplementary Info:39 ref

ISSN:0032-0935
Year:2000
Journal Title:Planta

399. Title:Identification and expression of three new Nicotiana plumbaginifolia genes which encode isoforms of a plasma-membrane H+-ATPase, and one of which is induced by mechanical stress

View Article: Planta. 2000. 210 (5). 715-722
CD Volume:334
Print Article: Pages: 715-722

Author(s):Oufattole M Arango M Boutry M
Author Affiliation:Unite de Biochimie Physiologique, Universite catholique de Louvain, Place Croix du Sud 2-20, B-1348 Louvain-la-Neuve, Belgium

Language:English

Abstract:To analyze in detail the multigene family encoding the plasma-membrane H+-ATPase [adenosinetriphosphatase] (pma) in Nicotiana plumbaginifolia, five new pma genes (pma5-pma9) were isolated. Three of these (pma6, pma8, pma9) were fully characterized and classified into new and independent subfamilies. Their cell-type expression was followed by the beta -glucuronidase (gusA) reporter-gene method. While the pma8-gusA transgene was not expressed in transgenic tobacco, expression of the two other transgenes (pma6-gusA and pma9-gusA) was found to be restricted to particular cell types. In the vegetative tissues, pma6-gusA expression was limited to the head cells of the leaf short trichomes, involved in secretion, and to the cortical parenchyma of the young nodes where the developing leaves and axillary flowering stalks join the stem. In the latter tissues, gene expression was enhanced by mechanical stress, suggesting that H+-ATPase might be involved in the strength of the tissues and their resistance to mechanical trauma. The pma9-gusA transgene was mainly expressed in the apical meristem of adventitious roots and axillary buds as well as in the phloem tissues of the stem, in which expression depended on the developmental stage. In flowers, pma9-gusA expression was limited to the mature pollen grains and the young fertilized ovules, while that of pma6-gusA was identified in most of the organs. Reverse transcription-polymerase chain reaction of leaf and stem RNA confirmed the expression of pma6 and pma9, while pma8 was found to be expressed in both organs at a lower level. In conclusion, although pma6 and pma9 had a more

restricted expression pattern than the previously characterized pma genes, they were nevertheless expressed in cell types in which H+-ATPase had not been previously detected
Descriptors:genes. genetic-transformation. genetic-engineering. adventitious-roots. flowering. gene-expression. ovules. parenchyma. phloem. phenylmercury-acetate. pollen. RNA. tobacco. transgenic-plants. trichomes. adenosinetriphosphatase. polymerase-chain-reaction. reporter-genes. stress. mechanically-induced-stress. stimulant-plants. biotechnology
Identifiers:beta -glucuronidase
Organism Descriptors:Nicotiana-tabacum. Nicotiana-plumbaginifolia. Nicotiana
Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. FF005. FF060
Supplementary Info:36 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

400. Title:Functional characterisation of LKT1, a K+ uptake channel from tomato root hairs, and comparison with the closely related potato inwardly rectifying K+ channel SKT1 after expression in Xenopus oocytes
View Article: Planta. 2000. 210 (5). 723-731
CD Volume:334
Print Article: Pages: 723-731
Author(s):Hartje S Zimmermann S Klonus D Mueller Roeber B
Author Affiliation:Max-Planck-Institut fur Molekulare Pflanzenphysiologie (MPI-MP) Am Muhlenberg 1, 14476 Golm, Germany
Language:English
Abstract:A cDNA encoding a novel inwardly rectifying potassium (Kin+) channel, LKT1, was cloned from a root-hair-specific cDNA library of tomato (Lycopersicon esculentum). The LKT1 mRNA was shown to be most strongly expressed in root hairs by northern blot analysis. The LKT1 channel is a member of the AKT family of Kin+ channels previously identified in Arabidopsis thaliana and potato (Solanum tuberosum). Moreover, LKT1 is closely related (97% identical amino acids) to potato SKT1. An electrophysiological comparison of the two channels should therefore assist the identification of possible molecular bases for functional differences. For this comparison, both channels were functionally expressed and electrophysiologically characterised within the same expression system, i.e. Xenopus laevis oocytes. Voltage-clamp measurements identified LKT1 as a K+-selective inward rectifier which activates with slow kinetics upon hyperpolarising voltage pulses to potentials more negative than -50 mV. The activation potential of LKT1 is shifted towards positive potentials with respect to SKT1 which might be due to single amino acid exchanges in the rim of the channel's pore region or in the S4 domain. Like SKT1, LKT1 reversibly activated upon shifting the external pH from 6.6 to 5.5, which indicates a physiological role for pH-dependent regulation of AKT-type Kin+ channels. The pharmacological inhibitor Cs+, applied externally, inhibited Kin+ currents mediated by LKT1 and SKT1 half-maximally with a concentration (IC50) of 21 micro M and 17 micro M, respectively. In conclusion, LKT1 may serve as a low-affinity influx pathway for K+ into root hair cells. Comparison of homologous Kin+ rectifiers from different plant species expressed in the same heterologous system allows conclusions to be drawn in respect to structure-function relationships

Descriptors:root-hairs. uptake. amino-acids. complementary-DNA. messenger-RNA. potassium. ion-transport. gene-expression. nucleotide-sequences. mineral-uptake. vegetables. biotechnology. tomatoes. potatoes
Organism Descriptors:Xenopus. Arabidopsis. Arabidopsis-thaliana. Lycopersicon. Lycopersicon-esculentum. Solanum. Solanum-tuberosum. Xenopus-laevis
Supplemental Descriptors:Pipidae. Anura. Amphibia. vertebrates. Chordata. animals. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Arabidopsis. Solanaceae. Solanales. Lycopersicon. Solanum. Xenopus
Subject Codes:FF020. WW000. FF003. FF005. FF060
Supplementary Info:40 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

401. Title:Water-selective and multifunctional aquaporins from Lotus japonicus nodules
View Article: Planta. 2000. 210 (5). 741-748
CD Volume:334
Print Article: Pages: 741-748
Author(s):Guenther J F Roberts D M
Author Affiliation:Department of Biochemistry, Cellular and Molecular Biology, University of Tennessee, Knoxville, TN 37996-0840, USA
Language:English
Abstract:By using reverse transcriptase-polymerase chain reaction, two cDNAs were isolated that encode major intrinsic membrane proteins (MIPs) that are expressed in nitrogen-fixing root nodules of Lotus japonicus. Lotus intrinsic membrane protein 1 (LIMP 1) is expressed at high levels in both nodule and root tissues and shows highest sequence similarity to members of the tonoplast intrinsic protein (TIP) subfamily of plant MIPs. Functional analysis of LIMP 1 by expression in Xenopus laevis oocytes show that it is a water-specific aquaporin. In contrast, LIMP 2 shows the highest sequence similarity to soyabean nodulin 26 (67.8% amino acid sequence identity). LIMP 2 is also a nodulin, showing expression only in mature nitrogen fixing nodules of L. japonicus. LIMP 2 is a multifunctional aquaglyceroporin, and displays the ability to flux both water as well as glycerol upon expression in Xenopus oocytes. Additionally, the carboxyl terminal region of LIMP 2 has a conserved phosphorylation motif that is phosphorylated by a calmodulin-like domain protein kinase. Overall, the data show that L. japonicus nodules contain two structurally and functionally distinct MIP proteins: one (LIMP 2) which appears to be the nodulin 26 orthologue of L. japonicus and another (LIMP 1) which appears to be a member of the TIP subfamily
Descriptors:kinases. surface-proteins. nitrogen-fixation. phosphorylation. protein-kinase. root-nodules. soyabeans. tonoplast. polymerase-chain-reaction. nucleotide-sequences. amino-acid-sequences. nodulins. gene-expression. fodder-plants. fodder-legumes. biotechnology
Identifiers:Lotus japonicus
Organism Descriptors:Glycine-max. Glycine-(Fabaceae). Xenopus. Xenopus-laevis. Lotus. Fabaceae
Supplemental Descriptors:Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Pipidae. Anura. Amphibia. vertebrates. Chordata. animals. Xenopus. Lotus
Subject Codes:FF020. WW000. FF007
Supplementary Info:35 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

402. Title:Identification of a signal peptide for oryzacystatin-I
View Article: Planta. 2000. 210 (5). 844-847
CD Volume:334
Print Article: Pages: 844-847
Author(s):Womack J S Randall J Kemp J D
Author Affiliation:Gene Lab, MSC 3GL, Department of Entomology, Plant Pathology and Weed Science, New Mexico State University, Box 30003, Las Cruces, New Mexico 88003, USA
Language:English
Abstract:A previously unidentified extension of an open reading frame from the genomic DNA of japonica rice (Oryza sativa) encoding oryzacystatin-I (OC-I; access. M29259, protein ID AAA33912.1) has been identified as a 5' gene segment coding for the OC-I signal peptide. The signal peptide appears to direct a preprotein (SPOC-I; Accession No. AF164378) to the endoplasmic reticulum, where it is processed into the mature form of OC-I. The start codon of SPOC-I begins 114 bp upstream from that previously published for OC-I. A putative proteolytic site, which may yield a mature OC-I approximately 12 residues larger than previously described, has been identified within SPOC-I between Ala-26 and Glu-27. The signal peptide sequence was amplified by polymerase chain reaction using genomic DNA from O. sativa seedlings and ligated to the 5' end of the truncated OC-I gene at the endogenous Sa/I site. Partially purified protein extracts from Escherichia coli expressing SPOC-I reacted with polyclonal antibodies raised against OC-I and revealed a protein of the expected molecular weight (15 355 Da). In vitro translation of SPOC-I in the presence of microsomal membranes yielded a processed product approximately 2.7 kDa smaller than the pre-protein. Nicotiana tabacum cv. Xanthi plants independently transformed with the SPOC-I gene processed SPOC-I and accumulated the mature form of OC-I (approximately 12.6 kDa), which co-migrated with natural, mature OC-I extracted from rice seed when separated by SDS-PAGE. Nucleotide sequence data reported here will appear in the Plant Gene Register database under accession number P6R99-175
Descriptors:antibodies. DNA. electrophoresis. endoplasmic-reticulum. genomes. genome-analysis. rice. polymerase-chain-reaction. amino-acid-sequences. seedlings. translation. open-reading-frames. SDS-PAGE. nucleotide-sequences. proteinase-inhibitors. cereals. biotechnology. tobacco
Identifiers:oryzacystatin
Organism Descriptors:Escherichia. Escherichia-coli. Nicotiana. Nicotiana-tabacum. Oryza-sativa. Oryza
Supplemental Descriptors:Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. Escherichia. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Nicotiana. Oryza. Poaceae. Cyperales. monocotyledons
Subject Codes:FF020. FF007. WW000. FF060
Supplementary Info:20 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

403. Title:The genes ABI1 and ABI2 are involved in abscisic acid- and drought-inducible expression of the Daucus carota L. Dc3 promoter in guard cells of transgenic Arabidopsis thaliana (L.) Heynh
View Article: Planta. 2000. 210 (6). 875-883
CD Volume:334

Print Article: Pages: 875-883
Author(s):Chak R K F Thomas T L Quatrano R S Rock C D
Author Affiliation:Department of Biology, Hong Kong University of Science and Technology, Clear Water Bay, Kowloon, Hong Kong, China
Language:English
Abstract:The ABA INSENSITIVE1 (ABI1) and ABI2 genes encode homologous type-2C protein phosphatases with redundant yet distinct functions in abscisic acid (ABA) responses. Results from Northern blot analysis showed that ABA- and mannitol-inducible expression of the COR47 and COR78/LTI78/RD29A (COR78) genes was more impaired in the abi2 mutant of Arabidopsis thaliana than in the abi1 mutant. Furthermore, ABA-plus-mannitol treatments were additive towards COR47 gene expression; however, the ABA-deficient aba1 mutant showed reduced COR expression relative to the wild type in response to mannitol and ABA-plus-mannitol treatments. These results support the notion that drought- and ABA-signalling pathways are separate yet overlapping. To facilitate quantitative analysis of the genetic control of tissue-specific ABA- and desiccation-response pathways, we analyzed ABA- and mannitol-inducible expression of a carrot (Daucus carota) Dc3 promoter:uidA (beta -glucuronidase; GUS) chimaeric reporter (Dc3-GUS) in transgenic wild-type, ABA-deficient aba1, and ABA-insensitive abi1 and abi2 mutants. The Dc3 promoter directed ABA- and mannitol-inducible GUS expression in Arabidopsis guard cells and the two treatments were additive. The aba1, abi1 and abi2 mutant genotypes had reduced GUS expression in guard cells of cotyledons in response to mannitol, whereas abi1 and abi2 mutants were reduced in ABA-inducible GUS expression, consistent with overlapping ABA- and drought-response pathways. Quantitative fluorometric GUS assays of leaf extracts showed that abi2 mutants responded less to exogenous ABA than did abi1 mutants, and abi2 mutants responded more to mannitol than did abi1 mutants. We concluded that Dc3-GUS Arabidopsis is a tractable system in which to study tissue-specific ABA and drought signalling and suggest that ABI2 functions predominantly over ABI1 in COR78 and COR47 gene expression and guard-cell Dc3-GUS expression
Descriptors:genes. guard-cells. abscisic-acid. carrots. cotyledons. gene-expression. plant-growth-regulators. mutants. genetic-transformation. water-stress. genetic-engineering. stomata. growth-inhibitors. vegetables. biotechnology
Identifiers:protein phosphatase
Organism Descriptors:Arabidopsis-thaliana. Daucus-carota. Daucus. Daucus-carota
Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Daucus. Apiaceae. Apiales
Subject Codes:FF020. FF060. FF900. FF003
Supplementary Info:59 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

404. Title:The auxin-resistant diageotropica mutant of tomato responds to gravity via an auxin-mediated pathway
View Article: Planta. 2000. 210 (6). 906-913
CD Volume:334
Print Article: Pages: 906-913
Author(s):Rice M S Lomax T L
Author Affiliation:Department of Botany and Plant Pathology, Center for Gene Research and Biotechnology, Oregon State University, Corvallis, OR 97331-2902, USA
Language:English

Abstract:Hypocotyls of the diageotropica (dgt) mutant of tomato (Lycopersicon esculentum) do not elongate in response to exogenous auxin, but can respond to gravity. This appears paradoxical in light of the Cholodny-Went hypothesis, which states that shoot gravicurvature results from asymmetric stimulation of elongation by auxin. While light-grown dgt seedlings can achieve correct gravitropic reorientation, the response is slow compared to wild-type seedlings. The sensitivity of dgt seedlings to inhibition of gravicurvature by immersion in auxin or auxin-transport inhibitors is similar to that of wild-type plants, indicating that both an auxin gradient and auxin transport are required for the gravitropic response and that auxin uptake, efflux, and at least one auxin receptor are functional in dgt. Furthermore, dgt gravicurvature is the result of asymmetrically increased elongation as would be expected for an auxin-mediated response. Our results suggest differences between elongation in response to exogenous auxin (absent in dgt) and elongation in response to gravistimulation (present but attenuated in dgt) and confirm the presence of two phases during the gravitropic response, both of which are dependent on functional auxin transport
Descriptors:mutants. auxins. gravitropism. mutations. tomatoes. tropisms. vegetables. plant-growth-regulators. fruit-vegetables
Organism Descriptors:Lycopersicon-esculentum. Solanaceae. Lycopersicon
Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF060. FF020. FF003
Supplementary Info:27 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

405. Title:12-Oxophytodienoate reductase 3 (OPR3) is the isoenzyme involved in jasmonate biosynthesis
View Article: Planta. 2000. 210 (6). 979-984
CD Volume:334
Print Article: Pages: 979-984
Author(s):Schaller F Biesgen C Mussig C Altmann T Weiler E W
Author Affiliation:Lehrstuhl fur Pflanzenphysiologie, Ruhr-Universitat, 44780 Bochum, Germany
Language:English
Abstract:In addition to OPR1 and OPR2, two isoenzymes of 12-oxophytodienoate reductase, a third isoform (OPR3) has recently been identified in Arabidopsis thaliana. The expression of the OPR3 gene is induced not only by a variety of stimuli, such as touch, wind, wounding, UV-light and application of detergent, but also by brassinosteroids. The three enzymes were expressed in a functional form in Escherichia coli, and OPR2 was additionally expressed in insect cell cultures and overexpressed in A. thaliana. Substrate conversion was analyzed using a stereospecific assay. The results show that OPR3 effectively converts the natural (9S,13S)-12-oxophytodienoic acid [Km=35 micro M, Vmax 53.7 nkat (mg protein)-1] to the corresponding 3-2(2'(Z)-pentenyl) cyclopentane-1-octanoic acid (OPC-8:0) stereoisomer while OPR1 and OPR2 convert (9S,13S)-12-oxophytodienoic acid with greatly reduced efficiency compared to OPR3. Thus, OPR3 is the isoenzyme relevant for jasmonate biosynthesis
Descriptors:biosynthesis. brassinosteroids. isoenzymes. jasmonic-acid. genetic-transformation. gene-expression. plant-growth-regulators. DNA-cloning. weeds. biotechnology. growth-inhibitors
Identifiers:oxophytodienoate reductase

Organism Descriptors:Arabidopsis-thaliana. Arabidopsis. Escherichia-coli
Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF020. WW000. FF060
Supplementary Info:25 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

406. Title:Isoforms of chalcone synthase in Daucus carota L. and their differential expression in organs from the European wild carrot and in ultraviolet-A-irradiated cell cultures
View Article: Planta. 2000. 210 (6). 993-998
CD Volume:334
Print Article: Pages: 993-998
Author(s):Hirner A A Seitz H U
Author Affiliation:Universitat Tubingen, Zentrum fur Molekularbiologie der Pflanzen (ZMBP), Lehrstuhl fur Pflanzenphysiologie, Auf der Morgenstelle 1, 72076 Tubingen, Germany
Language:English
Abstract:Two isoforms of chalcone synthase [naringenin-chalcone synthase] (CHS) were isolated from cDNA libraries derived from UV-A-irradiated anthocyanin-accumulating (DCb) and non-accumulating (DCs) cell cultures of carrot. The clones designated as DcCHS1, which were present only in the DCb library, had a deduced primary sequence of 389 amino acids and an expected molecular mass of 42.7 kDa. The second isoform (DcCHS2) was present in both libraries. It had the highest degree of similarity (97.7%) to parsley CHS over all 397 amino acids. The expected molecular mass of the corresponding protein was 43.6 kDa. Results obtained from Southern blot analysis indicated the existence of at least two CHS genes in carrot. A transient enhancement of the DcCHS1 mRNA level after continuous irradiation with UV-A light could only be observed in anthocyanin-accumulating cultures, whereas an increase in DcCHS2 mRNA was seen in both cell lines. The maximum accumulation of CHS mRNA occurred 48 h after the onset of UV-A irradiation. In the European wild carrot the accumulation of DcCHS1 mRNA was restricted to the red central flowers, whereas the DcCHS2 mRNA was detectable in all red and white petals, as well as leaves, but was absent in stems and roots. The expression of DcCHS1 was restricted to anthocyanin-accumulating cells or organs. The heterologous expression of both cDNAs in Escherichia coli resulted in immunostainable bands of different sizes on the Western blot and high levels of catalytic CHS activity. Nucleotide sequences reported here have been submitted to EMBL database under accession numbers AJ006779 (DcCHS1) and AJ006780 (DcCHS2)
Descriptors:carrots. naringenin-chalcone-synthase. alleles. amino-acids. complementary-DNA. cell-lines. genes. ultraviolet-radiation. messenger-RNA. parsley. DNA-cloning. gene-expression. isoenzymes. nucleotide-sequences. vegetables. biotechnology
Organism Descriptors:Daucus. Daucus-carota. Escherichia-coli. Petroselinum-crispum
Supplemental Descriptors:Apiaceae. Apiales. dicotyledons. angiosperms. Spermatophyta. plants. Daucus. Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. Petroselinum
Subject Codes:FF060. FF020. WW000. FF003
Supplementary Info:27 ref
ISSN:0032-0935
Year:2000

Journal Title:Planta
Copyright:Copyright CAB International

407. Title:Cloning and expression of UDP-glucose: flavonoid 7-O-glucosyltransferase from hairy root cultures of Scutellaria baicalensis
View Article: Planta. 2000. 210 (6). 1006-1013
CD Volume:334
Print Article: Pages: 1006-1013
Author(s):Hirotani M Kuroda R Suzuki H Yoshikawa T
Author Affiliation:School of Pharmaceutical Sciences, Kitasato University, Minato-ku, Tokyo 108-8641, Japan
Language:English
Abstract:A cDNA encoding UDP-glucose: baicalein 7-O-glucosyltransferase (UBGT) was isolated from a cDNA library from hairy root cultures of Scutellaria baicalensis probed with a partial-length cDNA clone of a UDP-glucose: flavonoid 3-O-glucosyltransferase (UFGT) from grape (Vitis vinifera). The heterologous probe contained a glucosyltransferase consensus amino acid sequence which was also present in the Scutellaria cDNA clones. The complete nucleotide sequence of the 1688-bp cDNA insert was determined and the deduced amino acid sequences are presented (GenBank/EBI databases accession number AB031274). The nucleotide sequence analysis of UBGT revealed an open reading frame encoding a polypeptide of 476 amino acids with a calculated molecular mass of 53 094 Da. The reaction product for baicalein and UDP-glucose catalyzed by recombinant UBGT in Escherichia coli was identified as authentic baicalein 7-O-glucoside using high-performance liquid chromatography and proton nuclear magnetic resonance spectroscopy. The enzyme activities of recombinant UBGT expressed in E. coli were also detected towards flavonoids such as baicalein, wogonin, apigenin, scutellarein, 7,4'-dihydroxyflavone and kaempferol and phenolic compounds. The accumulation of UBGT mRNA in hairy roots was in response to wounding or salicylic acid treatments
Descriptors:amino-acids. complementary-DNA. chromatography. DNA-cloning. flavonoids. messenger-RNA. nuclear-magnetic-resonance-spectroscopy. phenolic-compounds. salicylic-acid. injuries. nucleotide-sequences. gene-expression. medicinal-plants. biotechnology. grapes
Identifiers:glucosyltransferase. UDP-glucose:baicalein glucosyltransferase
Organism Descriptors:Scutellaria-baicalensis. Escherichia-coli. Escherichia. Vitis. Vitis-vinifera
Supplemental Descriptors:Scutellaria. Lamiaceae. Lamiales. dicotyledons. angiosperms. Spermatophyta. plants. Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. Vitidaceae. Rhamnales. Vitis
Subject Codes:FF060. FF020. WW000. FF003. FF900
Supplementary Info:37 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

408. Title:Expansion of transgenic tobacco protoplasts expressing pumpkin ascorbate oxidase is more rapid than that of wild-type protoplasts
View Article: Planta. 2000. 210 (6). 1018-1022
CD Volume:334
Print Article: Pages: 1018-1022
Author(s):Kato N Esaka M
Author Affiliation:Faculty of Applied Biological Science, Hiroshima University, Kagamiyama, Higashi-Hiroshima 739-8528, Japan
Language:English

Abstract:When pumpkin (Cucurbita spp., cv. Ebisu Nankin) ascorbate oxidase cDNA was introduced into cultured cells of tobacco BY-2 (Nicotiana tabacum cv. Bright Yellow No. 2) by Agrobacterium tumefaciens-mediated transformation, the transgenic cells expressed and secreted the recombinant pumpkin ascorbate oxidase into the culture medium. These transgenic cells showed no morphological difference from wild-type cells. However, in the presence of benzyladenine and NAA protoplasts prepared from the transgenic cells elongated more rapidly than those of wild-type cells. We propose that ascorbate oxidase may play a key role in the regulation of cell expansion perhaps by controlling transport processes through the plasma membrane, but not by affecting the cell wall
Descriptors:ascorbate-oxidase. protoplasts. pumpkins. tobacco. complementary-DNA. cell-walls. genetic-transformation. benzyladenine. NAA. plant-growth-regulators. genetic-engineering. gene-expression. vegetables. biotechnology. auxins. cytokinins
Organism Descriptors:Cucurbita. Nicotiana-tabacum. Agrobacterium-tumefaciens. Nicotiana
Supplemental Descriptors:Cucurbitaceae. Violales. dicotyledons. angiosperms. Spermatophyta. plants. Nicotiana. Solanaceae. Solanales. Agrobacterium. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF003. FF020. FF060. FF170. WW000
Supplementary Info:25 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

409. Title:Three maize root-specific genes are not correctly expressed in regenerated caps in the absence of the quiescent center
View Article: Planta. 2000. 211 (1). 23-33
CD Volume:334
Print Article: Pages: 23-33
Author(s):Ponce G Lujan R Campos M E Reyes A Nieto Sotelo J Feldman L J Cassab G I
Author Affiliation:Department of Plant Molecular Biology, Institute of Biotechnology, National Autonomous University of Mexico, PO Box 510-3, Cuernavaca, Mor., 62250, Mexico
Language:English
Abstract:The quiescent centre is viewed as an architectural template in the root apical meristem of all angiosperm and gymnosperm root tips. In roots of Arabidopsis thaliana, the quiescent centre inhibits differentiation of contacting initial cells and maintains the surrounding initial cells as stem cells. Here, the role of the quiescent centre in the development of the maize (Zea mays) root cap has been further explored. Three maize root-specific genes were identified. Two of these were exclusively expressed in the root cap and one of them encoded a GDP-mannose-4, 6-dehydratase. Most likely these two genes are structural, tissue-specific markers of the cap. The third gene, a putative glycine-rich cell wall protein, was expressed in the cap and in the root epidermis and, conceivably is a positional marker of the cap. Microsurgical and molecular data indicate that the quiescent centre and cap initials may regulate the positional and structural expression of these genes in the cap and thereby control root cap development
Descriptors:genes. maize. epidermis. root-tips. gene-expression. plant-development. cereals
Organism Descriptors:Zea-mays. Arabidopsis. Arabidopsis-thaliana

Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Brassicaceae. Capparidales. dicotyledons. Arabidopsis
Subject Codes:FF060. FF020
Supplementary Info:37 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta

410. Title:Decrease of phosphoribulokinase activity by antisense RNA in transgenic tobacco: definition of the light environment under which phosphoribulokinase is not in large excess
View Article: Planta. 2000. 211 (1). 112-119
CD Volume:334
Print Article: Pages: 112-119
Author(s):Paul M J Driscoll S P Andralojc P J Knight J S Gray J C Lawlor D W
Author Affiliation:Biochemistry and Physiology Department, IACR-Rothamsted, Harpenden, Hertfordshire, AL5 2JQ, UK
Language:English
Abstract:To test the hypothesis that the contribution of phosphoribulokinase (PRK) to the control of photosynthesis changes depending on the light environment of the plant, the response of tobacco (Nicotiana tabacum) transformed with antisense PRK constructs to irradiance was determined. In plants grown under low irradiance (330 micro mol m-2 s-1) steady-state photosynthesis was limited in plants with decreased PRK activity upon exposure to higher irradiance, with a control coefficient of PRK for CO2 assimilation of 0.25 at and above 800 micro mol m-2 s-1. The flux control coefficient of PRK for steady-state CO2 assimilation was zero at all irradiances in plant material grown at 800 micro mol m-2 s-1 and in plants grown in a glasshouse during mid-summer (alternating shade and sun 300-1600 micro mol m-2 s-1). To explain these differences between plants grown under low and high irradiances, Calvin cycle enzyme activities and metabolite content were determined. Activities of PRK and other non-equilibrium Calvin cycle enzymes fructose-1,6-bisphosphatase, sedoheptulose-1,7-bisphosphatase and ribulose-1,5-bisphosphate carboxylase-oxygenase were twofold higher in plants grown at 800 micro mol m-2 s-1 or in the glasshouse than in plants grown at 330 micro mol m-2 s-1. Activities of equilibrium enzymes transketolase, aldolase, ribulose-5-phosphate epimerase and isomerase were very similar under all growth irradiances. The flux control coefficient of 0.25 in plants grown at 330 micro mol m-2 s-1 can be explained by low ribulose-5-phosphate content in combination with low PRK activity limits the synthesis of ribulose-1,5-bisphosphate. This limitation is overcome in high-light-grown plants because of the large relative increase in activities of sedoheptulose-1,7-bisphosphatase and fructose-1,6-bisphosphatase under these conditions, which facilitates the synthesis of larger amounts of ribulose-5-phosphate. This potential limitation will have maintained evolutionary selection pressure for high concentrations of PRK within the chloroplast
Descriptors:tobacco. chloroplasts. control. isomerases. photosynthesis. light. genetic-transformation. gene-expression. antisense-DNA. enzyme-activity. stimulant-plants. biotechnology
Identifiers:phosphoribulokinase
Organism Descriptors:Nicotiana. Nicotiana-tabacum
Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Nicotiana
Subject Codes:WW000. FF020. FF060
Supplementary Info:24 ref

ISSN:0032-0935
Year:2000
Journal Title:Planta
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411. Title:Importance of sequences adjacent to the terminal tripeptide in the import of a peroxisomal Candida tropicalis protein in plant peroxisomes
View Article: Planta. 2000. 211 (1). 150-157
CD Volume:334
Print Article: Pages: 150-157
Author(s):Bongcam V Petetot J M C Mittendorf V Robertson E J Leech R M Qin YongMei Hiltunen J K Poirier Y
Author Variant:Qin-Y-M
Author Affiliation:Institut d'Ecologie-Biologie et Physiologie Vegetales, Universite de Lausanne, 1015 Lausanne, Switzerland
Language:English
Abstract:The peroxisome targeting signal (PTS) required for import of the rat acyl-CoA oxidase (AOX; EC 1.3.3.6) and the Candida tropicalis multifunctional protein (MFP) in plant peroxisomes was assessed in transgenic Arabidopsis thaliana. The native rat AOX accumulated in peroxisomes in A. thaliana cotyledons and targeting was dependent on the presence of the C-terminal tripeptide S-K-L. In contrast, the native C. tropicalis MFP, containing the consensus PTS sequence A-K-I was not targeted to plant peroxisomes. Modification of the carboxy terminus to the S-K-L tripeptide also failed to deliver the MFP to peroxisomes while addition of the last 34 amino acids of the Brassica napus isocitrate lyase, containing the terminal tripeptide S-R-M, enabled import of the fusion protein into peroxisomes. These results underline the influence of the amino acids adjacent to the terminal tripeptide of the C. tropicalis MFP on peroxisomal targeting, even in the context of a protein having a consensus PTS sequence S-K-L
Descriptors:peroxisomes. amino-acids. cotyledons. isocitrate-lyase. transgenic-plants. genetic-transformation. gene-expression. surface-proteins. weeds. biotechnology
Identifiers:acetyl-CoA oxidase
Organism Descriptors:Candida. Candida-tropicalis. Arabidopsis-thaliana. Arabidopsis. Brassica. Brassica-napus. rats
Supplemental Descriptors:Deuteromycotina. Eumycota. fungi. Candida. Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica. Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:FF020. WW000. FF060
Supplementary Info:48 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
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412. Title:Transgenic Nicotiana tabacum and Arabidopsis thaliana plants overexpressing allene oxide synthase
View Article: Planta. 2000. 211 (1). 163-165
CD Volume:334
Print Article: Pages: 163-165
Author(s):Laudert D Schaller F Weiler E W
Author Affiliation:Lehrstuhl fur Pflanzenphysiologie, Ruhr-Universitat, 44780 Bochum, Germany
Language:English
Abstract:Allene oxide synthase (AOS), encoded by a single gene in Arabidopsis thaliana, catalyses the first step specific to the octadecanoid

pathway. Enzyme activity is very low in control plants, but is upregulated by wounding, octadecanoids, ethylene, salicylate and coronatine. In order to study the consequences of constitutive expression of AOS on the level of jasmonates, a complete cDNA encoding the enzyme from A. thaliana was constitutively expressed in both A. thaliana and tobacco (Nicotiana tabacum). Over-expression of AOS did not alter the basal level of jasmonic acid; thus, output of the jasmonate pathway in the unchallenged plant appears to be strictly limited by substrate availability. In wounded plants overexpressing AOS, peak jasmonate levels were 2- to 3-fold higher compared to untransformed plants. More importantly, the transgenic plants reached the maximum jasmonate levels significantly earlier than wounded untransformed control plants. These findings suggest that overexpression of AOS might be a way of controlling defence dynamics in higher plants

Descriptors:complementary-DNA. enzyme-activity. ethylene. jasmonic-acid. tobacco. transgenic-plants. genetic-transformation. gene-expression. injuries. stimulant-plants. biotechnology

Identifiers:coronatine. allene oxidase

Organism Descriptors:Arabidopsis. Arabidopsis-thaliana. Nicotiana. Nicotiana-tabacum

Supplemental Descriptors:Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Arabidopsis. Solanaceae. Solanales. Nicotiana

Subject Codes:FF020. WW000. FF060

Supplementary Info:15 ref

ISSN:0032-0935

Year:2000

Journal Title:Planta

413. Title:Involvement of 14-3-3 proteins in the osmotic regulation of H+-ATPase in plant plasma membranes

View Article: Planta. 2000. 211 (3). 446-448

CD Volume:334

Print Article: Pages: 446-448

Author(s):Babakov A V Chelysheva V V Klychnikov O I Zorinyanz S E Trofimova M S Boer A H de

Author Variant:de-Boer-A-H

Author Affiliation:Institute of Agricultural Biotechnology RAAS, 42 Timiryazevskaya st., 127550 Moscow, Russia

Language:English

Abstract:Taking the binding of fusicoccin to plasma membranes as an indicator of complex formation between the 14-3-3 dimer and H+-ATPase, we assessed the effect of osmotic stress on the interaction of these proteins in suspension-cultured cells of sugarbeet (Beta vulgaris). An increase in osmolarity of the cell incubation medium, accompanied by a decrease in turgor, was found to activate the H+ efflux 5-fold. The same increment was observed in the number of high-affinity fusicoccin-binding sites in isolated plasma membranes; the 14-3-3 content in the membranes increased 2- to 3-fold, while the H+-ATPase activity changed only slightly. The data obtained indicate that osmotic regulation of H+-ATPase in the plant plasma membrane is achieved via modulation of the coupling between H+ transport and ATP hydrolysis, and that such regulation involves 14-3-3 proteins

Descriptors:plasma-membranes. ATP. efflux. fusicoccin. hydrolysis. sugarbeet. turgor. cell-cultures. enzymes. adenosinetriphosphatase

Identifiers:osmotic stress

Organism Descriptors:Beta-vulgaris. Beta-vulgaris-var.-saccharifera

Supplemental Descriptors:Beta. Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms. Spermatophyta. plants. Beta-vulgaris
Subject Codes:FF005. FF060
Supplementary Info:19 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

414. Title:A novel reverse-genetic approach (SIMF) identifies Mutator insertions in new Myb genes
View Article: Planta. 2000. 211 (6). 887-893
CD Volume:334
Print Article: Pages: 887-893
Author(s):Rabinowicz P D Grotewold E
Author Affiliation:Department of Plant Biology and Plant Biotechnology Center, The Ohio State University, Columbus, OH 43210, USA
Language:English
Abstract:We have developed a new strategy designated SIMF (systematic insertional mutagenesis of families), to identify DNA insertions in many members of a gene family simultaneously. This method requires only a short amino acid sequence conserved in all members of the family to make a degenerate oligonucleotide, and a sequence from the end of the DNA insertion. The SIMF strategy was successfully applied to the large maize R2R3 Myb family of regulatory genes, and Mutator insertions in several novel Myb genes were identified. Application of this technique to identify insertions in other large gene families could significantly decrease the effort involved in screening at the same time for insertions in all members of groups of genes that share a limited sequence identity
Descriptors:amino-acid-sequences. transcription-factors. maize. transposable-elements
Organism Descriptors:plants. Zea-mays
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. WW000
Supplementary Info:25 ref
ISSN:0032-0935
Year:2000
Journal Title:Planta
Copyright:Copyright CAB International

415. Title:Hydroxamate siderophores of root nodule bacteria
View Article: Soil Biology & Biochemistry. 2000. 32 (1). 11-21
CD Volume:330
Print Article: Pages: 11-21
Author(s):Carson K C Meyer J M Dilworth M J
Author Affiliation:Centre for Rhizobium Studies, School of Biological Sciences and Biotechnology, Murdoch University, South St., Murdoch, WA 6150, Australia
Language:English
Abstract:Sixty strains of root nodule bacteria were screened for siderophore production in low-iron broth, among them 40 strains from the Australian Inoculants Research and Control Service, which are the current commercial inoculants used in the pulse and legume pasture industries in Australia. Eleven new siderophore-producing strains were recognised including Sinorhizobium meliloti (WSM826, WSM352, SU47), Rhizobium leguminosarum biovar viciae (WU163, MNF3841, SU391), R. leguminosarum biovar trifolii (CB782, CC2483g, CC283b) and R. tropici (WSM1385,

CB3060). Siderophores were identified by chemical characterization for catecholate or hydroxamate, spectral studies, isoelectrofocusing and siderophore-mediated iron-uptake studies. The S. meliloti strains all produced dihydroxamate siderophores. Other siderophore-producing rhizobia, with the exception of R. tropici CB306c, excreted trihydroxamate-type siderophores. No bradyrhizobia were Chromazurol S-positive. 59Fe uptake studies revealed that all strains transported iron complexed to citrate. The sinorhizobia took up 5-10-fold more iron from dihydroxamate than trihydroxamate siderophores. Conversely, other rhizobia and the slow-growing bradyrhizobia transported iron complexed to trihydroxamates at rates 2-5 fold those of dihydroxamate siderophores. Rhizobactin 1021 was excreted by S. meliloti strains 1021, Rm2011 and SU47 and vicibactin by seven strains of R. leguminosarum (bv. viciae and bv. trifolii)
Descriptors:nodules. root-nodules. siderophores. characterization. citrates. iron. pastures. research. strains. uptake
Geographic Locator:Australia
Identifiers:inoculants. Rhizobium tropici. Sinorhizobium. Sinorhizobium meliloti
Organism Descriptors:Rhizobium. Rhizobium-leguminosarum. Rhizobiaceae
Supplemental Descriptors:Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Rhizobium. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries
Subject Codes:PP350. JJ100. JJ200
Supplementary Info:36 ref
ISSN:0038-0717
Year:2000
Journal Title:Soil Biology & Biochemistry
Copyright:Copyright CAB International

416. Title:Identification of tolerance to soil acidity in inoculant strains of Rhizobium leguminosarum bv. trifolii
View Article: Soil Biology & Biochemistry. 2000. 32 (10). 1393-1403
CD Volume:330
Print Article: Pages: 1393-1403
Author(s):Watkin E L J O'Hara G W Howieson J G Glenn A R
Author Affiliation:Centre For Rhizobium Studies, School of Biological Sciences and Biotechnology, Division of Science and Engineering, Murdoch University, Murdoch, WA 6150, Australia
Language:English
Abstract:The acid-soil tolerance of six strains (WU95, NA3001, WSM409, TA1, NA3025 and NA3039) of Rhizobium leguminosarum bv. trifolii was assessed in a three-year cross-row field experiment in an acid sandy soil of pH 4.2. Strains WSM409, NA3039 and WU95 were more acid-soil tolerant than strains NA3025, TA1 and NA3001. Strains WSM409 and NA3039 colonized and persisted in acid-soil to a greater degree than strains TA1 and NA3001. The data from this study identified strain WSM409 as having outstanding potential for improving the production of clovers on acid soils
Descriptors:tolerance. acidity. soil-acidity. strains. acid-soils. clovers. sandy-soils. soil
Organism Descriptors:Rhizobium. Rhizobium-leguminosarum. Trifolium
Supplemental Descriptors:Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Rhizobium. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:JJ100. JJ200
Supplementary Info:42 ref
ISSN:0038-0717
Year:2000
Journal Title:Soil Biology & Biochemistry
Copyright:Copyright CAB International

417. Title:Factors influencing the degradation of soil-applied endosulfan isomers
View Article: Soil Biology & Biochemistry. 2000. 32 (11/12). 1697-1705
CD Volume:331
Print Article: Pages: 1697-1705
Author(s):Niranjan Awasthi Rajiv Ahuja Ashwani Kumar
Author Variant:Awasthi-N. Ahuja-R. Kumar-A
Author Affiliation:Environmental Biotechnology Section, Industrial Toxicology Research Centre, Post Box No. 80, Mahatma Gandhi Marg, Lucknow 226 001, India
Language:English
Abstract:The addition of isolated bacterial cells to contaminated soils causes an enhanced degradation of endosulfan isomers. Various factors, including the additional presence of carbon sources, pH, moisture content, concentration of endosulfan, and size of inoculum, influenced the degradation of endosulfan isomers. The degradation was faster in wet soils, as compared with the flooded soils, and was inhibited by the presence of additional carbon sources such as sodium acetate and sodium succinate. The degradation of endosulfan was not detectable at acidic pH and increased gradually to reach an optimal activity at pH 8.5. It chemically converts into endosulfan diol at higher pH values. The rate of biodegradation progressed with the increase in endosulfan concentration up to 5.0 mg g-1 soil, followed by an inhibitory effect at higher concentrations, reaching a total loss of biodegradative activity at 10 mg g-1 soil. The addition of 2x106 bacterial cells g-1 soil was optimal for endosulfan degradation and any further increase in inoculum size was of no additional advantage. Initial optimization of these factors is, therefore, essential for successful bioremediation
Descriptors:degradation. endosulfan. biodegradation. bioremediation. carbon. contamination. moisture. moisture-content. optimization. sodium-acetate. soil. pollution. isomers. pH. soil-water-content. flooding
Identifiers:sodium succinate
Subject Codes:JJ100. HH430. PP600. JJ300
Supplementary Info:36 ref
ISSN:0038-0717
Year:2000
Journal Title:Soil Biology & Biochemistry

418. Title:Bioactivation of poorly soluble phosphate rocks with a phosphorus-solubilizing fungus
View Article: Soil Science Society of America Journal. 2000. 64 (3). 927-932
CD Volume:322
Print Article: Pages: 927-932
Author(s):Goenadi D H Siswanto Sugiarto Y
Author Affiliation:Indonesian Biotechnology Research Unit for Estate Crops, Bogor 16151, Indonesia
Language:English
Abstract:Many studies have demonstrated ineffectiveness of finely ground phosphate rock (PR) use due to the low solubility of its P contents. This study was conducted to develop a simple, effective, and environmentally sound process to improve P availability of PR to crops by using a phosphate-solubilizing fungus (PSF), Aspergillus niger BCC F.194, isolated from tropical acid soils. The optimum incubation period and the optimum level of PR were determined. The P-solubilizing effect of the supernatant of 9-d-old liquid culture supernatant (LCS) of the fungus was also determined by reacting it at various concentrations with Moroccan phosphate rock (MPR). The inoculation of

the growth media with the PSF A. niger resulted in the highest P solubility of the rock after 9 d of culturing at 2.5 g MPR litre-1. Up to a certain degree, direct inoculation of fungal biomass and its LCS onto MPR caused a marked increase in 2% citric acid-soluble P, but not in water-soluble P content. The possibilities of using the LCS instead of H2SO4 in superphosphate (SP) production and using both with lower H3PO4 concentrations were investigated with MPR as raw materials. Replacement of H2SO4 by the LCS in the SP production process yielded a comparable 2% citric acid-soluble P content. Combining the LCS and H2SO4 reduced the consumption of H3PO4 that occurs in standard SP production. This LCS technique provides a practical means for an effective bioactivation of PR intended for both as a P fertilizer and a raw material of the SP

Descriptors:phosphate. rocks. acid-soils. biomass. consumption. inoculation. phosphorus. soil. superphosphate. tropics. rock-phosphate. phosphorus-fertilizers. solubilization

Identifiers:phosphate solubilizing fungi

Organism Descriptors:fungi. Aspergillus. Aspergillus-niger

Supplemental Descriptors:Deuteromycotina. Eumycota. fungi. Aspergillus

Subject Codes:JJ700. JJ100

Supplementary Info:33 ref

ISSN:0361-5995

Year:2000

Journal Title:Soil Science Society of America Journal

419. Title:RAPD analysis of selected common bean (Phaseolus vulgaris L.) cultivars from three African countries

View Article: South African Journal of Plant and Soil. 2000. 17 (2). 93-94

CD Volume:323

Print Article: Pages: 93-94

Author(s):Mienie C M S Herselman L Terhlanche R E

Author Affiliation:ARC-Grain Crops Institute, Private Bag X1251, Potchefstroom 2520, South Africa

Language:English

Abstract:DNA from six dry bean cultivars was analysed with a total of 32 primers in RAPD analysis to develop a method to distinguish between the different cultivars. The varieties are cultivated in three African countries and belong to two different gene pools. The cultivars analysed were Lyamunga 85 and Lyamunga 90 from Tanzania, CAL 96 and K 20 from Uganda, and Awash I and Mexican 142 from Ethiopia. The two types of beans, the Mesoamerican white seeded and large seeded Andean calima types, were separated in the two genetic pools. RAPD analysis revealed a close relationship between Lyamunga 85 and CAL 96. All the cultivars tested could be distinguished with a minimum of six primers

Descriptors:cultivar-identification. random-amplified-polymorphic-DNA. grain-legumes. biotechnology

Geographic Locator:Ethiopia. Tanzania. Uganda. Africa

Organism Descriptors:Phaseolus-vulgaris. Fabaceae

Supplemental Descriptors:Phaseolus. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. East-Africa. Africa-South-of-Sahara. Africa. Least-Developed-Countries. Developing-Countries. ACP-Countries. Commonwealth-of-Nations. SADC-Countries. Anglophone-Africa

Subject Codes:FF005. FF020. WW000

Supplementary Info:6 ref

ISSN:0257-1862

Year:2000

Journal Title:South African Journal of Plant and Soil

420. Title:Genotype variation in regeneration and transient expression efficiencies of 14 South African wheat cultivars
View Article: South African Journal of Plant and Soil. 17 (4). October, 2000. 170- 174
CD Volume:323
Print Article: Pages: 170-174
Author(s):Lacock L Botha A M
Author Affiliation:Faculty of Natural and Agricultural Sciences, Forestry and Agriculture Biotechnology Institute, University of Pretoria, Pretoria, 0002: ambothao@postino.up.ac.za
Language:English
Language of Summary:Afrikaans (AF); English (EN)
Abstract:Fourteen spring and winter hard red South African wheat (Triticum aestivum L.) cultivars were compared for their regeneration and transient anthocyanin expression efficiencies. Embryonic and non-embryonic callus, as well as plantlets, were obtained from all the cultivars cultured on a modified Murashige and Skoog basal medium supplemented with 5 mg l-1 6-Benzylaminopurine. Gamtoos and Tugela Dn1 were the best cultivars for the development of both roots and shoots. None of the cultivars produced callus or plantlets on ML3 medium. Transient anthocyanin expression was obtained in winter, as well as spring, hard red wheat cultivars. Using the non-destructive anthocyanin reporter-gene, it was established that the spring wheat cultivars Palmiet Dn1, Palmiet Dn2 and Palmiet Dn5 were the most suitable cultivars for future transformation studies, determined by the percentage bombarded calli expressing anthocyanin after two to three weeks
Descriptors:regeneration: genotype variation; spring; winter. Agronomy (Agriculture); Development. 6-benzylaminopurine; anthocyanin: transient expression efficiency
Organism Descriptors:Triticum aestivum [South African wheat] (Gramineae): cultivar- Betta, cultivar-Betta Dn1, cultivar-Betta Dn2, cultivar-Gamtoos, cultivar-Gamtoos Dn2, cultivar-Gamtoos Dn5, cultivar-Palmiet, cultivar-Palmiet Dn1, cultivar-Palmiet Dn2, cultivar-Palmiet Dn5, cultivar-Palmiet Lr29, cultivar-Palmiet Lr34, cultivar-Tugela, cultivar-Tugela Dn1, grain crop. root: development; shoot: development
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Development
ISSN:0257-1862
Year:2000
Journal Title:South African Journal of Plant and Soil

421. Title:Introgression of Allium fistulosum into A. cepa mediated by A. roylei
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 17-26
CD Volume:335
Print Article: Pages: 17-26
Author(s):Khrustaleva L I Kik C
Author Affiliation:DLO-Centre for Plant Breeding and Reproduction Research (CPRO-DLO), Department of Vegetable and Fruit Crops, P.O. Box 16, NL-6700 AA Wageningen, Netherlands
Language:English
Abstract:Introgression of Allium fistulosum into the genome of A. cepa using A. roylei as a bridging species was studied by means of genomic in situ hybridization. It was demonstrated that A. fistulosum can be stably

introgressed into A. cepa with a bridge-cross. The first and second bridge-cross generations were fertile, although pollen was sterile in some individuals. Only occasionally were there translocations in the second generation bridge-cross. Recombination between the three genomes was frequently seen in meiotic anaphase 1 and prophase 2 chromosomes of the first generation bridge-cross, and in mitotic chromosomes of the second generation bridge-cross. The number of observed recombination points in anaphase 1 and prophase 2 significantly exceeded the value expected from chiasma frequency in metaphase 1. Recombination points were randomly distributed, thus the A. cepa or A. roylei type of random distribution prevails over the A. fistulosum type of proximally localised chiasmata
Descriptors:recombination. DNA-hybridization. introgression. onions. interspecific-hybridization. genomes. chiasmata. Welsh-onions. vegetables. biotechnology
Identifiers:Allium roylei. fluorescence in situ hybridization
Organism Descriptors:Allium-cepa. Allium-fistulosum. Allium
Supplemental Descriptors:Allium. Alliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants. Liliaceae
Subject Codes:FF020. FF003. WW000
Supplementary Info:45 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

422. Title:Locating introgressions of Hordeum bulbosum chromatin within the H. vulgare genome
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 27-31
CD Volume:335
Print Article: Pages: 27-31
Author(s):Pickering R A Malyshev S Kunzel G Johnston P A Korzun V Menke M Schubert I
Author Affiliation:New Zealand Institute for Crop & Food Research Limited, Private Bag 4704, Christchurch, New Zealand
Language:English
Abstract:Several disease resistant recombinants between barley (Hordeum vulgare) and bulbous barley grass (H. bulbosum) have been obtained in recent years, but the process of characterization is often laborious and time-consuming. In order to improve the identification and chromosomal location of introgressed chromatin from H. bulbosum into the barley (cv. Emir) genome, sequential genomic in situ hybridization (GISH) and fluorescence in situ hybridization (FISH) were used. GISH established that an introgression was present in the disease(Puccinia hordei) resistant recombinant line, and the subsequent use of FISH, with a short oligonucleotide sequence as probe, located the introgression on the long arm of barley chromosome 2H. These data were confirmed using RFLP probes that hybridize to barley chromosome 2HL
Descriptors:genomes. barley. DNA-hybridization. interspecific-hybridization. restriction-fragment-length-polymorphism. introgression. disease-resistance. plant-diseases. plant-pathogens. plant-pathogenic-fungi. fungal-diseases. wild-relatives. cereals. biotechnology. plant-genetic-resources. control. plant-pathology
Identifiers:fluorescence in situ hybridization
Organism Descriptors:Hordeum-vulgare. Hordeum-bulbosum. Puccinia-hordei
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Puccinia. Uredinales. Basidiomycotina. Eumycota. fungi
Subject Codes:FF005. FF020. WW000. FF610. HH600. PP720

Supplementary Info:21 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

423. Title:A genetic map of maritime pine based on AFLP, RAPD and protein markers
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 39-48
CD Volume:335
Print Article: Pages: 39-48
Author(s):Costa P Pot D Dubos C Frigerio J M Pionneau C Bodenes C Bertocchi E Cervera M T Remington D L Plomion C
Author Affiliation:INRA, Laboratoire de Genetique et Amelioration des Arbres Forestiers, BP45, F-33610 Cestas, France
Language:English
Abstract:The amplified fragment length polymorphism (AFLP) technique was adapted for genetic analysis in maritime pine (Pinus pinaster), a species characterized by a large genome size (24 pg/C). A genetic linkage map was constructed for one F1 individual based on 239 AFLP and 127 random amplified polymorphic DNA (RAPD) markers. Markers were scored on megagametophytes (1n) from 200 germinated F2 seedlings. Polymorphism rate, labour time and cost of both AFLP and RAPD techniques were compared. The AFLP technique was twice as fast and three-times less costly per marker than the RAPD technique. Thirteen linkage groups were identified with a LOD score more than or equal to 6 covering 1873 cM, which provided 93.4% of genome coverage. Proteins were extracted from needles (2n) of the F2 progeny and revealed by 2-dimensional electrophoresis. Thirty-one segregating proteins were mapped using a quantitative trait locus detection strategy based on the quantification of protein accumulation. Two framework maps of the same F1 individual are now available. The first map uses RAPD markers and the second map, presented in this study, uses mostly AFLP markers. Although the total genetic length of both maps was almost identical, differences among homologous groups were observed
Descriptors:genetic-markers. electrophoresis. labour-requirements. costs. biochemical-markers. gene-mapping. random-amplified-polymorphic-DNA. forest-trees. plant-proteins. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Pinus-pinaster. Pinopsida
Supplemental Descriptors:Pinus. Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants
Subject Codes:KK100. FF020. WW000. EE900. EE100
Supplementary Info:45 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

424. Title:A combined RFLP and AFLP linkage map of upland rice (Oryza sativa L.) used to identify QTLs for root-penetration ability
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 49-56
CD Volume:335
Print Article: Pages: 49-56
Author(s):Price A H Steele K A Moore B J Barraclough P B Clark L J
Author Affiliation:Department of Plant and Soil Science, University of Aberdeen, Aberdeen AB24 3UU, UK
Language:English

Abstract:A combined restriction fragment length (RFLP) and amplified fragment length polymorphism (AFLP) linkage map of an F6 recombinant inbred population, which was derived from a previously mapped F2 of a cross between the two drought resistant upland rice varieties Bala and Azucena, is presented. The map contains 101 RFLP and 34 AFLP markers on 17 linkage groups covering 1680 cM. Also presented is the approximate mapping position of a further 4 RFLP and 75 AFLP markers, which either could not be given a unique place on the map or for which the available data is not sufficient to allow confident positioning, and the result of quantitative trait locus (QTL) mapping of traits related to root-penetration ability. Root penetration was assessed by counting the number of root axes that penetrated a 3 mm-thick layer consisting of 80% wax and 20% white soft paraffin. Good root penetration would be expected to increase drought resistance where soil strength is high. Single-marker analysis revealed 7 QTLs for the number of roots which penetrate the wax layer. In identical locations were 7 QTLs for the ratio of penetrated to the total number of roots. Transgressive inheritance of positive alleles from Bala explained 4 of these QTLs. Comparison of the QTLs identified here with previous reports of QTLs for root morphology suggest that alleles which improve root penetration ability may also either make the roots longer or thicker
Descriptors:rice. restriction-fragment-length-polymorphism. drought-resistance. gene-mapping. roots. quantitative-trait-loci. inheritance. genetics. cereals. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF030. FF020. WW000. FF900
Supplementary Info:27 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

425. Title:Associations between anther-culture response and molecular markers on chromosomes 2H, 3H and 4H of barley (Hordeum vulgare L.)
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 57-62
CD Volume:335
Print Article: Pages: 57-62
Author(s):Manninen O M
Author Affiliation:Agricultural Research Centre of Finland, Plant Production Research, Crops and Soil, FIN-31600 Jokioinen, Finland
Language:English
Abstract:Segregation distortion is a common phenomenon among anther culture-derived plants and it has been suggested that the distorted areas may contain genes affecting survival in anther culture. Segregation of 111 markers was studied in an androgenetic barley (Hordeum vulgare) progeny and a linkage map was constructed. Thirty-one progeny lines were tested for their anther culture ability, and associations between molecular markers and anther culture traits were established. Two regions on chromosomes 2H and 4H were associated with anther response, three on 2H (two areas) and 3H with plant regeneration rate, and one on 4H with spontaneous diploidization. The chromosomal regions controlling anther culture response and the regions where distorted segregation was found were not always the same
Descriptors:barley. anther-culture. segregation-distortion. genetics. genetic-markers. gene-mapping. regeneration. chromosomes. cereals. biotechnology

Organism Descriptors:Hordeum-vulgare
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF170. FF020. WW000
Supplementary Info:34 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

426. Title:RAPD linkage mapping of the shell thickness locus in oil palm (Elaeis guineensis Jacq.)
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 63-70
CD Volume:335
Print Article: Pages: 63-70
Author(s):Moretzsohn M C Nunes C D M Ferreira M E Grattapaglia D
Author Affiliation:Laboratorio de Genetica de Plantas, Embrapa Recursos Geneticos e Biotecnologia C.P.02372, 70849-970 Brasilia DF, Brazil
Language:English
Abstract:Shell thickness is an important trait in oil palm breeding and is the basis for the classification of varieties of oil palm into the types dura, tenera and pisifera. This trait seems to be controlled by a single locus, with two alleles (sh+ and sh-) showing co-dominant expression. Two single-tree linkage maps were constructed for a maternal tenera (sh+ sh-) palm and for a paternal pisifera (sh- sh-) palm using the pseudo-test-cross mapping strategy in combination with random amplified polymorphic DNA (RAPD) markers through the analysis of an F1 tenera x pisifera progeny. A total of 308 arbitrary primers were screened in a sample of 8 F1 plants and 121 markers were detected in a testcross configuration. An average of 1.66 polymorphic markers per selected primer were identified in this cross. At LOD 5.0 (with a few exceptions) and theta =0.25, the maternal tenera map included 48 markers distributed in 12 linkage groups or pairs of markers (449.3 cM) while the paternal pisifera map included 42 markers distributed in 15 linkage groups or pairs of markers (399.7 cM). RAPD and bulked segregant analysis were used to identify markers more tightly linked to the sh+ locus. A total of 174 new primers not previously used in the linkage analysis were screened using bulks of DNA extracted from plants selected for the contrasting shell-thickness phenotypes. Two RAPD markers (R11-1282 and T19-1046) were identified to be linked on both sides of the sh+ locus on linkage group 4. The estimated map distances from sh+ to R11-1282 and to T19-1046 were 17.5 and 23.9 cM, respectively. The results demonstrate the usefulness of RAPD markers and the pseudo-testcross mapping strategy for developing genetic linkage information, and constitute an important step towards early marker-assisted selection for shell thickness in oil palm
Descriptors:linkage. gene-mapping. oil-palms. alleles. genes. random-amplified-polymorphic-DNA. genetic-markers. fruits. plant-morphology. fatty-oil-plants. oil-plants. biotechnology
Organism Descriptors:Elaeis-guineensis. Elaeis
Supplemental Descriptors:Elaeis. Arecaceae. Arecales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. FF030. WW000
Supplementary Info:34 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

427. Title:Identification of larch species (Larix decidua, Larix kaempferi and Larix x eurolepis) and estimation of hybrid fraction in seed lots by RAPD fingerprints
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 71-74
CD Volume:335
Print Article: Pages: 71-74
Author(s):Scheepers D Eloy M C Briquet M
Author Affiliation:Universite catholique de Louvain, Unite de Biochimie Physiologique, Place Croix du Sud 2/20, B-1348 Louvain-la-Neuve, Belgium
Language:English
Abstract:Species-specific RAPD markers were used to identify the larch species Larix decidua and L. kaempferi, and their interspecific hybrid (L. x eurolepis). Although morphological differences between pure species and the hybrids exist, differentiation is not always possible, especially at an early stage (seed or plantlet). Eleven random amplified polymorphic DNA (RAPD) markers differentiated the two larch species, and 4 species-specific markers were sufficient to estimate the F1 hybrid fraction in a seed lot. The species-specific markers were tested on individual trees of European and Japanese larches of diverse geographic origins, and on several seed lots of different origins (F1, F2 hybrids and pure species). The 4 specific markers found for European and Japanese larches were monomorphic and present in all provenances and in all F1 hybrid trees tested. Polymorphic sequence-characterized-amplified regions (SCAR) fragments were obtained for 3 of the 11 fragments originally selected for the RAPD screening phase. For 2 of them, the sequence had some homology with the mitochondrial genome of other organisms and is thus mitochondrial. The two mitochondrial fragments and the OPF-131000 fragment exhibited one polymorphic band, thereby maintaining its species-specific identity: OPF-131000 is specific to European larch. The 4 RAPD primers selected in this study offer a reliable, quick and cheap tool for the identification of different larch species (L. decidua and L. kaempferi) and their interspecific hybrid (L. x eurolepis)
Descriptors:hybrids. identification. interspecific-hybridization. forest-trees. random-amplified-polymorphic-DNA. biotechnology
Geographic Locator:Europe. Japan
Organism Descriptors:Larix-eurolepis. Larix-kaempferi. Larix-decidua. Pinopsida
Supplemental Descriptors:Larix. Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants. East-Asia. Asia. Developed-Countries. OECD-Countries
Subject Codes:KK100. FF020. WW000
Supplementary Info:13 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

428. Title:An integrated AFLP and RFLP Brassica oleracea linkage map from two morphologically distinct doubled-haploid mapping populations
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 75-81
CD Volume:335
Print Article: Pages: 75-81
Author(s):Sebastian R L Howell E C King G J Marshall D F Kearsey M J
Author Affiliation:Plant Genetics and Cell Biology Group, School of Biological Sciences, University of Birmingham, Birmingham B15 2TT, UK
Language:English
Abstract:Genetic maps of molecular markers in two very different F1-derived doubled-haploid populations of Brassica oleracea are compared and the integrated map described. The F1 crosses were: Chinese kale x calabrese

(var. alboglabra [B. alboglabra] x var. italica) and cauliflower x Brussels sprout (var. botrytis x var. gemmifera). Integration of the two component maps using Joinmap v.2.0 was based on 105 common loci including restriction fragment length polymorphisms, amplified fragment length polymorphisms and microsatellites. This provided an effective method of producing a high-density consensus linkage map of the B. oleracea genome. Based on 547 markers mapping to 9 linkage groups, the integrated map covers a total map length of 893 cM, with an average locus interval of 2.6 cM. Comparisons back to the component linkage maps revealed similar sequences of common markers, although significant differences in recombination frequency were observed between some pairs of homologous markers. Map integration resulted in an increased locus density and effective population size, providing a stronger framework for subsequent physical mapping and for precision mapping of quantitative trait loci using substitution lines

Descriptors:linkage. gene-mapping. restriction-fragment-length-polymorphism. Brussels-sprouts. broccoli. cauliflowers. microsatellites. interspecific-hybridization. vegetables. biotechnology

Identifiers:amplified fragment length polymorphism

Organism Descriptors:Brassica-oleracea-var.-gemmifera. Brassica-oleracea-var.-botrytis. Brassica-alboglabra. Brassica-oleracea-var.-italica. Brassica-oleracea

Supplemental Descriptors:Brassica-oleracea. Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF003. FF020. WW000

Supplementary Info:23 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

429. Title:Construction of a yeast artificial chromosome library of pepper (Capsicum annuum L.) and identification of clones from the Bs2 resistance locus

View Article: Theoretical and Applied Genetics. 2000. 100 (1). 112-117

CD Volume:335

Print Article: Pages: 112-117

Author(s):Tai T Staskawicz B J

Author Affiliation:Department of Plant Biology, 111 Koshland Hall, University of California, Berkeley, CA 94720, USA

Language:English

Abstract:A yeast artificial chromosome (YAC) library was constructed using high-molecular-weight DNA isolated from pepper (Capsicum annuum) leaf protoplasts. Insert DNA was prepared by partial digestion using EcoRI and subjected to electrophoretic fractionation before in-gel ligation to the pJS97/98 YAC vector. Prior to transformation of yeast spheroplasts, ligation products were subjected to a second electrophoretic size selection. The library consists of about 19 000 clones with an average insert size of 500 kb, thus representing approximately 3 haploid genome equivalents. Three PCR-based markers tightly linked to the pepper Bs2 resistance gene [for resistance to Xanthomonas vesicatoria] were used to assess the utility of this library for positional cloning. Three YAC clones containing pepper genomic DNA from the Bs2 resistance locus were isolated from the library. The clones ranged in size from 270 to 1.2 Mb and should prove useful for the cloning of the Bs2 gene

Descriptors:DNA-cloning. yeast-artificial-chromosomes. genes. disease-resistance. plant-pathogens. plant-diseases. plant-pathogenic-

bacteria. molecular-genetics. vegetables. biotechnology. fruit-vegetables. control. plant-pathology
Organism Descriptors:Capsicum-annuum. Xanthomonas-vesicatoria
Supplemental Descriptors:Capsicum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF003. FF610. HH600. FF020. WW000
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

430. Title:A genetic map of an interspecific cross in Allium based on amplified fragment length polymorphism (AFLPTM) markers
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 118-126
CD Volume:335
Print Article: Pages: 118-126
Author(s):Heusden A W van Ooijen J W van Vrielink van Ginkel R Verbeek W H J Wietsma W A Kik C
Author Variant:van-Heusden-A-W. van-Ooijen-J-W
Author Affiliation:DLO-Centre for Plant Breeding and Reproduction Research (CPRO-DLO), P.O. Box 16, 6700 AA Wageningen, Netherlands
Language:English
Abstract:Segregation of 692 polymorphic AFLPTM fragments was determined in an F2 of the interspecific cross A. roylei x A. cepa. A. roylei is a wild relative of onion. Two different enzyme combinations were used, PstI/MseI and EcoRI/MseI; in the latter, one extra selective nucleotide was added to the MseI primer. The map based on A. cepa markers consisted of 8 linkage groups with 262 markers covering 694 cM of the expected 800 cM. The map based on A. roylei markers comprised 15 linkage groups with 243 markers and had a length of 626 cM. The two maps were not integrated and 25% of the markers remained unlinked. One of the alliinase genes and a SCAR [sequence-characterized-amplified region] marker linked to the disease resistance gene to downy mildew (Peronospora destructor) are present on this map. Of the AFLP markers, 50-80% were polymorphic between A. cepa and A. roylei; the level of polymorphic markers between different A. cepa accessions was 4-8%
Descriptors:interspecific-hybridization. disease-resistance. genes. linkage. onions. wild-relatives. genetic-markers. gene-mapping. plant-diseases. plant-pathogens. plant-pathogenic-fungi. fungal-diseases. vegetables. plant-genetic-resources. biotechnology. control. plant-pathology
Identifiers:Allium roylei. amplified fragment length polymorphism
Organism Descriptors:Allium-cepa. Peronospora-destructor. Allium
Supplemental Descriptors:Allium. Alliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants. Peronospora. Peronosporales. Mastigomycotina. Eumycota. fungi. Liliaceae
Subject Codes:FF003. PP720. FF020. WW000. FF610. HH600
Supplementary Info:29 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

431. Title:A saturated genetic linkage map of rubber tree (Hevea spp.) based on RFLP, AFLP, microsatellite, and isozyme markers
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 127-138
CD Volume:335

Print Article: Pages: 127-138
Author(s):Lespinasse D Rodier Goud M Grivet L Leconte A Legnate H Seguin M
Author Affiliation:CIRAD, Centre de Cooperation Internationale en Recherche Agronomique pour le Developpement, avenue Agropolis, BP 5035, 34032 Montpellier cedex 1, France
Language:English
Abstract:A genetic map for Hevea spp. (2n = 36) is presented. It is based on the F1 progeny of 106 individuals, allowing the construction of a female, a male and a synthetic map according to the pseudo-testcross strategy. Progeny were derived from an interspecific cross between PB260, a H. brasiliensis cultivated clone, and RO38, a H. brasiliensis x H. benthamiana interspecific hybrid clone. The disomic inheritance observed for all the codominant markers scattered on the 2n = 36 chromosomes revealed that Hevea behaves as diploids. Homologous linkage groups between the two parental maps were merged using bridge loci. A total of 717 loci constituted the synthetic map, including 301 restriction fragment length polymorphisms, 388 amplified fragment length polymorphisms, 18 microsatellites and 10 isoenzymes. The markers were assembled into 18 linkage groups, thus reflecting the basic chromosome number, and covered a total distance of 2144 cM. Nine markers were unlinked. Segregation distortion was rare (1.4%). Average marker density was 1 per 3 cM. Comparison of the distance between loci in the parental maps revealed significantly less meiotic recombination in the interspecific hybrid male parent than in the female parent. Hevea origin and genome organisation are discussed
Descriptors:linkage. restriction-fragment-length-polymorphism. interspecific-hybridization. isoenzymes. microsatellites. recombination. gene-mapping. inheritance. genetic-markers. segregation-distortion. rubber-plants. genomes. biotechnology
Identifiers:Hevea benthamiana. amplified fragment length polymorphism
Organism Descriptors:Hevea-brasiliensis
Supplemental Descriptors:Hevea. Euphorbiaceae. Euphorbiales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:52 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

432. Title:Molecular analysis of introgressive breeding in coffee (Coffea arabica L.)
View Article: Theoretical and Applied Genetics. 2000. 100 (1). 139-146
CD Volume:335
Print Article: Pages: 139-146
Author(s):Lashermes P Andrzejewski S Bertrand B Combes M C Dussert S Graziosi G Trouslot P Anthony F
Author Affiliation:IRD (ex ORSTOM), GeneTrop, BP 5045, F-34032 Montpellier, France
Language:English
Abstract:Nineteen arabica coffee introgression lines (BC1F4) and two accessions derived from a spontaneous interspecific cross (i.e. Timor Hybrid (TH)) between Coffea arabica (2n = 4x = 44) and C. canephora (2n = 2x = 22) were analysed for the introgression of C. canephora genetic material. TH-derived genotypes were evaluated by amplified fragment length polymorphism (AFLP), using 42 primer combinations, and compared to 23 accessions of C. arabica and 8 accessions of C. canephora. A total of 1062 polymorphic fragments were scored among the 52 accessions analysed. Some 178 markers consisting of 109 additional bands (i.e.

introgressed markers) and 69 missing bands distinguished the group composed of the TH-derived genotypes from the accessions of C. arabica. AFLP therefore seemed to be an extremely efficient technique for DNA marker generation in coffee as well as for the detection of introgression in C. arabica. The genetic diversity observed in the TH-derived genotypes appeared to be approximately double that in C. arabica. Although representing only a small proportion of the genetic diversity available in C. canephora, TH obviously constitutes a considerable source of genetic diversity for arabica breeding. Analysis of genetic relationships among TH-derived genotypes suggested that introgression was not restricted to chromosome substitution but also involved chromosome recombinations. Furthermore, TH-derived genotypes varied considerably in the number of AFLP markers attributable to introgression. In this way, the introgressed markers identified in the analysed arabica coffee introgressed genotypes were estimated to represent from 9 to 29% of the C. canephora genome. Nevertheless, the amount of alien genetic material in the introgression arabica lines remains substantial and should justify the development of adapted breeding strategies

Descriptors:coffee. genetic-diversity. interspecific-hybridization. introgression. genetic-markers. chromosome-substitution. recombination. plant-breeding. stimulant-plants. biotechnology

Identifiers:amplified fragment length polymorphism

Organism Descriptors:Coffea-canephora. Coffea-arabica. Coffea

Supplemental Descriptors:Coffea. Rubiaceae. Rubiales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF003. FF020. WW000

Supplementary Info:29 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

433. Title:The use of self-pollinated progenies as 'in-groups' for the genetic characterization of cocoa germplasm

View Article: Theoretical and Applied Genetics. 2000. 100 (1). 160-166

CD Volume:335

Print Article: Pages: 160-166

Author(s):Charters Y M Wilkinson M J

Author Affiliation:Department of Agricultural Botany, School of Plant Sciences, P.O. Box 221, University of Reading, Whiteknights, Reading RG6 6AS, UK

Language:English

Abstract:The potential of inter-simple sequence repeat-polymerase chain reaction analysis is assessed for the maintenance and genetic characterisation of an international collection of cocoa (Theobroma cacao) genotypes. Six primers were sufficient to distinguish all but 3 pairs of the 62 accessions examined. A UPGMA dendrogram was used to provide a measure of the genetic variability between genotypes. The scale was supplied by the inclusion of Theobroma grandiflora as an 'out group' and also by the use of two contrasting progenies as 'in groups'. The 'in groups' were obtained from the self-pollination of one plant (SPEC 54.1) known to be highly homozygous and also of a second, highly heterozygous, clone (P 19B). These reference points allowed several documentation errors to be resolved and provided a basis for identifying unwanted or low-priority material. Implications of the work for the routine maintenance of large germplasm collections are briefly discussed

Descriptors:cocoa. germplasm. genetic-variation. gene-banks. plant-genetic-resources. polymerase-chain-reaction. maintenance. stimulant-plants. biotechnology

Organism Descriptors:Theobroma-cacao
Supplemental Descriptors:Theobroma. Sterculiaceae. Malvales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. PP720. FF020. WW000
Supplementary Info:11 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

434. Title:The distribution, organization and evolution of two abundant and widespread repetitive DNA sequences in the genus Hordeum
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 169-176
CD Volume:335
Print Article: Pages: 169-176
Author(s):Taketa S Ando H Takeda K Harrison G E Heslop Harrison J S
Author Affiliation:Research Institute for Bioresources, Okayama University, Chuo 2-20-1, Kurashiki 710-0046, Japan
Language:English
Abstract:The genomic organization and chromosomal distributions of two abundant tandemly repeated DNA sequences, dpTal and pSc119.2, were examined in six wild Hordeum taxa, representing the four basic genomes of the genus, by Southern and fluorescence in situ hybridization. The dpTal probe hybridized to between 30 and 60 sites on the chromosomes of all five diploid species studied, but hybridization patterns differed among the species. Hybridization of the pSc119.2 sequence to the chromosomes and Southern blots of digested DNA detected signals in H. bulbosum, H. chilense, H. marinum and H. murinum 4x, but not in H. murinum 2x and H. vulgare subsp. spontaneum [H. spontaneum]. A maximum of one pSc119.2 signal was observed in the terminal or subterminal region of each chromosome arm in the species carrying this sequence. The species carrying the same I-genome differed in the presence (H. bulbosum) or absence (H. vulgare subsp. spontaneum) of pSc119.2. The presence of pSc119.2 in the tetraploid cytotype of H. murinum, but its absence in the diploid cytotype, suggests that the tetraploid is not likely to be a simple autotetraploid of the diploid. Data about the inter- and intra-specific variation of the two independent repetitive DNA sequences give information about both the interrelationships of the species and the evolution of the repetitive sequences
Descriptors:repetitive-DNA. genomes. DNA-hybridization. wild-relatives. barley. polyploidy. Southern-blotting. evolution. cereals. plant-genetic-resources. biotechnology
Identifiers:fluorescence in situ hybridization
Organism Descriptors:Hordeum-bulbosum. Hordeum-marinum. Hordeum-murinum. Hordeum-spontaneum. Hordeum-vulgare. Hordeum-chilense
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. PP720. FF020. WW000
Supplementary Info:37 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

435. Title:The interspecific genome structure of cultivated banana, Musa spp. revealed by genomic DNA in situ hybridization
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 177-183
CD Volume:335
Print Article: Pages: 177-183

Author(s):D'Hont A Paget Goy A Escoute J Carreel F
Author Affiliation:CIRAD, BP 5035, 34032 Montpellier Cedex 1, France
Language:English
Abstract:In cultivated banana, Musa spp., there are four known genomes, A, B, S and T. These correspond to the genetic constitutions of wild Eumusa species M. acuminata, M. balbisiana, M. schizocarpa and the Australimusa species, respectively. Most cultivated clones are triploid or diploid, and have been classified into genomic groups according to chromosome numbers and morphological traits. Genomic in situ hybridization (GISH) enabled the differentiation of the chromosomes of these four genomes; however, a distal portion of the chromosomes remained unlabelled. GISH was used to determine the exact genome structure of interspecific cultivated clones. In most cases the results were consistent with the chromosome constitution estimated by means of phenotypic descriptors. The one notable exception, the clone 'Pelipita', has 8 A and 25 B chromosomes instead of the predicted 11 A and 22 B. GISH also enabled the determination of the chromosome complement of a few clones that could not be classified only on the basis of phenotypic descriptors and chromosome counts. Ribosomal DNA sites often appeared to be associated with satellites, which can be separated from chromosomes, representing a potential source of error for chromosome counting using classical techniques
Descriptors:bananas. genomes. genome-analysis. DNA-hybridization. interspecific-hybridization. chromosome-number. chromosomes. satellites. ribosomal-DNA. fruit-crops. fruits. biotechnology
Organism Descriptors:Musa
Supplemental Descriptors:Musaceae. Zingiberales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:27 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

436. Title:High-resolution linkage analysis and physical characterization of the EIX-responding locus in tomato
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 184-189
CD Volume:335
Print Article: Pages: 184-189
Author(s):Ron M Kantety R Martin G B Avidan N Eshed Y Zamir D Avni A
Author Affiliation:Department of Plant Sciences, Tel-Aviv University, Tel-Aviv 69978, Israel
Language:English
Abstract:An ethylene-inducing xylanase (EIX) from Trichoderma viride is a potent elicitor of ethylene biosynthesis, localized cell death and other defence responses in specific cultivars of tobacco (Nicotiana tabacum) and tomato (Lycopersicon esculentum). Wild species of tomato, such as L. cheesmanii and L. pennellii, do not respond to EIX treatment. F1 progeny of the crosses L. esculentum x L. cheesmanii and L. esculentum x L. pennellii responded to EIX treatment with an increase in ethylene biosynthesis and induction of localized cell death. The F2 progeny of these crosses segregated 3:1 (responding:non-responding). The EIX-responding locus (Eix) was mapped to the short arm of chromosome 7 using a population of introgression lines, containing small restriction fragment length polymorphism (RFLP)-defined chromosome segments of L. pennellii introgressed into L. esculentum. RFLP analysis of 990 F2 plants that segregated for the introgressed segment mapped the Eix locus 0.1 and 0.9 cM from the flanking markers TG61 and TG131,

respectively. Using marker TG61, a yeast artificial chromosome (YAC) clone was isolated that carries 300-kb DNA segments derived from the Eix region. Mapping the ends of this YAC clone showed that it spans the Eix locus. Thus, positional cloning of the Eix locus appears feasible
Descriptors:characterization. linkage. biosynthesis. ethylene. induction. gene-mapping. restriction-fragment-length-polymorphism. tomatoes. wild-relatives. plant-growth-regulators. elicitors. plant-pathogens. plant-diseases. plant-pathogenic-fungi. fungal-diseases. disease-resistance. yeast-artificial-chromosomes. interspecific-hybridization. glycosidases. vegetables. biotechnology. plant-genetic-resources
Identifiers:xylanase
Organism Descriptors:Lycopersicon-cheesmanii. Lycopersicon-pennellii. Lycopersicon-esculentum. Trichoderma-viride. Lycopersicon
Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Trichoderma. Deuteromycotina. Eumycota. fungi
Subject Codes:FF020. FF003. PP720. WW000. FF610. HH600
Supplementary Info:39 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

437. Title:Comparative mapping reveals a complex relationship between the pearl millet genome and those of foxtail millet and rice
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 190-198
CD Volume:335
Print Article: Pages: 190-198
Author(s):Devos K M Pittaway T S Reynolds A Gale M D
Author Affiliation:John Innes Centre, Norwich Research Park, Colney, Norwich NR4 7UH, UK
Language:English
Abstract:Comparative genetic maps were constructed of the pearl millet (Pennisetum glaucum) genome with foxtail millet (Setaria italica), and used to describe the homoeology between the genomes of pearl millet, foxtail millet and rice. Despite the close taxonomic relationship of pearl and foxtail millet, their genomes were highly rearranged. A comparison of the millet and rice genomes indicated that most of these rearrangements were likely to have taken place in pearl millet. Two duplications were identified in pearl millet. A duplication between the distal segments of linkage groups 1 and 4 corresponds to the ancient duplication previously identified between rice chromosome arms 11S and 12S, and foxtail millet chromosomes VII and VIII. The other putative duplication, also between regions of linkage groups 1 and 4, is likely to be species-specific. The exploitation of the comparative maps in pearl millet research is discussed
Descriptors:genomes. gene-mapping. millets. rice. chromosomes. linkage. foxtail-millet. pearl-millet. chromosome-maps. comparisons. cereals. biotechnology
Organism Descriptors:Setaria-italica. Pennisetum-glaucum. Oryza-sativa. Oryza
Supplemental Descriptors:Setaria-(Poaceae). Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Pennisetum. Oryza
Subject Codes:FF005. FF020. WW000
Supplementary Info:32 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

438. Title:Comparative molecular mapping in Ceratotropis species using an interspecific cross between azuki bean (Vigna angularis) and rice bean (V. umbellata)
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 207-213
CD Volume:335
Print Article: Pages: 207-213
Author(s):Kaga A Ishii T Tsukimoto K Tokoro E Kamijima O
Author Affiliation:Division of Science of Biological Resources, Graduate School of Science and Technology, Kobe University, Nada-ku, Kobe 657-8501, Japan
Language:English
Abstract:A genetic linkage map was developed with 86 F2 plants derived from an interspecific cross between azuki bean (Vigna angularis, 2n = 2x = 22) and rice bean (V. umbellata, 2n = 2x = 22). In total, 14 linkage groups, each containing more than 4 markers, were constructed with one phenotypic, 114 restriction fragment length polymorphism and 74 random amplified polymorphic DNA markers. The total map size was 1702 cM and the average distance between markers was 9.7 cM. Loci showing significant deviation from the expected ratio clustered in several linkage groups. Most of the skewed loci were due to the predominance of rice bean alleles. The azuki bean-rice bean linkage map was compared with other available maps of Vigna species in subgenus Ceratotropis. Based on the lineage of the common mapped markers, 7 and 16 conserved linkage blocks were found in the interspecific map of azuki bean x V. nakashimae and mung bean (V. radiata) map, respectively. Although the present map is not fully saturated, it may facilitate gene tagging, quantitative trait locus mapping and further useful gene transfer for azuki bean breeding
Descriptors:interspecific-hybridization. gene-mapping. linkage. mung-beans. grain-legumes. biotechnology. plant-genetic-resources
Identifiers:Vigna nakashimae
Organism Descriptors:Vigna-angularis. Vigna-umbellata. Vigna-radiata. Fabaceae
Supplemental Descriptors:Vigna. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:31 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

439. Title:The nad4L-orf25 gene cluster is conserved and expressed in sugar beet mitochondria
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 214-220
CD Volume:335
Print Article: Pages: 214-220
Author(s):Kubo T Yamamoto M P Mikami T
Author Affiliation:Laboratory of Genetic Engineering, Faculty of Agriculture, Hokkaido University, Sapporo 060-8589, Japan
Language:English
Abstract:It is reported that a gene coding for NADH dehydrogenase subunit 4L and a presumed gene, orf25, are linked and co-transcribed with each other in sugarbeet mitochondria. Ten and twelve C-to-U editing events were observed in the mRNAs of nad4L and orf25, respectively; the amino-acid sequence specified after editing is better-conserved in comparison with the homologues of other organisms. It is noted that the translation initiation codon of nad4L is created by editing. Conservation of the nad4L-orf25 linkage was examined by polymerase chain reaction (PCR)-

amplification of the intergenic region. Successful PCR products were obtained from 5 dicotyledons (spinach, apple, snapdragon, petunia and tobacco) and 2 monocotyledons (tulip and pineapple), but not in 2 poaceous plants, rice and maize. The intergenic region, when present, was well-conserved in its sequence, suggesting a monophyletic origin of this linkage. Theses results, together with previous reports of Arabidopsis and four poaceous species, favour the argument that the nad4L-orf25 linkage is conserved throughout angiosperms except in the Poaceae. Nucleotide sequence data of the sugarbeet nad4L-orf25 locus have been deposited under DDBJ/EMBL/GenBank accession number AB020062
Descriptors:mitochondrial-genetics. sugarbeet. linkage. NADH-dehydrogenase. polymerase-chain-reaction. evolution. nucleotide-sequences. RNA-editing. amino-acid-sequences. sugar-crops. biotechnology
Organism Descriptors:angiosperms. Beta-vulgaris-var.-saccharifera
Supplemental Descriptors:Spermatophyta. plants. Beta-vulgaris. Beta. Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms
Subject Codes:FF005. WW000. FF020. ZZ380
Supplementary Info:18 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

440. Title:Evolutionary features of chondriome divergence in Triticum (wheat) and Aegilops shown by RFLP analysis of mitochondrial DNAs
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 221-231
CD Volume:335
Print Article: Pages: 221-231
Author(s):Wang G Z Matsuoka Y Tsunewaki K
Author Affiliation:Department of Bioscience, Fukui Prefectural University, 4-1-1 Kenjyojima, Matsuoka, Yoshida-gun, Fukui 910-1195, Japan
Language:English
Abstract:A comprehensive analysis was made of restriction fragment length polymorphism (RFLP) of the mitochondrial (mt) DNA of two related genera, Triticum (wheat) and Aegilops. This led to clarification of the nature of mtDNA variability and the inference of the phylogeny of the mitochondrial genomes (chondriome). Forty-six alloplasmic lines and one euplasmic line of common wheat (2n = 42, genomes AABBDD) carrying plasmons (cytoplasmic genomes) of 47 accessions belonging to 33 species were used. This consisted of nearly all the Triticum and Aegilops species. RFLP analysis, carried out with 7 mitochondrial gene probes (7.0 kb in total) in combination with 3 restriction endonucleases, found marked variation. Of the 168 bands detected, 165 were variable (98.2%), indicating that there is extremely high mtDNA variability in these genera. This high variability is attributed to the variation present in the intergenic regions. Most of the variation was between chondriomes of different plasmon types; only 8 bands (4.8%) between those of the same plasmon types were variable, evidence of clear chondriome divergence between different plasmon types. Comprehensive phylogenetic trees of the chondriome were constructed on the basis of genetic distances. All but 1 of the polyploids had chondriomes closely related to those of 1 putative parent, indicating uniparental chondriome transmission at the time of polyploid formation. The chondriome showed parallel evolutionary divergence to the plastome (chloroplast genome). Use of a minimum set of 3 mtDNA probe-enzyme combinations is proposed for tentative plasmon type identification and the screening of new plasmon types in those genera
Descriptors:restriction-fragment-length-polymorphism. wheat. genomes. mitochondrial-DNA. mitochondrial-genetics. phylogenetics. phylogeny.

evolution. cytoplasm. wild-relatives. cereals. biotechnology. plant-genetic-resources
Organism Descriptors:Aegilops. Triticum
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. WW000. ZZ380. PP720
Supplementary Info:32 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

441. Title:Molecular mapping of chromosome segments introgressed from Solanum lycopersicoides into cultivated tomato (Lycopersicon esculentum)
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 232-241
CD Volume:335
Print Article: Pages: 232-241
Author(s):Chetelat R T Meglic V
Author Affiliation:Department of Vegetable Crops, University of California, One Shields Avenue, Davis, CA 95616, USA
Language:English
Abstract:Wild nightshade (Solanum lycopersicoides accession LA2951) was backcrossed to Lycopersicon esculentum cv. VF36, and then inbred through single-seed descent for several generations. Over 300 backcross-inbred families thereby derived were genotyped at 139 marker loci, consisting of restriction fragment length polymorphisms (RFLPs), alloenzymes and monogenic morphological markers, to identify introgressed S. lycopersicoides chromosomes and segments thereof. The pattern of genotypes observed in the lines indicated a high degree of overall synteny between the S. lycopersicoides genome and that of tomato. Two putative single-copy RFLP probes revealed secondary loci in this wide cross. Recovery of the L. esculentum genome was more rapid than expected, with an average value in the BC2 generation of 97.8%, versus the expected value of 87.5%. This was due to widespread segregation distortion that favoured L. esculentum alleles as well as a tendency for plants homozygous for introgressed segments to be partially or completely male-sterile, thereby preventing the fixation of S. lycopersicoides markers in many lines. Despite these difficulties, nearly every S. lycopersicoides marker (or approximately 98% of the genome, measured in cM) was represented in at least 1 backcross-inbred line, with only a region on chromosome 4L missing from the population as a whole. Although the extent of transmission and fixation of introgressed segments varied according to chromosome, overall approx equal to 66% of the S. lycopersicoides genome was represented by homozygous introgressions with sufficient fertility to reproduce by self-pollination. An excess of terminal (vs. interstitial) segments was noted, and putative heterozygous substitutions for chromosomes 6, 7, 8 and 10 were found. Recombination within certain introgressed regions was reduced over 100-fold. These backcross-inbred lines are expected to facilitate the genetic analysis of traits identified in S. lycopersicoides and their transfer into horticultural tomatoes
Descriptors:gene-mapping. wild-relatives. alloenzymes. restriction-fragment-length-polymorphism. tomatoes. introgression. intergeneric-hybridization. backcrossing. segregation-distortion. genetic-markers. recombination. vegetables. plant-genetic-resources. biotechnology
Organism Descriptors:Lycopersicon-esculentum. Solanum-lycopersicoides. Lycopersicon

Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Solanum
Subject Codes:FF003. PP720. FF020. WW000
Supplementary Info:45 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

442. Title:Application of microsatellites in wheat (Triticum aestivum L.) for studying genetic differentiation caused by selection for adaptation and use
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 242-248
CD Volume:335
Print Article: Pages: 242-248
Author(s):Stachel M Lelley T Grausgruber H Vollmann J
Author Affiliation:Institute for Agrobiotechnology, Department of Plant Biotechnology, Konrad Lorenz Strasse 20, A-3430 Tulln, Austria
Language:English
Abstract:For studying genetic differentiation caused by selection for adaptation and end-use, the allele frequencies of 42 microsatellites (MS), representative of the 3 wheat genomes, were analysed in 60 wheat cultivars. The cultivars originated from 3 agroecological areas (AEAs; Germany, Austria and Hungary) and represent equal numbers of quality wheats and feed wheats for each country. For the 42 loci, 202 alleles were detected using PAGE and silver staining. The average number of alleles per locus was 4.8, including 4 monomorphic loci. For 16 loci, null alleles were detected. Cluster analysis clearly differentiated the varieties according to the 3 AEAs and, within each AEA, into quality wheats from feed wheats. Analysis of variance revealed highly significant differences of distance data between AEAs as well as between quality groups. The correlation between genetic distance (GD) and pedigree data (coefficient of diversity, COD) was rs = 0.45. The results have proven the excellent resolving power of MS in varietal differentiation, which arises through breeding under specific environmental conditions, and for different end-use
Descriptors:microsatellites. wheat. alleles. cultivars. staining. PAGE. genetic-distance. environment. geography. crop-quality. cluster-analysis. cereals. biotechnology
Geographic Locator:Austria. Germany. Hungary
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Central-Europe. Europe. Developed-Countries. European-Union-Countries. OECD-Countries. Western-Europe
Subject Codes:FF005. FF100. FF020. WW000
Supplementary Info:27 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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443. Title:Identification and molecular mapping of loci controlling fruit ripening time in tomato
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 249-255
CD Volume:335
Print Article: Pages: 249-255
Author(s):Doganlar S Tanksley S D Mutschler M A

Author Affiliation:Department of Plant Breeding and Biometry, 352 Emerson Hall, Cornell University, Ithaca, NY 14853-1902, USA
Language:English
Abstract:Using RAPD marker analysis, two quantitative trait loci (QTLs) associated with earliness due to reduced fruit-ripening time (days from anthesis to ripening = DTR) were identified and mapped in an F2 population derived from a cross between Lycopersicon esculentum 'E6203' (normal ripening) and L. esculentum 'Early Cherry' (early ripening). One QTL, on chromosome 5, was associated with a reduction in both ripening time (5 days) and fruit weight (29.3%), and explained 15.8 and 13.0% of the total phenotypic variation for DTR and fruit weight, respectively. The other QTL, on chromosome 12, was primarily associated with a reduction only in ripening time (7 days) and explained 12.3% of the total phenotypic variation for DTR. The gene action at this QTL was partially dominant (d/a = 0.41). Together, these two QTLs explained 25.1% of the total phenotypic variation for DTR. Additionally, two QTLs associated with fruit weight were identified in the same F2 population and mapped to chromosomes 4 and 6, respectively. Together, these two QTLs explained 30.9% of the total phenotypic variation for fruit weight. For all QTLs, the 'Early Cherry' alleles caused reductions in both ripening time and fruit weight. The polymorphic band for the most significant RAPD marker (OPAB-06), linked to the reduced ripening time QTL on chromosome 12, was converted to a cleaved amplified polymorphism assay for marker-aided selection and further introgression of early ripening time (DTR) into cultivated tomato
Descriptors:gene-mapping. ripening. phenotypic-variation. random-amplified-polymorphic-DNA. genetic-markers. tomatoes. quantitative-trait-loci. growth-period. maturity. fruits. earliness. genetics. vegetables. biotechnology
Organism Descriptors:Lycopersicon-esculentum. Lycopersicon
Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF060. FF020. WW000
Supplementary Info:27 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

444. Title:Fgr, a major locus that modulates the fructose to glucose ratio in mature tomato fruits
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 256-262
CD Volume:335
Print Article: Pages: 256-262
Author(s):Levin I Gilboa N Yeselson E Shen S Schaffer A A
Author Affiliation:Department of Plant Genetics and Breeding, Institute of Field and Garden Crops, Volcani Center, P.O. Box 6, Bet Dagan 50250, Israel
Language:English
Abstract:A genetic trait determining the ratio of fructose to glucose in mature tomato fruits is described. A backcross breeding programme based on the interspecific cross of Lycopersicon hirsutum and L. esculentum yielded stable genotypes with a high ratio of fructose to glucose (>1.5:1) compared with the approximately equimolar ratios found in L. esculentum. Two inter-simple-sequence repeat (ISSR) DNA sequences, highly associated (20 < LOD score < 21) with the trait, were identified by polymerase chain reaction. The markers were less associated with either glucose or fructose levels individually (2 < LOD score < 3) and were statistically unlinked to total sugars and total soluble solids (TSS). These two ISSR bands segregated in a dominant fashion and were

allelic to each other, one associated in coupling and the other in repulsion with the trait of high fructose to glucose ratio. Both ISSR markers were mapped to the centromeric region of tomato chromosome 4. Quantitative analysis of the identified locus, based on data from segregating F2, BC and F3 populations from the cross between genotypes having high and low fructose to glucose ratios, suggested that the L. hirsutum-derived allele (FgrH), which increases the fructose to glucose ratio, is partially dominant. FgrH leads to an increase in fructose levels and a subsequent decrease in glucose levels, with no effect on total hexose levels. Accordingly, it is concluded that the Fgr locus modulates the partitioning of hexose sugars between fructose and glucose, with no effect on total sugars or TSS

Descriptors:fructose. fruits. interspecific-hybridization. sugars. tomatoes. hexoses. glucose. genes. genetics. genetic-markers. gene-mapping. wild-relatives. plant-composition. polymerase-chain-reaction. vegetables. plant-genetic-resources. biotechnology

Organism Descriptors:Lycopersicon-esculentum. Lycopersicon-hirsutum. Lycopersicon

Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. FF003. FF040. WW000. PP720

Supplementary Info:24 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

445. Title:Organisation and expression of mitochondrial atp9 genes from CMS and fertile carrots

View Article: Theoretical and Applied Genetics. 2000. 100 (2). 263-270

CD Volume:335

Print Article: Pages: 263-270

Author(s):Szklarczyk M Oczkowski M Augustyniak H Borner T Linke B Michalik B

Author Affiliation:Department of Genetics, Plant Breeding and Seed Science, Cracow Agricultural University, Al. 29-go Listopada 54, 31-425 Cracow, Poland

Language:English

Abstract:The F0-F1 ATPase [adenosinetriphosphatase] subunit 9 gene of carrot (Daucus carota) mitochondria has been isolated from both petaloid male-sterile (atp9-1) and normal fertile cytoplasms (atp9-3). The position occupied in atp9-3 by the TAA stop codon is, in the case of atp9-1, replaced by the CAA triplet coding for glutamine, which makes this latter open reading frame 13 amino acid residues longer than that of atp9-3. The 3' end of atp9-3 is flanked by a direct repeat of 42 bp. The sequence of the repeat unit is also present at the 3' end of atp9-1 but without reiteration. A truncated and presumably inactive version of atp9 (atp9-2) was present in cytoplasms regardless of the fertility phenotype which they condition. The atp9-1 gene from petaloid cytoplasm appeared to be co-transcribed with the gene coding for 5S rRNA, and nuclear background influenced the accumulation of the respective transcript. The results are discussed with respect to a potential role of atp9-1 in generating the petaloid form of CMS. Nucleotide sequence data are available in the EMBL/GenBank/DDBJ databases under accession numbers AJ009697 (atp9-1), AJ009982 (atp9-2) and AJ009824 (atp9-3)

Descriptors:carrots. genes. adenosinetriphosphatase. mitochondrial-genetics. cytoplasmic-male-sterility. gene-expression. nucleotide-sequences. vegetables. biotechnology

Organism Descriptors:Daucus-carota

Supplemental Descriptors:Daucus. Apiaceae. Apiales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF060. WW000. FF020
Supplementary Info:47 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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446. Title:A spelt-specific gamma -gliadin gene: discovery and detection
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 271-279
CD Volume:335
Print Article: Pages: 271-279
Author(s):Buren M von Luthy J Hubner P
Author Variant:von-Buren-M
Author Affiliation:Laboratory of Food Chemistry, Department of Chemistry and Biochemistry, University of Berne, Freiestrasse 3, 3012 Berne, Switzerland
Language:English
Abstract:Polymerase chain reaction (PCR) primers GAG5 and GAG6 were designed based on published gamma -gliadin gene sequences and applied to 35 cultivars of closely related spelt (Triticum spelta) and hexaploid wheat (T. aestivum). Eight tetraploid durum wheat (T. durum) cultivars were included in the analysis. The obtained PCR products originated from two gamma -gliadin genes which were mapped to homeologous chromosomes 1B and 1D and termed GAG56B and GAG56D, respectively. Two alleles of GAG56D differing in a 9-bp deletion/duplication and single nucleotide polymorphism were found. The 18 spelts tested and wheat cv. Chinese Spring were discovered to carry a previously unknown gamma -gliadin gene, while 16 wheat cultivars possessed its longer, already published allele. Two PCR-based detection systems for the diagnostic alleles were developed and applied. The occurrence of two alleles of GAG56B among the investigated durum wheats correlated with their expression of gluten quality markers gamma -gliadins 42 or 45. Nucleotide sequence data have been deposited under GenBank accession number AF120267
Descriptors:alleles. genes. polymerase-chain-reaction. wheat. gliadin. quality. nucleotide-sequences. cereals. biotechnology
Organism Descriptors:Triticum-durum. Triticum-aestivum. Triticum-spelta. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. FF005. FF040. QQ050. QQ500
Supplementary Info:48 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

447. Title:Application of AFLP, RAPD and ISSR markers to genetic mapping of European and Japanese larch
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 299-307
CD Volume:335
Print Article: Pages: 299-307
Author(s):Arcade A Anselin F Faivre Rampant P Lesage M C Paques L E Prat D
Author Affiliation:INRA, Unite Amelioration, Genetique et Physiologie forestieres, Avenue de la Pomme de Pin, BP 20619 Ardon, F-45166 Oliver Cedex, France
Language:English

Abstract:Single-tree genetic linkage maps of European larch (Larix decidua) and Japanese larch (L. kaempferi) were constructed using segregation data from 112 progeny individuals of an hybrid family. A total of 266 markers (114 amplified fragment length polymorphism, 149 random amplified polymorphic DNA and 3 inter-simple-sequence repeat loci) showing a testcross configuration, i.e. heterozygous in one parent and null in the other parent, were grouped at LOD 4.0, theta =0.3. The maternal parent map (L. decidua) consisted of 117 markers partitioned within 17 linkage groups (1152 cM) and the paternal parent map (L. kaempferi) had 125 markers assembled into 21 linkage groups (1206 cM). The map distance covered by markers was determined by adding a 34.7-cM independence distance at the end of each group and unlinked marker. It reached 2537 and 2997 cM, respectively, for European and Japanese larches, and represented, respectively, a 79.6 and 80.8% coverage of the overall genome. A few 3:1 segregating markers were used to identify homologous linkage groups between the European larch and Japanese larch genetic maps. The PCR-based molecular markers allowed the construction of genetic maps, thus ensuring a good coverage of the larch genome for further quantitative trait locus detection and mapping studies
Descriptors:genetic-mapping. gene-mapping. forest-trees. genomes. linkage. random-amplified-polymorphic-DNA. genetic-markers. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Larix-kaempferi. Larix-decidua. Pinopsida
Supplemental Descriptors:Larix. Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants
Subject Codes:KK100. FF020. WW000
Supplementary Info:36 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

448. Title:Silencing of HMW glutenins in transgenic wheat expressing extra HMW subunits
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 319-327
CD Volume:335
Print Article: Pages: 319-327
Author(s):Alvarez M L Guelman S Halford N G Lustig S Reggiardo M I Ryabushkina N Shewry P Stein J Vallejos R H
Author Affiliation:Centro de Estudios Fotosinteticos y Bioquimicos (CEFOBI), CONICET-UNR, Suipacha 531, 2000 Rosario, Argentina
Language:English
Abstract:Wheat HMW glutenin subunit genes 1Ax1 and 1Dx5 were introduced, and either expressed or overexpressed, into a commercial wheat cultivar (Pro INTA Federal) that already expresses 5 subunits. Six independent transgenic events were obtained and characterized by SDS-PAGE and Southern analysis. The 1Dx5 gene was overexpressed in two events without changes in the other endosperm proteins. Overexpression of 1Dx5 increased the contribution of HMW glutenin subunits to total protein up to 22%. Two events express the 1Ax1 subunit transgene with associated silencing of the 1Ax2* endogenous subunit. In SDS-PAGE, one of them showed a new HMW glutenin band of an apparent Mr lower than that of the 1Dx5 subunit. Southern analysis of the 4 events confirmed transformation and suggested that the transgenes are present in a low copy number. Silencing of all HMW glutenin subunits was observed in two different events of transgenic wheat expressing the 1Ax1 subunit transgene and overexpressing the Dx5 gene. Transgenes and expression patterns were stably transmitted to the progenies in all events, except one where in some of the segregating T2 seeds the silencing of all HMW

glutenin subunits was reverted associated with a drastic lost of transgenes from a high to a low copy number. The revertant T2 seeds expressed the 5 endogenous subunits plus the 1Ax1 transgene
Descriptors:glutenins. transgenic-plants. wheat. genetic-transformation. gene-expression. seeds. endosperm. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. WW000. QQ050. QQ500
Supplementary Info:32 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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449. Title:The applicability of consensus PCR primers across species and genera: the use of wheat Em sequences to develop markers for orthologues in rye
View Article: Theoretical and Applied Genetics. 2000. 100 (2). 328-336
CD Volume:335
Print Article: Pages: 328-336
Author(s):Campenhout S van Koebner R M D Volckaert G
Author Variant:van-Campenhout-S
Author Affiliation:Katholieke Universiteit Leuven, Laboratory of Gene Technology, K. Mercierlaan 92, B-3001 Leuven, Belgium
Language:English
Abstract:Two wheat consensus primer sets, directed to "early-methionine-labelled" (Em) gene sequences, were tested for their ability to amplify beyond their original source. A range of widely diverse templates, including other Triticeae species and sample monocot and dicot species, was assayed. Primer set EMC5/EMC3, amplifying the entire coding region with its intron and part of the 3' untranslated region, targets Triticeae and sorghum Em sequences. The other set, EMC5/EMCO31, directed to the coding region and its intron, amplifies templates from all the grass species. Both primer sets fail to amplify Em sequences from more distant monocots and the dicots. Using set EMC5/EMC3, ten members of the rye Em gene family were isolated from 5 rye sources and sequenced. Significant DNA sequence variation between wheat and rye sequences in the non-coding regions was found, and used to develop 7 sequence-specific primers. Twelve primer combinations were analysed, 7 of which were Em-R1-specific, amplifying a product in at least one of the tested rye or rye-carrying genotypes but not in wheat. Four sets exhibited clear amplification length polymorphisms which allowed discrimination between and within the rye sources. The primers also discriminated between wheat-rye recombinants with proximal 1RL rye chromatin and those carrying distal 1RL rye chromatin. These results show that wheat consensus primer sets can be used to isolate orthologous sequences, especially from species that are used for alien gene transfer in wheat. Subsequently, species-specific assays can be designed that are useful tools for this application
Descriptors:polymerase-chain-reaction. rye. wheat. cereals. biotechnology
Organism Descriptors:Secale-cereale. Triticum-aestivum. Triticum
Supplemental Descriptors:Secale. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum
Subject Codes:FF005. FF020. WW000
Supplementary Info:34 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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450. Title:Genomic in situ hybridization (GISH) analyses of Thinopyrum intermedium, its partial amphiploid Zhong 5, and disease-resistant derivatives in wheat

View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 344-352
CD Volume:335
Print Article: Pages: 344-352

Author(s):Tang S Li Z Jia X Larkin P J
Author Affiliation:State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics, Chinese Academy of Sciences, Beijing 100101, China

Language:English

Abstract:Genomic in situ hybridization (GISH) to root-tip cells at mitotic metaphase, using genomic DNA probes from Thinopyrum intermedium [Elymus hispidus] and Pseudoroegneria strigosa, was used to examine the genomic constitution of Th. intermedium, the 56-chromosome partial amphiploid to wheat called Zhong 5 and disease-resistant derivatives of Zhong 5, in a wheat background. Evidence from GISH indicated that Th. intermedium contained seven pairs of St, seven JS and 21 J chromosomes; three pairs of Th. intermedium chromosomes with satellites in their short arms belonging to the St, J, J genomes and homoeologous groups 1, 1, and 5 respectively. GISH results using different materials and different probes showed that seven pairs of added Th. intermedium chromosomes in Zhong 5 included three pairs of St chromosomes, two pairs of JS chromosomes and two pairs of St-JS reciprocal translocation chromosomes. A pair of chromosomes, which substituted a pair of wheat chromosomes in Yi 4212 and in HG 295 and was added to 21 pairs of wheat chromosomes in the disomic additions Z1, Z2 and Z6, conferred barley yellow dwarf virus-resistance and was identical to a pair of St-JS translocation chromosomes (StJS) in Zhong 5. The StJS chromosome had a special GISH signal pattern and could be easily distinguished from other added chromosomes in Zhong 5; it has not yet been possible to locate the BYDV-resistant gene(s) of this translocated chromosome either in the St chromosome portion belonging to homoeologous group 2 or in the JS chromosome portion whose homoeologous group relationship is still uncertain. Among 22 chromosome pairs in disomic addition line Z3, the added chromosome pair had satellites and belonged to the St genome and homoeologous group 1. Disomic addition line Z4 carried a pair of added chromosomes which was composed of a group-7 JS chromosome translocated with a wheat chromosome; this chromosome was different to 7 Ai-1, but was identical to 7 Ai-2. The leaf rust [Puccinia recondita f.sp. tritici] and stem rust [P. graminis f.sp. tritici] resistance genes were located in the distal region of the long arm, whereas the stripe rust [P. striiformis] resistance gene(s) was located in the short arm or in the proximal region of the long arm of 7 Ai-2. A pair of JS-wheat translocation chromosomes, which originated from the WJS chromosomes in Z4, was added to the disomic addition line Z5; the added chromosomes of Z5 carried leaf and stem rust resistance but not stripe rust resistance; Z5 is a potentially useful source for rust resistance genes in wheat breeding and for cloning these novel rust-resistant genes. GISH analysis using the St genome as a probe has proved advantageous in identifying alien Th. intermedium in wheat

Descriptors:DNA-hybridization. wheat. chromosomes. genes. genomes. genome-analysis. rust-diseases. satellites. wild-relatives. disease-resistance. plant-diseases. plant-pathogens. fungal-diseases. plant-pathogenic-fungi. addition-lines. chromosome-translocation. chromosome-addition. chromosome-substitution. translocation-lines. substitution-lines. intergeneric-hybridization. gene-location. cereals. biotechnology. plant-genetic-resources. plant-pathology

Identifiers:Pseudoroegneria strigosa. Pseudoroegneria
Organism Descriptors:Elymus-hispidus. Triticum-aestivum. barley-yellow-dwarf-luteovirus. plant-viruses. Puccinia-recondita. Puccinia-striiformis. Puccinia-graminis. Triticum
Supplemental Descriptors:Elymus. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum. luteovirus-group. plant-viruses. viruses. plant-pathogens. pathogens. Puccinia. Uredinales. Basidiomycotina. Eumycota. fungi
Subject Codes:FF020. WW000. FF005. FF610. HH600. PP720
Supplementary Info:52 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

451. Title:Identification of C-genome chromosomes involved in intergenomic translocations in Avena sativa L., using cloned repetitive DNA sequences
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 353-360
CD Volume:335
Print Article: Pages: 353-360
Author(s):Linares C Irigoyen M L Fominaya A
Author Affiliation:Department of Cell Biology and Genetics, University of Alcala, Campus Universitario, ES-28871 Alcala de Henares, Madrid, Spain
Language:English
Abstract:Four anonymous non-coding sequences were isolated from an Avena strigosa [A. nuda] (A genome) genomic library and subsequently characterized. These sequences, designated As14, As121, As93 and As111 (EMBL accession numbers AJ005499-AJ005502, respectively), were 639, 730, 668 and 619 bp long, respectively, and showed different patterns of distribution in diploid and polyploid Avena species. Southern hybridization showed that sequences with homology to sequences As14 and As121 were dispersed throughout the genome of diploid (A genome), tetraploid (AC genomes) and hexaploid (ACD genomes) Avena species but were absent in the C-genome diploid species. In contrast, sequences homologous to sequences As93 and As111 were found in diploid (A and C genomes), tetraploid (AC genomes) and hexaploid (ACD genomes) species. The chromosomal locations of the 4 sequences in hexaploid oat species were determined by fluorescent in situ hybridization (FISH) and found to be distributed over the length of the 28 chromosomes (except in the telomeric regions) of the A and D genomes. Furthermore, 2 C-genome chromosome pairs with the As14 sequence, and 4 with As121, were discovered to be involved in intergenomic translocations. These chromosomes were identified as 1C, 2C, 4C and 16C by combining the As14 or As121 sequences with two ribosomal sequences and a C-genome-specific sequence as probes in FISH. These sequences offer new tools for analysing possible intergenomic translocations in other hexaploid oat species
Descriptors:chromosomes. nucleotide-sequences. repetitive-DNA. DNA-hybridization. genomes. oats. chromosome-translocation. cereals. biotechnology
Identifiers:fluorescence in situ hybridization
Organism Descriptors:Avena. Avena-sativa. Avena-nuda
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Avena
Subject Codes:FF005. FF020. WW000
Supplementary Info:30 ref
ISSN:0040-5752
Year:2000

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452. Title:Cytological heterozygosity and the hybrid origin of sweet orange (Citrus sinensis (L.) Osbeck)
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 361-367
CD Volume:335
Print Article: Pages: 361-367
Author(s):Pedrosa A Schweizer D Guerra M
Author Affiliation:Department of Cytology and Genetics, Institute of Botany, University of Vienna, Rennweg 14, A-1030, Vienna, Austria
Language:English
Abstract:Citrus sinensis chromosomes, although small in size, present a remarkable differentiation of bands with the fluorochromes CMA and DAPI. These bands suggest that some heteromorphisms are fixed in this species. To investigate the extent of these heteromorphisms, ten cultivars of C. sinensis were analysed with CMA/DAPI staining and, in some of them, the 18S-5.8S-25S rRNA and 5S rRNA genes were located by in situ hybridization. CMA/DAPI staining showed exactly the same CMA+/DAPI- banding pattern for all cultivars. In situ hybridization revealed three 18S-5.8S-25S rRNA gene sites, two proximally located on two similar chromosomes and one terminally located on a third non-related chromosome. Two 5S rRNA gene sites were observed in this species, with one located proximal to the telomeric 18S-5.8S-25S rDNA site. Both cytological approaches revealed an invariable, heterozygotic karyotype among sweet orange cultivars. Based on these data, the putative hybrid origin of the species is discussed
Descriptors:heterozygosity. chromosomes. genes. DNA-hybridization. ribosomal-RNA. oranges. chromosome-banding. gene-location. gene-mapping. origin. fruit-crops. fruits. biotechnology
Organism Descriptors:Citrus-sinensis. Citrus
Supplemental Descriptors:Citrus. Rutaceae. Sapindales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:44 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

453. Title:RAPD and AFLP tagging and mapping of Beta (B) and Beta modifier (MoB), two genes which influence beta -carotene accumulation in fruit of tomato (Lycopersicon esculentum Mill.)
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 368-375
CD Volume:335
Print Article: Pages: 368-375
Author(s):Zhang Y Stommel J R
Author Affiliation:USDA-ARS, Vegetable Laboratory, Plant Sciences Institute, Beltsville, MD 20705, USA
Language:English
Abstract:The Beta (B) locus in tomato (Lycopersicon esculentum) increases fruit beta -carotene content at the expense of lycopene, resulting in orange-pigmented fruit. Expression of B is influenced by the beta-modifier (MoB) gene which segregates independently of B. RAPD and AFLP analyses were performed using near isogenic lines (NILs) unique for B and bulked segregant analysis (BSA) of a L. esculentum x L. cheesmanii-derived F2 population segregating for B. Using 1018 random primers for RAPD analysis and 64 primer pairs for AFLP analysis, we identified polymorphic products which distinguished the NILs and the two bulked

DNA samples constructed for BSA. A single 100 bp AFLP amplification product (E-ACA/M-CTG100) which distinguished the NILs cosegregated with MoB and was demonstrated to be tightly linked to the locus. E-ACA/M-CTG100 exhibited a recombination frequency of 1.7% in the F2 progeny derived from an initial cross between the isolines. The MoB locus was mapped to the long arm of chromosome 6. Two RAPD products (OPAR181100 and UBC792830) of 1100 bp and 830 bp, respectively, were polymorphic between orange- and red-fruited bulks constructed from F2 individuals in the L. esculentum and L. cheesmanii mating series. OPAR181100 and UBC792830 displayed recombination frequencies of 4.2% and 7.6%, respectively, in F2 progeny. The B-linked OPAR181100 marker was also mapped to the long arm of chromosome 6, proximal to MoB, and revealed linkage between B and MoB
Descriptors:genes. gene-mapping. random-amplified-polymorphic-DNA. tomatoes. interspecific-hybridization. modifier-genes. carotenes. linkage. wild-relatives. vegetables. biotechnology. plant-genetic-resources
Identifiers:beta -carotene. amplified fragment length polymorphism
Organism Descriptors:Lycopersicon-esculentum. Lycopersicon-cheesmanii. Lycopersicon
Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF003. FF040. PP720. WW000
Supplementary Info:36 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

454. Title:Structural differences in the vicinity of the waxy locus among the Oryza species with the AA-genome: identification of variable regions
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 376-383
CD Volume:335
Print Article: Pages: 376-383
Author(s):Nagano H Kawasaki S Kishima Y Sano Y
Author Affiliation:Laboratory of Plant Breeding, Faculty of Agriculture, Hokkaido University, 060-8589 Sapporo, Japan
Language:English
Abstract:We constructed a fine physical map for a 260-kb rice BAC contig surrounding the waxy locus. In order to identify variable regions within this 260-kb as to the restriction fragment length polymorphisms and copy numbers, sixty overlapping fragments derived from the 260-kb contig were used as probes to compare their corresponding structures among the Oryza species with AA-genome. According to the hybridization patterns, each fragment was classified into four types: true single copy (class 1), single copy with a smear background (class 2), multiple copy without a smear background (class 3) and only a smear background (class 4). Out of 16 single copy (class 1 and class 2) regions obtained in this map, the one site corresponding to wx gave rise to remarkable polymorphisms among AA-genome species in Oryza. In most of the fragments observed as repetitive segments (class 4), we could not find obvious differences in the hybridization pattern. However, interestingly, one site sorted into class-3 showed copy numbers varying among the lines. The lines belonging to O. sativa, O. rufipogon, O. meridionalis and O. longistaminata possessed high-copy numbers of this fragment, whereas only a few bands were detected in the lines from O. glaberrima, O. barthii and O. glumaepatula. The two variable regions found within the AA-genome species represented genomic dynamisms
Descriptors:DNA-hybridization. rice. wild-relatives. molecular-genetics. cereals. biotechnology. plant-genetic-resources

Identifiers:Oryza meridionalis. Oryza glumaepatula
Organism Descriptors:Oryza. Oryza-barthii. Oryza-glaberrima. Oryza-longistaminata. Oryza-rufipogon. Oryza-sativa
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Oryza
Subject Codes:FF020. FF005. WW000. PP720
Supplementary Info:26 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

455. Title:Anchored simple-sequence repeats as primers to generate species-specific DNA markers in Lolium and Festuca grasses
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 384-390
CD Volume:335
Print Article: Pages: 384-390
Author(s):Pasakinskiene I Griffiths C M Bettany A J E Paplauskiene V Humphreys M W
Author Affiliation:Lithuanian Institute of Agriculture, Dotnuva-Akademija, 5051 Kedainiai, Lithuania
Language:English
Abstract:Simple-sequence repeats (SSRs) comprising three tetranucleotide repeat sequences with two-base 'anchors', namely 5'-(AGAC)4GC, 5'-AC(GACA)4 and 5'-(GACA)4GT, were used in PCR reactions as primers to develop inter-SSR DNA fingerprints of the outbreeding grass species Lolium multiflorum, L. perenne, Festuca pratensis and F. arundinacea. Each species was represented by DNA samples from 3 to 6 varieties. In all four species distinctive species-specific DNA profiles were produced that were common across a number of varieties despite their diverse origin. While the fingerprints of the two ryegrasses, L. multiflorum and L. perenne, were the most similar, a number of inter-SSR DNA markers were generated that enabled them to be distinguished from each other. Some slight variations were found between varieties, which provided putative variety-specific markers for cultivar identification. In addition, variations in the DNA profiles of the genotypes of L. multiflorum and F. pratensis were examined, and the results showed that variety-specific fingerprints are integrated patterns made up from the profiles of individual genotypes. Amongst the primers used, AC(GACA)4 generated the best distinction between Lolium and Festuca individuals and provides an effective new tool for genome identification. A number of species-discriminating sequences, ranging in size between 550 bp and 1,600 bp, were cloned: three clones for F. pratensis, one clone for L. multiflorum and one clone for F. arundinacea. An F. pratensis fragment pFp 78H582 was sequenced. Southern hybridization confirmed the presence of this fragment in F. arundinacea (which contains one genome of F. pratensis), but no homology was found with L. multiflorum. However, an F. arundinacea clone amplified with (GACA)4GT, pFa 104H1350, was found to be unique to the F. arundinacea genome
Descriptors:genetic-markers. genomes. DNA-hybridization. polymerase-chain-reaction. cultivar-identification. pasture-plants. fodder-plants. biotechnology
Organism Descriptors:Festuca-arundinacea. Festuca-pratensis. Lolium-multiflorum. Lolium-perenne. grasses. Poaceae
Supplemental Descriptors:Festuca. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Lolium
Subject Codes:FF007. FF020. WW000
Supplementary Info:30 ref
ISSN:0040-5752

Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

456. Title:RAPD markers linked to a gene for resistance to pine needle gall midge in Japanese black pine (Pinus thunbergii)
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 391-395
CD Volume:335
Print Article: Pages: 391-395
Author(s):Kondo T Terada K Hayashi E Kuramoto N Okamura M Kawasaki H
Author Affiliation:Forest Tree Breeding Center, Ishi, Juo, Taga, Ibaraki 319-1301, Japan
Language:English
Abstract:Linkage of RAPD markers to a single dominant gene for resistance to pine needle gall midge (Thecodiplosis japonensis) was investigated in Japanese black pine (Pinus thunbergii). Three primers that generated linked markers were found after 1160 primers were screened by bulked segregant analysis. The distances between the resistance gene, R, and the marker genes OPC06580, OPD01700 and OPAX192100 were 5.1 cM, 6.7 cM and 13.6 cM, respectively. OPC06580 was in coupling phase to R, whereas OPD01700 and OPAX192100 were in repulsion phase to R. A linkage map for a resistant tree was constructed using 96 macrogametophytes. In linkage analysis, 98 out of 127 polymorphic markers were assigned to 17 linkage groups and six linked pairs. The total length of this map was 1469.8 cM, with an average marker density of 15.6 cM. The genome length was estimated to be 2138.3 cM and the derived linkage map covered 67.5% of the genome. Although the linked markers OPC06580, OPAX192100 and OPD01700 belonged to the same linkage group, no precise positions were found for OPC06580 or OPD01700
Descriptors:genes. genetic-markers. forest-trees. random-amplified-polymorphic-DNA. pest-resistance. plant-pests. insect-pests. linkage. biotechnology. control. agricultural-entomology
Organism Descriptors:Pinus-thunbergii. Thecodiplosis-japonensis. Pinopsida. arthropods
Supplemental Descriptors:Pinus. Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants. Thecodiplosis. Cecidomyiidae. Diptera. insects. arthropods. invertebrates. animals
Subject Codes:FF020. WW000. KK100. FF620. HH600
Supplementary Info:14 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

457. Title:QTL analysis of leaf morphology in tetraploid Gossypium (cotton)
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 409-418
CD Volume:335
Print Article: Pages: 409-418
Author(s):Jiang C Wright R J Woo S S DelMonte T A Paterson A H
Author Affiliation:Plant Genome Mapping Laboratory, Department of Soil and Crop Science, Texas A&M University, College Station, TX 77843-2474, USA
Language:English
Abstract:Molecular markers were used to map and characterize quantitative trait loci (QTLs) determining cotton leaf morphology and other traits, in 180 F2 plants from an interspecific cross between a Gossypium hirsutum genotype carrying four morphological mutants, and a wild-type Gossypium barbadense. The prominent effects of a single region of chromosome 15, presumably the classical "Okra-leaf" locus, were modified by QTLs on several other chromosomes affecting leaf size and shape. For most

traits, each parent contained some alleles with positive effects and others with negative effects, suggesting a large potential for adapting leaf size and shape to the needs of particular production regimes. Twenty-one QTLs/loci were found for the morphological traits at LODmore than or equal to 3.0 and Pless than or equal to 0.001, among which 14 (63.6%) mapped to D-subgenome chromosomes. Forty-one more possible QTLs/loci were suggested with 2.0less than or equal to LOD<3.0 and 0.001<Pless than or equal to 0.01. Among all of the 62 possible QTLs (found at LODmore than or equal to 2.0 and Pless than or equal to 0.01) for the 14 morphological traits in this study, 38 (61.3%) mapped to D-subgenome chromosomes. This reinforces the findings of several other studies in suggesting that the D-subgenome of tetraploid cotton has been subject to a relatively greater rate of evolution than the A-subgenome, subsequent to polyploid formation

Descriptors:cotton. interspecific-hybridization. plant-morphology. mutants. mutations. leaves. genetic-markers. quantitative-trait-loci. polyploidy. evolution. genomes. gene-mapping. fibre-plants. biotechnology

Organism Descriptors:Gossypium-barbadense. Gossypium-hirsutum. Gossypium

Supplemental Descriptors:Gossypium. Malvaceae. Malvales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF030. FF020

Supplementary Info:31 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

458. Title:AFLP-derived STS markers for the identification of sex in Asparagus officinalis L

View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 432-438

CD Volume:335

Print Article: Pages: 432-438

Author(s):Reamon Buttner S M Jung C

Author Affiliation:Institute of Crop Science and Plant Breeding, Christian-Albrechts-University of Kiel, Olshausenstrasse 40, D-24118 Kiel, Germany

Language:English

Abstract:For a simple, rapid and PCR-based screening of sex in the cultivated asparagus (Asparagus officinalis), we developed five sequence-tagged-site (STS) markers from previously mapped, low-copy, sex-linked amplified fragment length polymorphism (AFLP) markers. A male/female PCR assay was feasible with these STS markers either by direct amplification or by digestion with restriction enzymes. Similar to the AFLP markers from which they were derived, STS4150.1, STS4150.2, STS4150.3 and STS3156 did not give recombinants in five different populations. STS3660 could be scored co-dominantly, enabling the differentiation of XY from YY males in the screened F2 mapping population. The use of the sex-linked STS markers should allow early identification of sex, thus accelerating the breeding process for new asparagus varieties. Further, 10 additional AFLP markers obtained with PstI/MseI primer combinations have been mapped on the L5 chromosome, bringing the total number of known AFLP and STS markers flanking the sex locus to 24. These markers can be utilized for fine mapping of the sex gene in asparagus, which will pave the way for a map-based cloning approach

Descriptors:polymerase-chain-reaction. sex. genetic-markers. males. vegetables. biotechnology

Organism Descriptors:Asparagus-officinalis

Supplemental Descriptors:Asparagus. Liliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF060. WW000. FF020
Supplementary Info:26 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

459. Title:RAPD linkage map of the genomic region encompassing the root-knot nematode (Meloidogyne javanica) resistance locus in carrot
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 439-446
CD Volume:335
Print Article: Pages: 439-446
Author(s):Boiteux L S Belter J G Roberts P A Simon P W
Author Affiliation:Plant Breeding and Plant Genetics Program, 1575 Linden Drive, University of Wisconsin, Madison, WI 53706, USA
Language:English
Abstract:Inheritance studies have indicated that resistance to the root-knot nematode (Meloidogyne javanica) in carrot (Daucus carota) inbred line 'Brasilia-1252' is controlled by the action of one or two (duplicated) dominant gene(s) located at a single genomic region (designated the Mj-1 locus). A systematic search for randomly amplified polymorphic DNA (RAPD) markers linked to Mj-1 was carried out using bulked segregant analysis. Altogether 1000 ten-mer primers were screened with 69.1% displaying scorable amplicons. A total of approximately 2400 RAPD bands were examined. Four reproducible markers (OP-C21700, OP-Q6500, OP-U12700 and OP-AL15500) were identified, in coupling-phase linkage, flanking the Mj-1 region. The genetic distances between RAPD markers and the Mj-1 locus, estimated using an F2 progeny of 412 individuals from 'Brasilia 1252' x 'B6274', ranged from 0.8 to 5.7 cM. The two closest flanking markers (OP-Q6500 and OP-AL15500) encompassed a region of 2.7 cM. The frequency of these RAPD loci was evaluated in 121 accessions of a broad-based carrot germplasm collection. Only five entries (all resistant to M. javanica and genetically related to 'Brasilia 1252') exhibited the simultaneous presence of all four markers. An advanced line derived from the same cross, susceptible to M. javanica but relatively resistant to another root-knot nematode species (M. incognita), did not share three of the closest markers. These results suggest that at least some genes controlling resistance to M. incognita and M. javanica in 'Brasilia 1252' reside at distinct loci. The low number of markers suggests a reduced amount of genetic divergence between the parental lines at the region surrounding the target locus. Nevertheless, the low rate of recombination indicated these markers could be useful landmarks for positional cloning of the resistance gene(s). These RAPD markers could also be used to increase the Mj-1 frequency during recurrent selection cycles and in backcrossing programmes to minimize 'linkage drag' in elite lines employed for the development of resistant F1 hybrids
Descriptors:carrots. linkage. genes. germplasm. hybrids. pest-resistance. plant-parasitic-nematodes. genetic-markers. gene-mapping. vegetables. biotechnology. nematology. control. plant-nematology
Organism Descriptors:Meloidogyne-javanica. Meloidogyne-incognita. Daucus-carota
Supplemental Descriptors:Meloidogyne. Meloidogynidae. Nematoda. invertebrates. animals. Daucus. Apiaceae. Apiales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF620. HH600. FF020. WW000
Supplementary Info:30 ref
ISSN:0040-5752

Year:2000
Journal Title:Theoretical and Applied Genetics

460. Title:Genetic mapping of hypervariable minisatellite sequences in rice (Oryza sativa L.)
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 447-453
CD Volume:335
Print Article: Pages: 447-453
Author(s):Gustafson J P Yano M
Author Affiliation:USDA-ARS, Plant Genetics Research Unit, and Plant Science Unit, University of Missouri, Columbia, Missouri 65211, USA
Language:English
Abstract:Minisatellites, or DNA fingerprinting sequences, have been utilized in animal linkage studies for several years but have not been used as markers for plant genome mapping. In animal genome mapping they have resulted in limited success because they are evenly dispersed in some species but are often clustered near telomeric regions, as observed on human chromosomes. The purpose of the present study was to generate DNA fingerprints utilizing several rice-derived minisatellites containing different core sequences and numbers of repeat units, followed by assessing their potential for use as genetic markers when mapped to a rice recombinant inbred line (RIL) population. Sites of segregating minisatellite loci were mapped onto 11 of the 12 rice RIL linkage maps. The implications for the use of rice minisatellite core sequences as genetic markers on linkage maps in rice are discussed
Descriptors:gene-mapping. rice. DNA-fingerprinting. genetic-markers. microsatellites. linkage. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:28 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

461. Title:Molecular phylogeny of mangroves VII. PCR-RFLP of trnS-psbC and rbcL gene regions in 24 mangrove and mangrove-associate species
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 454-460
CD Volume:335
Print Article: Pages: 454-460
Author(s):Parani M Lakshmi M Ziegenhagen B Fladung M Senthilkumar P Parida A
Author Affiliation:M.S. Swaminathan Research Foundation, III Cross Street, Taramani Institution Area, Chennai 600 113, India
Language:English
Abstract:Chloroplast DNA (ctDNA) regions, trnS-psbC and rbcL, from 120 individuals of 24 mangrove and mangrove associate species belonging to 11 orders, 13 families and 17 genera of Angiospermae were amplified by the polymerase chain reaction (PCR) and restriction-digested with HaeIII. Analysis of polymorphism in the restriction fragments (PCR-RFLP) revealed 18 classes of restriction banding pattern in trnS-psbC region. This has provided molecular evidence for diversity in the mangrove floral component at the above-species level. Intra-generic variations were observed in three genera, viz. Rhizophora, Avicennia and Suaeda. Species-specific restriction patterns were found in the genera Rhizophora and Suaeda. A natural hybrid belonging to the genus Rhizophora was also analysed, and its restriction pattern was the same

as that of a putative parental species. PCR-RFLP analysis of rbcL gene region was less differentiating. However, it showed 13 different classes of restriction patterns and revealed the usefulness of these investigations for genome analysis at a higher taxonomic level. Intra-specific variation was not observed in any of the species in either of the ctDNA regions analysed. This is the first report which describes variations in the chloroplast genome of mangrove species
Descriptors:mangroves. phylogeny. chloroplast-DNA. polymerase-chain-reaction. restriction-fragment-length-polymorphism. taxonomy. chloroplast-genetics. genetic-variation. hybrids. forest-trees. broadleaves. biotechnology. plant-genetic-resources
Organism Descriptors:Avicennia. Rhizophora. Suaeda
Supplemental Descriptors:Verbenaceae. Lamiales. dicotyledons. angiosperms. Spermatophyta. plants. Rhizophoraceae. Rhizophorales. Chenopodiaceae. Caryophyllales
Subject Codes:FF020. WW000. KK100. MM300
Supplementary Info:35 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

462. Title:Evidence of multiple complex patterns of T-DNA integration into the rice genome
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 461-470
CD Volume:335
Print Article: Pages: 461-470
Author(s):Yin Z Wang G L
Author Affiliation:Institute of Molecular Agrobiology, 1 Research Link, National University of Singapore, Singapore 117604, Singapore
Language:English
Abstract:The transfer of the long T-DNA (T-DNA and non-T-DNA) of a binary plasmid from Agrobacterium into the rice genome was investigated at both molecular and genetic levels. Out of 226 independent transgenic plants, 33% of the transformants contained non-T-DNA sequences. There was no major difference in the frequency of non-T-DNA transfer among three Agrobacterium tumefaciens strains. Four T1 plants containing a single putative long T-DNA insertion were selected for Southern analysis. Three of them were confirmed to have a long T-DNA insertion with a size of greater-than-unit-length of the binary plasmid. This was further confirmed by rescuing the intact binary plasmid from these plants. Our results suggest that long T-DNA transfer by rolling-circle replication from Agrobacterium to rice occurs frequently, and that the high frequency of non-T-DNA transfer should be considered when producing transgenic rice for commercial production
Descriptors:rice. transgenic-plants. genetic-transformation. gene-transfer. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Agrobacterium-tumefaciens. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Agrobacterium. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF005. WW000. FF020
Supplementary Info:41 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

463. Title:AFLP linkage group assignment to the chromosomes of Allium cepa L. via monosomic addition lines
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 480-486
CD Volume:335
Print Article: Pages: 480-486
Author(s):Heusden A W van Shigyo M Tashiro Y Vrielink van Ginkel R Kik C
Author Variant:van-Heusden-A-W
Author Affiliation:DLO-Centre for Plant Breeding and Reproduction Research (CPRO-DLO), P.O. Box 16, 6700 AA Wageningen, Netherlands
Language:English
Abstract:Two complete sets of Allium fistulosum-A. cepa monosomic addition lines (2n = 2x + 1 = 17) together with an amplified fragment length polymorphism (AFLP) linkage map based on a cross between A. cepa and A. roylei were used to re-evaluate the eight A. cepa linkage groups identified in the mapping study. The linkage groups could be assigned to individual, physical chromosomes. The low level of molecular homology between A. cepa and A. fistulosum enabled the identification of 186 AFLP markers present in A. cepa and not in A. fistulosum with ten different primer combinations. With the monosomic addition lines, the distribution of the markers over the eight chromosomes of A. cepa could be determined. Of these 186 AFLP markers, 51 were absent in A. roylei and consequently used as markers in the mapping study (A. cepa x A. roylei cross). Therefore, these 51 AFLP markers could be used to assign the eight A. cepa linkage groups identified in the mapping study to physical chromosomes. Seven isozyme and three cleaved amplified polymorphic sequence (CAPS) markers were also included. Two of the linkage groups had to be split because they included two sets of markers corresponding to different chromosomes. A total of 20 (approx. 10%) of the A. cepa-specific AFLP markers were amplified in more than one type of the monosomic addition lines, suggesting unlinked duplications. The co-dominant isozyme and CAPS markers were used to identify the correspondence of linkage groups originating from A. cepa or from A. roylei
Descriptors:chromosomes. linkage. onions. addition-lines. chromosome-addition. gene-mapping. genetic-markers. Welsh-onions. vegetables. biotechnology
Identifiers:Allium roylei. amplified fragment length polymorphism
Organism Descriptors:Allium-cepa. Allium-fistulosum. Allium
Supplemental Descriptors:Allium. Alliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants. Liliaceae
Subject Codes:FF003. FF020. WW000
Supplementary Info:24 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

464. Title:High-frequency linkage of co-expressing T-DNA in transgenic Arabidopsis thaliana transformed by vacuum-infiltration of Agrobacterium tumefaciens
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 487-493
CD Volume:335
Print Article: Pages: 487-493
Author(s):Poirier Y Ventre G Nawrath C
Author Affiliation:Institut d'Ecologie-Biologie et Physiologie Vegetales, Batiment de Biologie, Universite de Lausanne, CH-1015 Lausanne, Switzerland
Language:English
Abstract:The efficiency of co-expression and linkage of distinct T-DNAs present in separate Agrobacterium tumefaciens was analysed in Arabidopsis

thaliana transformed by the vacuum infiltration method. Co-expression was monitored by the synthesis of three bacterial proteins involved in the production of polyhydroxybutyrate (PHB) in the plastids. Out of 80 kanamycin-resistant transgenic plants analysed, 13 plants were co-transformed with the two distinct T-DNAs and produced PHB. Of those, 7 lines had a kanamycin-resistance segregation ratio consistent with the presence of a single functional insert. Genetic linkage between the distinct T-DNAs was demonstrated for all 13 PHB-producing lines, while physical linkage between the distinct T-DNAs was shown for 12 out of 13 lines. T-DNAs were frequently linked in an inverted orientation about the left borders. Transformation of A. thaliana by the co-infiltration of two A. tumefaciens containing distinct T-DNAs is, thus, an efficient approach for the integration and expression of several transgenes at a single locus. This approach will facilitate the creation and study of novel metabolic pathways requiring the expression of numerous transgenes

Descriptors:linkage. plastics. genetic-transformation. transgenic-plants. gene-expression. polyhydroxybutyrate. weeds. biotechnology

Organism Descriptors:Agrobacterium-tumefaciens. Arabidopsis-thaliana

Supplemental Descriptors:Agrobacterium. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. WW000. SS200

Supplementary Info:27 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

465. Title:Microsatellite variability in grapevine cultivars from different European regions and evaluation of assignment testing to assess the geographic origin of cultivars

View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 498-505

CD Volume:335

Print Article: Pages: 498-505

Author(s):Sefc K M Lopes M S Lefort F Botta R Roubelakis Angelakis K A Ibanez J Pejic I Wagner H W Glossl J Steinkellner H

Author Affiliation:Zentrum fur Angewandte Genetik, Universitat fur Bodenkultur Wien, Muthgasse 18, A-1190 Vienna, Austria

Language:English

Abstract:Nine microsatellite markers (VVMD5, VVMD7, VVS2, ssrVrZAG21, ssrVrZAG47, ssrVrZAG62, ssrVrZAG64, ssrVrZAG79 and ssrVrZAG83) were chosen for the analysis of marker information content, the genetic structure of grapevine (Vitis) cultivar gene pools and differentiation among grapevines sampled from seven European vine-growing regions (Greece, Croatia, North Italy, Austria and Germany, France, Spain, and Portugal). The markers were found to be highly informative in all cultivar groups and therefore constitute a useful set for the genetic characterization of European grapevines. Similar and high levels of genetic variability were detected in all investigated grapevine gene pools. Genetic differentiation among cultivars from different regions was significant, even in the case of adjacent groups such as the Spanish and Portuguese cultivars. No genetic differentiation could be detected between vines with blue and white grapes, indicating that they have undergone the processes of cultivar development jointly. The observed genetic differentiation among vine-growing regions suggested that cultivars could possibly be assigned to their regions of origin according to their genotypes. This might allow one to determine the geographical origin of cultivars with an unknown background. The

assignment procedure proved to work for cultivars from the higher differentiated regions, as for example from Austria and Portugal
Descriptors:cultivars. grapes. genetic-variation. geography. microsatellites. fruit-crops. fruits. biotechnology
Geographic Locator:Europe
Organism Descriptors:Vitis
Supplemental Descriptors:Vitidaceae. Rhamnales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:30 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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466. Title:Hot spots of DNA instability revealed through the study of somaclonal variation in rye
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 506-511
CD Volume:335
Print Article: Pages: 506-511
Author(s):Linacero R Freitas Alves E Vazquez A M
Author Affiliation:Departamento de Genetica, Facultad de Biologia, Universidad Complutense, 28040 Madrid, Spain
Language:English
Abstract:RAPD analysis was performed to assess DNA variation among rye (Secale cereale) plants regenerated from immature embryos and inflorescences. From the studied plants, 40% showed at least one variation, and the number of mutations per plant was quite high, ranging from 1 up to 12. On some occasions (2.9% of the scored bands) the modified band was observed in only one plant or in several but originated from the same callus (variable band). In other cases (5.25%) the same band varied in several plants obtained from different calli. These hypervariable bands and could vary between plants belonging to different cultivars and/or with different origins, inflorescences or embryos. Thus, they must originate through independent mutational events. We assume that these bands represent hypervariable regions of the rye genome and so detect hot spots of DNA instability. Some of these bands proved to be unique sequences, others were present in a low copy number while the remaining ones were moderately or highly repetitive
Descriptors:random-amplified-polymorphic-DNA. rye. somaclonal-variation. callus. mutations. embryo-culture. tissue-culture. cereals. biotechnology
Organism Descriptors:Secale-cereale
Supplemental Descriptors:Secale. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:23 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

467. Title:Extended physical maps and a consensus physical map of the homoeologous group-6 chromosomes of wheat (Triticum aestivum L. em Thell.)
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 519-527
CD Volume:335
Print Article: Pages: 519-527
Author(s):Weng Y Tuleen N A Hart G E

Author Affiliation:Department of Soil and Crop Sciences, Texas A & M University, College Station, TX 77843, USA
Language:English
Abstract:Extended physical maps of chromosomes 6A, 6B and 6D of common wheat (Triticum aestivum, 2n = 6x = 42, AABBDD) were constructed with 107 DNA clones and 45 homoeologous group-6 deletion lines. Two-hundred-and-ten RFLP loci were mapped, including three orthologous loci with each of 34 clones, two orthologous loci with each of 31 clones, one locus with 40 clones, two paralogous loci with one clone, and four loci, including three orthologs and one paralog, with one clone. Fifty-five, 74 and 81 loci were mapped in 6A, 6B and 6D, respectively. The linear orders of the mapped orthologous loci in 6A, 6B and 6D appear to be identical, and 65 loci were placed on a group-6 consensus physical map. Comparison of the consensus physical map with eight linkage maps of homoeologous group-6 chromosomes from six Triticeae species disclosed that the linear orders of the loci on the maps are largely, if not entirely, conserved. The relative distributions of loci on the physical and linkage maps differ markedly, however. On most of the linkage maps, the loci are either distributed relatively evenly or clustered around the centromere. In contrast, approximately 90% of the loci on the three physical maps are located either in the distal one-half or the distal two-thirds of the six chromosome arms and most of the loci are clustered in two or three segments in each chromosome
Descriptors:wheat. restriction-fragment-length-polymorphism. gene-mapping. chromosome-maps. linkage. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:57 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

468. Title:QTL analysis of flower and fruit traits in sour cherry
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 535-544
CD Volume:335
Print Article: Pages: 535-544
Author(s):Wang D Karle R Iezzoni A F
Author Affiliation:Department of Horticulture, Michigan State University, East Lansing MI 48824, USA
Language:English
Abstract:The map locations and effects of quantitative trait loci (QTLs) were estimated for eight flower and fruit traits in sour cherry (Prunus cerasus) using a restriction fragment length polymorphism (RFLP) genetic linkage map constructed from a double pseudo-testcross. The mapping population consisted of 86 progeny from the cross between two sour cherry cultivars, Rheinische Schattenmorelle (RS) x Erdi Botermo (EB). The genetic linkage maps for RS and EB were 398.2 cM and 222.2 cM, respectively, with an average interval length of 9.8 cM. The RS/EB linkage map that was generated with shared segregating markers consisted of 17 linkage groups covering 272.9 cM with an average interval length of 4.8 cM. Eleven putatively significant QTLs (LOD >2.4) were detected for six characters (bloom time, ripening time, % pistil death, % pollen germination, fruit weight, and soluble solids concentration). The percentage of phenotypic variation explained by a single QTL ranged from 12.9% to 25.9%. Of the QTLs identified for the traits in which the two parents differed significantly, 50% had allelic

effects opposite to those predicted from the parental phenotype. Three QTLs affecting flower traits (bloom time, % pistil death, and % pollen germination) mapped to a single linkage group, EB 1. The RFLP closest to the bloom time QTL on EB 1 was detected by a sweet cherry cDNA clone pS141 whose partial amino acid sequence was 81% identical to that of a Japanese pear stylar ribonuclease
Descriptors:flowers. complementary-DNA. gene-mapping. gynoecium. pollen. pollen-germination. restriction-fragment-length-polymorphism. ripening. ribonucleases. fruits. cherries. quantitative-trait-loci. linkage. flowering-date. phenotypic-variation. fruit-crops. biotechnology
Organism Descriptors:Prunus-cerasus. Prunus
Supplemental Descriptors:Prunus. Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000. FF060
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

469. Title:Application of fluorescence-based semi-automated AFLP analysis in barley and wheat
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 545-551
CD Volume:335
Print Article: Pages: 545-551
Author(s):Schwarz G Herz M Huang X Q Michalek W Jahoor A Wenzel G Mohler V
Author Affiliation:Technische Universitat Munchen, Lehrstuhl fur Pflanzenbau und Pflanzenzuchtung, Alte Akademie 12, D-85350 Freising-Weihenstephan, Germany
Language:English
Abstract:Genetic mapping and the selection of closely linked molecular markers for important agronomic traits require efficient, large-scale genotyping methods. A semi-automated multifluorophore technique was applied for genotyping amplified fragment length polmorphism (AFLP) marker loci in barley and wheat. In comparison to conventional 33P-based AFLP analysis, the technique showed a higher resolution of amplicons, thus increasing the number of distinguishable fragments. Automated sizing of the same fragment in different lanes or different gels showed high conformity, allowing subsequent unambigous allele-typing. Simultaneous electrophoresis of different AFLP samples in one lane (multimixing), as well as simultaneous amplification of AFLP fragments with different primer combinations in one reaction (multiplexing), displayed consistent results with respect to fragment number, polymorphic peaks and correct size-calling. The accuracy of semi-automated codominant analysis for hemizygous AFLP markers in an F2 population was too low, proposing the use of dominant allele-typing defaults. Nevertheless, the efficiency of genetic mapping, especially of complex plant genomes, will be accelerated by combining the presented genotyping procedures
Descriptors:barley. wheat. gene-mapping. techniques. automation. genetic-markers. fluorescence. cereals. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Hordeum-vulgare. Triticum-aestivum. Triticum
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum
Subject Codes:FF005. FF020. WW000. ZZ900
Supplementary Info:21 ref
ISSN:0040-5752

Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

470. Title:Parental contribution and coefficient of coancestry among maize inbreds: pedigree, RFLP, and SSR data
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 552-556
CD Volume:335
Print Article: Pages: 552-556
Author(s):Bernardo R Romero Severson J Ziegle J Hauser J Joe L Hookstra G Doerge R W
Author Affiliation:Department of Agronomy, Purdue University, 1150 Lilly Hall of Life Sciences, West Lafayette, IN 47907-1150, USA
Language:English
Abstract:The genetic relationship between inbreds i and j can be estimated from pedigree or from molecular marker data. The objectives of this study were to: (1) determine whether pedigree, restriction fragment length polymorphism (RFLP), and simple sequence repeat (SSR) data give similar estimates of parental contribution and coefficient of coancestry (fij) among a set of maize (Zea mays) inbreds; and (2) compare the usefulness of RFLP and SSR markers for estimating genetic relationship. We studied 13 maize inbreds with known pedigrees. The inbreds were genotyped using 124 RFLP and 195 SSR markers. For each type of marker, parental contributions were estimated from marker similarity among an inbred and both of its parents, and were subsequently used to estimate fij. Estimates of parental contribution differed significantly (alpha <0.05) between pedigree data and either type of marker, but not between the marker systems. The RFLP estimates of parental contribution failed to sum to 1.0, reflecting a higher frequency of non-parental bands with RFLP than with SSR markers. The fij estimated from pedigree, RFLP, and SSR data were highly correlated (r = 0.87-0.97), although significant differences were found among the three sets of fij estimates. We concluded that pedigree and marker data often lead to different estimates of parental contribution and fij, and that SSR markers are superior to RFLP markers for estimating genetic relationship. A relevant question is whether or not the inbreds previously genotyped with an older marker system (e.g., RFLP) need to be re-analysed with a newer marker system (e.g., SSR) for the purpose of estimating genetic relationship. Such re-analysis seems unnecessary if data for the same type of marker are available for a given inbred and both of its parents
Descriptors:maize. restriction-fragment-length-polymorphism. inbred-lines. microsatellites. mathematics. estimation. pedigree. cereals. biotechnology
Organism Descriptors:Zea-mays
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. ZZ100
Supplementary Info:16 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

471. Title:Genetic mapping of the powdery mildew resistance gene Pm6 in wheat by RFLP analysis
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 564-568
CD Volume:335
Print Article: Pages: 564-568
Author(s):Tao W Liu D Liu J Feng Y Chen P

Author Affiliation:Key Open Laboratory of Agriculture Ministry for Crop Cytogenetics, Nanjing Agricultural University, Nanjing, Jiangsu 210095, China
Language:English
Abstract:Pm6 in bread wheat (Triticum aestivum), which was transferred from T. timopheevii, is a gene conferring resistance to the powdery mildew disease caused by Erysiphe graminis f.sp. tritici. Six near-isogenic lines (NILs) of Pm6 in a cultivar 'Prins' background were analysed to map this gene using restriction fragment length polymorphism (RFLP). Each of the six NILs possessed a T. timopheevii-derived segment, varying in length, and associated with powdery mildew resistance. Lines IGV1-465 (FAO163b/7*Prins) and IGV1-467 (Idaed 59B/7*Prins) had the shortest introgressed segments, which were detected only by DNA probes BCD135 and PSR934, respectively. The polymorphic loci detected by both probes were mapped to the long arm of chromosome 2B. Lines IGV1-458 (CI13250/7*Prins) and IGV1-456 (CI12559/8*Prins) contained the longest T. timopheevii segments involving both arms of donor chromosome 2G across the centromere. All these introgressed segments had an overlapping region flanked by the loci xpsr934 and xbcd135 on 2BL. Thus, Pm6 was located in this region since the powdery mildew resistance in all the NILs resulted from the introgressed fragments. Using the F2 mapping population from a cross of IGV1-463 (PI170914/7*Prins) x Prins, Pm6 was shown to be closely linked to the loci xbcd135 and xbcd266 at a genetic distance of 1.6 cM and 4.8 cM, respectively. BCD135 was successfully used in detecting the presence of Pm6 in different genetic backgrounds
Descriptors:gene-mapping. fungal-diseases. restriction-fragment-length-polymorphism. wheat. DNA-probes. plant-diseases. plant-pathogens. plant-pathogenic-fungi. disease-resistance. genes. cereals. biotechnology. plant-pathology
Organism Descriptors:Triticum-aestivum. Erysiphe-graminis. Triticum-timopheevii. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Erysiphe. Erysiphales. Ascomycotina. Eumycota. fungi
Subject Codes:FF005. FF020. WW000. FF610. HH600
Supplementary Info:27 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

472. Title:Genetic linkage mapping in Acacia mangium. 1. Evaluation of restriction endonucleases, inheritance of RFLP loci and their conservation across species
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 576-583
CD Volume:335
Print Article: Pages: 576-583
Author(s):Butcher P A Moran G F Bell R
Author Affiliation:CSIRO Forestry and Forest Products, PO Box E4008, Kingston ACT 2604, Australia
Language:English
Abstract:Random genomic probes were used to assess levels of restriction fragment length polymorphism (RFLP) in two 2-generation outbred pedigrees of Acacia mangium. Probes were evaluated for their ability to detect polymorphic loci in each pedigree and to determine the relative efficiency of different restriction enzymes in revealing polymorphisms. Sixty-two percent of the probes which detected single- or low-copy number sequences revealed polymorphisms with at least one restriction

enzyme. HpaII was the most efficient in detecting polymorphism among first-generation individuals. The recognition sequence of HpaII contains a CpG dimer, suggesting that cytosines in the CpG sequence may be hot spots for mutation in plant genomes, as previously reported in bacterial and mammalian genomes. Mendelian inheritance of 230 loci was demonstrated based on single-locus segregation in second-generation individuals. Less than 5% of loci showed evidence of segregation distortion. The proportion of fully informative loci (15%) was lower than previously reported in eucalypts reflecting the lower level of genetic diversity in A. mangium. The RFLP probes are suitable for the construction of a high-density genetic linkage map in A. mangium. Cross-hybridisation of the A. mangium RFLPs to DNA from species representing the three subgenera of the genus Acacia indicates that these markers could be used in breeding programmes of other diploid acacias, for comparative studies of genome organisation and for phylogenetic studies

Descriptors:inheritance. linkage. gene-mapping. restriction-fragment-length-polymorphism. genetic-diversity. mutations. forest-trees. genetics. tree-breeding. broadleaves. biotechnology

Organism Descriptors:Acacia-mangium

Supplemental Descriptors:Acacia. Mimosoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. WW000. KK100. KK600

Supplementary Info:37 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

473. Title:The use of microsatellites for detecting DNA polymorphism, genotype identification and genetic diversity in wheat

View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 584-592

CD Volume:335

Print Article: Pages: 584-592

Author(s):Prasad M Varshney R K Roy J K Balyan H S Gupta P K

Author Affiliation:Molecular Biology Laboratory, Department of Agricultural Botany, Ch. Charan Singh University, Meerut-250004, India

Language:English

Abstract:A set of 20 wheat microsatellite markers was used with 55 elite wheat genotypes to examine their utility (1) in detecting DNA polymorphism, (2) in the identifying genotypes and (3) in estimating genetic diversity among wheat genotypes. The 55 elite genotypes of wheat used in this study originated in 29 countries representing six continents. A total of 155 alleles were detected at 21 loci using the above microsatellite primer pairs (only 1 primer amplified 2 loci; all other primers amplified 1 locus each). Of the 20 primers amplifying 21 loci, 17 primers and their corresponding 18 loci were assigned to 13 different chromosomes (6 chromosomes of the A genome, 5 chromosomes of the B genome and 2 chromosomes of the D genome). The number of alleles per locus ranged from 1 to 13, with an average of 7.4 alleles per locus. The values of average polymorphic information content (PIC) and the marker index (MI) for these markers were estimated to be 0.71 and 0.70, respectively. The (GT)n microsatellites were found to be the most polymorphic. The genetic similarity (GS) coefficient for all possible 1485 pairs of genotypes ranged from 0.05 to 0.88 with an average of 0.23. The dendrogram, prepared on the basis of similarity matrix using the UPGMA algorithm, delineated the above genotypes into two major clusters (I and II), each with two subclusters (Ia, Ib and IIa, IIb). One of these subclusters (Ib) consisted of a solitary genotype (E3111)

from Portugal, so that it was unique and diverse with respect to all other genotypes belonging to cluster I and placed in subcluster Ia. Using a set of only 12 primer pairs, we were able to distinguish a maximum of 48 of the above 55 wheat genotypes. The results demonstrate the utility of microsatellite markers for detecting polymorphism leading to genotype identification and for estimating genetic diversity
Descriptors:genetic-diversity. microsatellites. genetic-polymorphism. wheat. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:36 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

474. Title:A first interspecific Oryza sativa x Oryza glaberrima microsatellite-based genetic linkage map
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 593-601
CD Volume:335
Print Article: Pages: 593-601
Author(s):Lorieux M Ndjiondjop M N Ghesquiere A
Author Affiliation:IRD, GeneTrop Laboratory, BP 5045, 34032 Montpellier cedex, France
Language:English
Abstract:Oryza glaberrima is an endemic African cultivated rice species. To provide a tool for evaluation and utilisation of the potential of O. glaberrima in rice breeding, we developed an interspecific O. glaberrima x O. sativa genetic linkage map. It was based on PCR markers, essentially microsatellites and sequence-tagged sites. Segregation of markers was examined in a backcross (O. sativa/O. glaberrima//O. sativa) population. Several traits were measured on the BC1 plants, and major genes and quantitative trait loci (QTLs) were mapped for these traits. Several of these genes correspond well to previously identified loci. The overall map length was comparable to those observed in indica x japonica crosses, indicating that recombination between the two species occurs without limitation. However, three chromosomes show discrepancies with the indica x japonica maps. The colinearity with intraspecific maps was very good, confirming previous cytological observations. A strong segregation-distortion hot spot was observed on chromosome 6 near the waxy gene, indicating the presence of s10, a sporo-gametophytic sterility gene previously identified by Sano (1990). The main interests of such a PCR-based map for African rice breeding are discussed, including gene and QTL localisation, marker-assisted selection, and the development of interspecific introgression lines
Descriptors:interspecific-hybridization. linkage. microsatellites. polymerase-chain-reaction. recombination. rice. genetic-markers. gene-mapping. genes. sterility. quantitative-trait-loci. cereals. biotechnology. plant-genetic-resources
Organism Descriptors:Oryza-sativa. Oryza-glaberrima. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:43 ref
ISSN:0040-5752
Year:2000

Journal Title:Theoretical and Applied Genetics
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475. Title:Are mapped markers more useful for assessing genetic diversity?
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 607-613
CD Volume:335
Print Article: Pages: 607-613
Author(s):Virk P S Newbury H J Jackson M T Ford Lloyd B V
Author Affiliation:School of Biological Sciences, University of Birmingham, PO Box 363, Birmingham B15 2TT, UK
Language:English
Abstract:Genetic diversity within populations of organisms and species is commonly measured using molecular-marker data. It has been claimed that more reliable diversity measurements can be obtained using selected genetically mapped markers to ensure that all regions of the genome are represented in the data sets employed. However, this has not been tested. In the present study, using rice (Oryza sativa) as a model species, we have shown that the use of unmapped amplified fragment length polymorphism markers reveals a pattern of diversity that is very similar to that obtained using a range of other marker types and which reflects the known crossability groups within this species. In contrast, we show that use of mapped-marker data can, in some cases, result in highly misleading patterns of diversity; the results obtained are critically related to the choice of parents used in the cross from which the mapping population was produced. For diversity analyses, we propose that it is appropriate to use unmapped markers provided that the marker-type has been shown to have a wide distribution over the genome
Descriptors:gene-mapping. rice. plant-genetic-resources. genetic-markers. genetic-diversity. cereals. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. PP720
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

476. Title:Development of SCAR markers linked to the gene Or5 conferring resistance to broomrape (Orobanche cumana Wallr.) in sunflower
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 625-632
CD Volume:335
Print Article: Pages: 625-632
Author(s):Lu Y H Melero Vara J M Garcia Tejada J A Blanchard P
Author Affiliation:Rustica Prograin Genetique, Unite marquage genetique, 7 rue Hermes, 31520 Ramonville Saint-Agne, France
Language:English
Abstract:A consensus molecular linkage map of 61.9 cM containing the Or5 gene, which confers resistance to race E of broomrape Orobanche cumana, five sequence-characterized amplified region (SCAR) markers (three dominant, two codominant) and one random amplified polymorphic DNA (RAPD) marker were identified based on segregation data scored from two F2 populations of susceptible x resistant sunflower (Helianthus annuus) line crosses. Bulked segregant analysis was carried out to generate the five SCAR markers, while the single RAPD marker in the group was identified from 61 segregating RAPD markers that were directly screened

on one of the two F2 populations. The five SCAR markers, RTS05, RTS28, RTS40, RTS29 and RTS41, were significantly (LODmore than or equal to 4.0) linked to the Or5 gene and mapped separately at 5.6, 13.6, 14.1, 21.4 and 39.4 cM from the Or5 locus on one side, while the RAPD marker, UBC120_660, was found at 22.5 cM (LOD=1.4) on the opposite side. These markers should facilitate the efficient transfer of the resistance gene among sunflower breeding lines. As the first report on molecular markers linked to a broomrape resistance gene, the present work provides a starting point to study other genes and to examine the hypothesis of the clustering of broomrape resistance genes in sunflower
Descriptors:sunflowers. genes. genetic-markers. random-amplified-polymorphic-DNA. resistance. parasitic-weeds. gene-mapping. fatty-oil-plants. oil-plants. biotechnology
Organism Descriptors:Orobanche-cumana. Helianthus-annuus
Supplemental Descriptors:Orobanche. Orobanchaceae. Scrophulariales. dicotyledons. angiosperms. Spermatophyta. plants. Helianthus. Asteraceae. Asterales
Subject Codes:FF005. FF020. WW000. FF500. HH600
Supplementary Info:49 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

477. Title:Estimating genetic diversity of Arabidopsis thaliana ecotypes with amplified fragment length polymorphisms (AFLP)
View Article: Theoretical and Applied Genetics. 2000. 100 (3/4). 633-640
CD Volume:335
Print Article: Pages: 633-640
Author(s):Erschadi S Haberer G Schoniger M Torres Ruiz R A
Author Affiliation:Institut fur Genetik, Technische Universitat Munchen, Lichtenbergstr. 4, 85747 Garching, Germany
Language:English
Abstract:The extensive natural variation of Arabidopsis thaliana ecotypes is being increasingly exploited as a source of variants of genes which control (agronomically) important traits. We have subjected 19 different A. thaliana ecotypes to an analysis using the amplified fragment length polymorphism (AFLP) technique in order to estimate their genetic diversity. The genetic diversity was estimated applying the method of Nei and Li (1979) and a modified version of it, and using 471 informative polymorphisms. The data obtained revealed that within this small set of ecotypes a group of three ecotypes and a further single ecotype exhibit considerable genetic diversity in comparison to the others. These ecotypes clustered at positions significantly separated from the bulk of the ecotypes in the generated similarity plots. The analysis demonstrated the usefulness of the AFLP method for determining intraspecies genetic diversity as exemplified with A. thaliana ecotypes. Results are discussed and compared with data obtained with other methods
Descriptors:ecotypes. genetic-diversity. weeds. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Arabidopsis-thaliana
Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. ZZ380
Supplementary Info:25 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

478. Title:Construction of an improved linkage map of diploid alfalfa (Medicago sativa)
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 641-657
CD Volume:335
Print Article: Pages: 641-657
Author(s):Kalo P Endre G Zimanyi L Csanadi G Kiss G B
Author Affiliation:Institute of Genetics, Biological Research Center of the Hungarian Academy of Sciences, P.O. Box 521, Szeged H-6701, Hungary
Language:English
Abstract:An improved genetic map of diploid (2n = 2x = 16) alfalfa has been developed by analysing the inheritance of more than 800 genetic markers on the F2 population of 137 plant individuals. The F2 segregating population derived from a self-pollinated F1 hybrid individual of the cross Medicago sativa subsp. quasifalcata x M. sativa subsp. coerulea. This mapping population was the same one which had been used for the construction of our previous alfalfa genetic map. The genetic analyses were performed by using maximum-likelihood equations and related computer programs. The improved genetic map of alfalfa in its present form contains 868 markers (four morphological, 12 isozyme, 26 seed protein, 216 RFLP, 608 RAPD and two specific PCR markers) in eight linkage groups. Of the markers, 80 are known genes, including 2 previously cytologically localized genes, the rDNA and the beta - tubulin loci. The genetic map covers 754 centimorgans (cM) with an average marker density of 0.8/cM. The correlation between the physical and genetic distances is about 1000-1300 kilobase pairs per cM. In this map, the linkage relationships of some markers on linkage groups 6, 7, and 8 are different from the previously published one. The cause of this discrepancy was that the genetic linkage of markers displaying distorted segregation (characterized by an overwhelming number of heterozygous individuals) had artificially linked genetic regions that turned out to be unlinked. To overcome the disadvantageous influence of the excess number of heterozygous genotypes on the recombination fractions, we used recently described maximum-likelihood formulas and colour-mapping, which allowed us to exclude the misleading linkages and to estimate the genetic distances more precisely
Descriptors:linkage. computer-software. genes. genetic-markers. gene-mapping. lucerne. fodder-legumes. wide-hybridization. inheritance. segregation-distortion. fodder-plants. biotechnology
Organism Descriptors:Medicago-sativa. Fabaceae. Medicago
Supplemental Descriptors:Medicago. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF007. FF020. WW000
Supplementary Info:74 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

479. Title:Iron accumulation and enhanced growth in transgenic lettuce plants expressing the iron-binding protein ferritin
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 658-664
CD Volume:335
Print Article: Pages: 658-664
Author(s):Goto F Yoshihara T Saiki H
Author Affiliation:Bio-Science Department, Central Research Institute of Electric Power Industry, 1646 Abiko, Abiko-shi, Chiba-ken 270-1194, Japan

Language:English
Abstract:Transgenic lettuce (Lactuca sativa) plants accumulating the iron storage protein ferritin were produced by transformation with Agrobacterium tumefaciens carrying soyabean ferritin cDNA. The integration of the ferritin gene and expression levels in leaves were examined by Southern- and western-blot analysis, respectively. It was shown that transgenic lettuce plants contained iron levels ranging from 1.2 to 1.7 times that of the control plants, however, the manganese content in transgenic lettuce plants was similar to that in the control. Enhanced growth of transgenic lettuces was observed at the early developmental stages, resulting in weights 27-42% greater than those of control plants. Transgenic lettuce had photosynthesis rates superior to those of the controls, and grew larger and faster compared with the controls during the period of 3 months from germination. These results demonstrate the possibility of producing lettuce plants with high yield, high iron content and rapid growth rate
Descriptors:binding-proteins. lettuces. transgenic-plants. growth-rate. iron. manganese. ferritin. genetic-transformation. gene-expression. soyabeans. genetic-engineering. photosynthesis. nutritive-value. vegetables. biotechnology
Organism Descriptors:Lactuca-sativa. Glycine-max. Glycine-(Fabaceae)
Supplemental Descriptors:Lactuca. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants. Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales
Subject Codes:FF003. FF020. WW000. FF061. FF040. QQ050. QQ500
Supplementary Info:31 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

480. Title:Detection of 5S and 25S rRNA genes in Sinapis alba, Raphanus sativus and Brassica napus by double fluorescence in situ hybridization
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 665-669
CD Volume:335
Print Article: Pages: 665-669
Author(s):Schrader O Budahn H Ahne R
Author Affiliation:Federal Centre for Breeding Research on Cultivated Plants, Institute for Breeding Methods in Vegetables, Neuer Weg 22/23, D-06484 Quedlinburg, Germany
Language:English
Abstract:Different ribosomal RNA (5S and 25S) genes were investigated simultaneously by fluorescence in situ hybridization (FISH) in Sinapis alba, Raphanus sativus and Brassica napus. The chromosomes of S. alba carried four 5S and six 25S gene sites, and those of R. sativus four sites of each gene, respectively. These two species have one chromosome pair with both rDNA genes; the two are closely located on a short arm of S. alba, while in R. sativus one is distal on the short arm (5S) and the other more proximal on the long arm (25S). In B. napus we have confirmed 12 sites of 25S rDNA. The detection of 5S rDNA genes revealed 14 signals on 12 chromosomes. Of these, six chromosomes had signals for both rDNA genes. The FISH with 5S rDNA probes detected two sites closely adjacent in four chromosomes of B napus. These results are discussed in relation to a probable homoeologous chromosome pair in B. oleracea
Descriptors:genes. ribosomal-RNA. DNA-hybridization. fatty-oil-plants. rape. oil-plants. biotechnology. radishes
Identifiers:fluorescence in situ hybridization

Organism Descriptors:Brassica-napus. Raphanus-sativus. Sinapis-alba. Brassica-napus-var.-oleifera
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Raphanus. Sinapis. Brassica-napus
Subject Codes:FF005. FF020. WW000
Supplementary Info:25 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

481. Title:A broad exploration of a transgenic population of citrus: stability of gene expression and phenotype
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 670-677
CD Volume:335
Print Article: Pages: 670-677
Author(s):Cervera M Pina J A Juarez J Navarro L Pena L
Author Affiliation:Departamento Proteccion Vegetal y Biotecnologia, Instituto Valenciano de Investigaciones Agrarias (IVIA), Apartado Oficial 46113-Moncada, Valencia, Spain
Language:English
Abstract:A collection of 70 transgenic citrus plants for the uidA (GUS) and nptII [kanamycin kinase] genes have been maintained under screenhouse conditions over a period of 4-5 years. A detailed scanning of the plants allowed us to detect four phenotypic off-type plants and a large variation of transgene integration and expression patterns among the population. Off-type plants were analysed and characterised as nucellar tetraploids, probably originating from tetraploid starting tissues rather than from somaclonal variation events. Transgene integration and expression analyses revealed that: (1) a significant negative correlation was found between copy number and GUS activity; (2) rearrangements of the T-DNA inserts did not imply low expression levels; and (3) stability of integration and expression of the transgenes was confirmed for all the transformants grown under natural environmental conditions. These combined features validate transformation as a tool for the genetic improvement of citrus
Descriptors:gene-expression. transgenic-plants. genes. genetic-transformation. reporter-genes. kinases. fruit-crops. fruits. biotechnology
Identifiers:beta -glucuronidase. kanamycin kinase. selectable markers
Organism Descriptors:Citrus
Supplemental Descriptors:Rutaceae. Sapindales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:40 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

482. Title:AFLP analysis of African cassava (Manihot esculenta Crantz) germplasm resistant to the cassava mosaic disease (CMD)
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 678-685
CD Volume:335
Print Article: Pages: 678-685
Author(s):Fregene M Bernal A Duque M Dixon A Tohme J
Author Affiliation:Biotechnology Research Unit, CIAT, Cali, Colombia
Language:English
Abstract:Amplified fragment length polymorphism (AFLP) was assessed in 20 landraces and nine elite lines of cassava from Africa, resistant and

susceptible to the cassava mosaic disease (CMD). Eleven accessions from a representative core collection from Latin America, previously studied by AFLPs, were included as a reference. AFLP data from all accessions was analysed by both unweighted pair group mean average (UPGMA) and multiple cluster (MCA) analyses. Genetic differentiation between clusters and the coefficient of genetic differentiation was also calculated. Results reveal a genetic divergence between African and Latin American accessions, although some overlap was found between them. African landraces resistant to CMD, were also found to be genetically differentiated from susceptible landraces and from resistant elite lines. AFLP analysis identified a considerable number of duplicates in the African accessions, suggesting a sizeable percentage of redundancy. A unique AFLP fragment, found in a relatively high frequency in African accessions, but absent in the Latin American accessions, was found to be associated with branching pattern by QTL mapping in an F1 progeny derived from African and Latin American parents. The likely source and the utility of the unique AFLP fragment in understanding the processes of genetic divergence in Africa is discussed

Descriptors:cassava. germplasm. landraces. cluster-analysis. statistical-analysis. plant-diseases. plant-pathogens. viral-diseases. disease-resistance. genetic-distance. root-crops. plant-genetic-resources. biotechnology. control. plant-pathology

Geographic Locator:Africa. Latin-America

Identifiers:amplified fragment length polymorphism

Organism Descriptors:Manihot-esculenta. cassava-mosaic-virus. plant-viruses

Supplemental Descriptors:Manihot. Euphorbiaceae. Euphorbiales. dicotyledons. angiosperms. Spermatophyta. plants. miscellaneous-plant-viruses. plant-viruses. viruses. plant-pathogens. pathogens

Subject Codes:FF020. FF005. WW000. FF610. HH600

Supplementary Info:31 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

483. Title:Microsatellite mapping of the induced sphaerococcoid mutation genes in Triticum aestivum

View Article: Theoretical and Applied Genetics. 2000. 100 (5). 686-689

CD Volume:335

Print Article: Pages: 686-689

Author(s):Salina E Borner A Leonova I Korzun V Laikova L Maystrenko O Roder M S

Author Affiliation:Institute of Cytology and Genetics, Lvrentiev ave. 10, Novosibirsk 630090, Russia

Language:English

Abstract:The sphaerococcoid mutation affects a set of characters formed during development. This set includes rigid short culm, straight flag leaf, dense spike, hemispherical glume and small, spherical grains. The S1, S2 and S3 genes of the induced sphaerococcoid mutation in common wheat (Triticum aestivum) were mapped using three different F2 populations consisting of 71-96 individual plants. Twenty-four microsatellite markers from homeologous group 3 of T. aestivum were used to map the S1, S2 and S3 genes on chromosomes 3D, 3B and 3A, respectively. The S1 locus was found to be closely linked to the centromeric marker Xgwm456 of the long arm (2.9 cM) and mapped not far (8.0 cM) from the Xgdm72 marker of the short arm of chromosome 3D. The S2 gene was tightly linked to 2 centromeric markers (Xgwm566, Xgwm845) of chromosome 3B. S3 was located between Xgwm2 (5.1 cM), the marker of the short arm, and Xgwm720 (6.6 cM), the marker of the long arm, both of chromosome 3A.

Mapping the S1, S2 and S3 loci of the induced sphaerococcoid mutation near the centromeric regions supports the hypothesis that the sphaerococcum type may be due to gene duplication resulting from DNA recombination in the centromeric region
Descriptors:genes. gene-mapping. mutations. wheat. chromosomes. plant-development. abnormal-development. plant-morphology. microsatellites. recombination. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060. FF030. FF020. WW000
Supplementary Info:20 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

484. Title:Mapping and genome organization of microsatellite sequences in rice (Oryza sativa L.)
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 697-712
CD Volume:335
Print Article: Pages: 697-712
Author(s):Temnykh S Park W D Ayres N Cartinhour S Hauck N Lipovich L Cho Y G Ishii T McCouch S R
Author Affiliation:Department of Plant Breeding, 252 Emerson Hall, Cornell University, Ithaca, NY 14853-1901, USA
Language:English
Abstract:In order to enhance the resolution of an existing genetic map of rice, and to obtain a comprehensive picture of marker utility and genomic distribution of microsatellites in this important grain species, rice DNA sequences containing simple sequence repeats (SSRs) were extracted from several small-insert genomic libraries and from the database. Some 188 new microsatellite markers were developed and evaluated for allelic diversity. The new simple sequence length polymorphisms (SSLPs) were incorporated into the existing map previously containing 124 SSR loci. The 312 microsatellite markers reported here provide whole-genome coverage with an average density of one SSLP per 6 cM. In this study, 26 SSLP markers were identified in published sequences of known genes, 65 were developed based on partial cDNA sequences available in GenBank, and 97 were isolated from genomic libraries. Microsatellite markers with different SSR motifs are relatively uniformly distributed along rice chromosomes regardless of whether they were derived from genomic clones or cDNA sequences. However, the distribution of polymorphism detected by these markers varies between different regions of the genome
Descriptors:genomes. rice. complementary-DNA. microsatellites. genetic-polymorphism. genetic-markers. gene-mapping. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:43 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

485. Title:Diversity of microsatellites derived from genomic libraries and GenBank sequences in rice (Oryza sativa L.)

View Article: Theoretical and Applied Genetics. 2000. 100 (5). 713-722
CD Volume:335
Print Article: Pages: 713-722
Author(s):Cho Y G Ishii T Temnykh S Chen X Lipovich L McCouch S R Park W D Ayres N Cartinhour S
Author Affiliation:Department of Plant Breeding, 252 Emerson Hall, Cornell University, Ithaca, NY 14853-1901, USA
Language:English
Abstract:The growing number of rice microsatellite markers warrants a comprehensive comparison of allelic variability between the markers developed using different methods, with various sequence repeat motifs, and from coding and non-coding portions of the genome. We have performed such a comparison over a set of 323 microsatellite markers; 194 were derived from genomic library screening and 129 were derived from the analysis of rice-expressed sequence tags (ESTs) available in public DNA databases. We have evaluated the frequency of polymorphism between parental pairs of six inter-subspecific crosses and one interspecific cross widely used for mapping in rice. Microsatellites derived from genomic libraries detected a higher level of polymorphism than those derived from ESTs contained in the GenBank database (83.8% versus 54.0%). Similarly, the other measures of genetic variability (the number of alleles per locus, polymorphism information content and allele size ranges) were all higher in genomic library-derived microsatellites than in their EST-database counterparts. The highest overall degree of genetic diversity was seen in GA-containing microsatellites of genomic library origin, while the most conserved markers contained CCG- or CAG-trinucleotide motifs and were developed from GenBank sequences. Preferential location of specific motifs in coding versus non-coding regions of known genes was related to observed levels of microsatellite diversity. A strong positive correlation was observed between the maximum length of a microsatellite motif and the standard deviation of the molecular-weight of amplified fragments. The reliability of molecular weight standard deviation as an indicator of genetic variability of microsatellite loci is discussed
Descriptors:microsatellites. rice. genetic-variation. genomes. genetic-polymorphism. genetic-markers. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:35 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

486. Title:Analysis of SSRs derived from grape ESTs
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 723-726
CD Volume:335
Print Article: Pages: 723-726
Author(s):Scott K D Eggler P Seaton G Rossetto M Ablett E M Lee L S Henry R J
Author Affiliation:Centre for Plant Conservation Genetics, PO Box 157, Southern Cross University, Lismore, NSW 2480, Australia
Language:English
Abstract:Some 124 microsatellites were isolated from analysis of 5000 Vitis expressed sequence tags (ESTs). A diversity of dinucleotide and trinucleotide simple sequence repeat (SSR) motifs were present. Primers were designed for 16 of these SSRs and they were tested on seven accessions. Ten of the sixteen primer pairs resulted in PCR

products of the expected size. All ten functional primers were polymorphic across the accessions studied. Polymorphisms were evident at the level of cultivars, Vitis species, and between related genera. SSRs that were from the 3' untranslated region (UTR) were most polymorphic at the cultivar level, the 5' UTR SSRs were most polymorphic between cultivars and species, and those SSRs within coding sequence were most polymorphic between species and genera. These results show that EST-derived SSRs in Vitis are useful as they are polymorphic and highly transferable. With EST SSRs being applicable to studies at several taxonomic levels, the large number of SSRs (approximately 1000) that will be available from an expanded EST database of 45 000 will have many potential applications in mapping and identity research

Descriptors:microsatellites. grapes. genetic-polymorphism. taxonomy. fruit-crops. fruits. biotechnology

Organism Descriptors:Vitis. Vitis-vinifera

Supplemental Descriptors:Vitidaceae. Rhamnales. dicotyledons. angiosperms. Spermatophyta. plants. Vitis

Subject Codes:FF003. FF020. WW000. ZZ380

Supplementary Info:12 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

487. Title:Molecular mapping of a rice gene conditioning thermosensitive genic male sterility using AFLP, RFLP and SSR techniques

View Article: Theoretical and Applied Genetics. 2000. 100 (5). 727-734

CD Volume:335

Print Article: Pages: 727-734

Author(s):Dong N V Subudhi P K Luong P N Quang V D Quy T D Zheng H G Wang B Nguyen H T

Author Affiliation:Molecular Biology Laboratory, Agricultural Genetics Institute, Tulieum, Hanoi, Vietnam

Language:English

Abstract:The discovery and application of the thermosensitive genic male sterility (TGMS) system has great potential for revolutionizing hybrid seed production technology in rice. An F2 population developed from a cross between a TGMS indica mutant, TGMS-VN1, and a fertile indica line, CH1, was used to identify molecular markers linked to the TGMS gene and to subsequently determine its chromosomal location on the linkage map of rice. Bulk segregant analysis was performed using the AFLP technique. From the survey of 200 AFLP primer combinations, four AFLP markers (E2/M5-600, E3/M16-400, E5/M12-600, and E5/M12-200) linked to the TGMS gene were identified. All the markers were linked to the gene in the coupling phase. All except E2/M5-200 were found to be low-copy sequences. However, the marker E5/M12-600 showed polymorphism in RFLP analysis and was closely linked to the TGMS gene at a distance of 3.3 cM. This marker was subsequently mapped on chromosome 2 using doubled-haploid mapping populations derived from the crosses IR64 x Azucena and CT9993 x IR62666. Linkage of microsatellite marker RM27 with the TGMS gene further confirmed its location on chromosome 2. The closest marker, E5/M12-600, was sequenced so that a PCR marker can be developed for the marker-assisted transfer of this gene to different genetic backgrounds. The new TGMS gene is tentatively designated as tms4(t)

Descriptors:male-sterility. gene-mapping. restriction-fragment-length-polymorphism. rice. mutants. polymerase-chain-reaction. genetic-markers. microsatellites. temperature. genes. cereals. biotechnology

Identifiers:amplified fragment length polymorphism
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060. WW000. FF020
Supplementary Info:25 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

488. Title:A- or C-chromosomes, does it matter for the transfer of transgenes from Brassica napus
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 750-754
CD Volume:335
Print Article: Pages: 750-754
Author(s):Tomiuk J Hauser T P Bagger Jorgensen R
Author Affiliation:Department of Plant Biology and Biogeochemistry, Riso National Laboratory, P.O. Box 49, DK-4000 Roskilde, Denmark
Language:English
Abstract:Introgression of genes from allotetraploid Brassica napus into its diploid wild relative B. rapa [B. campestris] is generally considered to be inevitable. As a means to minimize a potential ecological risk in environments where B. rapa is growing, the insertion of transgenes into chromosome regions of B. napus with a very low probability of transfer to backcross generations with B. rapa has been proposed. Recently, the progeny of four backcross generations between transgenic herbicide-tolerant B. napus and B. rapa was studied in selection experiments (Theoretical and Applied Genetics (1997) 95, 442-450). The rapid decrease in the frequency of herbicide-tolerant plants was explained by selection against the C-chromosomes of B. napus in favour of the homeologous A-chromosomes. Obviously, such C-chromosomes could be potential candidates as safe integration sites for transgenes. We considered these safety aspects using a simple population genetic model. Theory and experiments, however, do not favour the chromosomes of B. napus as safe candidates with respect to the introgression of transgenes into wild populations of B. rapa
Descriptors:chromosomes. gene-transfer. gene-flow. biosafety. transgenic-plants. interspecific-hybridization. herbicide-resistance. population-genetics. rape. genetic-transformation. weeds. fatty-oil-plants. oil-plants. biotechnology. plant-genetic-resources
Organism Descriptors:Brassica-campestris. Brassica-napus. Brassica-napus-var.-oleifera
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica-napus
Subject Codes:FF005. FF020. WW000. FF500. HH410
Supplementary Info:20 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

489. Title:Expression of active barley seed ribosome-inactivating protein in transgenic wheat
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 755-763
CD Volume:335
Print Article: Pages: 755-763
Author(s):Bieri S Potrykus I Futterer J

Author Affiliation:Institute of Plant Sciences, ETH Zurich, Universitatsstrasse 2, CH 8092 Zurich, Switzerland
Language:English
Abstract:Phenotypically normal, transgenic wheat (Triticum aestivum, cv. Frisal) plants expressing a barley seed ribosome-inactivating protein (RIP) were produced. Expression was controlled by an intron-enhanced cauliflower mosaic virus 35S promoter and has been completely stable over four generations so far, possibly due to matrix-associated regions (MARs) that flank the transgenes. An engineered fusion to a signal peptide derived from the barley seed beta -1,3-glucanase caused the transport of RIP to the apoplast. Activity of the accumulated protein could be shown by significant inhibition of a rabbit reticulocyte transcription/translation system. Plants expressing high levels of RIP were protected only moderately or not at all against infection by the fungal pathogen Erysiphe graminis
Descriptors:barley. transgenic-plants. wheat. plant-pathogens. plant-pathogenic-fungi. plant-diseases. ribosome-inactivating-proteins. genetic-transformation. gene-expression. genetic-engineering. cereals. biotechnology
Organism Descriptors:Hordeum-vulgare. Triticum-aestivum. Erysiphe-graminis. Triticum
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum. Erysiphe. Erysiphales. Ascomycotina. Eumycota. fungi
Subject Codes:FF005. FF020. WW000
Supplementary Info:50 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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490. Title:An analysis of genetic diversity in coconut (Cocos nucifera) populations from across the geographic range using sequence-tagged microsatellites (SSRs) and AFLPs
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 764-771
CD Volume:335
Print Article: Pages: 764-771
Author(s):Teulat B Aldam C Trehin R Lebrun P Barker J H A Arnold G M Karp A Baudouin L Rognon F
Author Affiliation:Burotrop, Agropolis International, Avenue Agropolis, 34394 Montpellier, Cedex 5, France
Language:English
Abstract:Genetic diversity in 31 individuals from 14 coconut populations across the entire geographic range (2-3 individuals per population) was assessed using sequence-tagged microsatellites (or simple sequence repeats, SSRs) and amplified fragment length polymorphism (AFLP). From the 39 SSR primer sets tested, only two gave patterns that could not be scored and used in the data analysis. The remainder included five SSRs that gave double-locus profiles in which one locus could still be scored separately. The 37 SSRs revealed between 2 and 16 alleles per locus and a total of 339 alleles in the 14 populations. Gene diversity (D = 1- SIGMA pi2) ranged from 0.47 to 0.90. Two of the four Dwarf populations were homozygous at all 37 loci, which is consistent with their autogamous (self-fertilising) reproduction. One Dwarf population was heterozygous at one locus but the other (Niu Leka Dwarf), which is known to be cross-pollinating, showed high levels of heterozygosity. Generally, diversity was higher in populations from the South Pacific and South East Asia. Three SSR loci (CNZ46, CN2A5, CN11E6) gave distinct genotypes for all but two populations. The East African

populations had higher heterozygosities than those from West Africa, and the populations from Tonga and Fiji generally had distinct alleles from those of the South Pacific. AFLP analysis with 12 primer combinations gave a total of 1106 bands, of which 303 were polymorphic (27%). Similarity matrices were constructed from the two data sets using the proportion of shared alleles for SSRs and a Jaccard coefficient for AFLPs. In each case cluster and principal coordinates analyses were performed, with the resultant dendrograms and plots revealing similar relationships among the populations for both approaches. There was generally a good separation of populations, and phenetic relationships were in agreement with those previously shown by RFLPs. The use of SSRs and AFLPs in genetic-diversity analysis for the establishment of germplasm collections is discussed
Descriptors:coconuts. genetic-diversity. microsatellites. heterozygosity. genetic-polymorphism. cluster-analysis. principal-component-analysis. fatty-oil-plants. oil-plants. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Cocos-nucifera
Supplemental Descriptors:Cocos. Arecaceae. Arecales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:23 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

491. Title:Differential accumulation of the S-adenosylmethionine decarboxylase transcript in rice seedlings in response to salt and drought stresses
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 782-788
CD Volume:335
Print Article: Pages: 782-788
Author(s):Li Z Y Chen S Y
Author Affiliation:Laboratory of Plant Biotechnology, Institute of Genetics, Chinese Academy of Sciences, Beijing 100101, China
Language:English
Abstract:Differences in gene expression between salinity-stressed and normally grown rice seedlings were compared by using the differential display (DD) technique. One DD-derived cDNA clone was characterized as a partial sequence of the rice S-adenosylmethionine decarboxylase (SAMDC) gene by sequence analysis and a homology search of GenBank databases. The full-length cDNA for the rice SAMDC gene, designated SAMDC1 (GenBank accession no. AF067194), was further isolated by the RT-PCR approach and was found to be different from another rice SAMDC gene released in GenBank. Comparison of the deduced polypeptide of SAMDC1 with SAMDC proteins from other plant species revealed several homologous regions, in particular the conserved proenzyme cleavage site and the putative PEST domain. Southern blot analysis indicated that the SAMDC1 gene was present as a single-copy sequence in the rice genome. Northern hybridization showed that the transcript of SAMDC1 was differentially accumulated in rice seedlings in response to salinity, drought and exogenous abscisic acid stresses. Furthermore, levels of the SAMDC1 transcript under saline conditions were compared between a salt-tolerant japonica rice variety, Lansheng, and a salt-sensitive japonica rice variety, 77-170. It was observed that elevation in the level of the SAMDC1 transcript occurred earlier in Lansheng than in 77-170 when both were affected by salinity stress. In addition, relative to the control, higher levels of the SAMDC1 transcript were detected in Lansheng under low salt conditions or salt-stressed for shorter times,

and also in 77-170 under high salt conditions or salt-stressed for prolonged times. The results suggest that expression of the SAMDC1 gene in seedlings is positively correlated with the salt tolerance of rice
Descriptors:rice. complementary-DNA. characterization. gene-expression. DNA-hybridization. salinity. salt-tolerance. stress. genes. nucleotide-sequences. adenosylmethionine-decarboxylase. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. FF900
Supplementary Info:31 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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492. Title:Genetic analysis of temperature-sensitive male sterility in rice
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 794-801
CD Volume:335
Print Article: Pages: 794-801
Author(s):Reddy O U K Siddiq E A Sarma N P Ali J Hussain A J Nimmakayala P Ramasamy P Pammi S Reddy A S
Author Affiliation:Crop Biotechnology Center, Texas A & M University, College Station, TX-77843-2123, USA
Language:English
Abstract:The present study of genetic analysis is an attempt to precisely characterize diverse temperature-sensitive genic male-sterile (TGMS) lines so as to explore the possibilities of utilizing the most promising in large-scale hybrid seed production. Genetical studies revealed that the TGMS segregants derived from crosses involving TGMS lines ID24 and SA2 expressed differential fertility levels at low-temperature conditions. A majority of these progenies expressed transgressive segregation towards either sterility of fertility, causing instability of sterility and low reversibility of fertility which may be due to large numbers of single-locus QTLs and their epistatic interactions. We identified two putative genes imparting temperature-sensitive male sterility after observing crosses involving diverse TGMS sources. To identify suitable molecular markers closely linked to the trait we used RAPD, AFLP and microsatellites which generated polymorphism through bulked segregant analysis. AFLP analysis using a smaller genome kit resulted in enormous polymorphism, out of which the combination EAA/MCAG amplified a 330-bp fragment, which closely segregated with the gene at a distance of 5.3 cM. This fragment was eluted for cloning and from the sequence a STS primer (TS200) was developed which produced a dominant polymorphism specific to TGMS. The microsatellite RM257, located earlier on chromosome 9, was linked with the TGMS trait in SA2 at a distance of 6.2 cM. RM257 produced a codominant polymorphism with 145-bp (sterile) and 132-bp (fertile) products. Both individually and collectively, the markers TS200 and RM257 located on either side of the TGMS locus are very useful for marker-assisted selection
Descriptors:rice. male-sterility. microsatellites. temperature. restriction-fragment-length-polymorphism. genetic-markers. genetics. gene-mapping. cereals. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF020. FF060. WW000
Supplementary Info:24 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

493. Title:Cytosine deaminase as a substrate-dependent negative selectable marker in Brassica napus
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 802-809
CD Volume:335
Print Article: Pages: 802-809
Author(s):Babwah A V Waddell C S
Author Affiliation:McGill University, Department of Biology, 1205 Dr. Penfield Avenue, Montreal, Quebec H3A 1B1, Canada
Language:English
Abstract:The enzyme cytosine deaminase, encoded by the codA gene, catalyses the deamination of the non-toxic compound 5-fluorocytosine (5-FC) to the highly toxic compound 5-fluorouracil (5-FU). Cytosine deaminase activity is not found in higher plants and Brassica napus seedlings are unaffected by the presence of 5-FC in the growth medium. In codA-transformed B. napus seedlings, expression of cytosine deaminase results in a reduction of root and hypocotyl lengths, and a severe suppression of true leaf development. This phenotype is dependent on the presence of the 5-FC substrate and no effects are seen in plants grown in the absence of the substrate or in sibling plants lacking the transgene. The codA transformants have been assessed over three generations of growth and in each generation the transgene is stably inherited and confers the same 5-FC-sensitive phenotype. Transfer of 5-FC-sensitive seedlings to soil results in the restoration of normal growth in up to 100% of the seedlings. These results indicate that codA is a versatile dominant marker gene that can be used effectively in B. napus for substrate-dependent negative selection
Descriptors:inheritance. plant-development. marker-genes. seedlings. genetic-transformation. gene-expression. transgenic-plants. selection. amidine-hydrolases. rape. fatty-oil-plants. oil-plants. biotechnology
Identifiers:selectable markers. cytosine deaminase
Organism Descriptors:Brassica-napus. Brassica-napus-var.-oleifera
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica-napus
Subject Codes:FF020. WW000. FF005
Supplementary Info:25 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

494. Title:Improved resistance to bacterial soft rot by protoplast fusion between Brassica rapa and B. oleracea
View Article: Theoretical and Applied Genetics. 2000. 100 (5). 810-819
CD Volume:335
Print Article: Pages: 810-819
Author(s):Ren J P Dickson M H Earle E D
Author Affiliation:Department of Horticultural Sciences, New York State Agricultural Experimental Station, Geneva, NY 14456, USA
Language:English
Abstract:Erwinia soft rot (E. carotovora subsp. carotovora) is a destructive disease of Brassica rapa subsp. pekinensis [B. pekinensis] vegetables. Reliable sources of resistance and control methods are limited, so

development of highly resistant breeding lines is desirable. Protoplasts from B. rapa and B. oleracea (broccoli and cauliflower) genotypes selected for resistance to soft rot were fused in order to combine different sources of resistance. Twelve somatic hybrids (synthetic B. napus) were obtained and confirmed by morphology, nuclear DNA content, and RAPD analysis. They were normal looking plants that easily set seeds following self-pollination and backcrossing to B. rapa. Assays of detached leaves or seedlings inoculated in a mist-chamber showed that most somatic hybrids had lower disease severity ratings than the B. rapa fusion partner and a commercial variety of B. napus. Some progeny from selfing or backcrossing of somatic hybrids to B. rapa showed much more resistance than either fusion partner. The offspring populations of the somatic hybrids (F1-S1 and F1-BC1) clearly moved to the resistant direction compared to the parents; the percentage of resistant plants increased from 21% (average of parents) to 36% (F1-S1) and 48% (F1-BC1). These results suggest that it may be possible to obtain highly resistant B. rapa lines by further backcrossing and selection

Descriptors:Chinese-cabbages. cauliflowers. broccoli. protoplast-fusion. interspecific-hybridization. somatic-hybridization. plant-pathogens. plant-diseases. bacterial-diseases. plant-pathogenic-bacteria. disease-resistance. vegetables. biotechnology. control. plant-pathology

Organism Descriptors:Brassica-oleracea-var.-botrytis. Brassica-oleracea-var.-italica. Brassica-pekinensis. Erwinia-carotovora-subsp.-carotovora. Brassica. Brassica-oleracea

Supplemental Descriptors:Brassica-oleracea. Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Erwinia-carotovora. Erwinia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes

Subject Codes:FF003. FF170. WW000. FF020

Supplementary Info:25 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

495. Title:AFLP and CAPS linkage maps of Cryptomeria japonica

View Article: Theoretical and Applied Genetics. 2000. 100 (6). 825-831

CD Volume:335

Print Article: Pages: 825-831

Author(s):Nikaido A M Ujino T Iwata H Yoshimura K Yoshimura H Suyama Y Murai M Nagasaka K Tsumura Y

Author Affiliation:Genetics Section, Bio-resources Technology Division, Forestry and Forest Products Research Institute, Kukizaki, Ibaraki 305-8687, Japan

Language:English

Abstract:Two DNA marker systems, AFLP and cleaved amplified polymorphic sequences (CAPS), were used in a two-way pseudo-testcross strategy applied to an F1 population to construct genetic linkage maps of two local sugi cultivars. The AFLP markers detected about eight polymorphisms per parent per primer combination. Using 38 primer combinations, 612 AFLPs were detected in 'Haara 4' and 'Kumotooshi', of which 305 segregated in a 1:1 ratio (P>0.05). A total of 91 markers (83 AFLP and 8 CAPS) in 'Haara 4' and 132 (123 AFLP and 9 CAPS) in 'Kumotooshi' were distributed among 19 and 23 linkage groups, respectively, each of which included 2-17 markers. Maps of 'Haara 4' and 'Kumotooshi' spanned 1266.1 cM and 1992.3 cM, and covered approximately 50% and 80% of the sugi genome, respectively. Sequences

derived from cDNA, which were previously used to construct a sugi linkage map, were also placed on these linkage maps as CAPS markers. Where a 'two-way pseudo-testcross' is used, more than half of the sugi CAPS developed can be used to construct linkage maps for each parental family. The saturation of mapped markers, and the integration of several linkage maps derived from different mapping populations, is anticipated in the near future
Descriptors:linkage. complementary-DNA. cultivars. DNA. genomes. gene-mapping. forest-trees. biotechnology
Identifiers:amplified fragment length polymorphism. cleaved amplified polymorphic sequences
Organism Descriptors:Cryptomeria. Cryptomeria-japonica
Supplemental Descriptors:Taxodiaceae. Pinopsida. gymnosperms. Spermatophyta. plants. Cryptomeria
Subject Codes:FF020. WW000. KK100
Supplementary Info:25 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

496. Title:Agrobacterium-mediated engineering for sheath blight resistance of indica rice cultivars from different ecosystems
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 832-839
CD Volume:335
Print Article: Pages: 832-839
Author(s):Datta K Koukolikova Nicola Z Baisakh N Oliva N Datta S K
Author Affiliation:Plant Breeding, Genetics and Biochemistry Division, International Rice Research Institute, MCPO Box 3127, 1271 Makati City, Philippines
Language:English
Abstract:A concise T-DNA element was engineered containing the rice class-I chitinase gene expressed under the control of CaMV35S and the hygromycin phosphotransferase gene (hph) as a selectable marker. The binary plasmid vector pNO1 with the T-DNA element containing these genes of interest was mobilized to Agrobacterium tumefaciens strain LBA4404 to act as an efficient donor of T-DNA in the transformation of three different indica rice cultivars from different ecosystems. Many morphologically normal, fertile transgenic plants from these rice cultivars were generated after Agrobacterium-mediated transformation using 3-week-old scutella calli as initial explants. Stable integration, inheritance and expression of the chimaeric chitinase gene were demonstrated by Southern blot and western blot analysis of the transformants. Bioassay data showed that transgenic plants can restrict the growth of the sheath blight pathogen Rhizoctonia solani. Bioassay results were correlated with the molecular analysis. Although similar results were obtained upon DNA-mediated transformation, this report shows the potential of the cost-effective, simple Agrobacterium system for genetic manipulation of rice cultivars with a pathogenesis-related (PR) gene
Descriptors:cultivars. ecosystems. rice. bioassays. chitinase. explants. genes. genetic-engineering. inheritance. genetic-transformation. transgenic-plants. southern-blotting. gene-expression. genetic-vectors. plant-pathogens. plant-pathogenic-fungi. plant-diseases. disease-resistance. varietal-reactions. fungal-diseases. cereals. biotechnology. plant-pathology
Identifiers:selectable markers. hygromycin phosphotransferase
Organism Descriptors:Oryza-sativa. Agrobacterium. Agrobacterium-tumefaciens. Rhizoctonia-solani. Oryza

Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Agrobacterium. Rhizoctonia. Deuteromycotina. Eumycota. fungi
Subject Codes:FF020. WW000. FF005. FF610. HH600
Supplementary Info:47 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

497. Title:Genomic regions affecting seed shattering and seed dormancy in rice
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 840-846
CD Volume:335
Print Article: Pages: 840-846
Author(s):Cai H W Morishima H
Author Affiliation:National Institute of Genetics, Mishima, 411-8540, Japan
Language:English
Abstract:Non-shattering of the seeds and reduced seed dormancy were selected consciously and unconsciously during the domestication of rice, as in other cereals. Both traits are quantitative and their genetic bases are not fully elucidated, though several genes with relatively large effects have been identified. In the present study, attempts were made to detect genomic regions associated with shattering and dormancy using 125 recombinant inbred lines obtained from a cross between cultivated (Taiwanese indica cv. Pei-kuh) and wild rice strains (Oryza rufipogon line W1944). A total of 147 markers were mapped on 12 rice chromosomes, and QTL analysis was performed by simple interval mapping and composite interval mapping. For seed shattering, two methods revealed the same four QTLs. On the other hand, for seed dormancy a number of QTLs were estimated by the two methods. Based on the results obtained with the intact and de-hulled seeds, QTLs affecting hull-imposed dormancy and kernel dormancy, respectively, were estimated. Some QTLs detected by simple interval mapping were not significant by composite interval mapping, which reduces the effects of residual variation due to the genetic background. Several chromosomal regions where shattering QTLs and dormancy QTLs are linked with each other were found. This redundancy of QTL associations was explained by "multifactorial linkages" followed by natural selection favouring these two co-adapted traits
Descriptors:rice. interspecific-hybridization. seed-dormancy. seed-shattering. cereals. chromosomes. genes. gene-mapping. natural-selection. seeds. shedding. domestication. inbred-lines. quantitative-traits. biotechnology. plant-genetic-resources
Organism Descriptors:Oryza-sativa. Oryza-rufipogon. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. ZZ380. WW000. FF060
Supplementary Info:34 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

498. Title:Transfer of amiprophosmethyl resistance from a Nicotiana plumbaginifolia mutant by somatic hybridisation
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 847-857
CD Volume:335
Print Article: Pages: 847-857

Author(s):Yemets A I Kundel'chuk O P Smertenko A P Solodushko V G Rudas V A Gleba Yu Yu Blume Ya B
Author Affiliation:Institute of Cell Biology and Genetic Engineering, National Academy of Sciences of Ukraine, Acad. Zabolotny Street 148, Kiev GSP-22, 252650, Ukraine
Language:English
Abstract:Transfer of resistance to the phosphorothioamidate herbicide, amiprophosmethyl [amiprofos-methyl] (APM), from the beta -tubulin mutant of Nicotiana plumbaginifolia to the interspecific N. plumbaginifolia (+) N. sylvestris and to the intertribal N. plumbaginifolia (+) Atropa belladonna somatic hybrids has been demonstrated. Transfer to the recipient species was accomplished by: (1) symmetric hybridization and (2) asymmetric hybridization using gamma -irradiation of donor protoplasts. Cytogenetic analysis confirmed the hybrid origin of the hybrids obtained. It was established that most of them typically inherited no more than three donor chromosomes, although it was possible to obtain symmetric hybrids in the case of symmetric fusion. Immunofluorescence microscopy analysis has shown that protoplasts of the mutant, and of the N. plumbaginifolia (+) N. sylvestris and N. plumbaginifolia (+) A. belladonna hybrids, retained the normal structure of interphase microtubule (MT) arrays and mitotic figures after treatment with 5 micro M APM, whereas MTs of protoplasts of the recipients were destroyed under these conditions. It was also shown that hybrid clones contained an altered beta -tubulin isoform originating from the N. plumbaginifolia mutant. The selected hybrid clones were characterized by cross-resistance to trifluralin, a dinitroaniline herbicide with the same mode of anti-MT action. Some of the somatic hybrids which could flower were fertile. It was established that seeds of some fertile hybrids were able to germinate in the presence of 5 micro M APM. The results obtained thus support the conclusion that the technique of somatic hybridization, especially asymmetric fusion, can be used to transfer APM resistance from the N. plumbaginifolia mutant to different (related and remote) plant species of the Solanaceae, including important crops
Descriptors:somatic-hybridization. mutants. intergeneric-hybridization. chromosomes. clones. flowers. herbicides. hybrids. inheritance. interspecific-hybridization. protoplasts. seeds. trifluralin. amiprofos-methyl. tubulin. gamma-radiation. irradiation. chromosome-pairing. mitosis. protoplast-fusion. mutations. chromosome-translocation. herbicide-resistance. stimulant-plants. biotechnology. plant-genetic-resources
Organism Descriptors:Nicotiana-sylvestris. Nicotiana-plumbaginifolia. Atropa-belladonna. Atropa. Solanaceae
Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Atropa
Subject Codes:FF020. FF003. WW000. FF170. HH410
Supplementary Info:35 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

499. Title:Microsatellite analysis of maternal half-sib families of Quercus robur, pedunculate oak: II. inferring the number of pollen donors from the offspring
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 858-865
CD Volume:335
Print Article: Pages: 858-865

Author(s):Lexer C Heinze B Gerber S Macalka Kampfer S Steinkellner H Kremer A Glossl J
Author Affiliation:Zentrum fur Angewandte Genetik, Universitat fur Bodenkultur Wien, Muthgasse 18, A-1190 Vienna, Austria
Language:English
Abstract:An approach is presented to infer the number of pollen donors directly from genotype data of open-pollinated progeny of Quercus robur (pedunculate oak), a highly outcrossing tree species. The approach is based on closely linked, highly polymorphic codominant microsatellite markers. Initially the close linkages between three previously mapped microsatellite loci were confirmed by studies of linkage disequilibrium (LD). Then an approach to track the pollen donors contributing to maternal half-sib families (open-pollinated families) was developed by analysing haplotype arrays of closely linked microsatellite markers transmitted from the fathers to the progeny. Simulated data of five linked microsatellite loci segregating in eight open-pollinated families were used to study the relationship between the number of paternal chromosomes detected by this "haplotype approach" and the number of diploid fathers contributing to the families. The results showed that the number of diploid pollen donors can be expressed as an exponential function of the number of paternal chromosomes inferred from the progeny. The 95% confidence interval of this regression function is used to determine the minimum number of fathers contributing to a genotyped open-pollinated family of Quercus robur. Finally this open-pollinated family is used to demonstrate the resolution obtained with the "haplotype approach". Six independent microsatellite loci were used to study relatedness among all pairs of pollen gametes that share a haplotype of three linked markers. The results suggest that the majority of such gametes are identical by descent from the same father. The "haplotype approach" presented here can be used to monitor the number of contributing pollen donors in commercial seedlot samples from oak or any other outcrossing tree species for which closely linked, highly polymorphic, codominant genetic markers are available
Descriptors:pollen. chromosomes. genetic-markers. genotypes. linkage. outcrossing. paternal-effects. microsatellites. gene-mapping. forest-trees. tree-breeding. broadleaves. biotechnology
Organism Descriptors:Quercus. Quercus-robur
Supplemental Descriptors:Fagaceae. Fagales. dicotyledons. angiosperms. Spermatophyta. plants. Quercus
Subject Codes:FF020. KK100. WW000
Supplementary Info:29 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

500. Title:Genetic mapping of the Lablab purpureus genome suggests the presence of 'cuckoo' gene(s) in this species
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 866-871
CD Volume:335
Print Article: Pages: 866-871
Author(s):Konduri V Godwin I D Liu C J
Author Affiliation:School of Land and Food, University of Queensland, St. Lucia, Qld. 4072, Australia
Language:English
Abstract:A linkage map of Lablab purpureus consisting of 127 RFLP and 91 RAPD loci was constructed in an F2 population of 119 individuals. This population was derived from a cross between 'Rongai' (an annual

cultivar) and CPI 24973 (a perennial wild accession). The map comprises 17 linkage groups and covers 1610 centiMorgans (cM) with an average distance of 7 cM between markers. Severe segregation distortions were observed, with the very extreme situation where no paternal type was recovered from the mapping population. These results strongly suggest the presence of a gene conferring preferential transmission from the maternal parent 'Rongai'. It was also clear that, while the majority of RAPD markers are valuable when used together with RFLP or other stringent marker systems, they could be problematic when used solely in mapping exercises

Descriptors:genes. genomes. gene-mapping. linkage. restriction-fragment-length-polymorphism. maternal-effects. random-amplified-polymorphic-DNA. grain-legumes. plant-genetic-resources. biotechnology

Organism Descriptors:Lablab. Lablab-purpureus. Fabaceae

Supplemental Descriptors:Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Lablab

Subject Codes:FF020. FF005. WW000

Supplementary Info:21 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

501. Title:Association of transgene integration sites with chromosome rearrangements in hexaploid oat

View Article: Theoretical and Applied Genetics. 2000. 100 (6). 872-880

CD Volume:335

Print Article: Pages: 872-880

Author(s):Svitashev S Ananiev E Pawlowski W P Somers D A

Author Affiliation:Department of Agronomy and Plant Genetics, University of Minnesota, 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

Language:English

Abstract:Transgene loci in 16 transgenic oat (Avena sativa) lines produced by microprojectile bombardment were characterized using phenotypic and genotypic segregation, Southern blot analysis, and fluorescence in situ hybridization (FISH). Twenty-five transgene loci were detected; 8 lines exhibited single transgene loci and 8 lines had 2 or 3 loci. Double FISH of the transgene and oat C- and A/D-genome-specific dispersed and clustered repeats showed no preferences in the distribution of transgene loci among the highly heterochromatic C genome and the A/D genomes of hexaploid oat, nor among chromosomes within the genomes. Transgene integration sites were detected at different locations along individual chromosomes, although the majority of transformants had transgenes integrated into subtelomeric and telomeric regions. Transgene integration sites exhibited different levels of structural complexity, ranging from simple integration structures of two apparently contiguous transgene copies to tightly linked clusters of multiple copies of transgenes interspersed with oat DNA. The size of the genomic interspersions observed in these transgene clusters was estimated from FISH results on prometaphase chromosomes to be megabases long, indicating that some transgene loci were significantly larger than previously determined by Southern blot analysis. Overall, 6 of the 25 transgene loci were associated with rearranged chromosomes. These results suggest that particle bombardment-mediated transgene integration may result from and cause chromosomal breakage and rearrangements

Descriptors:biolistics. southern-blotting. breakage. characterization. chromosomes. genomes. transgenic-plants. genetic-transformation.

genetic-engineering. chromosome-breakage. cereals. biotechnology. oats
Identifiers:fluorescence in situ hybridization
Organism Descriptors:Avena. Avena-sativa
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Avena
Subject Codes:FF020. FF005. WW000
Supplementary Info:28 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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502. Title:Localising QTLs for leaf rust resistance and agronomic traits in barley (Hordeum vulgare L.)
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 881-888
CD Volume:335
Print Article: Pages: 881-888
Author(s):Kicherer S Backes G Walther U Jahoor A
Author Affiliation:Federal Centre for Breeding Research, Institut for Epidemiology and Resistance, Theodor-Romor-Weg 4, 06449 Aschersleben, Germany
Language:English
Abstract:The Hordeum vulgare accession HOR 1063 was crossed with the barley cultivar Krona, and 220 doubled haploid lines were produced based on this cross. A molecular map was constructed based on RFLP markers. Field trials were performed over 2 years and at two locations. In field trials, resistance to leaf rust (Puccinia recondita) by means of artificial infection, heading date, plant height and kernel weight were assessed. For leaf rust resistance, 4 QTLs were localised, that explained 96.1% of the genetic variation. One QTL on chromosome 4H confirmed a position found in another genetic background and one mapped to the same position as Rph16 on chromosome 2H. All digenic effects decreased the effects of the respective QTLs. In addition to the denso-locus and the hex-v locus, other QTLs influencing heading date, plant length and kernel weight were found in this cross
Descriptors:barley. genetic-variation. heading-date. plant-height. restriction-fragment-length-polymorphism. plant-pathogens. plant-pathogenic-fungi. plant-diseases. disease-resistance. varietal-reactions. fungal-diseases. yield-components. quantitative-traits. gene-mapping. cereals. biotechnology. plant-pathology
Organism Descriptors:Hordeum-vulgare. Hordeum. Puccinia-recondita
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Puccinia. Uredinales. Basidiomycotina. Eumycota. fungi
Subject Codes:FF020. WW000. FF005. FF610. HH600
Supplementary Info:44 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

503. Title:Genetic distance as a predictor of heterosis and hybrid performance within and between heterotic groups in sunflower
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 889-894
CD Volume:335
Print Article: Pages: 889-894
Author(s):Cheres M T Miller J F Crane J M Knapp S J

Author Affiliation:Department of Crop and Soil Science, Oregon State University, Corvallis, OR 97331-3002, USA
Language:English
Abstract:Heterosis is significant for seed yield and is one of the driving forces behind the hybrid seed industry in cultivated sunflower (Helianthus annuus). Heterotic groups in sunflower, if any other than the female and male inbred line groups exist, have not been well studied or described. The primary aims of this study were to assess the utility and validity of a series of proposed heterotic groups and estimate correlations between genetic distance, heterosis, and hybrid performance for seed yield in sunflower. Forty-two female by male heterotic group (A x R) and 81 female by female heterotic group (A x B) single-cross hybrids were grown in Corvallis, Oregon, and Casselton, North Dakota, in 1996 and 1997. Heterosis was significant for seed yield and plant height but not for seed oil concentration and days to flowering. Genetic distances were significantly correlated with hybrid seed yield when estimated from AFLP fingerprints (GD) (r=0.63 for A x R and 0.79 for A x B hybrids), but not from coancestries (GC) (r=-0.02 for A x R and 0.54 for A x B hybrids). GD (R2=0.4) was a poor predictor of hybrid seed yield. The proposed heterotic groups in sunflower seem to have utility, but do not seem to be as strongly differentiated as those in maize (Zea mays). The highest-yielding hybrids were from the BC x RB heterotic pattern; however, several BC x BC hybrids (within-group hybrids) were among the top-yielding hybrids. The outstanding performance of certain BC x BC hybrids casts some doubt on the validity of the BC group. Substantial genetic diversity seems to be present within and between heterotic group in sunflower
Descriptors:heterosis. sunflowers. flowering. genetic-diversity. hybrids. plant-height. inbred-lines. genetic-distance. hybrid-seed-production. yield-components. seed-oils. fatty-oil-plants. oil-plants. biotechnology. biotechnology
Geographic Locator:Oregon. USA. North-Dakota
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Helianthus-annuus. Helianthus. Helianthus
Supplemental Descriptors:Helianthus. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants. Pacific-Northwest-States-of-USA. Pacific-States-of-USA. Western-States-of-USA. USA. North-America. America. Developed-Countries. OECD-Countries. Northern-Plains-States-of-USA. West-North-Central-States-of-USA. North-Central-States-of-USA. Great-Plains-States-of-USA. Northern-Plains-States-of-USA. West-North-Central-States-of-USA. North-Central-States-of-USA. Great-Plains-States-of-USA
Subject Codes:FF020. FF005. WW000. FF030
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

504. Title:Genetic analysis of shoot regeneration from cotyledonary explants in Brassica napus
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 895-898
CD Volume:335
Print Article: Pages: 895-898
Author(s):Ono Y Takahata Y
Author Affiliation:Faculty of Agriculture, Iwate University, Morioka 020-8550, Japan
Language:English

Abstract:Genetic analysis of shoot regeneration from cotyledonary explants of Brassica napus was carried out by 7 x 7 diallel crosses using cultivars showing a different ability for regeneration. Both additive and dominant effects were significant, with the additive effect being more important than the dominant one. Dominant genes had a positive effect on shoot regeneration. Non-allelic interaction and average maternal effects were not detected, while specific the maternal one was significant. In the 5 x 5 sub-diallel table, the maternal effect became non-significant. The mean degree of dominance was 0.759. Broad- and narrow-sense heritabilities were 0.973 and 0.819, respectively, indicating that shoot regeneration ability can be easily transferred into economically important cultivars showing a low or an unresponsive ability
Descriptors:rape. explants. in-vitro-regeneration. cultivars. genes. diallel-analysis. tissue-culture. in-vitro-culture. regenerative-ability. maternal-effects. dominance. heritability. fatty-oil-plants. oil-plants. biotechnology
Organism Descriptors:Brassica. Brassica-napus. Brassica-napus-var.-oleifera
Supplemental Descriptors:Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica. Brassica-napus
Subject Codes:FF020. FF005. FF170. WW000
Supplementary Info:26 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

505. Title:A gene-based RFLP map of petunia
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 899-905
CD Volume:335
Print Article: Pages: 899-905
Author(s):Strommer J Gerats A G M Sanago M Molnar S J
Author Affiliation:Department of Plant Agriculture and Department of Molecular Biology and Genetics, University of Guelph, Guelph, Ontario, N1G 2W1, Canada
Language:English
Abstract:Due in large part to the data accumulated from years of classic genetic analysis, petunia (Petunia hybrida) has remained a useful model system, particularly for studies of gene regulation and genome structure. Three segregating populations of petunia were used, including those serving as the source of an earlier actin gene RFLP map, for RFLP mapping of several additional genes. Twenty-seven loci have been merged with 11 previously mapped morphological and biochemical markers. These results contribute additional evidence to reports of a high degree of genome plasticity and segregation distortion in this species and suggest that petunia may be a useful plant system for detailed analysis of plant genome organization, activity and evolution
Descriptors:restriction-fragment-length-polymorphism. actin. genes. genetic-analysis. genomes. gene-mapping. morphology. ornamental-herbaceous-plants. segregation-distortion. ornamental-plants. biotechnology
Organism Descriptors:Petunia. Petunia-hybrida
Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Petunia
Subject Codes:FF020. FF003. WW000
Supplementary Info:39 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

506. Title:RAPD analysis: a method to investigate aspects of the reproductive biology of Hypericum perforatum L
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 906-911
CD Volume:335
Print Article: Pages: 906-911
Author(s):Arnholdt Schmitt B
Author Affiliation:Institut fur Pflanzenernahrung, Justus-Liebig-Universitat Giessen, Sudanlage 6, D-35390 Giessen, Germany
Language:English
Abstract:Recent interest in breeding strategies for Hypericum perforatum requires a better understanding of the floral biology of this medicinal plant. The aim of the present study was to check, whether RAPD fingerprinting may be a useful tool for research on the mode of reproduction of this species. Progenies from three defined single plants of two accessions, as well as progenies from a random sample of seeds of a wild population, of H. perforatum were characterized by RAPD analyses using six primers. The results obtained by DNA fingerprints indicate the predominance of an identical mode of reproduction for this species, obviously due to apomixis. Nevertheless, non-identical reproduction was evident as a minor effect in H. perforatum, as could be demonstrated by significant deviations in the RAPD fingerprints of progenies from one single plant. It is concluded that RAPD fingerprint analysis is a suitable technique to discover identity or non-identity in H. perforatum populations. Therefore, RAPDs may be used in addition to cytological studies to confirm the mode of reproduction by apomixis versus self-pollination, haploid parthenogenesis or cross-fertilization
Descriptors:apomixis. medicinal-plants. seeds. random-amplified-polymorphic-DNA. DNA-fingerprinting. sexual-reproduction. reproductive-behaviour. biotechnology
Organism Descriptors:Hypericum. Hypericum-perforatum
Supplemental Descriptors:Clusiaceae. Theales. dicotyledons. angiosperms. Spermatophyta. plants. Hypericum
Subject Codes:FF020. FF003. WW000
Supplementary Info:10 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

507. Title:Temporal trends in the diversity of UK wheat
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 912-917
CD Volume:335
Print Article: Pages: 912-917
Author(s):Donini P Law J R Koebner R M D Reeves J C Cooke R J
Author Affiliation:John Innes Centre, Norwich NR4 7UH, UK
Language:English
Abstract:The common assertion that scientific plant breeding leads to a narrowing in crop diversity has been examined. The dominant UK winter wheat varieties from the period 1934-1994 were characterized using two types of PCR-based DNA profiling (amplified fragment length polymorphisms (AFLP) and simple-sequence repeats (SSRs), microsatellites), seed storage protein analysis and morphological descriptors. The varieties were grouped into a series of decadal groups on the basis of their first appearance on the 'Recommended List', and by analysis of molecular variance it was shown that an overwhelming proportion of the overall observed variance occurred within, rather than between, decades. A further range of statistical indices provided little evidence for any significant narrowing of overall diversity over

the time studied. Principal co-ordinate analysis showed that the diversity in the time periods overlapped and that the most modern group of varieties encompassed the majority of the diversity found in earlier decades. The consistent indication is that plant breeding has resulted, over time, in a qualitative, rather than a quantitative, shift in the diversity of winter wheat grown in the UK
Descriptors:wheat. microsatellites. morphology. plant-protein. varieties. cultivars. repetitive-DNA. plant-breeding. history. genetic-diversity. genetic-markers. cereals. biotechnology
Geographic Locator:UK
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. British-Isles. Western-Europe. Europe. Developed-Countries. Commonwealth-of-Nations. European-Union-Countries. OECD-Countries
Subject Codes:FF020. FF005. WW000
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

508. Title:Assessment of genetic diversity within and among germplasm accessions in cultivated sorghum using microsatellite markers
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 918-925
CD Volume:335
Print Article: Pages: 918-925
Author(s):Dje Y Heuertz M Lefebvre C Vekemans X
Author Affiliation:Universite Libre de Bruxelles, Laboratoire de Genetique et d'Ecologie vegetales, 1850 Chaussee de Wavre, B-1160 Brussels, Belgium
Language:English
Abstract:Microsatellite markers are increasingly being used in crop plants to discriminate among genotypes and as tools in marker-assisted selection. Here, the use of microsatellite markers to quantify the genetic diversity within as well as among accessions sampled from the world germplasm collection of sorghum was evaluated. Considerable variation was found at the five microsatellite loci analysed, with an average number of alleles per locus equal to 2.4 within accessions and 19.2 in the overall sample of 25 accessions. The collection of sorghum appeared highly structured genetically with about 70% of the total genetic diversity occurring among accessions. However, differentiation among morphologically defined races of sorghum, or among geographic origins, accounted for less than 15% of the total genetic diversity. These results are in global agreement with those obtained previously with allozyme markers. It was also shown that microsatellite data are useful in identifying individual accessions with a high relative contribution to the overall allelic diversity of the collection
Descriptors:genetic-diversity. germplasm. alleles. genotypes. microsatellites. characterization. cereals. biotechnology. plant-genetic-resources
Organism Descriptors:Sorghum-bicolor
Supplemental Descriptors:Sorghum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. WW000. PP720
Supplementary Info:45 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

509. Title:Multiple-marker mapping of wood density loci in an outbred pedigree of radiata pine
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 926-933
CD Volume:335
Print Article: Pages: 926-933
Author(s):Kumar S Spelman R J Garrick D J Richardson T E Lausberg M Wilcox P L
Author Affiliation:New Zealand Forest Research Institute, Private Bag 3020, Rotorua, New Zealand
Language:English
Abstract:The objective of this study was to determine the gene location and effects of genomic regions controlling wood density at three stages, i.e., rings corresponding to ages 1-5 (WD1_5), rings corresponding to ages 6-10 (WD6_10), and outer wood density (WD14) in a full-sib pedigree (850.055 x 850.096) of Pinus radiata. The number of offspring measured at these three stages were 80, 93 and 93, respectively. Only a single linkage group of the parent 850.55 was considered for mapping quantitative trait loci (QTLs). A multiple-marker least-squares approach was employed for mapping QTLs for each of the three traits, using a single-QTL model. Logistic regression was used for multiple-trait QTL mapping. Critical values for test-statistic were calculated empirically by 'shuffling' the data. A putative QTL with large effect on WD1_5 appears to be segregating at the 73 cM position (experiment-wise P<0.01). The width of the 95% bootstrap confidence interval for this putative QTL was 40 cM (i.e. 56-96 cM). The effect of this QTL on the expression of wood density at later stages was diminished. From multiple-trait analysis, two marker locations (at 66 cM and 91 cM) were found to be significantly associated (experiment-wise P<0.05) with the expression of wood density at different ages. These results are encouraging for the application of marker information to early selection in order to increase juvenile wood density, although the putative QTLs detected in this study need to be verified in an independent population
Descriptors:gene-mapping. wood-density. early-selection. juvenile-wood. linkage. tree-breeding. quantitative-traits. forest-trees. biotechnology. pines
Organism Descriptors:Pinus. Pinus-radiata. Pinopsida
Supplemental Descriptors:Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants. Pinus
Subject Codes:FF020. WW000. KK100. KK510
Supplementary Info:30 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

510. Title:Origin of Scm1 and Scm2 - two loci conferring resistance to sugarcane mosaic virus (SCMV) in maize
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 934-941
CD Volume:335
Print Article: Pages: 934-941
Author(s):Xu M L Melchinger A E Lubberstedt T
Author Affiliation:Institute of Plant Breeding, Seed Science, and Population Genetics, University of Hohenheim, D-70593 Stuttgart, Germany
Language:English
Abstract:Sugarcane mosaic virus (SCMV) causes serious losses of grain and forage yield of maize (Zea mays) in Europe. Two dominant genes, Scm1 and Scm2, have been identified which confer resistance to SCMV. Scm1 is located on the short arm of chromosome 6 and Scm2 near the centromere region of

chromosome 3. In the present study, resistant, partially resistant, and susceptible maize inbred lines, together with their ancestral lines, were evaluated with molecular markers (RFLP, AFLP and SSR) to trace back the origin of Scm1 and Scm2. The banding patterns indicated that the Scm1 region, originally identified in resistant European line FAP1360A, was derived from its ancestral line FAP954A. The other two resistant European lines, D21 and D32, most likely carry the same Scm1 region, which originated from their common ancestral line A632. This Scm1 region was also present in three partially resistant lines, D09, FAP1396A and FAP693A, but not in the resistant U.S. inbred Pa405. Apart from FAP954A and A632, none of the remaining ancestral lines and none of the susceptible lines harboured the Scm1 region. The Scm2 region present in FAP1360A was obviously transmitted from its ancestral line Co125. However, the presence of the respective Scm2 region was not confirmed in the other three resistant lines (D21, D32 and Pa405), the remaining ancestral lines, and all partially resistant lines by using closely linked markers

Descriptors:maize. forage. genes. yields. inbred-lines. plant-pathogens. plant-diseases. disease-resistance. varietal-reactions. genetics. gene-mapping. gene-location. genetic-markers. restriction-fragment-length-polymorphism. repetitive-DNA. cereals. biotechnology. plant-pathology

Geographic Locator:Europe

Identifiers:amplified fragment length polymorphism

Organism Descriptors:Zea-mays. sugarcane-mosaic-potyvirus. plant-viruses

Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. potyvirus-group. plant-viruses. viruses. plant-pathogens. pathogens

Subject Codes:FF020. WW000. FF005. FF610. HH600

Supplementary Info:15 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

511. Title:Mitochondrial genome diversity in connection with male sterility in Allium schoenoprasum L

View Article: Theoretical and Applied Genetics. 2000. 100 (6). 942-948

CD Volume:335

Print Article: Pages: 942-948

Author(s):Engelke T Tatlioglu T

Author Affiliation:Abteilung Angewandte Genetik, Universitat Hannover, Herrenhauser Str. 2, D-30419 Hannover, Germany

Language:English

Abstract:Mitochondrial genome diversity in chives (Allium schoenoprasum) was investigated with respect to different forms of male sterility. Cytoplasmically male-sterile (CMS) and restored genotypes of the known CMS system, compared to plants of wi-, st1- and st2-sterility types and additional fertile plants of different origin were examined by means of RFLP analyses using mitochondrial gene probes. Besides the (S)-cytoplasm of the CMS system four additional cytoplasms were distinguished that differed in the organization of their mitochondrial genomes. There is consequently a high degree of variability of the mitochondrial genome in chives, especially when compared with the closely related onion. A possible function of the atp9 [adenosinetriphosphatase] gene in generating the different cytoplasm types of chives is discussed in relation to the origin of known CMS sequences in other plant species. The existence of different cytoplasm types offers the opportunity for further characterization of the wi-, st1- and st2-sterility systems with respect to cytoplasmic factors

which might be causally related to them. Whether these new sterilities are CMS or GMS (genic male sterilities) is of interest to plant breeders in order that restrictions on the genetic basis used in hybrid seed production be avoided
Descriptors:genomes. cytoplasmic-male-sterility. chives. genotypes. hybrid-seed-production. restriction-fragment-length-polymorphism. mitochondrial-genetics. mitochondrial-DNA. adenosinetriphosphatase. vegetables. biotechnology
Organism Descriptors:Allium. Allium-schoenoprasum
Supplemental Descriptors:Alliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants. Allium
Subject Codes:FF020. FF003. WW000. FF060
Supplementary Info:42 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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512. Title:Genetic analysis of fertility restoration and accumulation of ORF125 mitochondrial protein in the kosena radish (Raphanus sativus cv. Kosena) and a Brassica napus restorer line
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 949-955
CD Volume:335
Print Article: Pages: 949-955
Author(s):Koizuka N Imai R Iwabuchi M Sakai T Imamura J
Author Affiliation:Plantech Research Institute, 1000 Kamoshida, Aoba-ku, Yokohama, 227-0033, Japan
Language:English
Abstract:The genetics of fertility restoration (Rf) of kosena radish CMS has been characterized. The kosena CMS-Rf system is genetically the same as that of the ogura CMS-Rf system. Two dominant genes that act complementary to the restoration of fertility control fertility restoration in kosena CMS. One allele (Rf1) is associated with accumulation of the CMS-associated protein, ORF125. The interaction of Rf1 and another allele (Rf2) was essential for the restoration of fertility in radish, whereas Rf1 alone was sufficient for the complete restoration of fertility in the B. napus kosena CMS cybrid
Descriptors:radishes. alleles. genes. genetics. mitochondrial-genetics. mitochondrial-DNA. cytoplasmic-male-sterility. intergeneric-hybridization. somatic-hybridization. vegetables. biotechnology
Organism Descriptors:Brassica. Brassica-napus. Raphanus-sativus. Raphanus
Supplemental Descriptors:Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica. Raphanus
Subject Codes:FF020. FF003. FF005. WW000. FF060
Supplementary Info:23 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

513. Title:A genetic map of the Nicotiana alata S locus that includes three pollen-expressed genes
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 956-964
CD Volume:335
Print Article: Pages: 956-964
Author(s):Li J H Nass N Kusaba M Dodds P N Treloar N Clarke A E Newbigin E
Author Affiliation:Plant Cell Biology Research Centre, School of Botany, University of Melbourne, del Parkville, Victoria 3010, Australia
Language:English

Abstract:The S locus of solanaceous plants includes separate genes that control the self-incompatibility phenotype of the pistil and of the pollen. The gene controlling the self-incompatibility phenotype of the pistil encodes an extracellular ribonuclease, the S-RNase. The gene(s) controlling the self-incompatibility phenotype of pollen (the pollen-S gene) has yet to be identified. As part of a long-term strategy to clone the pollen-S gene by chromosome walking, a detailed map of the region near the S locus of Nicotiana alata was generated using a total of 251 F2 plants. The map spans an interval of approximately 2.6 cM and contains five markers as well as the S-RNase gene. Two markers were detected with heterologous probes that also detect sequences linked to the S locus of Solanum tuberosum and the homologous region of the Lycopersicon genome. Three markers were identified by differential display using N. alata pollen RNA as a template. One of these markers is a pollen-expressed sequence, 48A, which detects a polymorphic marker no more than 0.5 cM from the S locus. RNA blot analysis indicates that the 48A gene is expressed primarily during pollen development after the completion of meiosis and is therefore a candidate for the pollen-S gene. The utility of these markers and the possible involvement of 48A in the molecular mechanism of self-incompatibility are discussed
Descriptors:genes. genomes. meiosis. gynoecium. pollen. RNA. self-incompatibility. chromosome-pairing. ribonucleases. chromosome-walking. gene-mapping. polymerase-chain-reaction. stimulant-plants. biotechnology. potatoes
Organism Descriptors:Nicotiana. Nicotiana-alata. Lycopersicon. Solanum. Solanum-tuberosum
Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Nicotiana. Solanum
Subject Codes:FF020. FF005. WW000. FF060
Supplementary Info:40 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

514. Title:Development of markers linked to Diuraphis noxia resistance in wheat using a novel PCR-RFLP approach
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 965-970
CD Volume:335
Print Article: Pages: 965-970
Author(s):Venter E Botha A M
Author Affiliation:Forestry and Agricultural Biotechnology Institute (FABI) and Department of Genetics, University of Pretoria, Pretoria, 0002, South Africa
Language:English
Abstract:Through random amplified polymorphic DNA (RAPD) analysis a putative marker linked to the Dn5 resistance gene was identified. This marker was converted to a more reliable sequence-characterised-amplified regions (SCAR) marker. The initial SCAR marker amplified the correct amplification product but failed to discern between the susceptible and resistant individuals. Hence, it was utilised to sequence the internal fragment. All nested primers designed from the internal sequences were also unable to produce any polymorphism between the susceptible and resistant cultivars. Restriction digests were then performed on these fragments, and the restriction enzyme EcoRI was able to discern between the susceptible and resistant F2 individuals of the Dn5 population. This granted one marker amplified with the internal SCAR primer set OPF141083 the ability to differentiate between parental individuals carrying the Dn5 genes. This marker was tested in a segregating F2

population carrying the Dn5 resistance gene and proved able to differentiate between the segregating individuals. This marker may prove useful in marker assisted selection (MAS), although performing restriction digests may hamper the throughput of a high number of samples
Descriptors:wheat. DNA-amplification. cultivars. genes. random-amplified-polymorphic-DNA. genetic-markers. linkage. pest-resistance. insect-pests. cereals. biotechnology. control. agricultural-entomology
Organism Descriptors:Diuraphis. Diuraphis-noxia. Triticum-aestivum. arthropods. Triticum
Supplemental Descriptors:Aphididae. Aphidoidea. Sternorrhyncha. Homoptera. Hemiptera. insects. arthropods. invertebrates. animals. Diuraphis. Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. FF005. FF620. HH600
Supplementary Info:34 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

515. Title:Modelling the spread of pollen from Lolium perenne. The implications for the release of wind-pollinated transgenics
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 971-974
CD Volume:335
Print Article: Pages: 971-974
Author(s):Giddings G
Author Affiliation:Cledwyn Building, Institute of Biological Sciences, University of Wales, Aberystwyth, Ceredigion, UK
Language:English
Abstract:The dispersal of pollen from a Lolium perenne source has previously been described using various Gaussian plume models which take distance and wind direction into account. One of these models is used here to calculate, using integration, possible pollen deposition onto small conspecific populations a kilometre from the source. The percentage of immigrant pollen is compared for six different sets of parameter values previously estimated from pollen-dispersal experiments. The source size is then scaled up to simulate what might happen if transgenic ryegrass was grown on a large scale. In this case it is seen that small conspecific populations might, in some conditions, be swamped by immigrant pollen, even if they are not directly downwind of the source. The implications of this are discussed in terms of assessing and managing the risks of releasing wind-pollinated transgenic crops
Descriptors:pollen. transgenic-plants. gene-flow. biosafety. simulation-models. fodder-plants. biotechnology
Organism Descriptors:Lolium. Lolium-perenne. grasses. Poaceae
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Lolium
Subject Codes:FF020. FF007. WW000. FF060
Supplementary Info:18 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

516. Title:Identification of QTLs involved in the resistance to South American leaf blight (Microcyclus ulei) in the rubber tree
View Article: Theoretical and Applied Genetics. 2000. 100 (6). 975-984
CD Volume:335

Print Article: Pages: 975-984
Author(s):Lespinasse D Grivet L Troispoux V Rodier Goud M Pinard F Seguin M
Author Affiliation:CIRAD, Centre de Cooperation Internationale en Recherche Agronomique pour le Developpement, Avenue Agropolis, B.P. 5035, 34032 Montpellier Cedex 1, France
Language:English
Abstract:South American leaf blight (SALB) is a disease of the rubber tree caused by the fungus Microcyclus ulei. Quantitative trait loci (QTLs) for resistance were mapped using 195 F1 progeny individuals derived from the cross between a susceptible cultivated clone, PB260, and a resistant clone, RO38, derived from interspecific hybridization. The resistance level of the progeny individuals was evaluated in controlled conditions. The reaction type (RT) and the lesion diameter (LD) were measured on immature leaves after artificial inoculation of the fungus. Five different strains of the fungus were used, all highly sporulating on PB260. Among those, four did not sporulate and one sporulated partially on RO38. Both pseudo-testcross parental genetic maps and the consensus map were constructed. The search for QTLs was performed using the Kruskal-Wallis marker-by-marker test and the Interval-Mapping method for the three maps. Eight QTLs for resistance were identified on the RO38 map. Only one QTL was detected on the PB260 map. The analysis of the F1 consensus map confirmed results obtained with the parental maps. A common QTL was detected for resistance to the five strains for both RT and LD. Two QTLs were common for complete resistance to four strains, for RT and LD respectively. Resistance determinism for complete and partial resistance, and perspectives for breeding for durable resistance to SALB are discussed
Descriptors:interspecific-hybridization. plant-pathogens. plant-pathogenic-fungi. plant-diseases. disease-resistance. varietal-reactions. fungal-diseases. rubber-plants. quantitative-traits. gene-mapping. biotechnology. plant-pathology
Geographic Locator:South-America
Organism Descriptors:Microcyclus-ulei. Hevea-brasiliensis
Supplemental Descriptors:Microcyclus. Dothideales. Ascomycotina. Eumycota. fungi. Hevea. Euphorbiaceae. Euphorbiales. dicotyledons. angiosperms. Spermatophyta. plants. America
Subject Codes:FF020. FF003. WW000. FF610. HH600
Supplementary Info:45 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

517. Title:Phylogeny reconstruction and hybrid analysis in Allium subgenus Rhizirideum
View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1000-1009
CD Volume:335
Print Article: Pages: 1000-1009
Author(s):Raamsdonk L W D van Ginkel M V van Kik C
Author Variant:van-Raamsdonk-L-W-D. van-Ginkel-M-V
Author Affiliation:DLO Centre for Plant Breeding and Reproduction Research (CPRO-DLO), P.O. Box 16, 6700 AA Wageningen, Netherlands
Language:English
Abstract:Amplified fragment length polymorphisms (AFLPs) for assessing nuclear DNA diversity have been used for the reconstruction of the phylogeny and evolution of several sections of Allium subgenus Rhizirideum. A dataset of 355 characters for 33 accessions belonging to 20 species has been compiled. The band-sharing of five interspecific hybrids and of an F2 population between A. cepa and A. roylei with their parents

indicated a heterozygosity level between 6 and 14%, which allows the use of dominant markers such as AFLPs for phylogeny reconstruction. A majority rule consensus tree based on 56 most-parsimonious trees (CI = 0.53) revealed a separate clade for each of the sections, Cepa, Rhizirideum and Schoenoprasum, and one clade combining the sections Oreiprason and Petroprason. An unweighted pair group mean average (UPGMA)-based dendrogram showed the same subdivision. The trees and the 'Hybrid Distance' approach both supported the assumption of a hybrid origin for A. roylei with considerable subsequent secondary evolution. The establishment of three alliances in the section Cepa and the close relationship of sections Oreiprason and Petroprason are now confirmed. The predictions of the soyabean domestication scenario, i.e. selection of a crop from one progenitor with subsequent narrowing of the genetic diversity of the crop, which applies to the cultigens A. cepa and A. fistulosum, is supported by the Hybrid Distance approach
Descriptors:heterozygosity. hybrids. interspecific-hybridization. phylogeny. onions. Welsh-onions. vegetables. biotechnology. plant-genetic-resources
Identifiers:Allium roylei. amplified fragment length polymorphism
Organism Descriptors:Allium. Allium-cepa. Allium-fistulosum
Supplemental Descriptors:Alliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants. Allium. Liliaceae
Subject Codes:FF003. FF020. WW000. ZZ380
Supplementary Info:39 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

518. Title:Inheritance of citrus nematode resistance and its linkage with molecular markers
View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1010-1017
CD Volume:335
Print Article: Pages: 1010-1017
Author(s):Ling P Duncan L W Deng Z Dunn D Hu X Huang S Gmitter F G Jr
Author Affiliation:University of Florida, Department of Horticultural Science, IFAS, Citrus Research and Education Center, 700 Experiment Station Road, Lake Alfred, FL 33850, USA
Language:English
Abstract:Eleven random amplified polymorphic DNA markers linked to a gene region conferring resistance to citrus nematodes (Tylenchulus semipenetrans) in an intergeneric backcross family were identified. Two sequence-characterized amplified region markers linked to a citrus tristeza virus resistance gene and one selected resistance gene candidate marker were evaluated for their association with citrus nematode resistance. A nematode-susceptible citrus hybrid, LB6-2 (Clementine mandarin (Citrus reticulata) x Hamlin orange (C. sinensis)), was crossed with the citrus nematode-resistant hybrid Swingle citrumelo (C. paradisi x Poncirus trifoliata) to produce 62 hybrids that were reproduced by rooted cuttings. The plants were grown in a greenhouse and inoculated with nematodes isolated from infected field trees. The hybrids segregated widely for this trait in a continuous distribution, suggesting possible polygenic control of the resistance. Bulked segregant analysis was used to identify markers associated with resistance by bulking DNA samples from individuals at the phenotypic distribution extremes. Linkage relationships were established by the inheritance of the markers in the entire population. A single major gene region that contributes to nematode resistance was identified. The resistance was inherited in this backcross family from the grandparent Poncirus trifoliata as a

single dominant gene. QTL analysis revealed that 53.6% of the phenotypic variance was explained by this major gene region. The existence of other resistance-associated loci was suggested by the continuous phenotypic distribution and the fact that some moderately susceptible hybrids possessed the resistance-linked markers. The markers may be useful in citrus rootstock breeding programmes if it can be demonstrated that they are valid in other genetic backgrounds

Descriptors:citrumelos. random-amplified-polymorphic-DNA. hybrids. inheritance. intergeneric-hybridization. mandarins. plant-parasitic-nematodes. pest-resistance. genetics. genetic-markers. oranges. interspecific-hybridization. fruit-crops. biotechnology. nematology. fruits. control. plant-nematology

Organism Descriptors:Citrus-paradisi-x-Poncirus-trifoliata. Citrus-reticulata. Poncirus-trifoliata. Tylenchulus-semipenetrans. Citrus-sinensis. Citrus

Supplemental Descriptors:Citrus. Rutaceae. Sapindales. dicotyledons. angiosperms. Spermatophyta. plants. Poncirus. Tylenchulus. Tylenchulidae. Nematoda. invertebrates. animals

Subject Codes:FF003. FF620. HH600. FF020. WW000

Supplementary Info:40 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

519. Title:Somatic cell hybridization of 'oxy' CMS Brassica juncea (AABB) with B. oleracea (CC) for correction of chlorosis and transfer of novel organelle combinations to allotetraploid brassicas

View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1043-1049

CD Volume:335

Print Article: Pages: 1043-1049

Author(s):Arumugam N Mukhopadhyay A Gupta V Sodhi Y S Verma J K Pental D Pradhan A K

Author Affiliation:Center for Genetic Manipulation of Crop Plants, Department of Genetics, University of Delhi South Campus, Benito Juarez Road, New Delhi 110 021, India

Language:English

Abstract:Alloplasmic lines of cultivated Brassica species with B. oxyrrhina cytoplasm are male-sterile and suffer from severe chlorosis. We developed male-sterile lines corrected for chlorosis by fusing protoplasts of CMS B. juncea (AABB) with 'oxy' cytoplasm and normal B. oleracea (CC). A large number of male-sterile AABBCC somatic hybrids with desirable organelle combinations, i.e. chloroplasts of B. oleracea and mitochondria with recombinant genomes, were recovered. While no recombination was observed in the chloroplast genome, the mitochondrial genome showed extensive recombination that resulted in the appearance of totally novel banding patterns in some of the hybrids. Hybrids with a parental-type mitochondrial genome as well as recombinant patterns close to either of the parental types were also obtained. Using AABBCC somatic hybrids as bridging material, we transferred the desirable organelle combinations to B. juncea (AABB), B. napus (AACC), and B. carinata (BBCC). Many of these lines are now at advanced stages of backcrossing and show stable inheritance of the CMS character and do not suffer from chlorosis

Descriptors:chlorosis. interspecific-hybridization. somatic-hybridization. protoplast-fusion. male-sterility. Indian-mustard. recombination. mitochondrial-genetics. cytoplasmic-male-sterility. fatty-oil-plants. oil-plants. biotechnology

Organism Descriptors:Brassica-oleracea. Brassica-juncea. Brassica-carinata. Brassica-napus
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060. FF020. FF170. WW000
Supplementary Info:29 ref
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Journal Title:Theoretical and Applied Genetics
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520. Title:Genetic diversity and relationships of sweetpotato and its wild relatives in Ipomoea series Batatas (Convolvulaceae) as revealed by inter-simple sequence repeat (ISSR) and restriction analysis of chloroplast DNA
View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1050-1060
CD Volume:335
Print Article: Pages: 1050-1060
Author(s):Huang J C Sun M
Author Affiliation:Department of Zoology, University of Hong Kong, Pokfulam Road, Hong Kong, China
Language:English
Abstract:Genetic diversity and relationships of 40 accessions of Ipomoea, representing ten species of series Batatas, were examined using ISSR markers and restriction-site variation in four non-coding regions of chloroplast DNA. A total of 2071 ISSR fragments were generated with 15 primers in these accessions and, on average, 52 bands per accession were amplified. Most of the primers contained dinucleotide repeats. The ISSR fragments were highly polymorphic (62.2%) among the 40 accessions studied. Restriction analysis of chloroplast (cp) DNA revealed 47 informative restriction-site and length mutations. Phylogenetic analyses of ISSR and cpDNA datasets generally revealed similar relationships at the interspecific level, but the high polymorphism of ISSRs resulted in a better separation of intraspecific accessions. However, the combined ISSR and cpDNA dataset appeared to be appropriate in resolving both intra- and interspecific relationships. Of the species examined, I. trifida was found to be the most closely related to cultivated sweet potato, the hexaploid I. batatas, while I. ramosissima and I. umbraticola were the most distantly related to I. batatas within the series. Ipomoea triloba, hitherto considered to be one of the ancestors of sweet potato, was only distantly related to sweet potato based on ISSR similarity index
Descriptors:chloroplast-DNA. sweet-potatoes. interspecific-hybridization. wild-relatives. genetic-markers. genetic-diversity. restriction-fragment-length-polymorphism. chloroplast-genetics. root-crops. biotechnology. plant-genetic-resources
Identifiers:Ipomoea trifida. Ipomoea ramosissima. Ipomoea umbraticola
Organism Descriptors:Ipomoea-batatas. Ipomoea-triloba
Supplemental Descriptors:Ipomoea. Convolvulaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. PP720. WW000
Supplementary Info:36 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

521. Title:Assessment of genetic relationships between Setaria italica and its wild relative S. viridis using AFLP markers

View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1061-1066
CD Volume:335
Print Article: Pages: 1061-1066
Author(s):Thierry d'Ennequin M le Panaud O Toupance B Sarr A
Author Variant:le-Thierry-d'Ennequin-M
Author Affiliation:Laboratoire Evolution et Systematique, UPRESA-CNRS 8079, Universite PARIS XI, Batiment 362, 91405 Orsay Cedex, France
Language:English
Abstract:Amplified fragment length polymorphism markers were used to assess genetic diversity and patterns of geographic variation among 39 accessions of foxtail millet (Setaria italica) and 22 accessions of green foxtail millet (S. viridis), its putative wild progenitor. Accessions originated mainly from China and Europe. A high level of polymorphism was revealed. Dendrograms based on Nei and Li distances from a neighbour joining procedure were constructed using 160 polymorphic bands. Bootstrap values revealed that no specific geographic structure can be extracted from these data. The high level of diversity among Chinese accessions was consistent with the hypothesis of a centre of domestication in China. The results also showed that accessions from Eastern Europe and Africa form two distinct clusters. The narrow genetic basis of these two gene pools may be the result of local-adaptation
Descriptors:millets. wild-relatives. geography. genetic-diversity. genetic-distance. cereals. plant-genetic-resources. biotechnology
Geographic Locator:China. Europe
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Setaria-viridis. Setaria-italica
Supplemental Descriptors:Setaria-(Poaceae). Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. East-Asia. Asia. Developing-Countries
Subject Codes:FF005. FF020. PP720. WW000
Supplementary Info:36 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

522. Title:Molecular characterisation of the inactive allele of the gene Glu-A1 and the development of a set of AS-PCR markers for HMW glutenins of wheat
View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1085-1094
CD Volume:335
Print Article: Pages: 1085-1094
Author(s):Bustos A de Rubio P Jouve N
Author Variant:de-Bustos-A
Author Affiliation:Department of Cell Biology and Genetics, University of Alcala, 28871 Alcala de Henares, Madrid, Spain
Language:English
Abstract:The present work reports new PCR markers that amplify the complete coding sequence of the specific alleles of the high molecular weight (HMW) glutenin genes. A set of AS-PCR molecular markers was designed which use primers from nucleotide sequences of the Glu-A1 and Glu-D1 genes, making use of the minor differences between the sequences of the x1, x2* of Glu-A1, and the x5 and y10 of Glu-D1. These primers were able to distinguish between x2* and the x1 or xNull of Glu-A1. Also x5 was distinguishable from x2, and y10 from y12. The primers amplified the complete coding regions and corresponded to the upstream and downstream flanking positions of Glu-A1 and Glu-D1. Primers designed to amplify the Glu-A1 gene amplified a single product when used with

genomic DNA of common wheats and the xNull allele of this gene. This work also describes the cloning and characterisation of the nucleotide sequence of this allele (EMBL/GenBank/DDBJ accession no. AF145590). It possesses the same general structure as x2 and x1 (previously determined) and differs from these alleles in the extension of the coding sequence for a presumptive mature protein with only 384 residues. This is due to the presence of a stop codon (TAA) 1215-bp downstream from the start codon. A further stop codon (TAG), 2280-bp downstream from the starting codon is also found. The open reading frame of xNull and x1 alleles has the same size in bp. Both are larger than x2* which shows two small deletions. The reduced size of the presumptive mature protein encoded by xNull could explain the negative effect of this allele on grain quality

Descriptors:alleles. glutenins. wheat. genes. polymerase-chain-reaction. genetic-markers. nucleotide-sequences. genetic-polymorphism. baking-quality. cereals. biotechnology

Organism Descriptors:Triticum-aestivum. Triticum

Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF040. FF020. WW000

Supplementary Info:36 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

523. Title:The detection and molecular mapping of a major gene for non-specific adult-plant disease resistance against stripe rust (Puccinia striiformis) in wheat

View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1095-1099

CD Volume:335

Print Article: Pages: 1095-1099

Author(s):Borner A Roder M S Unger O Meinel A

Author Affiliation:Institut fur Pflanzengenetik und Kulturpflanzenforschung (IPK), Correnstrasse 3, D-06466 Gatersleben, Germany

Language:English

Abstract:A major gene determining non-specific adult-plant disease resistance against stripe rust (Puccinia striiformis), designated Yrns-B1, was mapped by using a cross between 'Lgst. 79-74' (resistant) and 'Winzi' (susceptible). Analysing F3 lines of two consecutive experimental years (1997 and 1998), contrary modes of inheritance were observed due to the intermediate character of the gene and the difference in the disease pressure during the seasons. Using the disease scoring data of both experimental years independently, two maps were constructed detecting Yrns-B1 20.5 and 21.7 cM, respectively, proximal to the wheat microsatellite (WMS) marker Xgwm493 on the short arm of chromosome 3BS. The genetic relationships to other major genes or to quantitative trait loci controlling adult plant disease resistance against rusts in wheat are discussed

Descriptors:disease-resistance. gene-mapping. rust-diseases. wheat. genes. genetics. plant-diseases. plant-pathogens. fungal-diseases. plant-pathogenic-fungi. cereals. biotechnology. plant-pathology

Geographic Locator:Germany

Organism Descriptors:Puccinia-striiformis. Triticum-aestivum. Triticum

Supplemental Descriptors:Puccinia. Uredinales. Basidiomycotina. Eumycota. fungi. Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Western-Europe. Europe. Developed-Countries. European-Union-Countries. OECD-Countries

Subject Codes:FF005. FF610. HH600. FF020. WW000

Supplementary Info:19 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

524. Title:Fine mapping and DNA marker-assisted pyramiding of the three major genes for blast resistance in rice
View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1121-1128
CD Volume:335
Print Article: Pages: 1121-1128
Author(s):Hittalmani S Parco A Mew T V Zeigler R S Huang N
Author Affiliation:International Rice Research Institute, P.O. Box 933, Manila, Philippines
Language:English
Abstract:Three major genes (Pi1, Piz-5 and Pita) for blast (Magnaporthe grisea) resistance on chromosomes 11, 6 and 12, respectively, were fine-mapped and closely linked RFLP markers identified. New markers for Pi1 and Pita were found that were flanking the genes. The three genes were pyramided using RFLP markers. A PCR-based SAP (sequence amplified polymorphism) marker was used to identify Piz-5 in the segregating population. The plants carrying the two- and three-gene combinations that were tested for resistance to leaf blast in the Philippines and India indicated that combinations including Piz-5 have enhanced resistance than when it is present alone. The genes from the pyramided lines are at present being deployed into agronomically superior rice varieties by marker-aided selection
Descriptors:genes. gene-mapping. rice. restriction-fragment-length-polymorphism. disease-resistance. plant-pathogens. genetic-markers. plant-diseases. plant-pathogenic-fungi. fungal-diseases. cereals. biotechnology. plant-pathology
Organism Descriptors:Oryza-sativa. Magnaporthe-grisea. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Magnaporthe. Polystigmatales. Ascomycotina. Eumycota. fungi
Subject Codes:FF005. FF610. HH600. FF020. WW000
Supplementary Info:34 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

525. Title:The cystathionine- gamma -synthase gene involved in methionine biosynthesis is highly expressed and auxin-repressed during wild strawberry (Fragaria vesca L.) fruit ripening
View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1129-1136
CD Volume:335
Print Article: Pages: 1129-1136
Author(s):Marty I Douat C Tichit L Jungsup K Leustek T Albagnac G
Author Affiliation:INRA Avignon-Station de Technologie Produits Vegetaux, Domaine Saint-Paul, Site Agroparc, 84914 Avignon Cedex 09, France
Language:English
Abstract:Differential screening of a cDNA library from ripe wild-strawberry (Fragaria vesca) receptacles allowed the isolation of a cDNA clone for an mRNA which accumulated to high levels in ripe strawberry receptacles. Sequence analysis of this cDNA (1940 bp) and the corresponding gene (4330 bp) indicated the presence of an ORF coding for a predicted protein of 545 amino acids (MWt 58.3 kDa) showing 91% identity with an Arabidopsis thaliana cystathionine gamma -synthase [O-

succinylhomoserine (thiol)-lyase] (CGS), an enzyme involved in methionine biosynthesis. Up to now, CGS activity was reported only in leaves from various plants and in microorganisms. In this study, a much stronger expression was observed in receptacles from strawberries compared to other organs (leaves, flowers, etc.). Accumulation of CGS transcripts in receptacles of both wild and commercial strawberries was highly correlated with the progress of ripening. Immunoblot experiments with an A. thaliana CGS antibody demonstrated a similar profile of accumulation for CGS protein and transcripts. Southern-blot analysis of genomic DNA indicated that the CGS protein was encoded by a single gene in Fragaria species and in some climacteric fruits, e.g. peach and apricot. In addition to the ripening-related genes identified in strawberries, the treatment of receptacles (de-achenated or not) with the auxin NAA significantly reduced CGS gene expression

Descriptors:methionine. ripening. strawberries. fruits. gene-expression. genes. wild-relatives. lyases. fruit-crops. biotechnology. plant-genetic-resources. plant-growth-regulators. auxins. temperate-fruits

Identifiers:O-succinylhomoserine (thiol)-lyase

Organism Descriptors:Fragaria-vesca. Fragaria

Supplemental Descriptors:Fragaria. Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF003. FF060. FF020. WW000. PP720

Supplementary Info:34 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

526. Title:Development of PCR markers for the wheat leaf rust resistance gene Lr47

View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1137-1143

CD Volume:335

Print Article: Pages: 1137-1143

Author(s):Helguera M Khan I A Dubcovsky J

Author Affiliation:Department of Agronomy and Range Science, University of California, One Shields Avenue, Davis CA 95616-8515, California, USA

Language:English

Abstract:The leaf rust [Puccinia recondita f.sp. tritici] resistance gene Lr47 confers resistance to a wide spectrum of leaf rust strains. This gene was recently transferred from chromosome 7S of Triticum speltoides [Aegilops speltoides] to chromosome 7A of hexaploid wheat Triticum aestivum. To facilitate the transfer of Lr47 to commercial varieties, the completely linked restriction fragment length polymorphism (RFLP) locus Xabc465 was converted into a PCR-based marker. Barley clone ABC465 is orthologous to the type-I wheat sucrose synthase gene and primers were designed for the conserved regions between the two sequences. These conserved primers were used to amplify, clone and sequence different alleles from T. speltoides and T. aestivum. This sequence information was then used to identify the T. speltoides sequence, detect allele-specific mutations, and design specific primers. Cosegregation of the PCR product of these primers and the T. speltoides chromosome segment was confirmed in four backcross-populations. To complement this dominant marker, a cleavage amplified polymorphic sequence (CAPS) was developed for the 7A allele of Xabc465. This CAPS marker is useful to select homozygous Lr47 plants from F2 or back-cross-F2 segregating populations, and in combination with the T. speltoides-specific primers is expected to facilitate the deployment of Lr47 in new bread wheat varieties

Descriptors:polymerase-chain-reaction. rust-diseases. wheat. restriction-fragment-length-polymorphism. wild-relatives. intergeneric-hybridization. plant-diseases. plant-pathogens. plant-pathogenic-fungi. fungal-diseases. genetic-markers. cereals. biotechnology. plant-genetic-resources. plant-pathology
Organism Descriptors:Triticum-aestivum. Aegilops-speltoides. Puccinia-recondita. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Aegilops. Puccinia. Uredinales. Basidiomycotina. Eumycota. fungi
Subject Codes:FF005. FF610. HH600. PP720. FF020. WW000
Supplementary Info:25 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

527. Title:The maize rp1 rust resistance gene identifies homologues in barley that have been subjected to diversifying selection
View Article: Theoretical and Applied Genetics. 2000. 100 (7). 1144-1154
CD Volume:335
Print Article: Pages: 1144-1154
Author(s):Ayliffe M A Collins N C Ellis J G Pryor A
Author Affiliation:CSIRO Plant Industry, P.O. Box 1600, Canberra, ACT 2601, Australia
Language:English
Abstract:A number of agronomically important grasses (sorghum, wheat, panicum, sugarcane, oats, rice and barley) are shown to contain sequences homologous to rp1, a maize gene that confers race-specific resistance to the rust fungus Puccinia sorghi. Mapping of rp1-related sequences in barley identified three unlinked loci on chromosomes 1HL, 3HL and 7HS. The locus located on chromosome 7HS comprises a small gene family of at least four members, two of which were isolated and are predicted to encode nucleotide binding site-leucine-rich repeat (NBS-LRR) proteins that are, respectively, 58% and 60% identical to the maize rp1 protein. Evidence of positive selection for sequence diversification acting up-on these two barley genes was observed; however, diversifying selection was restricted to the carboxy terminal half of the LRR domain. One of these rp1 homologous genes cosegregated with the barley Rpg1 stem rust resistance gene amongst 148 members of the SteptoexMorex double haploid mapping family. Three other unrelated resistance gene-like sequences, potentially encoding NBS-LRR proteins, are also shown to be linked to the Rpg1 locus but not cosegregating with the gene
Descriptors:barley. rust-diseases. gene-mapping. plant-diseases. plant-pathogens. plant-pathogenic-fungi. disease-resistance. genes. natural-selection. cereals. biotechnology. plant-pathology
Organism Descriptors:Hordeum-vulgare. Puccinia-sorghi
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Puccinia. Uredinales. Basidiomycotina. Eumycota. fungi
Subject Codes:FF005. FF610. HH600. FF020. WW000
Supplementary Info:40 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

528. Title:Citrus phylogeny and genetic origin of important species as investigated by molecular markers

View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1155-1166
CD Volume:335
Print Article: Pages: 1155-1166
Author(s):Nicolosi E Deng Z N Gentile A Malfa S la Continella G Tribulato E
Author Variant:la-Malfa-S
Author Affiliation:Istituto di Coltivazioni arboree, University of Catania, Via Valdisavoia, 5, 95123 Catania, Italy
Language:English
Abstract:Citrus phylogeny was investigated using RAPD, SCAR and ctDNA markers. The genotypes analysed included 36 accessions belonging to Citrus together with one accession from each of the related genera Poncirus, Fortunella, Microcitrus and Eremocitrus. Phylogenetic analysis with 262 RAPDs and 14 SCARs indicated that Fortunella is phylogenetically close to Citrus while the other three related genera are distant from Citrus and from each other. Within Citrus, the separation into two subgenera, Citrus and Papeda, designated by Swingle, was clearly observed, except for C. celebica and C. indica. Almost all the accessions belonging to subgenus Citrus fell into three clusters, each including one genotype that was considered to be a true species. Different phylogenetic relationships were revealed with ctDNA data. Citrus genotypes were separated into subgenera Archicitrus and Metacitrus, as proposed by Tanaka, while the division of subgenera Citrus and Papeda disappeared. C. medica and C. indica were quite distant from other citrus as well from related genera. C. ichangensis appeared to be the ancestor of the mandarin cluster, including C. tachibana. Lemon and Palestine sweet lime were clustered into the Pummelo cluster led by C. latipes. C. aurantifolia was located in the Micrantha cluster. Furthermore, genetic origin was studied on 17 cultivated citrus genotypes by the same molecular markers, and a hybrid origin was hypothesized for all the tested genotypes. The assumptions are discussed with respect to previous studies; similar results were obtained for the origin of orange and grapefruit. Hybrids of citron and sour orange were assumed for lemon, Palestine sweet lime, bergamot and Volkamer lemon, while a citron x mandarin hybrid was assumed for Rangpur lime and Rough lemon. For Mexican lime our molecular data indicated C. micrantha to be the female parent and C. medica as the male one
Descriptors:phylogeny. citrons. grapefruits. hybrids. mandarins. phylogenetics. pummelos. sour-oranges. chloroplast-DNA. chloroplast-genetics. random-amplified-polymorphic-DNA. taxonomy. molecular-genetics. interspecific-hybridization. fruit-crops. biotechnology. fruits. subtropical-fruits. citrus-fruits
Identifiers:Citrus indica. Citrus latipes. Citrus celebica. Citrus micrantha. Rutales
Organism Descriptors:Citrus-medica. Citrus. Fortunella. Poncirus. Microcitrus. Eremocitrus. Citrus-paradisi. Citrus-reticulata. Citrus-maxima. Citrus-aurantium. Citrus-tachibana. Citrus-ichangensis
Supplemental Descriptors:Citrus. Rutaceae. Sapindales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. ZZ380. FF003
Supplementary Info:35 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

529. Title:QTL analysis of bread-making quality in wheat using a doubled haploid population
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1167-1175

CD Volume:335
Print Article: Pages: 1167-1175
Author(s):Perretant M R Cadalen T Charmet G Sourdille P Nicolas P Boeuf C Tixier M H Branlard G Bernard S Bernard M
Author Affiliation:INRA Station d'Amelioration des Plantes, 234 av. du Brezet, 63039 Clermont-Ferrand, France
Language:English
Abstract:A set of 187 doubled haploid wheat lines derived from a cross between cultivars Courtot and Chinese Spring was explored for QTLs for three bread-making quality tests: hardness, protein content and strength of the dough (W of alveograph). The scores of the parental lines were quite different except for protein content, and the doubled haploid population showed a wide range of variation. About 350 molecular and biochemical markers were used to establish the genetic map, and technological criteria were evaluated in 1 to 3 years. QTL detection was performed by the 'marker regression' method. The most significant unlinked markers were used in the model as covariates, and the results were tested by bootstrap resampling. For hardness, we confirmed a previously tagged major QTL on chromosome 5DS, and two additional minor QTLs were found on chromosome 1A and 6D, respectively. For protein content two main QTLs were identified on chromosomes 1B and 6A, respectively. For W, three consistent QTLs were detected: two at the same location as those for hardness, on chromosomes 1A and 5D; the third one on chromosome 3B. Therefore, it appeared that except for the Glu-1A locus, storage protein loci were not clearly involved in the genetic control of the criteria studied in the present work. Despite the reasonable size of the population no QTL with interactive effects could be substantially established as measured. All computations were carried out using home-made programmes in Splus language, and these are available upon request
Descriptors:wheat. chromosomes. proteins. quantitative-traits. quantitative-trait-loci. gene-location. baking-quality. gene-mapping. genetic-markers. quality. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. QQ500. FF005. WW000
Supplementary Info:44 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

530. Title:Mapping quantitative trait loci (QTLs) for resistance to Cercospora leaf spot disease (Cercospora beticola Sacc.) in sugar beet (Beta vulgaris L.)
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1176-1182
CD Volume:335
Print Article: Pages: 1176-1182
Author(s):Setiawan A Koch G Barnes S R Jung C
Author Affiliation:Institute of Crop Science and Plant Breeding, Christian-Albrechts-University Kiel, Olshausenstr. 40, D-24118 Kiel, Germany
Language:English
Abstract:The breeding of sugarbeet varieties that combine resistance to A QTL analysis of Cercospora resistance in sugarbeet was carried out using a linkage map based on AFLP and RFLP markers. Two different screening methods for Cercospora resistance (a field test at Copparo, Italy, under natural infection, and a newly-developed leaf disc test) were used to estimate the level of Cercospora resistance; the correlation

between scores from the field (at 162 days after sowing) and the leaf disc test was significant. QTL analysis was based on F2 and F3 (half-sib family) generations derived from crosses between diploid single plants of 93164P (resistant to Cercospora leaf spot disease) and 95098P (susceptible). Four QTLs associated with Cercospora resistance (based on Lsmean (least squares means for genotypic effect) data of the leaf disc test) on chromosomes III, IV, VII and IX were revealed using Composite interval mapping. To produce populations segregating for leaf spot resistance as a single Mendelian factor, we selected for plants heterozygous for only one of the QTLs (on chromosome IV or IX) but homozygous for the others

Descriptors:sugarbeet. linkage. gene-mapping. restriction-fragment-length-polymorphism. screening. quantitative-trait-loci. quantitative-traits. genetic-markers. gene-location. plant-pathogens. plant-diseases. disease-resistance. plant-pathogenic-fungi. fungal-diseases. sugar-crops. biotechnology. plant-pathology

Geographic Locator:Italy

Identifiers:amplified fragment length polymorphism

Organism Descriptors:Beta-vulgaris. Cercospora-beticola. Beta-vulgaris-var.-saccharifera

Supplemental Descriptors:Beta. Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms. Spermatophyta. plants. Cercospora. Deuteromycotina. Eumycota. fungi. Beta-vulgaris. Southern-Europe. Europe. Mediterranean-Region. Developed-Countries. European-Union-Countries. OECD-Countries

Subject Codes:FF005. FF020. HH600. FF610. WW000

Supplementary Info:31 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

531. Title:Genetic mapping of jointless-2 to tomato chromosome 12 using RFLP and RAPD markers

View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1183-1189

CD Volume:335

Print Article: Pages: 1183-1189

Author(s):Zhang H B Budiman M A Wing R A

Author Affiliation:Department of Soil and Crop Sciences, Texas A & M University, College Station, TX 77843-2123, USA

Language:English

Abstract:Abscission zones are specialized regions in plants, usually located at the base of most plant parts, such as flowers, fruit and leaves, where organs are shed. Although a great deal of information is known about the physiological and biochemical events that lead to organ shedding, very little is known of the molecular events that lead to the formation of the abscission zone itself. In tomato, two recessive mutations have been discovered that completely suppress the formation of flower and fruit pedicel abscission zones, i.e., jointless (j) and jointless-2 (j-2), both tentatively localized to chromosome 11 about 30 cM apart. Because the study of the control of abscission zone development is important for both basic and applied research, we are using a map-based cloning approach to identify the jointless genes. The first step in any positional cloning experiment is to establish segregating mapping populations for the target gene and identify closely linked molecular markers that flank the locus. In this study, bulked segregant analysis was used to identify an RAPD marker associated with the j-2 locus, RPD140. To determine the chromosome location of RPD140, we converted it to an RFLP marker that was then mapped on the Cornell reference tomato

map in a marker-dense region of chromosome 12. To verify that the j-2 locus was located on tomato chromosome 12, we used nine chromosome 12 RFLP markers linked with RPD140 to map the j-2 gene in an interspecific F2 mapping population of 151 plants segregating for j-2. The j-2 gene was localized to a 3.0-cM interval between RPD140 and TG618 on tomato chromosome 12
Descriptors:gene-mapping. restriction-fragment-length-polymorphism. abscission. flowers. genes. interspecific-hybridization. mutations. plant-development. gene-location. genetic-markers. random-amplified-polymorphic-DNA. tomatoes. vegetables. biotechnology
Organism Descriptors:Lycopersicon-esculentum. Lycopersicon
Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:24 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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532. Title:Recombinant chromosomes of advanced backcross plants between Allium cepa L. and A. fistulosum L. revealed by in situ hybridization
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1190-1196
CD Volume:335
Print Article: Pages: 1190-1196
Author(s):Hou A Peffley E B
Author Affiliation:Department of Plant and Soil Science, and the Institute of Biotechnology, Texas Tech University, Lubbock, TX79409, USA
Language:English
Abstract:Cytological analysis of (Allium cepa x Allium fistulosum) x A. cepa F1BC3 plants revealed that most plants were diploid with 16 chromosomes. Karyotypes of these plants showed recombinant chromosomes. Fluorescence and genomic in situ hybridization patterns of the interspecific F1 hybrid and F1BC3 plants revealed A. fistulosum chromosomes or chromosomal segments. A highly repetitive 376-bp DNA sequence and genomic DNA of A. fistulosum revealed similar telomeric hybridization sites when hybridized onto A. fistulosum chromosomes. Cytogenetic evidence showed that A. fistulosum DNA has recombined into the A. cepa genome
Descriptors:chromosomes. DNA-hybridization. DNA. fluorescence. genomes. genome-analysis. interspecific-hybridization. karyotypes. recombination. introgression. backcrosses. vegetables. Welsh-onions. onions
Organism Descriptors:Allium-fistulosum. Allium. Allium-cepa
Supplemental Descriptors:Allium. Alliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF003. WW000
Supplementary Info:28 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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533. Title:QTLs for cell-membrane stability mapped in rice (Oryza sativa L.) under drought stress
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1197-1202
CD Volume:335
Print Article: Pages: 1197-1202
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Author Affiliation:Plant Molecular Genetics Laboratory, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409-2122, USA
Language:English
Abstract:Cell-membrane stability (CMS) is considered to be one of the major selection indices of drought tolerance in cereals. In order to determine which genomic region is responsible for CMS, 104 rice (Oryza sativa) doubled haploid (DH) lines derived from a cross between CT9993-5-10-1-M and IR62266-42-6-2 were studied in the greenhouse in a slowly developed drought stress environment. Drought stress was induced on 50-day-old plants by withholding water. The intensity of stress was assessed daily by visual scoring of leaf wilting and by measuring leaf relative water content (RWC). The leaf samples were collected from both control (well-watered) and stressed plants (at 60-65% of RWC), and the standard test for CMS was carried out in the laboratory. There was no significant difference (P>0.05) in RWC between the two parental lines as well as among the 104 lines, indicating that all the plants were sampled at a uniform stress level. However, a significant difference (P<0.05) in CMS was observed between the two parental lines and among the population. No significant correlation was found between CMS and RWC, indicating that the variation in CMS was genotypic in nature. The continuous distribution of CMS and its broad-sense heritability (34%) indicates that CMS should be polygenic in nature. A linkage map of this population comprising of 145 RFLPs, 153 AFLPs and 17 microsatellite markers was used for QTL analysis. Composite interval mapping identified nine putative QTLs for CMS located on chromosomes 1, 3, 7, 8, 9, 11 and 12. The amount of phenotypic variation that was explained by individual QTLs ranged from 13.4% to 42.1%. Four significant (P<0.05) pairs of digenic interactions between the detected QTLs for CMS were observed. The identification of QTLs for this important trait will be useful in breeding for the improvement of drought tolerance in rice. This is the first report of mapping QTLs associated with CMS under a natural water stress condition in any crop plants
Descriptors:drought. rice. chromosomes. drought-resistance. heritability. identification. linkage. gene-mapping. gene-location. phenotypic-variation. water-content. water-stress. quantitative-traits. quantitative-trait-loci. cell-membranes. restriction-fragment-length-polymorphism. genetic-markers. cereals. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Oryza. Oryza-sativa
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Oryza
Subject Codes:FF020. FF005. FF900. FF060. WW000
Supplementary Info:64 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

534. Title:An assessment of genetic relationships within the genus Digitalis based on PCR-generated RAPD markers
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1209-1216
CD Volume:335
Print Article: Pages: 1209-1216
Author(s):Nebauer S G Castillo Agudo L del Segura J
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Author Affiliation:Departamento de Biologia Vegetal, Facultad de Farmacia, Universitat de Valencia, Av. V.A. Estelles s/n, 46100-Burjassot, Valencia, Spain
Language:English

Abstract:RAPD markers were used to study inter-specific variation among six species of the genus Digitalis: D. obscura, D. lanata, D. grandiflora, D. purpurea, D. thapsi and D. dubia, and the hybrid D. excelsior (D. purpurea x D. grandiflora). A total of 91 highly reproducible bands amplified with four arbitrarily chosen decamer primers were obtained. Homology of the co-emigrating RAPD markers was tested by blot hybridization and sequencing of selected bands. The application of a range of statistical approaches for RAPD data analysis, including distance and parsimony methods, family clustering and the analysis of molecular variance (AMOVA), indicated that these molecular markers were taxonomically informative in Digitalis. The species relationships revealed were fully consistent with those previously obtained using morphological affinities. The hybrid D. excelsior seems to have stronger affinity to the section Digitalis than to Grandiflorae. This is the first known report of the application of RAPD markers for the study of genetic relationships among species of the genus Digitalis
Descriptors:assessment. interspecific-hybridization. morphology. random-amplified-polymorphic-DNA. phylogeny. taxonomy. medicinal-plants. biotechnology
Organism Descriptors:Digitalis. Digitalis-purpurea. Digitalis-lanata. Digitalis-grandiflora. Digitalis-thapsi
Supplemental Descriptors:Scrophulariaceae. Scrophulariales. dicotyledons. angiosperms. Spermatophyta. plants. Digitalis
Subject Codes:FF020. WW000. ZZ380
Supplementary Info:43 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

535. Title:Location and mapping of the powdery mildew resistance gene MlRE and detection of a resistance QTL by bulked segregant analysis (BSA) with microsatellites in wheat
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1217-1224
CD Volume:335
Print Article: Pages: 1217-1224
Author(s):Chantret N Sourdille P Roder M Tavaud M Bernard M Doussinault G
Author Affiliation:I.N.R.A. Station d'Amelioration des Plantes, Domaine de la Motte, 35653 Le Rheu Cedex, France
Language:English
Abstract:Powdery mildew (Blumeria graminis [Erysiphe graminis] f.sp. tritici) is one of the most damaging diseases of wheat (Triticum aestivum). The objective of this study was to locate and map a recently identified powdery mildew resistance gene, MlRE, carried by the resistant line RE714 using microsatellites uniformly distributed among the whole genome together with a bulked segregant analysis (BSA). The bulks consisted of individuals with an extreme phenotype taken from a population of 140 F3 families issued from the cross between RE714 (resistant) and Hardi (susceptible). The population had been tested with three powdery mildew isolates at the seedling stage. Qualitative interpretation of the resistance tests located the MlRE gene on the distal part of the long arm of chromosome 6A. A subsequent quantitative interpretation of the resistance permitted us to detect another resistance factor on a linkage group assigned to chromosome 5D, which was constructed with microsatellites for which a polymorphism of intensity between bulks was observed. This quantitative trait locus (QTL) explained 16.8-25.3% of the total variation. An interaction between both the resistant factor (MlRE and the QTL) was found for only one of the isolates tested. This study shows the advantage of making a

quantitative interpretation of resistant tests and that the use of microsatellites combined with BSA is a powerful strategy to locate resistance genes in wheat
Descriptors:gene-mapping. microsatellites. fungal-diseases. wheat. genes. linkage. polymorphism. seedlings. gene-location. plant-pathogens. plant-diseases. disease-resistance. plant-pathogenic-fungi. cereals. biotechnology. plant-pathology
Organism Descriptors:Triticum-aestivum. Erysiphe-graminis. Erysiphe-graminis-f.sp.-tritici. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Erysiphe. Erysiphales. Ascomycotina. Eumycota. fungi. Erysiphe-graminis
Subject Codes:FF020. WW000. FF610. HH600
Supplementary Info:37 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

536. Title:Identification of genomic regions associated with stay green in sorghum by testing RILs in multiple environments
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1225-1232
CD Volume:335
Print Article: Pages: 1225-1232
Author(s):Tao Y Z Henzell R G Jordan D R Butler D G Kelly A M McIntyre C L
Author Affiliation:CSIRO Tropical Agriculture, 306 Carmody Rd, St. Lucia, QLD 4067, Australia
Language:English
Abstract:Stay green is an important drought resistance trait for sorghum production. QTLs for this trait with consistent effects across a set of environments would increase the efficiency of selection because of its relatively low heritability. One hundred and sixty recombinant inbreds, derived from a cross between QL39 and QL41, were used as a segregating population for genome mapping and stay green evaluation. Phenotypic data were collected in replicated field trials from five sites and in three growing seasons, and analysed by fitting appropriate models to account for spatial variability and to describe the genotype by environment interaction. Interval mapping and non-parametric mapping identified three regions, each in a separate linkage group, associated with stay green in more than one trial, and two regions in single trial. The regions on linkage groups B and I were both consistently identified from three trials. The multiple environment testing was very helpful for correctly identifying QTLs associated with the trait. The utilisation of molecular markers for stay green in sorghum breeding is also discussed
Descriptors:drought. drought-resistance. genotypes. heritability. linkage. gene-mapping. gene-location. quantitative-trait-loci. colour. cereals. biotechnology
Organism Descriptors:Sorghum-bicolor
Supplemental Descriptors:Sorghum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. FF900. FF030. WW000
Supplementary Info:35 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

537. Title:Assessment of interspecific hybridization between transgenic oilseed rape and wild radish under normal agronomic conditions
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1233-1239
CD Volume:335
Print Article: Pages: 1233-1239
Author(s):Chevre A M Eber F Darmency H Fleury A Picault H Letanneur J C Renard M
Author Affiliation:Station d'Amelioration des Plantes, INRA BP 35327, 35653 Le Rheu cedex, France
Language:English
Abstract:In order to assess the hybridization rate between oilseed rape (Brassica napus, AACC, 2n=38) and wild radish (Raphanus raphanistrum, RrRr, 2n=18) under normal agronomic conditions, three 1-ha field experiments were performed at Rennes, France in 1996 and at Dijon, France in 1996 and 1997. In each case, wild radish plants were transplanted at different densities in the middle, the border or the margin of a herbicide-tolerant oilseed rape field. Among the 189 084 seedlings obtained from seeds harvested on wild radish plants, only one herbicide-tolerant interspecific hybrid (RrRrAC, 2n=37) was characterized from seeds harvested on an isolated plant growing in the margin of the field. Thus, for the wild radish total harvest, with a 95% confidence limit, the frequency of interspecific hybrids was assessed to range from 10-7 to 3.10-5. Interspecific hybrids were detected in all cases among the smallest seeds with a diameter less than 1.6 mm harvested on oilseed rape, but the highest frequency was obtained from oilseed rape close to wild radish plants growing as clusters in the border or the margin of the field. Most hybrids had the expected triploid genomic structure (ACRr, 2n=28), except for four amphidiploids (AACCRrRr, 2n=56) and one hybrid from a wild radish unreduced gamete (ACRrRr, 2n=37). Among the 73 847 seedlings observed on the oilseed rape total harvest, the frequency of interspecific hybrids was assessed to range from 2.10-5 to 5.10-4, with a 95% confidence limit. The results are discussed with regard to the type of oilseed rape variety used and the characteristics of the interspecific hybrids
Descriptors:hybridization. intergeneric-hybridization. rape. radishes. transgenics. characterization. hybrids. seedlings. seeds. gene-flow. transgenic-plants. biosafety. fatty-oil-plants. oil-plants. biotechnology
Geographic Locator:France
Organism Descriptors:Raphanus-sativus. Brassica-napus. Brassica-napus-var.-oleifera
Supplemental Descriptors:Raphanus. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica. Brassica-napus. Western-Europe. Europe. Mediterranean-Region. Developed-Countries. European-Union-Countries. OECD-Countries
Subject Codes:FF020. WW000. FF005
Supplementary Info:18 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

538. Title:Development and incorporation of microsatellite markers into the linkage map of sugar beet (Beta vulgaris spp.)
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1240-1248
CD Volume:335
Print Article: Pages: 1240-1248
Author(s):Rae S J Aldam C Dominguez I Hoebrechts M Barnes S R Edwards K J

Author Affiliation:IACR, Long Ashton Research Station, Institute of Arable Crop Research, Department of Agricultural Sciences, University of Bristol, Long Ashton, Bristol BS41 9AF, UK
Language:English
Abstract:A set of informative simple sequence repeat markers has been identified for use in the marker-assisted breeding of Beta vulgaris. Highly enriched small insert genomic libraries of sugarbeet were constructed, consisting of 1536 clones (with inserts of between 250-900 bp). Screening the clones with CA, CT, CAA, CATA and GATA nucleotide-repeat probes revealed positive hybridization to over 50% of the clones. Three-hundred-and-forty clones were sequenced. Primer pairs were designed for sequences flanking the repeats and, of these, 57 pairs revealed length polymorphism with 12 Beta accessions. Heterozygosity levels of the SSR loci ranged from 0.069 to 0.809. Heterozygosity levels were found to be similar to those detected using RFLP probes with the same accessions. Phenetic analysis using the markers indicated relationships in accordance with known pedigrees. Twenty-three of the SSR markers were polymorphic in one or both of two F2 mapping populations, and were placed relative to a framework of RFLP probes. The markers are distributed over all nine linkage groups of sugarbeet
Descriptors:linkage. sugarbeet. heterozygosity. gene-mapping. polymorphism. restriction-fragment-length-polymorphism. genetic-markers. microsatellites. sugar-crops. biotechnology
Organism Descriptors:Beta-vulgaris. Beta-vulgaris-var.-saccharifera
Supplemental Descriptors:Beta. Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms. Spermatophyta. plants. Beta-vulgaris
Subject Codes:FF020. FF005. WW000
Supplementary Info:42 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

539. Title:An integrated genetic map of Populus deltoides based on amplified fragment length polymorphisms
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1249-1256
CD Volume:335
Print Article: Pages: 1249-1256
Author(s):Wu R L Han Y F Hu J J Fang J J Li L Li M L Zeng Z B
Author Affiliation:Program in Statistical Genetics, Department of Statistics, North Carolina State University, Raleigh, NC 27695-8203, USA
Language:English
Abstract:Amplified fragment length polymorphism (AFLP) is an efficient molecular technique for generating a large number of DNA-based genetic markers in Populus. We have constructed an integrated genetic map for a Populus backcross population derived from two selected P. deltoides clones using AFLP markers. A traditional strategy for genetic mapping in outcrossing species, such as forest trees, is based on two-way pseudo-testcross configurations of the markers (testcross markers) heterozygous in one parent and null in the other. By using the markers segregating in both parents (intercross markers) as bridges, the two parent-specific genetic maps can be aligned. In this study, we detected a number of non-parental heteroduplex markers resulting from the PCR amplification of two DNA segments that have a high degree of homology to one another but differ in their nucleotide sequences. These heteroduplex markers detected have served as bridges to generate an integrated map which includes 19 major linkage groups equal to the Populus haploid chromosome number and 24 minor groups. The 19 major

linkage groups cover a total of 2927 cM, with an average spacing between two markers of 23.3 cM. The map developed in this study provides a first step in producing a highly saturated linkage map of the Populus deltoides genome
Descriptors:poplars. DNA. gene-mapping. genetic-markers. linkage. nucleotide-sequences. outcrossing. polymerase-chain-reaction. polymorphism. forest-trees. broadleaves. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Populus. Populus-deltoides
Supplemental Descriptors:Salicaceae. Salicales. dicotyledons. angiosperms. Spermatophyta. plants. Populus
Subject Codes:FF020. KK100. WW000
Supplementary Info:32 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

540. Title:Microsatellites and microsynteny in the chloroplast genomes of Oryza and eight other Gramineae species
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1257-1266
CD Volume:335
Print Article: Pages: 1257-1266
Author(s):Ishii T McCouch S R
Author Affiliation:Department of Plant Breeding, 252 Emerson Hall, Cornell University, Ithaca, NY 14853-1901, USA
Language:English
Abstract:Primer pairs flanking ten chloroplast microsatellite loci, originally identified in Oryza sativa cv. Nipponbare, were evaluated for amplification and allelic diversity using a panel of 13 diverse cultivars of rice (O. sativa), 19 accessions of wild rice (three O. officinalis, five O. latifolia, five O. minuta, four O. australiensis, one O. brachyantha and one O. ridleyi) and eight other Gramineae species (maize, teosinte, wheat, oat, barley, pearl millet, sorghum and sugarcane). Amplified products were obtained for all samples at nine out of ten loci. Among the rice cultivars, the number of alleles per locus ranged from one to four, with monomorphic patterns observed at five loci. The average polymorphism information content (PIC) value at the other five (polymorphic) loci was 0.54 among the 13 cultivars. When wild rice and the other Gramineae species were compared based on the proportion of shared alleles, their phylogenetic relationships were in agreement with previous studies using different types of markers; however, the magnitude of the differences based on chloroplast microsatellites underestimated the genetic distance separating these divergent species and genera. A sequence-based comparison of homologous regions of the rice and maize chloroplast genomes revealed that, while a high level of microsynteny is evident, the occurrence of actively evolving microsatellite motifs in specific regions of the rice chloroplast genome appears to be mainly a species or genome-specific phenomenon. Thus, the chloroplast primer pairs used in this study bracketed mutationally active microsatellite motifs in rice but degenerate, interrupted motifs or highly conserved, mutationally inert motifs in distantly related genera
Descriptors:chloroplasts. genomes. alleles. amplification. barley. maize. microsatellites. millets. rice. phylogenetics. polymorphism. sugarcane. wheat. wild-relatives. oats. chloroplast-genetics. chloroplast-DNA. repetitive-DNA. gene-mapping. cereals. biotechnology. pearl-millet
Identifiers:Oryza ridleyi

Organism Descriptors:Poaceae. Oryza. Hordeum-vulgare. Zea-mays. Oryza-australiensis. Oryza-brachyantha. Oryza-minuta. Oryza-officinalis. Oryza-sativa. Pennisetum-glaucum. Sorghum. Saccharum-officinarum. Zea. Triticum-aestivum. Oryza-latifolia. Sorghum-bicolor. Avena-sativa. Saccharum. Triticum
Supplemental Descriptors:Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Poaceae. Hordeum. Zea. Oryza. Pennisetum. Saccharum. Triticum. Sorghum. Avena
Subject Codes:FF020. WW000. FF005
Supplementary Info:47 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

541. Title:The genetic basis of seed-weight variation: tomato as a model system
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1267-1273
CD Volume:335
Print Article: Pages: 1267-1273
Author(s):Doganlar S Frary A Tanksley S D
Author Affiliation:Department of Plant Breeding, 252 Emerson Hall, Cornell University, Ithaca, NY 14853-1902, USA
Language:English
Abstract:QTL mapping experiments conducted in tomato during the past decade have allowed the identification of many seed-weight QTLs and have also revealed that only a few loci are responsible for the majority of the seed-weight changes that accompanied the domestication of tomato. This review presents a consensus map for seed weight QTL identified in previously published reports and in unpublished results from our laboratory
Descriptors:genes. tomatoes. gene-mapping. seed-weight. seedlings. seeds. gene-location. quantitative-trait-loci. quantitative-traits. vegetables. biotechnology
Organism Descriptors:Lycopersicon-esculentum. Lycopersicon
Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF030. FF003. WW000
Supplementary Info:26 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

542. Title:A newly identified barley gene, Dhn12, encoding a YSK2 DHN, is located on chromosome 6H and has embryo-specific expression
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1274-1278
CD Volume:335
Print Article: Pages: 1274-1278
Author(s):Choi D W Close T J
Author Affiliation:Department of Botany and Plant Sciences, University of California, Riverside, CA 92521-0124, USA
Language:English
Abstract:Dehydrins are water-soluble lipid-associating proteins that accumulate during low-temperature or water-deficit conditions, and are thought to play a role in freezing- and drought-tolerance in plants. Dhn genes exist as multi-gene families in plants. Previously, we screened lambda genomic libraries of two barley cultivars in an effort to isolate all of the barley Dhn genes. We identified 11 unique Dhn genes and estimated a total of 13 Dhn genes in the barley genome. To extend the

collection, we used an alternative source of clones, a 1.5xMorex barley BAC library. In this library, we found nine Dhn genes that we had described previously and one new Dhn gene, Dhn12. The Dhn12 gene encodes an acidic YSK2 dehydrin. The Dhn12 gene is located on chromosome 6H, and shows a different expression pattern from all other Dhn genes identified previously. RT-PCR results show that Dhn12 expression is embryo-specific. Dhn12 is not expressed in seedling shoots under any of the conditions tested, including non-stressed as well as dehydrated, or cold-, abscisic acid- or NaCl-treated seedlings
Descriptors:barley. genes. seedlings. gene-expression. nucleotide-sequences. gene-mapping. gene-location. plant-embryos. cereals. biotechnology
Identifiers:dehydrins
Organism Descriptors:Hordeum-vulgare
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. FF005
Supplementary Info:15 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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543. Title:Targeted resistance gene mapping in soybean using modified AFLPs
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1279-1283
CD Volume:335
Print Article: Pages: 1279-1283
Author(s):Hayes A J Maroof M A S
Author Affiliation:Department of Crop and Soil Environmental Sciences, Virginia Tech, Blacksburg, VA 24061-0404, USA
Language:English
Abstract:The soyabean (Glycine max) linkage group F contains a vital region of clustered genes for resistance to numerous pathogens including the soybean mosaic virus [soybean mosaic potyvirus] resistance gene, Rsv1. In order to develop new genetic markers that map to this gene cluster, we employed a targeted approach that utilizes the speed and high-throughput of AFLP, but modified it to incorporate sequence information from the highly conserved nucleotide binding site (NBS) region of cloned disease resistance genes. By using a labelled degenerate primer corresponding to the p-loop portion of the NBS region of resistance genes, such as N, L6 and Rps2, we were able to quickly amplify numerous polymorphic bands between parents of a population segregating for resistance to Rsv1. Of these polymorphic bands, bulk segregant analysis revealed four markers that were closely linked to Rsv1. These markers were cloned and used as probes for RFLP analysis. The four clones mapped to within a 6 cM region surrounding Rsv1, the closest being 0.4 cM away from the gene. Sequence analysis showed that all four clones contain the p-loop sequence corresponding to the degenerate primer and that one of the four clones contains an open reading frame sequence which when translated is related to the NBS region of other cloned disease resistance genes. The rapid identification of four markers closely linked to Rsv1 in soyabean demonstrates the utility of this method for generating markers tightly linked to important plant disease resistance genes
Descriptors:gene-mapping. soyabeans. binding-sites. disease-resistance. genes. genetic-markers. linkage. plant-pathogens. restriction-fragment-length-polymorphism. grain-legumes. biotechnology. plant-pathology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Glycine-max. Glycine-(Fabaceae). soybean-mosaic-potyvirus. plant-viruses. Fabaceae

Supplemental Descriptors:Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. potyvirus-group. plant-viruses. viruses. plant-pathogens. pathogens
Subject Codes:FF020. FF005. HH600. FF610. WW000
Supplementary Info:28 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

544. Title:Identification of eight chromosomes and a microsatellite marker on 1AS associated with QTL for grain weight in bread wheat
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1290-1294
CD Volume:335
Print Article: Pages: 1290-1294
Author(s):Varshney R K Prasad M Roy J K Kumar N Harjit Singh Dhaliwal H S Balyan H S Gupta P K
Author Affiliation:Molecular Biology Laboratory, Department of Agricultural Botany, Ch. Charan Singh University, Meerut-250004, India
Language:English
Abstract:The present study in bread wheat was undertaken (1) to identify chromosomes carrying QTLs controlling 1000-grain weight (GW) and (2) to develop molecular marker(s) linked with this trait. Using the genotype Rye Selection111 (RS111), we carried out a monosomic analysis that suggested that 8 chromosomes (1A, 1D, 2B, 4B, 5B, 6B, 7A and 7D) carried QTLs controlling GW, with only 3 of these (1A, 2B and 7A) carrying alleles for high GW. To tag the QTLs present on these chromosomes, we crossed the genotype RS111 with high GW (56.83 g) with the genotype Chinese Spring (CS) with low GW (23.74 g) and obtained 100 RILs. These RILs showed normal distribution for GW. The parental genotypes were analysed with as many as 346 STMS primer pairs for detection of polymorphism. Of these, 267 primer pairs gave scorable amplification products, 63 of which detected polymorphism between the parents. Using each of these 63 primer pairs, we carried out bulked segregant analysis on RILs representing two extremes of the distribution. One primer pair (WMC333) showed an association of the marker locus Xwmc333 with grain weight. This was confirmed through selective genotyping, and the co-segregation data on molecular marker locus Xwmc333 and GW were analysed following a single marker linear regression approach. Significant regression suggested linkage between Xwmc333 and a QTL for GW. The results showed that the above QTL accounted for 15.09% of the variation for GW between the parents. The marker has been located on chromosome arm 1AS, and the QTL was designated QGw1.ccsu-1A
Descriptors:chromosomes. grain. seeds. wheat. alleles. linkage. polymorphism. rye. genetic-markers. gene-location. gene-mapping. seed-weight. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Secale-cereale. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Secale
Subject Codes:FF020. FF005. QQ050. WW000
Supplementary Info:20 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

545. Title:QTLs and epistasis for aluminum tolerance in rice (Oryza sativa L.) at different seedling stages

View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1295-1303
CD Volume:335
Print Article: Pages: 1295-1303
Author(s):Wu P Liao C Y Hu B Yi K K Jin W Z Ni J J He C
Author Affiliation:Department of Biological Science, College of Life Science, Zhejiang University, Hua Jia Chi Campus, Hangzhou, 310029, China
Language:English
Abstract:To investigate the genetic background for aluminium (Al) tolerance in rice, a recombinant inbred (RI) population, derived from a cross between an Al-sensitive lowland indica rice variety, IR1552, and an Al-tolerant upland japonica rice variety, Azucena, was used in culture solution. A molecular linkage map, together with 104 amplified fragment length polymorphism (AFLP) markers and 103 restriction fragment length polymorphism (RFLP) markers, was constructed to map quantitative trait loci (QTLs) and epistatic loci for Al tolerance based on the segregation for relative root length (RRL) in the population. RRL was measured after stress for 2 and 4 weeks at a concentration of 1 mM of Al3+ and a control with a pH of 4.0, respectively. Two QTLs were detected at both the 2nd and the 4th weeks on chromosomes 1 and 12 from unconditional mapping, while the QTL on chromosome 1 was only detected at the 2nd stress week from conditional mapping. The effect of the QTL on chromosome 12 was increased with an increase of the stress period from 2 to 4 weeks. The QTL on chromosome 1 was expressed only at the earlier stress, but its contribution to tolerance was prolonged during growth. At least one different QTL was detected at the different stress periods. Mean comparisons between marker genotypic classes indicated that the positive alleles at the QTLs were from the Al-tolerant upland rice Azucena. An important heterozygous non-allelic interaction on Al tolerance was found. The results indicated that tolerance in the younger seedlings was predominantly controlled by an additive effect, while an epistatic effect was more important to the tolerance in older seedlings; additionally the detected QTLs may be multiple allelic loci for Al tolerance and phosphorus-uptake efficiency, or for Al and Fe2+ tolerance
Descriptors:aluminium. rice. seedlings. alleles. chromosomes. linkage. gene-mapping. polymorphism. restriction-fragment-length-polymorphism. quantitative-trait-loci. genetic-markers. roots. genetic-variance. toxic-substances. toxicity. stress. cereals. biotechnology
Organism Descriptors:Oryza. Oryza-sativa
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Oryza
Subject Codes:FF020. FF005. FF900. WW000
Supplementary Info:34 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

546. Title:Chloroplast DNA diversity within and among populations of the allotetraploid Prunus spinosa L
View Article: Theoretical and Applied Genetics. 2000. 100 (8). 1304-1310
CD Volume:335
Print Article: Pages: 1304-1310
Author(s):Mohanty A Martin J P Aguinagalde I
Author Affiliation:Departamento de Biologia Vegetal, Escuela Tecnica Superior de Ingenieros Agronomos, Universidad Politecnica de Madrid, Ciudad Universitaria s/n, 28040 Madrid, Spain
Language:English

Abstract:High chloroplast DNA (ctDNA) diversity was found within and among populations of Prunus spinosa sampled from seven European deciduous forests. A study of 12% of the total chloroplast genome detected 44 mutations, which were distributed over 24 haplotypes; four were common to two or more populations and the rest were unique haplotypes. The most-abundant and widely distributed haplotype was H2 (frequency of approximately 41%). Six of the seven populations were polymorphic. All of the six polymorphic populations had "private" haplotypes (frequency <5%) in addition to common haplotypes. The UPGMA dendrogram demonstrated a correlation between populations and their geographical locations. The total diversity was high (hT=0.824) and a major portion of it was within populations (hs=0.663). The level of population subdivision for unordered alleles was low (GST=19.5%) and for ordered alleles was lower (NST=13.6%). No phylogeographic structure could be demonstrated in the present geographical scale. High polymorphism in the ctDNA of P. spinosa has to be considered carefully when planning phylogenetic studies involving this species
Descriptors:DNA. alleles. chloroplasts. chloroplast-DNA. chloroplast-genetics. deciduous-forests. haplotypes. mutations. phylogenetics. polymorphism. wild-relatives. fruit-crops. biotechnology. biotechnology
Geographic Locator:Europe
Organism Descriptors:Prunus. Prunus-spinosa
Supplemental Descriptors:Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants. Prunus
Subject Codes:FF020. KK100. WW000. FF003
Supplementary Info:40 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

547. Title:Selection of transgenic meristematic cells utilizing a herbicidal molecule results in the recovery of fertile transgenic soybean (Glycine max (L.) Merrill) plants at a high frequency
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 1-6
CD Volume:335
Print Article: Pages: 1-6
Author(s):Aragao F J L Sarokin L Vianna G R Rech E L
Author Affiliation:Laboratorio de Introducao e Expressao de Genes, Embrapa Recursos Geneticos e Biotecnologia, Parque Estacao Biologica, Final Av. W3 Norte, Brasilia, DF 70770-900, Brazil
Language:English
Abstract:Imazapyr is a herbicidal molecule that concentrates in the apical meristematic region of the plant. Its mechanism of action is the inhibition of the enzymatic activity of acetohydroxyacid synthase [acetolactate synthase], which catalyses the initial step in the biosynthesis of isoleucine, leucine and valine. The selectable marker gene, ahas, was previously isolated from Arabidopsis thaliana and contains a mutation at position 653 bp. Combining the use of imazapyr, the ahas gene and a multiple shooting induction protocol has allowed us to develop a novel system to select transgenic meristematic cells after the physical introduction of foreign genes. In this study, we describe a protocol to obtain a high frequency of fertile transgenic soyabean plants that is variety-independent
Descriptors:transgenic-plants. genes. imazapyr. soyabeans. genetic-transformation. genetic-engineering. gene-expression. herbicides. herbicide-resistance. acetolactate-synthase. grain-legumes. biotechnology

Organism Descriptors:Arabidopsis-thaliana. Glycine-max. Fabaceae. Glycine-(Fabaceae)
Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales
Subject Codes:FF005. HH410. FF020. WW000
Supplementary Info:19 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

548. Title:The contribution of short repeats of low sequence complexity to large conifer genomes
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 7-14
CD Volume:335
Print Article: Pages: 7-14
Author(s):Schmidt A Doudrick R L Heslop Harrison J S Schmidt T
Author Affiliation:Institute of Crop Science and Plant Breeding, Olshausenstrasse 40, D-24118 Kiel, Germany
Language:English
Abstract:The abundance and genomic organization of six simple sequence repeats, consisting of di-, tri-, and tetranucleotide sequence motifs, and a minisatellite repeat have been analysed in different gymnosperms by Southern hybridization. Within the gymnosperm genomes investigated, the abundance and genomic organization of micro- and minisatellite repeats largely follows taxonomic groupings. We found that only particular simple sequence repeat motifs are amplified in gymnosperm genomes, while others such as (CAC)5 and (GACA)4 are present in only low copy numbers. The variation in abundance of simple sequence motifs reflects a similar situation to that found in angiosperms. Species of the two- and three-needle pine section Pinus are relatively conserved and can be distinguished from Pinus strobus which belongs to the five-needle pine section Strobus. The hybridization pattern of Picea species, bald cypress (Taxodium distichum) and gingko (Gingko biloba) were different from the patterns detected in the Pinus species. Furthermore, sequences with homology to the plant telomeric repeat (TTTAGGG)n have been analysed in the same set of gymnosperms. Telomere-like repeats are highly amplified within two- and three-needle pine genomes, such as slash pine (Pinus elliottii var. elliottii), compared to P. strobus, Picea species, bald cypress and gingko. P. elliottii var. elliottii was used as a representative species to investigate the chromosomal organization of telomere-like sequences by fluorescence in situ hybridization (FISH). The telomere-like sequences are not restricted to the ends of chromosomes; they form large intercalary and pericentric blocks showing that they are a repeated component of the slash pine genome. Conifers have genomes larger than 20 000 Mbp, and our results clearly demonstrate that repeats of low sequence complexity, such to (CA)8, (GA)8, (GGAT)4 and (GATA)4, and minisatellite- and telomere-like sequences represent a large fraction of the repetitive DNA of these species. The striking differences in abundance and genome organization of the various repeat motifs suggest that these repetitive sequences evolved differently in the gymnosperm genomes investigated
Descriptors:DNA-hybridization. repetitive-DNA. taxonomy. phylogeny. microsatellites. forest-trees. biotechnology. plant-genetic-resources
Identifiers:fluorescence in situ hybridization
Organism Descriptors:Pinopsida. Pinus-elliottii. Picea. Pinus-strobus. Ginkgo-biloba. gymnosperms. Taxodium-distichum

Supplemental Descriptors:gymnosperms. Spermatophyta. plants. Pinus. Pinaceae. Pinopsida. Ginkgo. Ginkgoaceae. Ginkgoopsida. Taxodium. Taxodiaceae
Subject Codes:FF020. WW000. KK100. ZZ380
Supplementary Info:38 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

549. Title:The pachytene chromosomes of maize as revealed by fluorescence in situ hybridization with repetitive DNA sequences
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 30-36
CD Volume:335
Print Article: Pages: 30-36
Author(s):Chen C C Chen C M Hsu F C Wang C J Yang J T Kao Y Y
Author Affiliation:Department of Botany, National Taiwan University, Taipei, Taiwan
Language:English
Abstract:A repetitive DNA sequence, ZmCR2.6c, was isolated from maize based on centromeric sequence CCS1 of the wild grass Brachypodium sylvaticum. ZmCR2.6c is 309 bp in length and shares 65% homology to bases 421-721 of the sorghum centromeric sequence pSau3A9. Fluorescence in situ hybridization (FISH) localized ZmCR2.6c to the primary constrictions of pachytene bivalents and to the stretched regions of MI/AI chromosomes, indicating that ZmCR2.6c is an important part of the centromere. Based on measurements of chromosome lengths and the positions of FISH signals of several cells, a pachytene karyotype was constructed for maize inbred line KYS. The karyotype agrees well with those derived from traditional analyses. Four classes of tandemly repeated sequences were mapped to the karyotype by FISH. Repeats 180 bp long are present in cytologically detectable knobs on 5L, 6S, 6L, 7L, and 9S, as well as at the termini and in the interstitial regions of many chromosomes not reported previously. A most interesting finding is the presence of 180-bp repeats in the NOR-secondary constriction. TR-1 elements co-exist with 180-bp repeats in the knob on 6S and form alone a small cluster in 4L. 26S and 5S rRNA genes are located in the NOR and at 2L.88, respectively. The combination of chromosome length, centromere position, and distribution of the tandem repeats allows all chromosomes to be identified unambiguously. The results presented form an important basis for using FISH for physical mapping and for investigating genome organization in maize
Descriptors:chromosome-morphology. DNA-hybridization. fluorescence. maize. repetitive-DNA. gene-mapping. chromosomes. cereals. biotechnology
Identifiers:fluorescence in situ hybridization
Organism Descriptors:Zea-mays. Brachypodium-sylvaticum
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Brachypodium
Subject Codes:FF005. FF020. WW000
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

550. Title:Fine physical mapping of the rice stripe resistance gene locus, Stvb-i
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 59-63
CD Volume:335
Print Article: Pages: 59-63

Author(s):Hayano Saito Y Saito K Nakamura S Kawasaki S Iwasaki M
Author Affiliation:Hokkaido National Agricultural Experiment Station (HNAES), Hitsujigaoka 1, Toyohira-ku, Sapporo 062-8555, Japan
Language:English
Abstract:The Stvb-i gene confers stripe disease resistance to rice. For positional cloning, we constructed a physical map spanning 1.8-cM distance between flanking markers, consisting of 18 bacterial artificial chromosome (BAC) clones, around the Stvb-i locus on rice chromosome 11. The 18 clones were isolated by screening a BAC library derived from a japonica cultivar, Shimokita, with three Stvb-i-linked RFLP markers and DraI-digested DNAs of a yeast artificial chromosome (YAC) clone. The results of Southern hybridization and restriction enzyme analyses indicated that these BAC clones are contiguous and cover about a 700-kb region containing the Stvb-i allele. Utilizing end and internal fragments of the BAC insert DNAs, 33 molecular markers were generated within a small chromosomal region including the Stvb-i locus. Genotyping analysis with these markers for a resistant cultivar and four nearby recombinants selected from 120 F2 individuals indicated that Stvb-i is contained within an approximately 286-kb region covered with two overlapping BAC clones
Descriptors:genes. gene-mapping. rice. disease-resistance. plant-diseases. plant-pathogens. cereals. biotechnology
Organism Descriptors:Oryza-sativa. rice-stripe-tenuivirus. plant-viruses. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. tenuivirus-group. plant-viruses. viruses. plant-pathogens. pathogens
Subject Codes:FF005. FF610. HH600. FF020. WW000
Supplementary Info:16 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

551. Title:Molecular characterization of the SCAR markers tightly linked to the Tm-2 locus of the genus Lycopersicon
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 64-69
CD Volume:335
Print Article: Pages: 64-69
Author(s):Sobir Ohmori T Murata M Motoyoshi F
Author Affiliation:Research Institute for Bioresources, Okayama University, Kurashiki 710-0046, Japan
Language:English
Abstract:The Tm-2 gene and its alleles conferring tomato mosaic virus resistance in tomato originate from Lycopersicon peruvianum, a wild relative of tomato. DNA fragments of several RAPD (random amplified polymorphic DNA) markers tightly linked with the Tm-2 locus in tomato were successfully cloned and sequenced. Subsequently, the 24-mer oligonucleotide primer pairs of the SCAR (sequence characterized amplified region) markers corresponding to the RAPD markers were designed based on the 5'-endmost sequences. A fragment of the same size as that of a SCAR marker was amplified in the ToMV-susceptible tomato line with no Tm-2, but the digests of the PCR fragments by AccI exhibited polymorphism in fragment length between the two lines. We chose three SCAR markers and three RAPD markers tightly linked with the Tm-2 locus, and examined whether the same-sized fragments corresponding to these markers were also present in three other lines carrying Tm-2a or one of the other Tm-2 alleles. The fragments corresponding to the three SCAR markers were present in all of the three lines, but the other markers (three RAPDs) were absent in one or two lines, suggesting

that the three SCAR markers are closer to Tm-2 than the other markers. Comparison of the nucleotide sequences of these fragments revealed that they are all homologous to the corresponding SCAR markers
Descriptors:tomatoes. disease-resistance. plant-diseases. plant-pathogens. genetic-markers. vegetables. biotechnology
Organism Descriptors:Lycopersicon-esculentum. plant-viruses. tomato-mosaic-tobamovirus. Lycopersicon
Supplemental Descriptors:Lycopersicon. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. viruses. plant-pathogens. pathogens. tobamovirus-group. plant-viruses
Subject Codes:FF003. FF610. HH600. FF020. WW000
Supplementary Info:20 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

552. Title:Physical distances between S-locus genes in various S haplotypes of Brassica rapa and B. oleracea
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 80-85
CD Volume:335
Print Article: Pages: 80-85
Author(s):Suzuki G Watanabe M Nishio T
Author Affiliation:Laboratory of Plant Breeding, Graduate School of Agricultural Science, Tohoku University, Tsutsumidori-Amamiyamachi 1-1, Aoba-ku, Sendai 981-8555, Japan
Language:English
Abstract:In Brassica, self-incompatibility genes SLG (for S-locus glycoprotein) and SRK (for S-receptor kinase) are located in the S-locus complex region with several other S-linked genes. The S locus is a highly polymorphic region: polymorphism has been observed not only in sequences of SLG and SRK but also in the location of the S-locus genes. In order to compare the physical location of the S-locus genes in various S haplotypes, we used six class-I S haplotypes of B. rapa [B. campestris] and seven class-I S haplotypes of B. oleracea in this study. DNA gel blot analysis using pulsed-field gel electrophoresis (PFGE) showed that the physical distances between SLG and SRK in B. rapa are significantly shorter than those in B. oleracea and that the sizes of MluI and BssHII fragments harbouring SLG and SRK are less variable within B. rapa than within B. oleracea. We concluded that several large genomic fragments might have been inserted into the S-locus region of B. oleracea after allelic differentiation of S-locus genes
Descriptors:genes. haplotypes. polymorphism. gene-location. self-incompatibility. gene-mapping. vegetables. biotechnology
Organism Descriptors:Brassica-oleracea. Brassica-campestris
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF060. FF020. WW000
Supplementary Info:23 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

553. Title:A computerised algorithm for selecting a subset of multiplex molecular markers and optimising linkage map construction
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 90-94
CD Volume:335

Print Article: Pages: 90-94
Author(s):Charmet G Bert P F Balfourier F
Author Affiliation:INRA station d'amelioration des plantes, 234 avenue du Brezet, F-63039 Clermont-Ferrand, France
Language:English
Abstract:A computer algorithm is presented which allows selection of a subset of multiplex markers based on the minimisation of an optimality criterion for a genetic linkage map. It could be applied for choosing a subset of primers (e.g. RAPD, IMA or AFLP), each of which provides several unevenly spaced genetic markers. The goal is to achieve a saturated map of evenly spaced markers, using as few primers as possible to minimise cost and labour. Minimising the average map distance between markers is trivial, but simply leads to selection of those primers which provide the greatest number of markers. However, minimising the standard deviation of interval length ensures that weight is given both to the number of markers and to the evenness of their distribution on the linkage map. This criterion was found empirically to give a result fairly close to the optimum. A stepwise-like selection procedure is therefore implemented, which stops when the optimality criterion does not decrease any more. An example is given of a molecular map of perennial ryegrass with 463 markers obtained from 17 AFLP primers. It is demonstrated that this can be safely reduced to a 175 marker map with only 6 primers. Genetic diversity studies may also benefit from using such a subset of less-redundant markers in genetic distance estimation
Descriptors:linkage. genetic-markers. computer-software. computer-techniques. algorithms. gene-mapping. biotechnology
Organism Descriptors:Lolium-perenne
Supplemental Descriptors:Lolium. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:ZZ100. WW000. FF020. FF007
Supplementary Info:6 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

554. Title:Microsatellites confirm the authenticity of inter-varietal chromosome substitution lines of wheat (Triticum aestivum L.)
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 95-99
CD Volume:335
Print Article: Pages: 95-99
Author(s):Pestsova E Salina E Borner A Korzun V Maystrenko O I Roder M S
Author Affiliation:Institut fur Pflanzengenetik und Kulturpflanzenforschung (IPK), Corrensstrasse 3, 06466 Gatersleben, Germany
Language:English
Abstract:Ninety-five wheat microsatellite markers (WMS) were used to verify the authenticity of the set of Saratovskaya 29/Yanetzkis Probat inter-varietal wheat chromosome substitution lines developed using Saratovskaya 29 as the recipient variety. Polymorphic markers were available for all chromosome arms except 4DS, 6DS and 7DS. Each chromosome substitution line was tested by 2-8 microsatellite markers. The results demonstrate that most of the lines are correct. Out of 21 lines tested, 17 showed the expected microsatellite pattern of the donor variety. Two entire chromosomes, 1B and 7A, and two chromosome arms, 3AL and 6DS, were not substituted with Yanetzkis Probat in their respective lines. Three microsatellite markers located in the distal regions of chromosome arms 4AL, 3BS and 5BL in the corresponding substitution lines did not reveal the expected microsatellite pattern

of the recipient variety. The possible causes of the incorrect substitution line development and the appearance of incorrect distal microsatellite markers are discussed. The data confirm the idea that microsatellite markers provide ideal tools for testing the authenticity of genetic stocks of wheat
Descriptors:wheat. chromosome-substitution. substitution-lines. microsatellites. genetic-markers. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:19 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

555. Title:Risk of alfalfa transgene dissemination and scale-dependent effects
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 107-114
CD Volume:335
Print Article: Pages: 107-114
Author(s):St Amand P C Skinner D Z Peaden R N
Author Affiliation:USDA/ARS and Kansas State University, Throckmorton Hall, Manhattan, KS 66506, USA
Language:English
Abstract:Pollen can function as a vehicle to disseminate introduced, genetically engineered genes throughout a plant population or into a related species. The measurement of the risk of inadvertent dispersal of transgenes must include the assessment of accidental dispersion of pollen. Factors to be considered include the rate of pollen spread, the maximal dispersion distance of pollen, and the spatial dynamics of pollen movement within seed production fields; none of which are known for alfalfa (Medicago sativa), an insect-pollinated crop species. Using a rare, naturally occurring molecular marker, alfalfa pollen movement was tracked from seed and hay production fields. Results indicated that leafcutter bees (Megachile spp.) used in commercial seed production show a directional, non-random bias when pollinating within fields, primarily resulting in the movement of pollen directly towards and away from the bee domicile. Within-field pollen movement was detected only over distances of 4 m or less. Dispersal of pollen from alfalfa hay and seed production fields occurs at distances up to 1000 m. By examining widely dispersed, individual escaped alfalfa plants and their progeny using RAPD markers, gene movement among escaped alfalfa plants has been confirmed for distances up to 230 m. The outcrossing frequency for large fields was nearly 10-times greater than that of research-sized plots. A minimum isolation distance of 1557 m may be required to prevent gene flow in alfalfa. Data suggest that complete containment of transgenes within alfalfa seed or hay production fields would be highly unlikely using current production practices
Descriptors:dispersal. gene-flow. lucerne. fodder-legumes. transgenic-plants. biosafety. pollination. pollinators. outcrossing. genetic-transformation. fodder-plants. biotechnology
Organism Descriptors:Medicago-sativa. Megachile. Fabaceae. Medicago
Supplemental Descriptors:Medicago. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Megachilidae. Hymenoptera. insects. arthropods. invertebrates. animals
Subject Codes:FF007. FF020. WW000
Supplementary Info:20 ref
ISSN:0040-5752

Year:2000
Journal Title:Theoretical and Applied Genetics
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556. Title:Use of 5'-anchored primers for the enhanced recovery of specific microsatellite markers in Brassica napus L
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 115-119
CD Volume:335
Print Article: Pages: 115-119
Author(s):Varghese J P Rudolph B Uzunova M I Ecke W
Author Affiliation:Department of Botany, CMS College, Kottayam 686001, Kerala, India
Language:English
Abstract:Microsatellite markers have assumed great significance in biological research. The isolation and characterisation of microsatellites involves DNA library construction and screening, DNA sequencing, primer design and PCR optimisation. When a microsatellite is situated close to the beginning or end of a cloned fragment, specific primers cannot be designed for one of the flanking sequences, thus hindering the utilisation of such microsatellites as markers. The present approach was to use one 5'-anchored primer complementary to the microsatellite sequence in combination with one specific Cy5-labelled primer with a view to retrieving useful microsatellites, which would otherwise be lost. Six pairs of a 5' anchored primer and a specific primer were used across a set of 31 Brassica napus winter cultivars and one accession each of five additional Brassica species. Using laser fluorometry a single labelled product was observed after amplification with each of four primer pairs, and one primer pair gave two labelled products. Three products corresponded in size with the products expected if 5' anchoring was effective, indicating the amplification of locus-specific full-length products including all of the microsatellite repeats. All six primer pairs showed polymorphisms across the Brassica species examined, but only one primer pair showed polymorphisms within B. napus, making it useful for genetic analysis in rapeseed cultivars. The other primer pairs could be useful in studying gene introgression into B. napus or for investigating interspecific crosses involving different Brassica species
Descriptors:microsatellites. rape. genetic-markers. fatty-oil-plants. oil-plants. biotechnology
Organism Descriptors:Brassica-napus. Brassica-napus-var.-oleifera
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica-napus
Subject Codes:FF005. FF020. WW000
Supplementary Info:12 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

557. Title:Linkage analysis of anther-derived monoploids showing distorted segregation of molecular markers
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 126-130
CD Volume:335
Print Article: Pages: 126-130
Author(s):Tai G C C Seabrook J E A Aziz A N
Author Affiliation:Potato Research Centre, Agriculture and Agri-Food Canada, P.O. Box 20280, Fredericton, N.B., E3B 4Z7, Canada
Language:English

Abstract:Monoploids can be obtained from several diploid plant species by anther culture. Mapping of molecular markers using monoploids is greatly facilitated by the simple 1:1 segregation ratio expected from all heterozygous loci in the genome. Distorted segregation of molecular markers, however, appears to be a common phenomenon in many crop species and hinders the use of monoploids for mapping purposes. This report examines the segregation pattern of two marker genes linked together with one locus or separately with two independent loci which are responsible for the observed distortion. Each of the loci exhibiting distorted segregation has one of the two alleles which inhibits regeneration of the gametic cells in vitro and disrupts the expected segregation ratio of the linked markers. All possible situations in which linkage occurs between markers and distortion-causing genes are considered. Theoretical results outlining the segregation pattern among these linkage types indicate that the distinguishable distorted ratios can be used for mapping purposes. A protocol is given for the mapping of distorted gene markers based on existing gene mapping software. An example is presented of the mapping of distorted RAPD markers of monoploids obtained from a diploid potato genotype
Descriptors:gene-mapping. genes. linkage. haploidy. potatoes. segregation-distortion. genetics. root-crops. biotechnology
Organism Descriptors:Solanum-tuberosum
Supplemental Descriptors:Solanum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. WW000. FF005
Supplementary Info:15 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

558. Title:Identification of AFLP fragments linked to seed coat colour in Brassica juncea and conversion to a SCAR marker for rapid selection
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 146-152
CD Volume:335
Print Article: Pages: 146-152
Author(s):Negi M S Devic M Delseny M Lakshmikumaran M
Author Affiliation:Plant Molecular Biology Division, Tata Energy Research Institute, Habitat Place, Lodhi Road, New Delhi 110 003, India
Language:English
Abstract:A Brassica juncea mapping population was generated and scored for seed coat colour. A combination of bulked segregant analysis and AFLP methodology was employed to identify markers linked to seed coat colour in B. juncea. AFLP analysis using 16 primer combinations revealed seven AFLP markers polymorphic between the parents and the bulks. Individual plants from the segregating population were analysed, and three AFLP markers were identified as being tightly linked to the seed coat colour trait and specific for brown-seeded individuals. Since AFLP markers are not adapted for large-scale application in plant breeding, our objective was to develop a fast, cheap and reliable PCR-based assay. Towards this goal, we employed PCR-walking technology to isolate sequences adjacent to the linked AFLP marker. Based on the sequence information of the cloned flanking sequence of marker AFLP8, primers were designed. Amplification using the locus-specific primers generated bands at 0.5 kb and 1.2 kb with the yellow-seeded parent and a 1.1-kb band with the brown-seeded parent. Thus, the dominant AFLP marker (AFLP8) was converted into a simple codominant SCAR (sequence characterized amplified region) marker and designated as SCM08. Scoring

of this marker in a segregating population easily distinguished yellow- and brown-seeded B. juncea and also differentiated between homozygous (BB) and heterozygous (Bb) brown-seeded individuals. Thus, this marker will be useful for the development of yellow seed B. juncea cultivars and facilitate the map-based cloning of genes responsible for seed coat colour trait
Descriptors:testas. genetic-markers. colour. seeds. fatty-oil-plants. oil-plants. biotechnology. Indian-mustard
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Brassica-juncea
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. FF060
Supplementary Info:37 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

559. Title:Onion microsatellites for germplasm analysis and their use in assessing intra- and interspecific relatedness within the subgenus Rhizirideum
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 153-164
CD Volume:335
Print Article: Pages: 153-164
Author(s):Fischer D Bachmann K
Author Affiliation:Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstrasse 3, D-06466 Gatersleben, Germany
Language:English
Abstract:We have identified a set of informative STMS markers in onion (Allium cepa) and report on their application for genotyping and for determining genetic relationships. The markers have been developed from a genomic library enriched for microsatellites. Integrity of the microsatellite polymorphism was confirmed by amplicon sequencing. The microsatellite genotypes of 83 onion accessions and landraces from living onion collections were compared. As few as four primer pairs were sufficient to assign unique microsatellite patterns to the 83 accessions. Some of the microsatellite markers can be used for interspecific taxonomic analyses among close relatives of Allium cepa. Generally, our data support and extend results obtained from recently performed analyses using ITS, RAPD and morphology
Descriptors:germplasm. microsatellites. genetic-polymorphism. taxonomy. onions. vegetables. plant-genetic-resources. biotechnology
Organism Descriptors:Allium-cepa. Allium
Supplemental Descriptors:Allium. Alliaceae. Liliales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000. ZZ380
Supplementary Info:37 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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560. Title:Mapping of simple sequence repeat (SSR) DNA markers in diploid and tetraploid alfalfa
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 165-172
CD Volume:335
Print Article: Pages: 165-172
Author(s):Diwan N Bouton J H Kochert G Cregan P B

Author Affiliation:Soybean and Alfalfa Research Laboratory, USDA-ARS, Bldg. 006, Rm. 100, BARC-West, Beltsville, MD 20705, USA
Language:English
Abstract:Cultivated alfalfa (Medicago sativa) is an autotetraploid. However, all three existing alfalfa genetic maps resulted from crosses of diploid alfalfa. The current study was undertaken to evaluate the use of simple sequence repeat (SSR) DNA markers for mapping in diploid and tetraploid alfalfa. Ten SSR markers were incorporated into an existing F2 diploid alfalfa RFLP map and also mapped in an F2 tetraploid population. The tetraploid population had two to four alleles in each of the loci examined. The segregation of these alleles in the tetraploid mapping population generally was clear and easy to interpret. Because of the complexity of tetrasomic linkage analysis and a lack of computer software to accommodate it, linkage relationships at the tetraploid level were determined using a single-dose allele (SDA) analysis, where the presence or absence of each allele was scored independently of the other alleles at the same locus. The SDA diploid map was also constructed to compare mapping using SDA to the standard co-dominant method. Linkage groups were generally conserved among the tetraploid and the two diploid linkage maps, except for segments where severe segregation distortion was present. Segregation distortion, which was present in both tetraploid and diploid populations, probably resulted from inbreeding depression. The ease of analysis together with the abundance of SSR loci in the alfalfa genome indicated that SSR markers should be a useful tool for mapping tetraploid alfalfa
Descriptors:lucerne. fodder-legumes. gene-mapping. microsatellites. polyploidy. segregation. linkage. segregation-distortion. inbreeding-depression. fodder-plants. biotechnology
Organism Descriptors:Medicago-sativa. Fabaceae. Medicago
Supplemental Descriptors:Medicago. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF007. FF020. WW000
Supplementary Info:21 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

561. Title:Assessment of genetic diversity in three subsets constituted from the ICRISAT sorghum collection using random vs non-random sampling procedures. B. Using molecular markers
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 197-202
CD Volume:335
Print Article: Pages: 197-202
Author(s):Grenier C Deu M Kresovich S Bramel Cox P J Hamon P
Author Affiliation:CIRAD, TA 70/03, Avenue Agropolis, F-34398 Montpellier Cedex 5, France
Language:English
Abstract:The large size of the sorghum (Sorghum bicolor) landrace collection maintained by ICRISAT lead to the establishment of a core collection. Thus, three subsets of around 200 accessions were established from: (1) a random sampling after stratification of the entire landrace collection (L), (2) a selective sampling based on quantitative characters (PCS), and (3) a selection based on the geographical origin of landraces and the traits under farmers' selection (T). An assessment was done of the genetic diversity retained by each sampling strategy using the polymorphisms at 15 microsatellite loci. The landraces of each subset were genotyped with three multiplex polymerase chain reactions (PCRs) of five fluorescent primer-pairs each with semi-

automated allele sizing. The average allelic richness for each subset was equivalent (16.1, 16.3 and 15.4 alleles per locus for the subsets PCS, L, and T, respectively). The average genetic diversity was also comparable for the three subsets (0.81, 0.77 and 0.80 for the subsets PCS, L, and T, respectively). Allelic frequency distribution for each subset was compared with a chi-square test but few significant differences were observed. A high percentage of rare alleles (71 to 76% of 206 total rare alleles) was maintained in the three subsets. The global molecular diversity retained in each subset was not affected by a sampling procedure based upon phenotypic characters
Descriptors:genetic-diversity. plant-genetic-resources. gene-banks. microsatellites. sampling. characterization. cereals. biotechnology
Organism Descriptors:Sorghum-bicolor
Supplemental Descriptors:Sorghum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. PP720. WW000
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

562. Title:Molecular marker assisted genetic analysis of head shattering in six-rowed barley
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 203-210
CD Volume:335
Print Article: Pages: 203-210
Author(s):Kandemir N Kudrna D A Ullrich S E Kleinhofs A
Author Affiliation:Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164-6420, USA
Language:English
Abstract:Head shattering in barley (Hordeum vulgare) has two forms; brittle rachis and weak rachis. Brittle rachis is not observed in cultivated barley since all cultivars carry non-brittle alleles at one of the two complementary brittle rachis loci (Btr1;Btr2). Weak rachis causes head shattering in barley cultivars and may be confused with brittle rachis. Brittle rachis has been mapped to the chromosome 3 (3H) short arm while map position(s) of the weak rachis is unknown. Two major and a putative minor QTL for head shattering were mapped using the Steptoe x Morex doubled haploid line population. The largest QTL, designated Hst-3, located on the chromosome 3 (3H) centromeric region, is associated with a major yield QTL. The Steptoe Hst-3 region, when transferred into Morex, resulted in a substantial decrease in head shattering. High-resolution mapping of Hst-3 was achieved using isogenic lines. Brittle rachis was mapped with molecular markers and shown to be located in a different position from that of Hst-3. The second major QTL, designated Hst-2 S, is located on chromosome 2 S. This locus is associated with an environmentally sensitive yield QTL
Descriptors:barley. gene-mapping. shedding. seed-shattering. genes. quantitative-trait-loci. cereals. biotechnology
Organism Descriptors:Hordeum-vulgare
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. FF060. WW000
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

563. Title:Restriction fragment length polymorphism (RFLP) for protein disulfide isomerase (PDI) gene sequences in Triticum and Aegilops species
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 220-226
CD Volume:335
Print Article: Pages: 220-226
Author(s):Ciaffi M Dominici L Umana E Tanzarella O A Porceddu E
Author Affiliation:Department of Agrobiology and Agrochemistry, University of Tuscia, 01100 Viterbo, Italy
Language:English
Abstract:RFLP variation revealed by protein disulfide isomerase (PDI) coding gene sequences was assessed in 170 accessions belonging to 23 species of Triticum and Aegilops. PDI restriction fragments were highly conserved within each species and confirmed that plant PDI is encoded either by single-copy sequences or by small gene families. The wheat PDI probe hybridized to single EcoRI or HindIII fragments in different diploid species and to one or two fragments per genome in polyploids. Four Aegilops species in the Sitopsis section showed complex patterns and high levels of intraspecific variation, whereas Ae. searsii possessed single monomorphic fragments. T. urartu and Ae. squarrosa [Ae. tauschii] showed fragments with the same mobility as those in the A and D genomes of Triticum polyploid species, respectively, whereas differences were observed between the hybridization patterns of T. monococcum and T. boeoticum and that of the A genome. The single fragment detected in Ae. squarrosa was also conserved in most accessions of polyploid Aegilops species carrying the D genome. The five species of the Sitopsis section showed variation for the PDI hybridization fragments and differed from those of the B and G genomes of emmer and timopheevi groups of wheat, although one of the Ae. speltoides EcoRI fragments was similar to those located on the 4B and 4G chromosomes. The similarity between the EcoRI fragment located on the 1B chromosome of common and emmer wheats and one with a lower hybridization intensity in Ae. longissima, Ae. bicornis and Ae. sharonensis support the hypothesis of a polyphyletic origin of the B genome
Descriptors:isomerases. restriction-fragment-length-polymorphism. wheat. wild-relatives. phylogeny. cereals. biotechnology. plant-genetic-resources
Organism Descriptors:Aegilops. Triticum-boeoticum. Triticum-monococcum. Triticum-urartu. Triticum-aestivum. Aegilops-tauschii. Aegilops-speltoides. Aegilops-longissima. Aegilops-bicornis. Aegilops-sharonensis. Triticum
Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Triticum. Aegilops
Subject Codes:FF005. FF020. WW000. PP720. ZZ380
Supplementary Info:33 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

564. Title:Genetic structure in cultivated and wild carrots (Daucus carota L.) revealed by AFLP analysis
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 227-233
CD Volume:335
Print Article: Pages: 227-233
Author(s):Shim S I Jorgensen R B
Author Affiliation:Institute of Natural Resources, Korea University, Seoul 136-701, Korea Republic
Language:English

Abstract:Genetic variation within and among five Danish populations of wild carrot and five cultivated varieties was investigated using amplified fragment length polymorphism (AFLP). Ten AFLP primer combinations produced 116 polymorphic bands. Based on the marker data an UPGMA-cluster analysis and principal component analysis (PCA) separated the Daucus collections into three groups, consisting of the wild populations, the old varieties, and the recently bred varieties. The genetic distance between the wild populations reflected the physical distance between collection sites. Analysis of genetic diversity showed that the old varieties released between 1974 and 1976 were more heterogeneous than the newly developed F1 hybrid varieties. The analysis of molecular variation (AMOVA) showed that the major part of the genetic variation in the plant material was found within populations/varieties. The presence of markers specific to the cultivated carrot makes it possible to detect introgression from cultivated to wild types
Descriptors:carrots. genetic-polymorphism. genetic-variation. vegetables. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Daucus-carota
Supplemental Descriptors:Daucus. Apiaceae. Apiales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:30 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

565. Title:Characterization and linkage mapping of R-gene analogous DNA sequences in pea (Pisum sativum L.)
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 241-247
CD Volume:335
Print Article: Pages: 241-247
Author(s):Timmerman Vaughan G M Frew T J Weeden N F
Author Affiliation:New Zealand Institute for Crop & Food Research Limited, Private Bag 4704, Christchurch, New Zealand
Language:English
Abstract:Pea (Pisum sativum) sequences that are analogous to the conserved nucleotide binding site (NBS) domain found in a number of plant disease resistance genes (R-genes) were cloned. Using redundant oligonucleotide primers and the polymerase chain reaction (PCR), we amplified nine pea sequences and characterised their sequences (GenBank accession numbers AF123695-AF123703). The pea R-gene analog (RGA)-deduced amino acid sequences demonstrated significant sequence similarity with known R-gene sequences lodged in public databases. The genomic locations of eight of the pea RGAs were determined by linkage mapping. The eight RGAs identified ten loci that mapped to six linkage groups. In addition, the genomic organization of the RGAs was inferred. Both single-copy and multicopy sequence families were present among the RGAs, and the multicopy families occurred most often as tightly linked clusters of related sequences. Intraspecific copy number variability was observed in three of the RGA sequence families, suggesting that these sequence families are evolving rapidly. The genomic locations of the pea RGAs were compared with the locations of known pea R-genes and sym genes involved in the pea-rhizobia symbiosis. Two pea RGAs mapped in the genomic region containing a pea R-gene, Fw, and four pea RGAs mapped in regions of the genome containing sym genes

Descriptors:nucleotide-sequences. gene-mapping. binding-sites. disease-resistance. plant-diseases. plant-pathogens. genes. grain-legumes. biotechnology
Organism Descriptors:Pisum-sativum. Fabaceae
Supplemental Descriptors:Pisum. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. HH600. FF020. FF610. WW000
Supplementary Info:35 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

566. Title:Analyzing quantitative trait loci for yield using a vegetatively replicated F2 population from a cross between the parents of an elite rice hybrid
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 248-254
CD Volume:335
Print Article: Pages: 248-254
Author(s):Li J X Yu S B Xu C G Tan Y F Gao Y J Li X H Zhang QiFa
Author Variant:Zhang-Q-F
Author Affiliation:National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan 430070, China
Language:English
Abstract:Although F2s are the most informative populations for genetic analysis, it has been difficult to use F2 populations directly for QTL analysis because it is usually difficult to assess the reliability of the data, due to an inability to estimate the experimental errors. In this study, we performed a QTL analysis for yield and yield-component traits of an F2 population based on data from replicated field trials over 2 years using vegetative shoots of ratooned plants, making use of the ratooning habit of rice. The objective of this study was to explore the possibility of conducting QTL analyses directly based on an F2 population by means of ratooning plants. The experimental population was from a cross between 'Zhenshan 97' and 'Minghui 63', the parents of 'Shanyou 63', an elite rice hybrid widely grown in China. A genetic linkage map containing 151 molecular markers was constructed for QTL mapping. A total of 20 distinct QTLs were detected; eight of these were detected in both years and remaining 12 in only 1 year. Compared with the results of our previous analysis of the F2:3 families from the same cross, it was shown that most of the QTLs detected in the ratooned F2 population were also detected in the F2:3 population. However, the estimates of both additive and dominant types of genetic effects for many of the QTLs based on F2 ratoons were substantially larger than those based on F2:3 families. The results indicate that vegetatively ratooned F2 populations may have considerable utility in the mapping of QTLs, especially if dominant types of gene actions are of concern, although there were certain technical limitations in making use of such populations in the experiments
Descriptors:rice. hybrids. quantitative-trait-loci. yields. yield-components. gene-mapping. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020
Supplementary Info:20 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

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567. Title:High-resolution genetic mapping of the pepper resistance locus Bs3 governing recognition of the Xanthomonas campestris pv vesicatoria AvrBs3 protein
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 255-263
CD Volume:335
Print Article: Pages: 255-263
Author(s):Pierre M Noel L Lahaye T Ballvora A Veuskens J Ganal M Bonas U
Author Affiliation:Centre National de la Recherche Scientifique, Institute des Sciences Vegetales, Avenue de la Terrasse, 91190 Gif-sur-Yvette Cedex, France
Language:English
Abstract:The pepper (Capsicum annuum) Bs3 gene confers resistance to Xanthomonas campestris pv. vesicatoria [X. vesicatoria] strains expressing the avirulence protein AvrBs3. Using amplified fragment length polymorphism (AFLP) and bulked DNA templates from resistant and susceptible plants we identified markers linked to Bs3 and defined a 2.1-cM interval containing the target gene. Bs3-linked AFLP fragments were cloned and conformity of isolated PCR products with the desired markers was determined by hybridisation to membrane-bound AFLP reactions. AFLP markers flanking the target gene were converted into locus-specific PCR-based markers. These markers were employed for the analysis of 790 plants segregating for Bs3, resulting in a linkage map with a genetic resolution of 0.13 cM. Mapping of Bs3-linked markers in tomato placed them to a syntenic interval on tomato chromosome 2
Descriptors:gene-mapping. plant-pathogens. plant-diseases. plant-pathogenic-bacteria. disease-resistance. genes. bacterial-diseases. genetic-markers. vegetables. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Xanthomonas-vesicatoria. Capsicum-annuum
Supplemental Descriptors:Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes. Capsicum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF610. HH600. FF020. WW000
Supplementary Info:61 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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568. Title:Conservation and variability of sequence-tagged microsatellite sites (STMSs) from chickpea (Cicer arietinum L.) within the genus Cicer
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 269-278
CD Volume:335
Print Article: Pages: 269-278
Author(s):Choumane W Winter P Weigand F Kahl G
Author Affiliation:ICARDA, P.O. Box 5466, Aleppo, Syria
Language:English
Abstract:The conservation of 90 microsatellite-flanking sequences from chickpea in 39 accessions of 8 annual and 1 accession of a perennial species of the genus Cicer was investigated. All of the primer sequences successfully amplified microsatellites in related species, indicating the conservation of microsatellite-flanking sequences in chickpea's relatives. However, the degree of conservation of the primer sites varied between species depending on their known phylogenetic relationship to chickpea, ranging from 92.2% in C. reticulatum, chickpea's closest relative and potential ancestor, down to 50% for C. cuneatum. A phylogenetic tree revealed that chickpea and the other

members of its crossability group were more closely related to the perennial C. anatolicum than to other annual species of the genus. Considerable variation in size and number of amplification products between and within species was observed. Sequence analysis of highly divergent amplification products proved that variation is either due to large differences in the number of microsatellite repeats or to the amplification of a locus unrelated to the one amplified from chickpea. Sequence information and bootstrapping using PAUP suggested that STMSs derived from chickpea may be efficiently and reliably used for synteny studies in chickpea's crossability group, including C. anatolicum. However, care should be taken when applying these markers to other species of the genus. Considering the data presented here and the known historical record, the age of section Monocicer, including chickpea, is estimated to be about 100 000 years

Descriptors:chickpeas. microsatellites. phylogenetics. phylogeny. grain-legumes. biotechnology. plant-genetic-resources

Identifiers:Cicer reticulatum. Cicer cuneatum. Cicer anatolicum

Organism Descriptors:Cicer-arietinum. Cicer. Fabaceae

Supplemental Descriptors:Cicer. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. ZZ380. FF020. WW000

Supplementary Info:43 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

569. Title:Mapping of QTLs conferring resistance to bacterial leaf streak in rice

View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 286-291

CD Volume:335

Print Article: Pages: 286-291

Author(s):Tang D Wu W Li W Lu H Worland A J

Author Affiliation:College of Crop Sciences, Fujian Agricultural University, Fuzhou, Fujian, China

Language:English

Abstract:A large F2 and a recombinant inbred (RI) population were separately derived from a cross between two indica rice varieties, one of which was highly resistant (Acc8558) to bacterial leaf streak (BLS, Xanthomonas oryzae pv. oryzicola) and the other highly susceptible (H359). Following artificial inoculation of the RI population and over 2 years of testing, 11 QTLs were mapped by composite interval mapping (CIM) on six chromosomes. Six of the QTLs were detected in both seasons. Eight of the QTLs were significant following stepwise regression analysis, and of these, 5 with the largest effects were significant in both seasons. The detected QTLs explained 84.6% of the genetic variation in 1997. Bulked segregant analysis (BSA) of the extremes of the F2 population identified 3 QTLs of large effect. The 3 QTLs were identical to 3 of the 5 largest QTLs detected by CIM. The independent detection of the same QTLs using two methods of analysis in separate mapping populations verifies the existence of the QTLs for BLS and provides markers to ease their introduction into elite varieties

Descriptors:rice. gene-mapping. quantitative-trait-loci. disease-resistance. plant-pathogens. plant-diseases. plant-pathogenic-bacteria. bacterial-diseases. cereals. biotechnology

Organism Descriptors:Oryza-sativa. Xanthomonas-oryzae-pv.-oryzicola. Oryza

Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Xanthomonas-oryzae. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes

Subject Codes:FF005. FF610. HH600. FF020. WW000
Supplementary Info:25 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

570. Title:Linkage mapping and QTL analysis in coconut (Cocos nucifera L.)
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 292-300
CD Volume:335
Print Article: Pages: 292-300
Author(s):Herran A Estioko L Becker D Rodriguez M J B Rohde W Ritter E
Author Affiliation:Neiker, Apartado 46, 01080 Vitoria, Spain
Language:English
Abstract:Different DNA marker types were used to construct linkage maps in coconut (Cocos nucifera; 2n = 32) for the two parents of the cross Malayan Yellow Dwarf (MYD) x Laguna Tall (LAGT). A total of 382 markers was sufficient to generate 16 linkage groups for each parent. The total genome length corresponded to 2226 cM for the LAGT map and 1266 cM for the MYD map with 4-32 markers per linkage group. Common markers allowed the association of 9 linkage groups for the two parents MYD and LAGT. QTL analysis for the trait early germination identified six loci. These QTLs correlate with early flowering and yield, representing characters which are important in coconut breeding. The co-segregation of markers with these QTLs provides the first opportunity for marker-assisted selection in coconut breeding programmes
Descriptors:coconuts. genetic-markers. linkage. quantitative-trait-loci. gene-mapping. seed-germination. fatty-oil-plants. oil-plants. biotechnology
Organism Descriptors:Cocos-nucifera
Supplemental Descriptors:Cocos. Arecaceae. Arecales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000. FF060
Supplementary Info:37 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

571. Title:Development and characterization of microsatellite markers in black poplar (Populus nigra L.)
View Article: Theoretical and Applied Genetics. 2000. 101 (1/2). 317-322
CD Volume:335
Print Article: Pages: 317-322
Author(s):Schoot J van der Pospiskova M Vosman B Smulders M J M
Author Variant:van-der-Schoot-J
Author Affiliation:Plant Research International, P.O. Box 16, NL-6700 AA Wageningen, Netherlands
Language:English
Abstract:Using an enrichment procedure, we have cloned and sequenced microsatellite loci from black poplar (Populus nigra) and developed primers for sequence-tagged microsatellite (STMS) analysis. Twelve primer pairs for dinucleotide repeats produced fragments of sufficient quality which were polymorphic in P. nigra. Some of them also showed amplification in other Populus species (P. deltoides, P. trichocarpa, P. tremula, P. tremuloides, P. candicans [P. balsamifera], and/or P. lasiocarpa). The best nine and (GT) (GA) microsatellite markers were tested on a set of 23 P. nigra genotypes from all over Europe. The microsatellites were highly polymorphic, with 10-19 different alleles

per microsatellite locus among these 23 genotypes. WPMS08 sometimes amplified three fragments. Using the other eight marker loci, the level of heterozygosity among the plants was on average 0.71 (range 0.25-1.00). The microsatellite markers developed will be useful for screening the genetic diversity in natural populations and in gene bank collections
Descriptors:characterization. poplars. heterozygosity. microsatellites. genetic-polymorphism. forest-trees. genetic-diversity. broadleaves. biotechnology
Identifiers:Populus lasiocarpa
Organism Descriptors:Populus-nigra. Populus-deltoides. Populus-trichocarpa. Populus-tremula. Populus-tremuloides. Populus-balsamifera
Supplemental Descriptors:Populus. Salicaceae. Salicales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:KK100. FF020. WW000
Supplementary Info:16 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

572. Title:Linkage disequilibrium and fingerprinting in sugar beet
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 323-326
CD Volume:335
Print Article: Pages: 323-326
Author(s):Kraft T Hansen M Nilsson N O
Author Affiliation:Novartis Seeds AB, P.O. Box 302, S-261 23 Landskrona, Sweden
Language:English
Abstract:It has been suggested that map information for molecular markers can be used to strengthen fingerprinting analyses. The success of this strategy depends on the distribution of linkage disequilibrium over the genome. Using 451 mapped AFLP markers, we investigated the occurrence of linkage disequilibrium in nine sugar beet breeding lines. A low but significant level of linkage disequilibrium was found for unlinked markers. Only for very tightly linked (<3 cM) markers was this level substantially higher. This implies that little is gained in utilising the map position of the markers in fingerprinting applications
Descriptors:sugarbeet. linkage. genetic-markers. gene-mapping. DNA-fingerprinting. sugar-crops. biotechnology
Identifiers:amplified fragment length polymorphism
Organism Descriptors:Beta-vulgaris-var.-saccharifera
Supplemental Descriptors:Beta-vulgaris. Beta. Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. WW000
Supplementary Info:17 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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573. Title:Analysis of the plastome and chondriome origin in plants regenerated after asymmetric Solanum ssp. protoplast fusions
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 336-343
CD Volume:335
Print Article: Pages: 336-343
Author(s):Rasmussen J O Lossl A Rasmussen O S
Author Affiliation:Department of Molecular and Structural Biology, Aarhus University, C.F. Mollers Alle Building 130, DK-8000 Aarhus, Denmark
Language:English

Abstract:Protoplasts from potato cultivars used as recipient parents were fused with irradiated protoplasts from wild Solanum donor species. Regenerated plants were analysed by RAPDs to identify hybrids. Irradiation of donor protoplasts with ionizing irradiation induced a broad range of donor nuclear DNA elimination in the asymmetric hybrids. Usage of chloroplast (cp)- and mitochondrial (mt)-specific PCR markers made it possible to trace the different origins of the cp genome in seven fusion combinations, as well as the mt genomes in two fusion combinations. Regenerated plants with recipient nucleus and plastome markers from the donors were found in six of the seven analysed fusion combinations. Protoplast fusion has generated novel mt genome combinations consisting of different portions of the mt genomes from the fusion partners. Selection of heterofusion products based on fluorescence markers is an efficient method to obtain asymmetric Solanum hybrids and cybrids from most fusion combinations. Possible models for cybrid formation are discussed
Descriptors:protoplasts. chloroplast-genetics. hybrids. ionizing-radiation. irradiation. nuclei. polymerase-chain-reaction. protoplast-fusion. somatic-hybridization. mitochondrial-genetics. potatoes. wild-relatives. interspecific-hybridization. root-crops. plant-genetic-resources. biotechnology
Organism Descriptors:Solanum. Solanum-tuberosum
Supplemental Descriptors:Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Solanum
Subject Codes:FF005. FF020. FF170. WW000. PP720
Supplementary Info:31 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

574. Title:Identification of self-incompatibility genotypes of almond by allele-specific PCR analysis
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 344-349
CD Volume:335
Print Article: Pages: 344-349
Author(s):Tamura M Ushijima K Sassa H Hirano H Tao R Gradziel T M Dandekar A M
Author Affiliation:Department of Pomology, University of California, 1 Shields Avenue, Davis, CA 95616, USA
Language:English
Abstract:In almond, gametophytic self-incompatibility is controlled by a single multiallelic locus (S-locus). In styles, the products of S-alleles are ribonucleases, the S-RNases. Cultivated almonds in California have four predominant S-alleles (Sa, Sb, Sc, Sd). We previously reported the cDNA cloning of three of these alleles, namely Sb, Sc and Sd. In this paper we report the cloning and DNA sequence analysis of the Sa allele (DDBJ/EMBL/GenBank accession no. AB026836). The Sa-RNase displays approximately 55% similarity at the amino-acid level with other almond S-RNases (Sb, Sc, and Sd) and this similarity was lower than that observed among the Sb, Sc and Sd-RNases. Using the cDNA sequence, a PCR-based identification system using genomic DNA was developed for each of the S-RNase alleles. Five almond cultivars with known self-incompatibility (SI) genotypes were analysed. Common sequences among four S-alleles were used to create four primers, which, when used as sets, amplify DNA bands of unique size that corresponded to each of the four almond S-alleles; Sa (602 bp), Sb (1083 bp), Sc (221 bp) and Sd (343 bp). All PCR products obtained from genomic DNA isolated from the five almond cultivars were cloned and their DNA sequence obtained. The nucleotide sequence of these genomic DNA fragments matched the

corresponding S-allele cDNA sequence in every case. The amplified products obtained for the Sa- and Sb-alleles were both longer than that expected for the coding region, revealing the presence of an intron of 84 bp in the Sa-allele and 556 bp in the Sb-allele. Both introns are present within the site of the hypervariable region common in S-RNases from the Rosaceae family and which may be important for S specificity. The exon portions of the genomic DNA sequences were completely consistent with the cDNA sequence of the corresponding S-allele. A useful application of these primers would be to identify the S-genotype of progeny in a breeding program, new varieties in an almond nursery, or new grower selections at the seedling stage
Descriptors:almonds. polymerase-chain-reaction. alleles. complementary-DNA. nucleotide-sequences. ribonucleases. self-incompatibility. genes. nut-crops. biotechnology
Organism Descriptors:Prunus-dulcis
Supplemental Descriptors:Prunus. Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. FF060. WW000
Supplementary Info:27 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

575. Title:Map locations of barley Dhn genes determined by gene-specific PCR
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 350-354
CD Volume:335
Print Article: Pages: 350-354
Author(s):Choi D W Koag M C Close T J
Author Affiliation:Department of Botany and Plant Sciences, University of California, Riverside, CA 92521-0124, USA
Language:English
Abstract:We previously identified 11 unique barley Dhn (dehydrins, stress-induced proteins) genes and found, using wheat-barley addition lines, that these genes are dispersed on four chromosomes 3H, 4H, 5H, 6H. In the present work, more precise positions of barley Dhn genes were determined using gene-specific PCR and 100 doubled haploid lines developed from a cross of Dicktoo and Morex barley. Dhn10 is located on 3H between saflp 106 and ABG4. Dhn6 is at the previously determined position on 4H between SOLPRO and BCD265a. Dhn1 and Dhn2 are at the previously determined position on 5H between mR and saflp172. The Dhn locus previously called Dhn4a on barley 5H or Dhn2.2 on T. monococcum 5A is in fact Dhn9 and maps to a revised position between BCD265b and saflp218. Dhn3, Dhn4, Dhn7 and Dhn5 each map to the same position on chromosome 6H, suggesting that the previously reported separation of Dhn3, Dhn4 and Dhn5 may reflect limitations in the accuracy of Southern blot data. In addition to clarifying the map positions of these important stress-related genes, these results illustrate the advantage of gene-specific probes for the mapping of individual genes in a multi-gene family
Descriptors:barley. genes. stress. gene-mapping. gene-location. polymerase-chain-reaction. cereals. biotechnology
Identifiers:dehydrins
Organism Descriptors:Hordeum-vulgare
Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. FF900
Supplementary Info:27 ref
ISSN:0040-5752

Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

576. Title:Cold stress-induced calcium-dependent protein kinase(s) in rice (Oryza sativa L.) seedling stem tissues
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 355-363
CD Volume:335
Print Article: Pages: 355-363
Author(s):Li W G Komatsu S
Author Affiliation:Department of Molecular Biology, National Institute of Agrobiological Resources, 2-1-2 Kannondai, Tsukuba 305-8602, Japan
Language:English
Abstract:Ca2+-dependent protein kinases (CDPKs) play an important role in plant signal transduction. Protein kinase(s) activities induced by 5 deg C cold stress in rice (Oryza sativa) seedlings were investigated in both leaf and stem tissues in an early (up to 45 min) and late (up to 12 h) response study. The leaf had 37-, 47- and 55-kDa protein kinase activities, and the stem had 37-, 47- and 55-kDa protein kinase activities. A 16-kDa protein showed constitutive kinase activity in the rice seedling leaf and stem. It was further identified that the 47-kDa protein kinase activity induced by cold in both the cytosolic and membrane fractions of the stem was strictly Ca2+-dependent. This CDPK activity increased in the presence of the Ca2+ ionophore A23187 in stem segments, whereas it was decreased by the Ca2+ channel blocker, LaCl3, and the Ca2+ chelator, EGTA. The general protein kinase inhibitor, staurosporine, completely inhibited this CDPK activity in vitro, and both W7, a calmodulin antagonist, and H7, a protein kinase C inhibitor, could only partially decrease this activity. The protein phosphatase inhibitor, okadaic acid, increased CDPK activity. This CDPK activity was also induced by salt, drought stress and the phytohormone abscisic acid. Among the 18 rice varieties tested, this cold-induced 47-kDa CDPK activity was stronger in the cold-tolerant varieties than in the sensitive ones
Descriptors:rice. seedlings. calmodulin. cold-stress. protein-kinase. gene-expression. cold-resistance. leaves. stems. cold. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. FF900
Supplementary Info:35 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

577. Title:PCR-based molecular markers for the fragrance gene in rice (Oryza sativa L.)
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 364-371
CD Volume:335
Print Article: Pages: 364-371
Author(s):Garland S Lewin L Blakeney A Reinke R Henry R
Author Affiliation:Centre for Plant Conservation Genetics, Southern Cross University (SCU), Lismore, NSW 2480, Australia
Language:English
Abstract:The genomic DNA clone RG28, linked to the major fragrance gene of rice (fgr), was assessed for polymorphism in order to produce a PCR-based marker for fragrance. A small mono-nucleotide repeat, that was

polymorphic between a pair of fragrant and non-fragrant cultivars, was identified and developed into a co-dominant PCR-based marker. The polymorphism-information-content determinations for three microsatellite markers, that have been genetically mapped near RG28, are also presented. These PCR-based markers will be highly useful in distinguishing fragrance-producing alleles from non-fragrance-producing alleles at the fgr locus
Descriptors:fragrance. rice. aroma. genes. genetic-markers. polymerase-chain-reaction. microsatellites. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000. QQ050. QQ500
Supplementary Info:16 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

578. Title:Mapping the jp (jumbo pollen) gene and QTLs involved in multinucleate microspore formation in diploid alfalfa
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 372-378
CD Volume:335
Print Article: Pages: 372-378
Author(s):Tavoletti S Pesaresi P Barcaccia G Albertini E Veronesi F
Author Affiliation:Dipartimento di Biotecnologie Agrarie ed Ambientali, Universita degli Studi di Ancona, Via Brecce Bianche, 60131 Ancona, Italy
Language:English
Abstract:The objective of this research was to map the jumbo-pollen trait in diploid alfalfa [lucerne]. Homozygous recessive (jpjp) plants are characterized by the complete failure of post-meiotic cytokinesis during microsporogenesis resulting in 100% 4n-pollen formation. Three F1 segregating populations were produced and analysed for pollen-grain production and the segregation of RFLP markers. The first cross combination did not segregate for the jumbo-pollen trait, but showed a clear segregation for multinucleate (bi-, tri- and tetra-nucleate)-microspore formation. Cytological analysis showed that few plants produced 100% normal (uninucleate) microspores, whereas most of them produced multinucleate microspores at a variable frequency (0-75%). Plants with multinucleate microspores always showed a prevalence of binucleated microspores, even though some plants showed a background presence of tri- and tetra-nucleate microspores. QTL analysis based on ANOVA I and step-wise multiple regression identified three QTLs with a highly significant effect on multinucleate-microspore formation. Two cross combinations, subsequently executed, showed Mendelian segregation for the jumbo-pollen trait and were effective in locating the jp gene on linkage group 6 close to the Vg1G1b RFLP locus. Interestingly, this RFLP locus was also linked to one QTL for multinucleate-microspore formation. Genetic models are discussed concerning the presence in linkage group 6 of a cluster of genes involved in multinucleate-microspore formation together with possible relationships between the jp gene and the Vg1G1b QTL
Descriptors:pollen. genes. linkage. restriction-fragment-length-polymorphism. gene-mapping. quantitative-trait-loci. lucerne. unreduced-gametes. genetic-models. fodder-plants. fodder-legumes. biotechnology
Organism Descriptors:Medicago-sativa. Fabaceae. Medicago
Supplemental Descriptors:Medicago. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF007. FF020. WW000
Supplementary Info:36 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

579. Title:Transgenic rice as a system to study the stability of transgene expression: multiple heterologous transgenes show similar behaviour in diverse genetic backgrounds
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 388-399
CD Volume:335
Print Article: Pages: 388-399
Author(s):Gahakwa D Maqbool S B Fu X Sudhakar D Christou P Kohli A
Author Affiliation:Molecular Biotechnology Unit, John Innes Centre, Colney Lane, Norwich NR4 7UH, UK
Language:English
Abstract:The success of contemporary breeding programmes involving genetic engineering depends on the stability of transgene expression over many generations. We studied the stability of transgene expression in 40 independent rice plant lines representing 11 diverse cultivated varieties. Each line contained three or four different transgenes delivered by particle bombardment, either by cotransformation or in the form of a cointegrate vector. Approximately 75% of the lines (29/40) demonstrated Mendelian inheritance of all transgenes, suggesting integration at a single locus. We found that levels of transgene expression varied among different lines, but primary transformants showing high-level expression of the gna, gusA, hpt and bar transgenes faithfully transmitted these traits to progeny. Furthermore, we found that cry1Ac and cry2A transgene expression was stably inherited when primary transformants showed moderate or low-level expression. Our results show that six transgenes (three markers and three insect-resistance genes) were stably expressed over four generations of transgenic rice plants. We showed that transgene expression was stable in lines of all the rice genotypes we analysed. Our data represent a step forward in the transfer of rice genetic engineering technology from model varieties to elite breeding lines grown in different parts of the world
Descriptors:rice. reporter-genes. genetic-engineering. inheritance. transgenic-plants. genetic-transformation. gene-expression. cereals. biotechnology
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:82 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

580. Title:Molecular mapping of the wheat powdery mildew resistance gene Pm24 and marker validation for molecular breeding
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 407-414
CD Volume:335
Print Article: Pages: 407-414
Author(s):Huang X Q Hsam S L K Zeller F J Wenzel G Mohler V

Author Affiliation:Technische Universitat Munchen, Lehrstuhl fur Pflanzenbau und Pflanzenzuchtung, Alte Akademie 12, D-85350 Freising-Weihenstephan, Germany
Language:English
Abstract:Molecular markers were identified in common wheat for the Pm24 locus conferring resistance to different isolates of the powdery mildew pathogen, Erysiphe graminis f.sp. tritici. Bulked segregant analysis was used to identify amplified fragment length polymorphism (AFLP) markers and microsatellite markers linked to the gene Pm24 in an F2 progeny from the cross Chinese Spring (susceptible) x Chiyacao (resistant). Two AFLP markers XACA/CTA-407 and XACA/CCG-420, and three microsatellite markers Xgwm106, Xgwm337 and Xgwm458, were mapped in coupling phase to the Pm24 locus. The AFLP marker locus XACA/CTA-407 co-segregated with the Pm24 gene, and XACA/CCG-420 mapped 4.5 cM from this gene. Another AFLP marker locus XAAT/CCA-346 co-segregated in repulsion phase with the Pm24 locus. Pm24 was mapped close to the centromere on the short arm of chromosome 1D, contrary to the previously reported location on chromosome 6D. Pm24 segregated independently of gene Pm22, also located on chromosome 1D. An allele of microsatellite locus Xgwm337 located 2.4 plus or minus 1.2 cM from Pm24 was shown to be diagnostic and therefore potentially useful for pyramiding two or more genes for powdery mildew resistance in a single genotype
Descriptors:gene-mapping. fungal-diseases. wheat. genes. plant-pathogens. plant-diseases. plant-pathogenic-fungi. disease-resistance. cereals. biotechnology
Organism Descriptors:Triticum-aestivum. Erysiphe-graminis-f.sp.-tritici. Triticum
Supplemental Descriptors:Triticum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Erysiphe-graminis. Erysiphe. Erysiphales. Ascomycotina. Eumycota. fungi
Subject Codes:FF005. FF020. WW000. FF610. HH600
Supplementary Info:42 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

581. Title:S1 analysis of long PCR heteroduplexes: detection of chloroplast indel polymorphisms in Fragaria
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 415-420
CD Volume:335
Print Article: Pages: 415-420
Author(s):Lin J Davis T M
Author Affiliation:Plant Biology Department, Rudman Hall, University of New Hampshire, Durham, NH 03824, USA
Language:English
Abstract:S1 analysis of long PCR heteroduplexes was found to be an effective method for detecting phylogenetically informative indel (insertion/deletion) polymorphisms in the highly conserved strawberry chloroplast genome. In this broadly applicable method, long-range PCR products containing heteroduplex DNA molecules generated from mixed-template amplifications are subjected to S1 nuclease digestion followed by separation and visualization on an agarose gel. The presence of fragments resulting from S1 digestion of mismatch loops in heteroduplex molecules is indicative of indel polymorphism between the template sources. Upon analysis of 13-kb heteroduplex-containing PCR products spanning the petA-psbB chloroplast genome region in Fragaria vesca and Fragaria moschata, two indels distinguishing these species were

detected, and subsequently localized to the psbJ-psbL and rpl20-rps18 intergenic regions. Comparative sequencing of these regions revealed that F. moschata resembled Fragaria viridis, but differed from F. vesca, Fragaria nubicola, and a closely related outgroup representative, Duchesnea indica, by a 10-bp deletion in the psbJ-psbL region and a 10-bp insertion in the rpl20-rps18 region. Thus, of the three diploids (2n = 2x = 14) examined, F. viridis is favored over F. vesca and F. nubicola as the most likely chloroplast genome donor to hexaploid (2n = 6x = 42) F. moschata
Descriptors:chloroplast-genetics. polymerase-chain-reaction. strawberries. phylogeny. genes. fruit-crops. plant-genetic-resources. biotechnology
Identifiers:Fragaria nubicola
Organism Descriptors:Fragaria-moschata. Duchesnea-indica. Fragaria-vesca. Fragaria
Supplemental Descriptors:Fragaria. Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants. Duchesnea
Subject Codes:FF003. FF020. WW000. ZZ380
Supplementary Info:22 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics

582. Title:Characterization of microsatellite markers in peach (Prunus persica (L.) Batsch)
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 421-428
CD Volume:335
Print Article: Pages: 421-428
Author(s):Sosinski B Gannavarapu M Hager L D Beck L E King G J Ryder C D Rajapakse S Baird W V Ballard R E Abbott A G
Author Affiliation:Department of Biological Sciences, Clemson University, Clemson, SC 29634, USA
Language:English
Abstract:Microsatellites have emerged as an important system of molecular markers. We evaluated the potential of microsatellites for use in genetic studies of peach (Prunus persica). Microsatellite loci in peach were identified by screening a pUC8 genomic library, a lambda ZAPII leaf cDNA library, as well as through database searches. Primer sequences for the microsatellite loci were tested from the related Rosaceae species apple (Malus x domestica [M. pumila]) and sour cherry (Prunus cerasus). The genomic library was screened for CT, CA and AGG repeats, while the cDNA library was screened for (CT)n- and (CA)n-containing clones. Estimates of microsatellite frequencies were determined from the genomic library screening, and indicate that CT repeats occur every 100 kb, CA repeats every 420 kb, and AGG repeats every 700 kb in the peach genome. Microsatellite-containing clones were sequenced, and specific PCR primers were designed to amplify the microsatellite-containing regions from genomic DNA. The level of microsatellite polymorphism was evaluated among 28 scion peach cultivars which displayed one to four alleles per primer pair. Five microsatellites were found to segregate in intraspecific peach-mapping crosses. In addition, these microsatellite markers were tested for their utility in cross-species amplification for use in comparative mapping both within the Rosaceae, and with the unrelated species Arabidopsis thaliana
Descriptors:peaches. microsatellites. genetic-markers. fruit-crops. biotechnology
Organism Descriptors:Prunus-persica

Supplemental Descriptors:Prunus. Rosaceae. Rosales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. WW000
Supplementary Info:38 ref
ISSN:0040-5752
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Journal Title:Theoretical and Applied Genetics
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583. Title:alpha -Keto acid elongation and glucosinolate biosynthesis in Arabidopsis thaliana
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 429-437
CD Volume:335
Print Article: Pages: 429-437
Author(s):Campos de Quiros H Magrath R McCallum D Kroymann J Scnabelrauch D Mitchell Olds T Mithen R
Author Affiliation:John Innes Centre, Norwich Research Park, Colney Lane, Norwich NR4 7UH, UK
Language:English
Abstract:QTL mapping of glucosinolates in a recombinant inbred population derived from an F1 hybrid between the Arabidopsis thaliana ecotypes Columbia and Landsberg erecta identified a single major QTL coincident with the GSL-ELONG locus which regulates side chain elongation. Physical mapping and sequencing identified two members of an isopropylmalate synthase-like gene family within the region of maximum LOD score for the QTL and the GSL-ELONG non-recombinant region. These genes are prime candidates for regulating glucosinolate biosynthesis
Descriptors:biosynthesis. ecotypes. genes. glucosinolates. gene-mapping. quantitative-trait-loci. wide-hybridization. amino-acid-sequences. lyases. weeds. biotechnology
Identifiers:isopropylmalate synthase
Organism Descriptors:Arabidopsis-thaliana
Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF060. WW000
Supplementary Info:22 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

584. Title:Characteristics, linkage-map positions, and allelic differentiation of Sorghum bicolor (L.) Moench DNA simple-sequence repeats (SSRs)
View Article: Theoretical and Applied Genetics. 2000. 101 (3). 438-448
CD Volume:335
Print Article: Pages: 438-448
Author(s):Kong L Dong J Hart G E
Author Affiliation:Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77843, USA
Language:English
Abstract:Fifty-one clones isolated from a size-fractionated genomic DNA library of Sorghum bicolor, that had been probed with four radiolabelled di- and tri-nucleotide oligomers, were sequenced. Fifty of the clones contained one or more simple-sequence repeats (SSRs) (72% of which were (AG/TC)n SSRs) and, following analysis of the clones, polymerase-chain-reaction primer sets that amplify 38 unique SSR loci were developed. Genotyping of the 38 loci in 18 sorghum accessions, including the parents of a recombinant inbred (RI) mapping population, revealed polymorphism at 36 of the loci among the 18 accessions and at 31 of the

loci (not including null alleles at two loci) between the parents of the RI population. All of the latter 31 loci were mapped. The genotypes at 17-mapped SSR loci were assayed in 190 S. bicolor accessions in order to determine delta T*, the estimated level of allelic differentiation (the estimated probability that two members of a population, chosen at random and without replacement, differ in allelic composition), at each of the loci. The mean delta T* value determined for S. bicolor overall was 0.89, the range of mean delta T* values for ten S. bicolor races was from 0.88 to 0.83, and the range of mean delta T* values for ten working groups (= sub-races) of the race caudatum, with only two exceptions, was from 0.87 to 0.79. The lowest delta T* values for six of the loci among the ten race-caudatum working groups ranged from 0.86 to 0.70; thus, the probability that different alleles will be present at one or more of these loci in two accessions chosen at random from a working group is >0.996 when three of the loci are genotyped, and >0.9999 when all six of the loci are genotyped. The results of this study confirm that most S. bicolor SSR loci are sufficiently polymorphic to be useful in marker-assisted selection programmes and they indicate that the levels of polymorphism at some loci are high enough to allow the vast majority of S. bicolor accessions, even accessions within working groups, to be distinguished from one another by determining the genotypes at a small number, perhaps as few as a half-dozen, SSR loci

Descriptors:alleles. gene-mapping. polymorphism. microsatellites. genetic-markers. cereals. biotechnology

Organism Descriptors:Sorghum-bicolor

Supplemental Descriptors:Sorghum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF020. WW000

Supplementary Info:33 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

585. Title:A chloroplast DNA hypervariable region in eucalypts

View Article: Theoretical and Applied Genetics. 2000. 101 (3). 473-477

CD Volume:335

Print Article: Pages: 473-477

Author(s):Vaillancourt R E Jackson H D

Author Affiliation:Cooperative Research Centre for Sustainable Production Forestry and School of Plant Science, University of Tasmania, GPO Box 252-55, Hobart, Tasmania 7001, Australia

Language:English

Abstract:Eucalypt chloroplast DNA (cpDNA) provides useful markers for phylogenetic and population research including gene flow and maternity studies. All cpDNA studies in Eucalyptus to date have been based on the RFLP technique, which requires relatively large amounts of clean DNA. The objective of this study was to develop PCR-based cpDNA markers for Eucalyptus. The chloroplast genome of Eucalyptus, like that of most angiosperms, possesses inverted repeats (IR). The two junctions between the IRs and the large single copy (LSC) regions are defined as JLA and JLB. The region surrounding the JLA junction was sequenced from 26 Eucalyptus DNA samples (21 of E. globulus, plus 5 other species), and the JLB region was sequenced using 5 of these samples. The samples were chosen to represent all major haplotypes identified in previous cpDNA RFLP studies. The JLA products were 150-210 bp in size, while those from JLB were approximately 500 bp in size. Eighteen mutations were scored in total. Extensive variation was found in the IR within

the intergenic spacer between rpl2 and the IR/LSC junctions. Many of these characters were complex indels. One sample of E. globulus possessed a relatively large (38 bp) insertion which caused displacement of the IR/LSC junctions. This is the first report of intraspecific variation in the position of IR/LSC junctions; interspecific variation was also found. The LSC region near JLB had a low rate of mutation and none were informative. The LSC region near JLA possessed 2 informative mutations. The variation revealed from these sequences reflects the differentiation previously uncovered in an extensive RFLP analysis on the same samples. These results suggest that the JLA region will provide very useful cpDNA polymorphisms for future studies in Eucalyptus

Descriptors:chloroplast-genetics. chloroplast-DNA. genetic-markers. polymerase-chain-reaction. polymorphism. forest-trees. broadleaves. biotechnology

Organism Descriptors:Eucalyptus-globulus. Eucalyptus

Supplemental Descriptors:Eucalyptus. Myrtaceae. Myrtales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:KK100. FF020. WW000

Supplementary Info:18 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

586. Title:Mapping quantitative and qualitative disease resistance genes in a doubled haploid population of barley (Hordeum vulgare)

View Article: Theoretical and Applied Genetics. 2000. 101 (4). 580-589

CD Volume:335

Print Article: Pages: 580-589

Author(s):Toojinda T Broers L H Chen X M Hayes P M Kleinhofs A Korte J Kudrna D Leung H Line R F Powell W Ramsay L Vivar H Waugh R

Author Affiliation:DNA Fingerprinting Unit, National Center for Genetic Engineering and Biotechnology, Kasetsart University, Kampangsaen Campus, Nakorn Pathom, Thailand

Language:English

Abstract:Stripe rust (Puccinia striiformis), leaf rust (P. hordei) and barley yellow dwarf virus (BYDV) are important diseases of barley (Hordeum vulgare). Using 94 doubled-haploid lines (DH) from the cross of Shyri x Galena, multiple disease phenotype datasets, and a 99-marker linkage map, we determined the number, genome location, and effects of genes conferring resistance to these diseases. We also mapped resistance gene analog polymorphism (RGAP) loci, based on degenerate motifs of cloned disease resistance genes, in the same population. Leaf rust resistance was determined by a single gene on chromosome 1 (7H). QTLs on chromosomes 2 (2H), 3 (3H), 5 (1H), and 6 (6H) were the principal determinants of resistance to stripe rust. Two-locus QTL interactions were significant determinants of resistance to this disease. Resistance to the MAV and PAV serotypes of BYDV was determined by coincident QTLs on chromosomes 1 (7H), 4 (4H), and 5 (1H). QTL interactions were not significant for BYDV resistance. The associations of molecular markers with qualitative and quantitative disease resistance loci will be a useful information for marker-assisted selection

Descriptors:barley. disease-resistance. genes. chromosomes. genomes. gene-mapping. plant-pathogenic-fungi. plant-diseases. plant-pathogens

Organism Descriptors:Hordeum-vulgare. Hordeum. Puccinia-striiformis. Puccinia-hordei. barley-yellow-dwarf-luteovirus. plant-viruses

Supplemental Descriptors:Hordeum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Puccinia. Uredinales. Basidiomycotina. Eumycota. fungi. luteovirus-group. plant-viruses. viruses. plant-pathogens. pathogens
Subject Codes:FF005. FF020. WW000. FF610
Supplementary Info:51 ref
ISSN:0040-5752
Year:2000
Journal Title:Theoretical and Applied Genetics
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587.Title:Genetic control of early events in protoplast division and regeneration pathways in sunflower
View Article: Theoretical and Applied Genetics. 2000. 101 (4). 606-612
CD Volume:335
Print Article: Pages: 606-612
Author(s):Berrios E F Gentzbittel L Mokrani L Alibert G Sarrafi A
Author Affiliation:Department of Biotechnology and Plant Breeding, Pole de Biotechnologie Vegetale, BAP, INP-ENSAT 18 Chemin de Borde Rouge, B.P. 107, 31326 Castanet, France
Language:English
Abstract:Experiments were conducted to identify the genetic factors controlling protoplast division and to determine eventual relations between genetic factors involving organogenesis, somatic embryogenesis and protoplast division in sunflower. The present study involved protoplast culture and two traits: total divisions per 100 protoplasts (TOTD) and asymmetric divisions per 100 protoplasts (ASYD) were scored in 52 recombinant inbred lines (RILs) from a cross between PAC-2 and RHA-266. Asymmetric division is an early event in the formation of embryoids from protoplasts. Analysis of variance indicated the existence of highly significant differences among parental genotypes and their RILs. Heritability for the two protoplast division parameters (TOTD and ASYD) was high (0.87 and 0.89, respectively) and genetic gain expressed as percentage of the best parent for 10% of the selected RILs was significant. Twelve putative loci associated with total divisions per 100 protoplasts were identified. Eleven QTLs were also detected for asymmetric divisions per 100 protoplasts. The QTLs present high significant LOD scores and sum to a high percentage of phenotypic variance. The percentage of phenotypic variation explained by each QTL ranged from 2% to 24%. Some segments of the linkage groups I, XV and XVII are likely to contain genes important for organogenesis, somatic embryogenesis and protoplast division, as clustering of QTLs for these characters were described. The QTLs identified in these three linkage groups should be involved in cell division and in early events associated with cell differentiation
Descriptors:protoplasts. in-vitro-regeneration. sunflowers. cell-differentiation. cell-division. heritability. protoplast-culture. somatic-embryogenesis
Organism Descriptors:Helianthus-annuus
Supplemental Descriptors:Helianthus. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF170. FF020. FF005
Supplementary Info:40 ref
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Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

588. Title:Genetic mapping of resistance to bacterial blight disease in cassava (Manihot esculenta Crantz)
View Article: Theoretical and Applied Genetics. 2000. 101 (5/6). 865-872
CD Volume:336
Print Article: Pages: 865-872
Author(s):Jorge V Fregene M A Duque M C Bonierbale M W Tohme J Verdier V
Author Affiliation:Biotechnology Research Unit, Centro Internacional de Agricultura Tropical, (CIAT) A.A. 6713, Cali, Colombia
Language:English
Abstract:Cassava bacterial blight (CBB), caused by Xanthomonas axonopodis pv. manihotis (Xam), is a major disease of cassava (Manihot esculenta) in Africa and South America. Planting resistant varieties is the preferred method of disease control. Recent genetic mapping of an F1 cross (TMS 30572 x CM 2177-2) led to the construction of the first molecular genetic map of cassava. To better understand the genetics of resistance to CBB, we evaluated individuals of the F1 cross for CBB resistance by controlled greenhouse inoculations and visually assessed symptoms on days 7, 15, and 30 days after inoculation, using a scale where 0=no disease and 5=maximum susceptibility. Five Xam strains were used: CIO-84, CIO-1, CIO-136, CIO-295, and ORST X-27. Area under the disease progress curve (AUDPC) was used as a quantitative measure of resistance in QTL analysis by single-marker regression. Based on the AUDPC values, eight QTLs (quantitative trait loci), located on linkage groups B, D, L, N and X of the female-derived framework map, were found to explain 9-20% of the phenotypic variance of the crop's response to the five Xam strains. With the male-derived framework map, four QTLs on linkage groups G and C explained 10.7-27.1% of the variance. A scheme to confirm the usefulness of these markers in evaluating segregating populations for resistance to CBB is proposed
Descriptors:cassava. genetics. quantitative-trait-loci. genetic-markers. plant-pathogenic-bacteria. plant-pathogens. plant-diseases. disease-resistance. gene-mapping
Organism Descriptors:Manihot-esculenta. Xanthomonas-axonopodis. Xanthomonas-axonopodis-pv.-manihotis
Supplemental Descriptors:Manihot. Euphorbiaceae. Euphorbiales. dicotyledons. angiosperms. Spermatophyta. plants. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes. Xanthomonas-axonopodis
Subject Codes:FF020. WW000. HH600. FF610. FF005
Supplementary Info:many ref
ISSN:0040-5752
Year:2000
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589. Title:Molecular phylogeny of Gossypium species by DNA fingerprinting
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Print Article: Pages: 931-938
Author(s):Khan S A Hussain D Askari E Stewart J M Malik K A Zafar Y
Author Affiliation:National Institute for Biotechnology and Genetic Engineering (NIBGE), P.O. Box 577, Jhang Road, Faisalabad, Pakistan
Language:English
Abstract:Total genomic DNA from 31 available Gossypium species, three subspecies and one interspecific hybrid, were analysed to evaluate genetic diversity by RAPD, using 45 random decamer primers. A total of 579 amplified bands were observed, with 12.9 bands per primer, of which 99.8% were polymorphic. OPJ-17 produced the maximum number of fragments while the minimum number of fragments was produced with primer OPA-08. Cluster analysis by the unweighted paired group method of arithmetic

means (UPGMA) showed six main clusters. Cluster 'A' consisted of two species and one subspecies of the A-genome, with a 0.78-0.92 Nei's similarity range. Cluster B, composed of all available tetraploid species and one interspecific hybrid, showed the same sister cluster. Nei's similarity ranged from 0.69 to 0.84. The B-genome formed the UPGMA sister cluster to the E-genome species. Cluster 'C' consisted of five Gossypium species of which three belong to the B-genome, with Nei's similarity values of 0.81 to 0.86. Although there was considerable disagreement at lower infra-generic ranks, particularly among the D-genome (diploid New World species) and C-genome (diploid Australian species) species. The sole F-genome species Gossypium longicalyx was resolved as a sister group to the D-genome species. Gossypium herbaceum and G. herbaceum Africanum showed the maximum Nei's similarity (0.93). Minimum similarity (0.29) was observed between Gossypium trilobum and Gossypium nelsonii. The average similarity among all studied species was 50%. The analysis revealed that the interspecific genetic relationship of several species is related to their centre of origin. As expected, most of the species have a wide genetic base range. The results also revealed the genetic relationships of the species Gossypium hirsutum to standard cultivated Gossypium barbadense, G. herbaceum and Gossypium arboreum. These results correspond well with previous reported results. The level of variation detected in closely related genotypes by RAPD analysis indicates that it may be a more efficient marker than morphological marker, isozyme and RFLP technology for the construction of genetic linkage maps

Descriptors:cotton. phylogeny. random-amplified-polymorphic-DNA. cluster-analysis. centres-of-origin. isoenzymes. restriction-fragment-length-polymorphism. linkage

Identifiers:Gossypium longicalyx. Gossypium trilobum. Gossypium nelsonii

Organism Descriptors:Gossypium. Gossypium-herbaceum. Gossypium-hirsutum. Gossypium-barbadense. Gossypium-arboreum

Supplemental Descriptors:Malvaceae. Malvales. dicotyledons. angiosperms. Spermatophyta. plants. Gossypium

Subject Codes:FF005. FF020. WW000. ZZ380

Supplementary Info:43 ref

ISSN:0040-5752

Year:2000

Journal Title:Theoretical and Applied Genetics

590. Title:Characterization and molecular analysis of transgenic plants obtained by microprotoplast fusion in sunflower

View Article: Theoretical and Applied Genetics. 2000. 101 (8). 1250-1258

CD Volume:336

Print Article: Pages: 1250-1258

Author(s):Binsfeld P C Wingender R Schnabl H

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Language:English

Abstract:Asymmetric somatic hybrid (ASH) plants were obtained by polyethylene glycol-mediated mass fusion of microprotoplasts from perennial Helianthus species and hypocotyl protoplasts of Helianthus annuus. The formation of micronuclei in perennial sunflower cell cultures was induced at early log phase by the addition of the herbicides amiprophosmethyl or oryzalin. Sub-diploid microprotoplasts were isolated by high-speed centrifugation and the smallest enriched by sequential filtration through nylon sieves of decreasing pore size. Fusion products were cultured and the regenerated plants phenotypically, genetically and cytologically characterized. DNA

analysis using RAPD markers revealed that 28 out of 53 regenerated plants were asymmetric hybrids. Subsequent nuclear-DNA flow cytometric analysis showed that these plants had a higher DNA content than the receptor H. annuus, suggesting that they represented addition lines. Cytological investigation of the metaphase cells of 16 hybrids revealed an addition of 2-8 extra chromosomes in these plants. The phenotype of most ASH plants resembled H. annuus. These results indicate that micronuclear induction and asymmetric somatic hybridization represent a potent tool for partial genome transfer aimed at the specific transfer of economically important traits in breeding programmes

Descriptors:cell-cultures. characterization. chromosomes. DNA. hypocotyls. in-vitro-culture. in-vitro-regeneration. microcell-hybrids. nuclei. oryzalin. protoplast-culture. protoplast-fusion. protoplasts. random-amplified-polymorphic-DNA. somatic-hybridization. sunflowers. transgenic-plants

Organism Descriptors:Helianthus-annuus. plants

Supplemental Descriptors:Helianthus. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF020. FF170. WW000

Supplementary Info:31 ref

ISSN:0040-5752

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Journal Title:Theoretical and Applied Genetics

591. Title:AFLP mapping of QTLs for in vitro organogenesis traits using recombinant inbred lines in sunflower (Helianthus annuus L.)

View Article: Theoretical and Applied Genetics. 2000. 101 (8). 1299-1306

CD Volume:336

Print Article: Pages: 1299-1306

Author(s):Flores Berrios E Gentzbittel L Kayyal H Alibert G Sarrafi A

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Language:English

Abstract:Genetic control for two in vitro organogenesis traits, the number of shoots per explant plated (S/E) and the number of shoots per regenerating explant (S/RE), was investigated in 75 recombinant inbred lines (RILs) of sunflower and their two parents (PAC-2 and RHA-266). Genetic variability was observed among the 75 RILs for the organogenesis traits studied. Some RILs presented significant differences when compared with the best parental line (RHA-266). Genetic gain, in terms of the percentage of the best parent, for 32% of the selected RILs was significant. A set of 99 RILs from the same cross including the 75 mentioned above was screened with 333 AFLP markers and a linkage map was constructed based on 264 linked loci. Six putative QTLs for the S/RE (tentatively named osr) and seven QTLs for the S/E (ose) trait were detected using composite interval mapping. For each trait, the QTLs explained 52% (ose) and 67% (osr) of the total phenotypic variance. These results suggested that additive gene effects predominate in explaining a large proportion of the observed genetic variation associated with regeneration ability. The coincidental location of QTLs for S/E and S/RE is discussed

Descriptors:explants. gene-mapping. genetic-gain. genetic-markers. genetic-variation. in-vitro-culture. in-vitro-regeneration. inbred-lines. organogenesis. quantitative-trait-loci. regenerative-ability. shoots. sunflowers. tissue-culture

Identifiers:amplified fragment length polymorphism

Organism Descriptors:Helianthus-annuus

Supplemental Descriptors:Helianthus. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. FF170. WW000
Supplementary Info:44 ref
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Year:2000
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592. Title:Genotypic variation and chromosomal location of QTLs for somatic embryogenesis revealed by epidermal layers culture of recombinant inbred lines in the sunflower (Helianthus annuus L.)
View Article: Theoretical and Applied Genetics. 2000. 101 (8). 1307-1312
CD Volume:336
Print Article: Pages: 1307-1312
Author(s):Flores Berrios E Sarrafi A Fabre F Alibert G Gentzbittel L
Author Affiliation:Department of Biotechnology and Plant Breeding, BAP, INP-ENSAT 18, Chemin de Borde Rouge, BP 107, 31326 Castanet, France
Language:English
Abstract:The present study was conducted to identify the genetic factors controlling somatic embryogenesis in the sunflower. Two traits, the number of embryogenic explants per 40 explants plated (EE/40 E) and the number of embryos per 40 explants (E/40 E), were scored in 74 recombinant inbred lines (RILs) from a cross between 'PAC-2' and 'RHA-266'. The experiment was designed as a randomized complete block with 76 genotypes (74 recombinant inbred lines and two parents) and three replications. Each replication consisted of three Erlenmeyer flasks with 40 epidermal layers (explants). Analyses of variance indicated the existence of highly significant differences among parental genotypes and their RILs. Heritabilities for the somatic embryogenesis traits studied, EE/40 E and E/40 E, were high (0.64 and 0.77, respectively) and the genetic gain, in percentage of the best parent for 10% of selected RILs, was significant. Four QTLs for EE/40 E (tee) and seven for E/40 E (ete) were detected using composite interval mapping and AFLP mapping. The QTLs for EE/40 E explained 48% of the phenotypic variation while the QTLs for E/40 E explained about 89% of the variation
Descriptors:chromosomes. epidermis. explants. gene-mapping. genetic-factors. genetic-gain. genetic-variation. genotypes. in-vitro-culture. inbred-lines. plant-embryos. quantitative-trait-loci. somatic-embryogenesis. sunflowers. tissue-culture
Organism Descriptors:Helianthus-annuus
Supplemental Descriptors:Helianthus. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. FF170. WW000
Supplementary Info:44 ref
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Journal Title:Theoretical and Applied Genetics
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593. Title:Effect of the environment on the bacterial bleaching of corals
View Article: Water Air and Soil Pollution. 123 (1-4). October, 2000. 337-352
CD Volume:310
Print Article: Pages: 337-352
Author(s):Banin E Ben Haim Y Israely T Loya Y Rosenberg E
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Language:English

Language of Summary:English (EN)
Abstract:Bleaching in stony-corals is the result of disruption of symbiosis between the coral hosts and photosynthetic microalgal endosymbionts (zooxanthellae). Coral bleaching events of unprecedented frequency and global extent have been reported during the last two decades. Recently, we demonstrated that bleaching of the coral Oculina patagonica in the Mediterranean Sea is caused by the bacterium Vibrio shiloi, when seawater temperature rises and allows the bacterium to become virulent. The first step in the infection process is host-specific adhesion of V. shiloi to O. patagonica via a beta-galactoside receptor on the coral surface. The bacterium then penetrates into the coral tissue and produces extracellular materials which rapidly inhibit photosynthesis of zooxanthellae and bleach and lyse the algae. The inhibition of photosynthesis is due to a low molecular weight, heat stable toxin and ammonia. Bleaching and lysis are due to a heat-labile, high molecular weight materials, probably lytic enzymes. Elevated temperature induces different virulence factors within the infectious agent of the disease, V. shiloi. Adhesion was found to be temperature-regulated. When the bacteria were grown at 16degreeC there was no adhesion to corals maintained at either 25degreeC or 16degree. However, when the bacteria were grown at 25degreeC they adhered avidly to corals maintained at 16degreeC and 25degreeC. In addition, the production of lytic enzymes and the photosynthesis inhibitor was also found to be temperature dependent. Production of the latter toxin was ten times greater at 29degreeC than at 16degreeC, and extracellular protease was 5-fold higher in cultures grown at 29degreeC than at 16degreeC. The data presented here suggest an explanation for the correlation between elevated seawater temperatures and seasonal coral bleaching
Descriptors:algal lysis; bacterial adhesion; environmental bleaching effects; photosynthesis inhibition; seasonal bacterial coral bleaching; seawater temperature infection. Marine Ecology (Ecology, Environmental Sciences); Infection; Toxicology. bacterial infection: bacterial disease. ammonia: photosynthesis inhibitor; beta-galactoside receptor; heat stable toxin: low molecular weight, photosynthesis inhibitor, toxin; lytic enzymes: algal bleaching agent, algal lysis agent, heat-labile, high molecular weight material, toxin
Geographic Locator:Mediterranean Sea (North Atlantic, Atlantic Ocean)
Organism Descriptors:Oculina patagonica [coral] (Cnidaria): symbiont host; Vibrio shiloi (Vibrionaceae): pathogen; zooxanthellae (Pyrrophyta): endosymbiont, host, photosynthetic microalgae
Supplemental Descriptors:Cnidaria: Invertebrata, Animalia; Pyrrophyta: Algae, Plantae; Vibrionaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Algae; Animals; Bacteria; Eubacteria; Invertebrates; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Marine Ecology (Ecology, Environmental Sciences); Infection; Toxicology
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Journal Title:Water, Air, and Soil Pollution