SUMBER DARI TEEAL

BIOTEKNOLOGI DAN SUMBER DAYA GENETIKA PERTANIAN

KEDELAI

1. **Poultry litter enhances soybean productivity in field infested with soybean cyst nematode**

   Source: Journal of Sustainable Agriculture. 1997. 11 (1). 39-51

   Author(s): Morant-M-A. Casasola-J-L. Brooks-C-B. Philip-E-T. Mitchell-V-G. Orr-

   Soil infested with Heterodera glycines was amended with poultry litter in a 3-year study designed to evaluate the effectiveness of the organic amendment for improving soyabean productivity and reducing damage by the nematode. Poultry litter was split-applied at V2 and V5 stages of soyabean development, at rates of 0, 5 or 10 t ha-1. The experimental plots were in Wicomico County, Maryland, and sown to Manokin (resistant) and Essex (susceptible) soyabean cultivars. Cyst index was inversely correlated with poultry litter, although the difference between the 5 t ha-1 and 10 t ha-1 treatments was not significant. Poultry litter had a greater impact on reducing cyst infestation in Essex. Over the 3-year period, cyst index increased incrementally on Manokin but this was significantly lower than on Essex. Nodule number and foliar N content were depressed by application of poultry litter. Shoot and root dry weight were improved by amending soil with 5 t ha-1 poultry litter, but were reduced by the 10 t ha-1 rate. Seed yield of both cultivars also tended to be reduced by 10 t ha-1 poultry litter treatment, but stimulated by the 5 t ha-1 treatment. The results indicated that 5 t ha-1 poultry litter is an effective means of improving productivity when soyabean is grown in H. glycines-infested soil

   Descriptors:Chemical-control. Control. Grain-legumes. Nematicides. Nematology. Organic-amendments. Plant-nematology. Plant-parasitic-nematodes. Poultry-manure. Soyabeans

2. **Impact of fly ash and phosphate solubilising bacteria on soybean productivity**

   Source: Bioresource Technology. 2002. 85 (3). 313-315

   Author(s): Sunita-Gaind. Gaur-A-C

   Abstract:

   Fly ash was characterized for the leaching potential of some major and minor constituents and then added to soil at 20, 40, 60 and 80 tonnes/ha with N and P fertilizer to evaluate its effect on nutrient uptake and soyabean yield singly as well as in combination with an efficient phosphate solubilizer Pseudomonas striata. The application of fly ash at 40 tonnes/ha in conjunction with P. striata inoculation improved the bean yield and P uptake by grain. The available phosphorus of soil also showed an upward trend. The fly ash did not exert any detrimental effect on the population of inoculated bacteria. However, the uptake of trace elements did not improve significantly

Descriptors:Crop-yield. Fly-ash. Leaching. Nitrogen-fertilizers. Nutrient-uptake. Phosphorus-fertilizers. Soil-amendments. Soyabeans. Trace-elements

3. **Mitigating climate change impact on soybean productivity in India: a simulation study**
   Source: Agricultural and Forest Meteorology. 2004. 121 (1-2). 113-125
   Author(s): Mall-R-K. Lal-M. Bhatia-V-S. Rathore-L-S. Ranjeet-Singh
   Abstract:

   Field experiments with soyabean were conducted over a period of 1990-1998 in diverse Indian locations ranging in latitude, longitude, and elevation. These locations provided a wide range of environments for testing and validation of the crop growth (CROPGRO) model considered in this study with observed changes in soils, rainfall and other weather parameters. Model predicted satisfactorily the trends of days to flowering, maturity and grain yields. The deviations of simulated results were within plus or minus 15% of the measurements. Validated CROPGRO model has been used to simulate the impact of climate change on soyabean production in India. The projected scenarios for the Indian subcontinent as inferred from three state-of-the-art global climate models (GCMs) have been used in the present study. There was a decrease (ranging between about 10 and 20%) in soyabean yield in all the three future scenarios when the effect of rise in surface air temperature at the time of the doubling of CO2 concentration was considered. The results obtained on the mitigatory option for reducing the negative impacts of temperature increases indicate that delaying the sowing dates would be favorable for increased soyabean yields at all the locations in India. Sowing in the second season would also be able to mitigate the detrimental effects of future increases in surface temperature due to global warming at some locations

   Descriptors:Air-temperature. Carbon-dioxide. Climatic-change. Computer-simulation. Crop-yield. Flowering. Flowering-date. Maturity. Productivity. Rain. Simulation. Simulation-models. Solar-radiation. Sowing-date. Soyabeans

4. **Predicting corn and soybean productivity for Illinois soils**
   Source: Agricultural Systems. 2000. 64 (3). 151-170
   Author(s): Garcia-Paredes-J-D. Olson-K-R. Lang-J-M
   Abstract:

   An approach based on multiple regression was used to evaluate the relationship between 16 selected soil properties of 34 major soils and established 1970s (1967-76) maize and soyabean yields for Illinois, USA. Statistical models developed from major soils were tested by calculating the 10-year average maize and soyabean yields for each of the 34 major soils. The coefficients generated from multiple regression were further tested using the soil property values for the additional 165 soils identified in 9 counties representing the crop reporting districts and weather districts in Illinois. The 10-year average crop yield trends were determined for 66 counties in the northern region and for 36 counties in the southern region for 1976-95. These 20-year yield trend increases were added to the established and model-predicted 1970s crop yields to estimate 1990s (1986-95) maize and soyabean yields for the average management level for all 199 Illinois soil types in 9 selected counties. The 1990s crop yield estimates for the selected counties were weighted by extent of each soil type in the county and compared against 10-year county averages for the 1990s farmer-reported Illinois Agricultural Statistics (IAS) maize and soyabean yields. Predicted 1990s county crop yields were statistically similar to IAS county crop yields

Descriptors: M**aize. Soyabeans. Simulation-models. Statistics. Yield-forecasting**

5. **The incidence of benefits from U.S. soybean productivity gains in a context of world trade**

Source: American Journal of Agricultural Economics. 1993. 75 (1). 169-180

Author(s): Cooke S C. Sundquist W B

Abstract:

A new procedure for measuring the 'K-shift' in the supply function from new technology is introduced. This procedure is used to show that US soyabean total factor productivity increased by 1.6% per year between 1974 and 1983. Brazilian and Argentine soyabean productivity increased 2.4% per year during this period. Total economic surplus in the USA and the rest of the world increased between $1700 and $3200 million. Of this total, US resource owners received between $1300 and $1500 million and US consumers received an increase in income of between $100 and $200 million from increased soyabean productivity

Descriptors:Soyabeans. Productivity. Technical-progress. Supply-response. Income-distribution. Economics

JAGUNG

1. **Maize seed supply systems and implications for seed sector development in Southwestern Nigeria**

Source: Journal of Sustainable Agriculture. 2006. 28 (2). 25-40

Author(s): Daniel-I-O. Adetumbi-J-A

Abstract:

This study examines the seed supply system for maize production in Southwestern Nigeria in order to characterise the local seed system and to assess the potentials of the maize seed sector in the development of sustainable crop improvement and enhanced agricultural productivity. Using structured questionnaires, a seed survey was conducted among 94 farmers randomly sampled from 5 farm settlement locations covering 3 states in the region. The data collected were subjected to descriptive analysis of simple proportions and percentages. All improved varieties on the sampled farms were the IITA elite varieties. At all locations, the percentage of total land area cultivated with the seeds of improved varieties ranged from 71 to 100%, while percentage of land area sown with local varieties ranged from 0 to 29%. Seed use in terms of volume followed the same pattern. The highest proportion of farmers (about 50%) who planted improved varieties used seeds from previously saved harvests, while 25% procured them from extension agents, 17% bought them from seed dealers, 5% from research institutes and the farmer-to-farmer exchange was negligible. About 39% of farmers used improved varieties for high crop yields, 24% for disease resistance and 22% for market preferences, whereas local varieties were cultivated by 37% of farmers because of market preferences and availability, 16% because of low cost and 12% because of disease resistance. The implications of the results on sustainable economic development of the seed industry and suggestions for strengthening of the commercial seed sector are discussed

Descriptors:Crop-production. Cultivars. Improved-varieties. Maize. Seed-industry. Seeds. Surveys

2. Some properties of corn grains and their flours I: physicochemical, functional and chapati-making properties of flours

Source: Food Chemistry. 2007. 101 (3). 938-946

Author(s): Sandhu-K-S. Narpinder-Singh. Malhi-N-S

Abstract:

The variability in physical (1000 kernel weight and bulk density) and mechanical (rupture force) properties of grains from different Indian corn varieties (African tall, Ageti, Early composite, Girja, Navjot, Parbhat, Partap, Pb sathi and Vijay) were studied. The functional (colour, gelatinization, retrogradation and pasting) and chapati-making properties of flours milled from corn varieties were evaluated. African tall flour showed the highest enthalpy of gelatinization (DELTA Hgel), peak-, trough-, breakdown-, final-, and setback viscosities, and L* (84.4) value and resulted in chapaties with higher extensibility (5.76 mm) and of light colour. African tall flour, with the lowest protein content, showed the lowest grain rupture force. Amylose content and hardness of starch gel from African tall were found to be the lowest among all corn varieties. Girja flour, with the lowest transition temperatures and DELTA Hgel, showed the lowest extensibility of chapaties made from it. Pearson correlations between physical and textural properties of corn grains and the functional properties of their flours were established. Rupture force of corn grain and protein content of flour showed a negative correlation with peak viscosity of flour ($r=-0.917$, and -0.863, $p<0.01$). The protein content of flours was negatively correlated with L* ($r=-0.759$, $p<0.01$) value and positively with b* ($r=0.635$, $p<0.01$) value. Pasting temperature of flours showed a significant negative correlation with peak, trough, breakdown, final and setback viscosities ($r=-0.836$, -0.846, -0.778, -0.871, and -0.847, respectively, $p<0.01$). Pearson correlation was also established between the grain and starch properties. Rupture force of corn grains was positively correlated with the amylose content of starch ($r=0.950$, $p<0.01$)

Descriptors:Amylose. Corn-flour. Cultivars. Flours. Functional-properties. Hardness. Mechanical-properties. Physicochemical-properties. Protein-content

3. Tillage x maize hybrid interactions

Source: Agronomy Journal. 2006. 98 (3). 436-442

Author(s): Duiker-S-W. Haldeman-J-F-Jr. Johnson-D-H

Abstract:

Continuous maize (Zea mays L.) yields may be depressed with no-tillage (NT) compared with conventional chisel and disking systems (CD). Shallow or deep in-row tillage (ST and DT, respectively) may help alleviate this yield reduction, whereas some hybrids may be better adapted to NT. We therefore evaluated five maize hybrids with NT, ST, DT, and CD from 2002 to 2004 on a Hagerstown silt loam (fine, mixed, semiactive, mesic Typic Hapludalf) in southeastern Pennsylvania. Residue cover, penetration resistance, bulk density, and soil temperature were measured as well as maize emergence, mid-season height, and yield. Residue cover varied in the order NT > ST and DT > CD. Bulk density and penetration resistance in NT were higher than in ST, DT, and CD to the depth of tillage. In 2002, the average soil temperature during the first month after planting varied in the order NT < ST and DT < CD, but did not vary between tillage systems in 2004. Emergence was slower in NT than the other tillage systems in 2002 only. Emergence varied between hybrids, but there was no tillage x hybrid interaction. Mid-season maize height was not lower in NT than the other tillage systems. Tillage systems did not affect yield, and there was no tillage x hybrid interaction for yield, although some hybrids yielded better than others. The study suggests continuous maize yields with NT will be similar to tilled systems on well-drained soils in the northeastern USA and that tillage system is not important for hybrid selection

Descriptors:Bulk-density. Chiselling. Crop-yield. Discing. Hybrid-varieties. Maize. No-tillage. Penetration. Plant-height. Row-tillage. Seedling-emergence. Soil-temperature. Tillage

4. Additive mean effects and multiplicative interaction analysis of maize yield trials in South Africa

Source: South African Journal of Plant and Soil. 2008. 25 (4). 185-193

Author(s): Ma'ali-S-H

Abstract:

Thirty five maize hybrids were evaluated over 98 environments for genotype * environment interaction (GEI) and yield stability under dry land conditions during the 2003 to 2006 seasons in the eastern and western maize production regions of South Africa. The Additive Mean Effects and Multiplicative Interaction (AMMI) statistical model was used to describe the GEI, yield stability and adaptation to certain environments. This model has shown to be effective in understanding complex GEI's in the national cultivar trials. The AMMI 2 combined analysis of variance (ANOVA) indicated highly significant differences among hybrids and environments as main effects. The environment and GEI contributed more towards the total variation. This demonstrated a high influence of the environment on the yield performance of maize hybrids in both regions. CRN 3604 and PAN 6611 were the most stable hybrids in the eastern region while PAN 6966 and PAN 6146 were the most stable hybrids in the western region. DKC 80-12B and DKC 80-10 were the best adapted hybrids for high potential environments in the eastern region while DKC 78-15B and DKC 80-12B were the best adapted hybrids for high potential environments in the western region. Caracal and to lesser extend Saffier were the best adapted hybrids for low potential environments in both the eastern and western regions

Descriptors:Crop yield; genotype environment interaction; hybrid varieties; maize; mathematical models Southern Africa; Africa South of Sahara; Africa; Developing Countries; Threshold Countries; Anglophone Africa; Commonwealth of Nations; Zea; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants; eukaryotes

5. **Performance of corn hybrids obtained from crosses of lines with different dry matter degradabilities**

Source: Bragantia. 2008. 67 (2). 285-297

Author(s): Mendes-M-C. Pinho-R-G-von. Pereira-M-N. Faria-Filho-E-M. Souza-Filho--

Abstract:

In order to recommend maize hybrids for silage, it is not enough to have high dry matter. It is also necessary that the silage presents high effective matter degradation (DEF) of the whole plant. Field studies were conducted in Minas Gerais, Brazil, during the 2003/04 cropping season, to evaluate the agronomic, bromatologic and rumen degradability of dry matter of 5 commercial maize hybrids, recommended for silage production, and 18 experimental hybrids from crosses of lines of high and low degradability. Maize plants were harvested at 20 cm from soil level at milk line at half grain stage. The silages were incubated in situ for 0, 6, 12, 24 and 96 h in the rumen of 3 fistulated cows. Effective degradability was calculated based on 0.05%/h of passage rate. It was observed that among the cultivars, there were hybrids that presented good potential for silage production with high DEF of the whole plant, independent of grain texture. The strategy of synthesizing hybrids aiming at high dry matter effective degradability based on lines with high DEF is correct. The low correlation between effective degradability with the agronomic and bromatologic characteristics indicate the need for better use of DEF in order to select maize hybrids of high quality of silage production

Descriptors:Hybrid-varieties. Maize. Rumen-digestion. Silage. Variety-trials

6. **A Bayesian approach for assessing the stability of genotypes**

Source: Crop Science. 2006. 46 (6). 2654-2665

Author(s): Cotes-J-M. Crossa-J. Sanches-A. Cornelius-P-L

Abstract:

Several statistical models can be used for assessing genotype x environment interaction (GEI) and studying genotypic stability. The objectives of this research were to show how (i) to use Bayesian methodology for computing Shukla's phenotypic stability variance and (ii) to incorporate prior information on the parameters for better estimation. Potato [Solanum tuberosum subsp. andigenum (Juz. & Bukasov) Hawkes], wheat (Triticum aestivum L.), and maize (Zea mays L.) multi environment trials (MET) were used for illustrating the application of the Bayes paradigm. The potato trial included 15 genotypes, but prior information for just three genotypes was used. The wheat trial used prior information on all 10 genotypes included in the trial, whereas for the maize trial, noninformative priors for the nine genotypes was used. Concerning the posterior distribution of the genotypic means, the maize MET with 20 sites gave less disperse posterior distributions of the genotypic means than did the posterior distribution of the genotypic means of the other METs, which included fewer environments. The Bayesian approach allows use of other statistical strategies such as the normal truncated distribution (used in this study). When analyzing grain yield, a lower bound of zero and an upper bound set by the researcher's experience can be used. The Bayesian paradigm offers plant breeders the possibility of computing the probability of a genotype being the best performer. The results of this study show that although some genotypes may have a very low probability of being the best in all sites, they have a relatively good chance of being among the five highest yielding genotypes

Descriptors:Crop yield; genetic stability; genotype environment interaction; genotypes; high yielding varieties; maize; mathematical models; potatoes; wheat Solanum; Solanaceae; Solanales; dicotyledons; angiosperms; Spermatophyta; plants; eukaryotes; Triticum; Poaceae; Cyperales; monocotyledons; Zea

7. Corn seed germination and vigor following freezing during seed development

Source: Crop Science. 2006. 46 (4). 1526-1535

Author(s): Woltz-J. TeKrony-D-M. Egli-D-B

Abstract:

The potential for an early autumn frost to reduce corn (Zea mays L.) seed quality is a concern for seed producers. This study evaluated the effect of freezing rate, freezing temperature (-6, -11 deg C) and duration (4, 6 h), ear attachment, and endosperm composition on seed germination and vigor (accelerated aging [AA] and cold test) during seed development and maturation of six corn hybrids in 1998, 1999, and 2000. Severe reductions in seed germination and vigor occurred for the most immature seeds frozen at >400 g kg-1 seed moisture content (SMC). The effect was reduced as seed developed for all hybrids resulting in a linear increase in germination and vigor to maximum levels at less than or equal to 300 g kg-1 seed moisture, which was slightly after physiological maturity (PM, maximum dry seed weight). The effect of freezing on seed germination and vigor was the same when (i) ears were frozen attached or detached from the plant; (ii) ears were exposed to different freezing rates; or (iii) seeds with sugary and starchy endosperm were frozen. The degree of freezing injury at a given temperature and duration of freezing was similar across four F1 hybrids, but seed from one F2 hybrid was injured slightly less at a given moisture content. Thus, the stage of seed development must be considered by seed companies before making harvesting decisions when facing a potential predicted freezing event. Our results suggest that a seed producer will have higher germination and vigor if they harvest immature seeds (less than or equal to 400 g kg-1 SMC) before the freezing event instead of after they are exposed to freezing temperatures

Descriptors:Accelerated aging; cold injury; cold stress; endosperm; freezing; hybrid varieties; maize; maize ears; seed development; seed germination; seed maturation; seed moisture; seed quality; starch; sugar content; vigour Zea; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants; eukaryotes

8. **Background and importance of Troyer Reid corn**

Source: Crop Science. 2006. 46 (6). 2460-2467

Author(s): Troyer-A-F. Palmer-L-S

Abstract:

Corn (Zea mays L.) history and American westward expansion were intertwined when several hundred newer, better adapted, open-pollinated corn varieties were developed by human and natural selection. Chester E. Troyer was a pioneer corn breeder who bred 'Troyer Reid', an improved 'Reid Yellow Dent' variety. We relate how Chester got to the particular Indiana farm whose pervious, river-bottom soil affected natural selection. Better, deeper rooting probably helped Troyer Reid obtain more nutrients and water. Chester's formative years were spent as a teacher, and his later achievements included being honored four times as Corn King of the World and also as a successful corn breeder of productive corn varieties and proprietary hybrids. He was first to produce and sell hybrid seed corn in Indiana in 1925, received the Purdue University Certificate of Distinction and was a successful seed corn businessman and employer, successful gladiolus (Gladiolus x gandavensis Van Houtte) breeder of award winning varieties, successful banker, and beloved civic philanthropist. Troyer Reid accounts for about 15% of the background of documented U.S. Corn Belt hybrid corn through inbreds developed by Purdue University, Pioneer Hi-Bred International, University of Minnesota, and Iowa State University corn breeders

Descriptors:Cultivars; hybrid varieties; maize Iridaceae; Liliales; monocotyledons; angiosperms; Spermatophyta; plants; eukaryotes; Gladiolus; Zea; Poaceae; Cyperales; North America; America; Developed Countries; OECD Countries

9. **Bt protein rhizosecreted from transgenic maize does not accumulate in soil**

Source: Electronic Journal of Biotechnology. 2008. 11 (2). 1-10

Author(s): Margarit-Ezequiel. Reggiardo-Martin-I. Permingeat-Hugo-R.

Abstract:

The persistence of CryIAb protein rhizosecreted in soil is important in the assessment of its environmental risk. Here we report that CryIAb protein from transgenic maize does not accumulate at high levels in soils. Levels of CryIAb protein rhizosecreted by three maize transgenic events (BT11, MON810 and 176) were studied in hydroponic cultures and found only in the MON810 and BT11 events but not in event 176 or control plants. Under field conditions, the cryIAb gene and a basal level of CryIAb protein was detected in soils from plots cultivated with transgenic and non-transgenic maize, possibly from Bacillus thuringiensis present in the soils

Descriptors: Molecular Genetics (Biochemistry and Molecular Biophysics)

10. **The maize Activator/Dissociation system is functional in hexaploid wheat through successive generations**

Source: Functional Plant Biology. 2007. 34 (9). 835-843

Author(s): Pastori-G-M. Huttly-A. West-J. Sparks-C. Pieters-A. Luna-C-M. Jones-H-D. Foyer-C-H

Abstract:

The aim of the present study was to provide useful background information and evidence of the functionality of the maize Activator/Dissociation (Ac/Ds) system in hexaploid wheat. Two transgenic parental wheat lines, one harbouring the immobilised Ac element (iAc) and the other the Ds element (pUbi[Ds-uidA]bar), were crossed. Transient GUS assays confirmed that the iAc transposase is active in hexaploid wheat. Selected F1 and F2 lines were analysed by PCR using primers specific to Ac, uidA and bar genes. The primer pair Ubi/bar-tag was used to detect excision of the Ds-uidA sequence, which occurred at a frequency of 39% in the F1 generation. Lines free of Ac and showing evidence of Ds excision were subject to Southern analysis, which indicated that at least one transposition event might have occurred in these lines. Although more evidence is required to unequivocally support the reintegration of the Ds element in the wheat genome, the evidence presented here nevertheless demonstrates the effectiveness and potential value of using this system to tag genes in wheat

Descriptors:Beta-glucuronidase. Enzymes. Gene-tagging. Genetic-transformation.Hexaploidy. Lines. Maize. Transgenic-plants. Transposition. Wheat

11. **Preference tests with collembolas on isogenic and Bt-maize**

Source: European Journal of Soil Biology. 2006. 42 (S1). S132-S135

Author(s): Bakonyi-G. Szira-F. Kiss-I. Villanyi-I. Seres-A. Szekacs-A

Abstract:

Collembolas are important members of belowground food webs. There is little information available on the effects of the plant residues of transgenic maize expressing Bacillus thuringiensis (Bt) toxin on soil animals, including collembola. This is why two questions were addressed in laboratory feeding experiments with three collembolan species: (i) Are collembola equally distributed on residues of isogenic and Bt-maize? and (ii) Do collembola show feeding preference to either of the maize types? Bt-maize (producing Cry1Ab toxin) proved to be a less preferred food source for Folsomia candida than the isogenic one. No similar phenomenon was found in the case of Heteromurus nitidus and Sinella caeca. F. candida reacted to as low as 3.45 (plus or minus 0.8 mg g-1) Bt-toxin content of the maize. Our results show that the effect of the Bt-toxin producing maize on the collembolan is species specific

Descriptors: bacterial-toxins. Feeding-preferences. Maize. Transgenic-plants

12. The digestive fate of Escherichia coli glutamate dehydrogenase deoxyribonucleic acid from transgenic corn in diets fed to weanling pigs

Source: Journal of Animal Science. 2006. 84 (3). 597-607

Author(s): Beagle-J-M. Apgar-G-A. Jones-K-L. Griswold-K-E. Radcliffe-J-S. Qiu-X. Lightfoot-D-A. Iqbal-M-J

Abstract:

Corn containing genetically engineered plasmid DNA encoding an Escherichia coli glutamate dehydrogenase (gdhA) was fed to 19-d-old weanling swine to trace the digestive fate of the transgenic DNA. Eight pens of 8 pigs were fed a commercial (nongdhA) starter for 2 wk. One pig was randomly selected from each pen for 0-h control samples. The remaining 56 pigs were transitioned onto a corn-soybean meal diet and fed a diet containing 58% gdhA corn for approximately 1 wk; immediately thereafter, liver, 10th rib muscle, white blood cells, and plasma from the hepatic portal vein and ingesta from the stomach, distal ileum, and large intestine were collected. The DNA was extracted and the concentration determined via spectrophotometry. Polymerase chain reaction and gel electrophoresis were performed with primers designed to amplify 490 bp that included the plasmid's ligation site between the maize ubiquitin and the gdhA genes. The gdhA corn-derived DNA and diet served as positive assay controls, and conventional corn DNA and distilled water acted as negative assay controls. Detection limits were 0.99 fg of target DNA confounded with 500 ng of conventional corn DNA per each 20 micro L reaction. Transgenic DNA was detected in 71.43% of the stomach and 1.79% of the ileal ingesta samples from treatment animals but was not detected in the large intestine, white blood cells, plasma, liver, or muscle samples. Transgenic DNA was not detected in any sample from 0-h control animals. Stomach and ileal ingesta samples were further analyzed using real-time PCR. With an estimated limit of detection of 1.049 ag/ micro L, 89.29% of the stomach ingesta samples were positive (average 1.56 fg target DNA). The proportion of transgenic DNA to total DNA differed between diet and stomach ingesta samples (P<0.001). Despite the greater sensitivity of real-time PCR, target DNA was detected in only 1.79% of ileal ingesta. These data suggest that the gdhA transgene began degradation in the stomach and was nondetectable in the large intestine

13. **Induction of the maize GapC4 promoter in transgenic potato under anaerobiosis and in Erwinia carotovora-inoculated tuber tissue**

Source: Molecular Plant Microbe Interactions. 1999. 12 (3). 182-188

Author(s): Bulow-L. Kohler-U. Cerff-R. Hehl-R. During-K

Abstract:

The induction pattern of the GapC4 promoter from maize in transgenic potato has been analysed by fusion to the beta -glucuronidase (gus) gene. Under anaerobic conditions this promoter confers high level expression not only in leaves, stems, and roots but also in tubers. After inoculation of potato tuber disks with E. carotovora subsp. atroseptica, beta -glucuronidase (GUS) activity could be detected in macerated tissue as well as in surrounding intact tissue. In mock controls no induction was detected, ruling out any induction due to an overall limitation in oxygen in the experimental system. In addition, it could be proven that no diffusion of GUS protein from macerated into intact tissue occurred. The promoter was shown to be aerobically induced even in the absence of live bacteria by incubation with purified Erwinia spp. pectolytic enzymes alone. Therefore, promoter induction seems to be mediated by a mobile factor instead of by limitation in oxygen. These results demonstrated that the maize GapC4 promoter is suitable for directing foreign genes encoding antibacterial proteins in transgenic potato

Descriptors:A**naerobiosis. Maize. Transgenics. Diffusion. Genes. Induction. Inoculation. Beta-glucuronidase. Plant-pathogenic-bacteria. Plant-pathogens. Disease-resistance. Root-crops. Cereals. Plant-pathology**

14. **Activation of latent transgenes in Arabidopsis using a hybrid transcription factor**

Source: Genetics. 1998. 149 (2). 633-639

Author(s): Guyer-D. Tuttle-A. Rouse-S. Volrath-S. Johnson-M. Potter-S. Gorlach-J. Goff-S. Crossland-L. Ward-E

Abstract:

A hybrid transcription factor comprising a fusion of the DNA-binding domain of Saccharomyces cerevisiae GAL4 and the transcription activation domain of maize C1 was expressed in stably transformed Arabidopsis. Additional transgenic lines were created containing test genes controlled by a synthetic promoter consisting of concatemeric copies of the cis-acting site recognized by GAL4 (UASG) fused to a minimal promoter. The GAL4/CI effector line was crossed to two lines containing a synthetic promoter/GUS fusion. Both histochemical staining and GUS activity assays indicate strong activation of GUS expression was achieved only after crossing. The GAL4/C1 effector line was also crossed to 15 lines containing a synthetic promoter/antisense adenylosuccinate synthetase gene. Severely retarded growth, and in some cases lethality, was observed in 40% of the F1 lines. This system of activation by crossing is generally useful for activating expression of test transgenes

Descriptors:Weeds. Transcription-factors. Maize. Transgenic-plants. Promoters. Genetic-transformation. Reporter-genes. Enzyme-activity. Biotechnology

15. **Pollen control during transgenic hybrid maize development in Mexico**

Source: Crop Science. 1998. 38 (6). 1597-1602

Author(s): Garcia-C-M. Figueroa-M-J. Gomez-L-R. Townsend-R. Schoper-J

Abstract:

Pollen containment may be necessary to prevent the dissemination of novel genes from transgenic crops into sexually compatible land races or wild relatives in locations where these are grown or occur naturally in the same vicinity. Routine maize (Zea mays) breeding activities employ controlled pollinations and are sometimes done in areas where land races or wild relatives are known to occur. The ability of researchers to control pollen movement and to thereby control the potential flow of novel genes from transgenic maize to land races or wild relatives was investigated at Puerto Vallarta, Mexico. Using white- and yellow-seeded inbreds, pollen control was measured in two mating designs. The ability to control pollen was assessed by observing seed colour in pollinations on adjacent plantings intended to trap uncontrolled pollen. In one experiment, the yellow-seeded maize contained a transgene. In this experiment contaminant seeds observed in the white maize were analysed for the presence of recombinant DNA and the gene expression product. The results from these experiments indicated that routine plant breeding activities can be conducted with completely effective pollen containment if the transgenic line is detasselled and serves as the female for pollination with a non-transgenic male inbred. However, precautions in addition to those used in these experiments are necessary to provide complete control of pollen dissemination if a transgenic male is used to make crosses and approx equal to 0.1% outcrossing to adjacent rows is deemed unacceptable

Descriptors:Maize. Transgenics. Gene-expression. Outcrossing. Pollen. Pollination. Seeds. Colour. Testas. Transgenic-plants. Biosafety. Genetic-engineering. Cereals. Biotechnology

KELAPA SAWIT

1. **Crystallization properties of palm oil by dry fractionation**

Source: Food Chemistry. 2004. 86 (2). 245-250

Author(s): Zaliha-O. Chong-C-L. Cheow-C-S. Norizzah-A-R. Kellens-M-J

Abstract:

The crystallization, thermal, physical, chemical and morphological properties of palm oil were investigated using differential scanning calorimetry, polarized microscopy, pulsed nuclear magnetic resonance (NMR) and gas chromatography (GC). The palm oil was fractionated into various stearin and olein (with iodine values (IV) >63) fractions by means of a dry fractionation process. During the cooling sequence, samples were taken at regular intervals from the crystallizer and analyzed for their iodine values, chemical compositions and physical behaviour. The physical properties of olein and stearin fractions, such as cloud point, slip melting point and solid fat content, were dependent on the crystallization temperatures. The iodine values of the olein and stearin fractions increased as the crystallization temperature decreased and both fractions started to cloud at lower temperatures. The palmitic acid content of stearin and olein fractions was also affected by the crystallization temperatures

Descriptors:Chemical-composition. Crystallization. Food-processing. Fractionation. Olein. Palm-oils. Physicochemical-properties. Stearin

2. **Expression of Bacillus thuringiensis insecticidal protein gene in transgenic oil palm**

Source: Electronic Journal of Biotechnology. 2006. 9 (2). 117-126

Author(s): Lee-Mei-Phing. Yeun-Li-Huey. (Abdullah-Ruslan. (russzn@ukm.my)

Abstract:

Oil palm, like all other crops, is susceptible to attack from several insect pests causing significant reduction in productivity. In the past, cry genes from Bacillus thuringiensis have been reported to be effective in conferring resistance towards insect pests in crops such as corn and rice. One of the advantages of these toxin proteins is their specificity towards certain harmful insects. A rapid and efficient method was developed for the transformation and evaluation of CryIA(b) expression in oil palm. A recombinant vector was introduced into immature embryos (IEs) of oil palm via the biolistic method. More than 700 putative transformed IEs from independent transformation events were generated. Transient transformation efficiency of 81-100 % was achieved. We found that pretreatment of target tissues with phytohormones is essential for increasing the transformation efficiency. This finding could enable higher transformation rate in oil palm that was previously difficult to transform. PCR analysis further confirmed the presence of the CryIA(b) in the transformed tissues. Expression of CryIA(b) from PCR-positive samples was further confirmed using a rapid gene expression detection system. This novel and rapid detection system could serve as a good opportunity to analyze the impact of transgenes upon transfer to the new environment, especially for crops with long generation cycle, such as oil palm

Descriptors:Molecular Genetics (Biochemistry and Molecular Biophysics); Pest Assessment Control and Management insect resistance, transformation efficiency, long generation cycle

3. **Development of transformation vectors for the production of potentially high oleate transgenic oil palm**

Source: Electronic Journal of Biotechnology. 2008. 11 (3). 1-9

Author(s): Yunus-Abdul-Masani-MatKadir-Ahmad-Parveez-Ghulam.

Abstract:

The main target of Malaysian Palm Oil Board (MPOB) genetic engineering programme is to produce high oleate transgenic palms. The availability of effective transformation vector is one of the pre-requisites for genetic manipulation of oil palm through recombinant DNA technology. Here, we describe the construction of a series of transformation vectors that have a maize ubiquitin promoter (UbiPro)-driven bar gene for selection of transformants on herbicide (Basta or Bialaphos), and mesocarp-specific promoter (MSP1) for expression of the transgenes [antisense palmitoyl-ACP-thioesterase (PAT) and sense beta-ketoacyl-ACP-synthase II (KASII) and sense Delta 9-stearoyl-ACP-desaturase (SAD)] potentially responsible for high oleate content in oil palm mesocarp. The transformation vectors constructed in this study are suitable for use in both particle bombardment (biolistic) and Agrobacterium-based transformation protocols

Descriptors: Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)

4. **Immature embryo: A useful tool for oil palm (Elaeis guineensis Jacq.) genetic transformation studies**

Source: Electronic Journal of Biotechnology. 2005. 8 (1). 24-34

Author(s): Abdullah-Ruslan. Zainal-Aliza. Heng-Wee-Ye. Li-Leaw-Chu. Beng-Yeap-Che. Phing-Lee-Mei. (Sirajuddin-Salwa-AbdullahPing-Winnie-Yap-Soo. Joseph-Juanita-Lourdes. Jusoh-Siti-Azma.

Abstract:

Oil palm (Elaeis guineensis Jacq.) is the highest yielding oil-bearing crop. However, being a perennial crop, genetic improvement of oil palm is extremely slow. Indeed, compared to other annual oil crops such as soybean and rapeseed, genetic manipulations remained less important. Therefore, to remain competitive, oil palm growers and breeders need new and novel approaches. In this report, the potential of immature embryos (IE) as a useful tool for oil palm genetic transformation studies was evaluated. It was evident that IEs were amenable to both direct and Agrobacterium-mediated gene transfer. Due to the abundant supply of IE, optimization of biolistic and Agrobacterium-mediated gene transfer into IEs were easily carried out. Transient transformation frequencies were comparable to other plant systems reported, with as high as 97.4% recorded for biolistic and 64.4% for Agrobacterium-mediated gene transfer. Like most moncots, oil palm tissues were less sensitive to kanamycin, geneticin and chloramphenicol. Instead, both hygromycin and phosphinotrycin were toxic 20 mg/l, making both suitable candidates for selecting putative transformants. IEs were also more responsive to in vitro manipulations as compared to other explants such as leaf and root tissues. Rapid in vitro response to callusing and embryogenesis or rapid and highly efficient direct germination resulted in a shorter culture period. This would minimize the production of abnormal clonal palms, which has been associated to chromosomal aberration due to prolonged time in culture. In addition, IEs also allows rapid and direct introduction of elite genes into breeding programs and in biclonal seed production

Descriptors: Toxicology; Methods and Techniques; Development; Genetics; Agronomy (Agriculture) embryogenesis, germination, chromosomal aberration, genetic transformation, plant regeneration, perennial crop, immature embryo

PADI

1. **Yield performance and adaptation of some Australian-grown rice varieties through multivariate analysis**

   Source: Australian Journal of Agricultural Research. 2007. 58 (9). 874-883
   Author(s): Sivapalan-S. Batten-G. Goonetilleke-A. Kokot-S
   Abstract:

   Rice breeders are involved in developing new varieties for a diverse range of production environments to increase average yields. Interpretation of performance of several varieties evaluated in a broad range of environments is usually affected by variety x environment interactions. Application of multivariate analyses, especially multi-criteria decision making (MCDM) methods in variety x environment interaction studies can benefit interpretation of yield performance and adaptation of varieties in response to different environments. The case study discussed in this paper highlights the significant advantages of using MCDM methods to overcome constraints imposed by having to investigate a large number of variables inherent in such analysis. The grain yield of 13 rice varieties with varying characteristics, grown in 4 different regions in southern New South Wales (NSW), Australia, during the 2000-06 growing seasons was analysed using classification techniques and preference ranking organization method for enrichment evaluation (PROMETHEE) analysis. Significant variety x environment interaction was found to influence the yield performance of individual varieties across a range of environmental conditions. Classification of environments and geometrical analysis for interactive aid (GAIA) plot of PROMETHEE analysis identified the Murrumbidgee Irrigation Area (MIA) and Coleambally Irrigation Area (CIA) as higher yielding regions compared with the Eastern Murray Valley (EMV) and Western Murray Valley (WMV). Turbid water and cold weather conditions are suggested to explain the lower yield obtained in the WMV environment. In terms of varieties, Amaroo and Opus were identified as widely adaptable to most of the environments, while Jarrah was the least adaptable. Illabong can be considered as best adapted to the EMV or WMV regions, while Paragon and Reiziq can be regarded as best adapted to the MIA and CIA regions. Partial and complete ranking showed the interrelationships between the varieties for their yield performance and adaptation across all environments. Amaroo, Illabong, and Opus were ranked as the most preferred varieties, while Koshihikari, Kyeema, and Jarrah were ranked as the least preferred ones. Partial pre-order with 13 classes from PROMETHEE I analysis identified varieties with similar characteristics and aided the selection of suitable alternative varieties. The outcomes from the analyses reported here allow rice varieties or genotypes to be rated for yield stability for a specific or a range of different environments

   Descriptors:Adaptation. Crop-yield. Cultivars. Decision-making. Farming-systems. Genotype-environment-interaction. Multivariate-analysis. Plant-breeding. Rice. Variety-trials

2. **Non-starch polysaccharide compositions of rice grains with respect to rice variety and degree of milling**

   Source: Food Chemistry. 2007. 101 (3). 1205-1210
   Author(s): Lai-V-M-F. Lu-Shin. He-WenHsien. Chen-HuaHan
   Abstract:

   The chemical compositions of cell wall materials (CWM) in brown and milled rice were investigated using four rice varieties, Taichung Sen 10 (TCS10, indica), Tainung 67 (TNu67, japonica), Taichung Sen Waxy 1 (TCSW1, indica waxy), and Taichung Waxy 70 (TCW70, japonica waxy). The yield of CWM preparation, equivalent to total dietary fiber content, followed the order of TNu67 > TCS10 > the waxy cultivars. This order also held for the water solubility and pectic substance content of the CWM preparations and the compositional ratio of arabinose to xylose of all CWM samples. Comparatively, the nonwaxy CWM were rich in pectic substances and glucans; whereas the waxy CWM counterparts were dominant with hemicellulose plus cellulose and arabinoxylan-related polysaccharides. These results were more significant for the hot-water-soluble than insoluble parts and mainly dependent of rice variety rather than the degree of milling

   Descriptors:Arabinose. cell-wall-components. cellulose. cereal-grains. chemical-composition. cultivars. hemicelluloses. milling. rice. xylose

3. **Effect of organic fertilizer and effective microorganisms on growth, yield and quality of paddy-rice varieties**

   Source: Journal of Crop Production. 2000. 3 (1). 269-273
   Author(s): Iwaishi-S
   Abstract:

   The effect of an organic fertilizer inoculated with Effective Microorganisms (EM) on the growth, yield and quality of 13 paddy-rice varieties varying with maturation period was studied. EM inoculation increased kernel enlargement after the panicle formation stage and also increased ear number and length and kernel number. The yield of brown rice from EM inoculation was higher for the standard fertilizer rate and lower for the higher rate of organic fertilizer. EM inoculation increased the glutinousness and the total quality index of glutinous rice varieties. Under 1993 weather conditions at Matsumoto, Japan, early and medium-ripening non-glutinous varieties and glutinous varieties were suitable for nature farming with EM-inoculated organic fertilizer

   Descriptors:Crop-yield. Cultivars. Fertilizers. Grain. Inoculation. Microorganisms. Organic-farming. Organic-fertilizers. Quality. Rice

4. **Analysis of food composition data on rice from a plant genetic resources perspective**

   Source: Food Chemistry. 2003. 80 (4). 589-596
   Author(s): Kennedy-G. Burlingame-B

Abstract:

Rice accounts for 21, 14 and 2% of global energy, protein and fat supply, respectively. There are thousands of different rice varieties; some have been in the diet for centuries, while others are new hybrids promoted for qualities such as high yield and drought and disease resistance. Little is known about the nutrient composition of many of the world's rice varieties. This paper investigates the literature on nutrient composition of rice varieties. Standardization of data to 100 g samples of unpolished rice (dry matter basis), showed intra-varietal ranges of; 9 g protein, 5.65 mg iron, 3.34 mg zinc, 1.6 mg thiamin, 0.392 mg riboflavin and 7.2 mg niacin. Currently, several research institutions are working toward improving the nutrient content of rice through greater utilization of rice genetic resources. The results section discusses in detail the magnitude of intra-varietal differences and highlights practical applications of genetic diversity in rice

Descriptors:Cultivars. Iron. Nicotinic-acid. Nutritive-value. Protein-content. Riboflavin. Rice. Thiamin. Zinc

5. Comparison of allelopathic potential of rice leaves, straw, and hull extracts on barnyardgrass

Source: Agronomy Journal. 2003. 95 (4). 1063-1070
Author(s): Chung-I-M. Kim-K-H. Ahn-J-K. Lee-S-B. Kim-S-H. Hahn-S-J
Abstract:

The use of rice (Oryza sativa L.) allelopathy for weed control is a new technology in agronomy. A laboratory bioassay using water extracts was conducted to determine the allelopathic potential of rice body parts on seed germination and growth of barnyardgrass (Echinochloa crus-galli P. Beauv. var. oryzicola Ohwi) and to determine rapid and simple methods for selecting allelopathic rice varieties using genetic characters and phenotypes. In this study, the highest inhibition rate was for 'Danganeuibangju' (76.9%) in straw extracts, 'Dongobyeo' (74.1%) in the leaves, and 'Baek' (31.7%) in the hull. 'CUBA 65-v-58' (38.6%) had the highest inhibition as a whole (average of leaves, straw, and hull), and there was a higher average inhibitory effect for straw extracts (21.6%) than for hulls (8.2%) and leaves (12.4%). With regard to classification by phenotypic and genetic characteristics, these groups showed a higher inhibitory effect in domestic varieties (14.2%), middle-maturing varieties (15.3%), varieties of hull colour (15.1%), and varieties of awn colour (16.0%). These results suggest that rice body parts may be a source of natural herbicides and that it is necessary to develop acceptable selection standards. There may also be genetic variation in rice varieties for their allelopathic potential on barnyardgrass. In the future, it might be possible to develop rice varieties with high allelopathic potential

Descriptors:Allelopathins. Allelopathy. Cultivars. Husks. Leaves. Rice. Straw. Weed-control. Weeds

6. **Impact of allelochemical exuded from allelopathic rice on soil microbial community**

Source: Soil Biology & Biochemistry. 2008. 40 (7). 1862-1869

Author(s): Kong-C-H. Wang-P. Zhao-H. Xu-X-H. Zhu-Y-D

Abstract:

Allelopathic rice releases allelochemicals from its roots to paddy soils at early growth stages to inhibit neighboring weeds. However, little is currently known about the effects of allelochemicals on soil microbes. In this study, we show that allelopathic rice can have great impact on the population and community structure of soil microbes. Allelopathic rice PI312777 seedlings reduced the culturable microbial population and total PLFA when compared to non-allelopathic rice Liaojing-9. Similar results were observed when, instead of growing seedlings, soils were incubated with plant root exudates. This result demonstrates that the composition of root exudates from the rice varieties tested contributes to the soil microbial community. Further experiments showed that the microbial community was affected by the allelochemical 5,4'-dihydroxy-3',5'-dimethoxy-7-O- beta -glucopyranosylflavone exuded from allelopathic rice roots, through immediately hydrolyzing glucose with stimulation on soil bacteria and aglycone (5,7,4'-trihydroxy-3',5'-dimethoxyflavone) with inhibition on soil fungi. This result indicates that the flavone O-glycoside can provide carbon and interact with soil microbes. PC analysis of the fatty acid data clearly separated the allelopathic PI312777 and the non-allelopathic Liaojing-9 variety (PC1=46.4%, PC2=20.3%). Similarly, the first principal component (PC1=37.4%) together with the second principal component (PC2=17.3%) explained 54.7% of the variation between the allelopathic and non-allelopathic root exudates. Furthermore, the canonical correlation between allelopathic root exudates and the flavone O-glycoside was statistically significant (Canonical R=0.889, chi 2 (25)=69.72, p=0.0041). Although the data generated in this study were not completely consistent between culturable microbes and PLFA profile, it is a fact that variation in soil microbial populations and community structures could be distinguished by the allelopathic and non-allelopathic rice varieties tested. Our results suggest that individual components of rice root exudates, such as allelochemicals from allelopathic rice, can modify the soil microbial community

Descriptors: **Allelochemicals. Allelopathy. Fatty-acids. Glycosides. Microbial-flora. Microorganisms. Rhizosphere. Rice. Root-exudates. Soil-bacteria. Soil-flora. Soil-fungi**

7. **Nutrient composition and physicochemical properties of Indian medicinal rice - Njavara**

Source: Food Chemistry. 2008. 106 (1). 165-171

Author(s): Deepa-G. Singh-Vasudev. Naidu-K-Akhilender. (kanaidu@mailcity.com)

Abstract:

Njavara, a medicinal rice, was assessed for its nutrient composition and physicochemical properties, in order to understand its therapeutic properties. Dehusked Njavara rice consisted of 73% carbohydrates, 9.5% protein, 2.5% fat, 1.4% ash and 1628 0 per 100 g of energy. Physicochemical properties and nutritive components of dehusked rice of Njavara were evaluated and compared with two commonly consumed non-medicinal rice varieties - Jyothi (red coloured) and IR 64 (brown coloured). The carbohydrates, fats, apparent amylose equivalent, fatty acid profile and triglycerides of Njavara were comparable to Jyothi and IR 64. However, Njavara rice had 16.5% higher protein, and contained higher amounts of thiamine (27-32%), riboflavin (4-25%) and niacin (2-36%) compared to the other two rice varieties. The total dietary fibre content in Njavara was found to be 34-44% higher than that of Jyothi and IR 64. Significantly higher phosphorus, potassium, magnesium, sodium and calcium levels were found in Njavara rice, compared to the other two varieties. The cooking time of dehusked Jyothi and IR 64 varieties were found to be 30 min, while Njavara needed longer time to cook, (38 min). The cooked rice of Njavara was slimy in nature, probably due to the presence of non-starch polysaccharides. (c) 2007 Published by Elsevier Ltd

Descriptors: Biochemistry and Molecular Biophysics; Foods

8. **Structure-viscosity relationships for rice varieties during starches from different heating**

Source: Food Chemistry. 2008. 106 (3). 1105-1112

Author(s): Li-Yu. Shoemaker-Charles-F. Ma-Jiangu. Moon-Kim-Ji. Zhong-Fang.

Abstract:

The effects of starch particle size and leached amylose on the viscosity of rice starch dispersions and changes of short-range structure and amylose content in starch granules of different rice varieties during heating were investigated. It was found that starch granule swelling increased rice starch dispersion viscosity during heating. The viscosities of the starch dispersions during heating were principally dependent on granular volume fraction and independent of starch variety. A distinct correlation between the amount of leached amylose and swelling of starch granules was also found. High initial amylose concentrations in starch granules reduced swelling during heating, thereby reducing rice dispersion viscosities. Fourier-transform IR spectroscopy indicated that the loss of short-range order was significant when the temperature reached the pasting onset temperature. The short-range order of waxy and medium grain rice starches was higher than that of long grain rice starches before gelatinization. The loss of order of waxy and medium grain rice starches was greater than that of long grain rice starches during heating, which was due to the presence of amylose, restraining the swelling and disruption of starch granules during heating. (c) 2007 Published by Elsevier Ltd

Descriptors: Biochemistry and Molecular Biophysics; Agronomy (Agriculture); Foods heating, structure-viscosity relationship

9. **Assessment of genetic diversity in Venezuelan rice cultivars using simple sequence repeats markers**

Source: Electronic Journal of Biotechnology. 2008. 11 (5). 1-14

Author(s) Herrera-Thaura-Ghneim. Duque-Duina-Poss. Almeida-Iris-Perez. Nunez-Gelis-Torrealba.. Pieters-Alejandro-J. Martinez-Cesar-P. Tohme-Joe-M.

Abstract:

In Venezuela, pedigree analyses indicate that the rice varieties currently under cultivation are closely related. Effective breeding programs, based on knowledge of the genetic diversity of cultivars, are needed to broaden the genetic bases of rice germplasm in the country. In this study, we used a set of 48 simple-sequence-repeat (SSR) markers to assess the genetic diversity of 11 Venezuelan rice cultivars, released by the National Rice Breeding Program between 1978 and 2007. A total of 203 alleles were detected, the number of alleles (NA) per marker ranged from 2 to 9, with an average of 4.23. The average genic diversity (H) over all SSR loci for the 18 genotypes was 0.524, ranging from 0.105 to 0.815. Positive correlations were found between H at each locus, NA, the allele size range and the maximum number of repeats. Venezuelan cultivars showed lower H (mean = 0.37) and NA (total = 124, mean = 2.58) than the whole sample. UPGMA-cluster-analysis based on genetic distance coefficients clearly separated all the genotypes, and showed that the Venezuelan rice varieties are closely related. Molecular identification of 7 Venezuelan cultivars could be done with 9 primers pairs which produced 10 genotype-specific-alleles. Although the genetic diversity was low, SSRs proved to be an efficient tool in assessing the genetic diversity of rice genotypes. Implications of the low genetic diversity detected and relatedness of Venezuelan cultivars are discussed

Descriptors:Population Genetics (Population Studies) genotype, genetic diversity, National Rice Breeding Program

10. **Identification and quantification of methyl nicotinate in rice (Oryza sativa L.) by gas chromatography-mass spectrometry**

Source: Food Chemistry. 2007. 105 (2). 736-741

Author(s): Rao-B-M. Saradhi-U-V-R-V. Rani-N-S. Prabhakar-S. Prasad-G-S-V. Ramanjaneyulu-G-S. Vairamani-M

Abstract:

During the course of analysis of popular rice varieties cultivated in India towards identification of their aroma compounds, methyl nicotinate (MN), a medicinal and flavour additive compound, was identified for the first time in rice samples. A simple direct solvent extraction method using 300 mg of the sample is developed to extract MN in rice samples and detected by capillary gas chromatography-mass spectrometry analysis. Quantitative analysis of MN is performed for polished rice, brown rice and rice bran samples from five rice varieties that are widely produced in India by using GC-MS operating under SIM mode (m/z 106). The quantity of MN is in the range of 0.63-1.30 micro g/g, 1.37-3.99 micro g/g and 1.87-12.04 micro g/g for polished rice, brown rice and rice bran samples, respectively. Breeding programmes for rice with high concentrations of MN can be greatly facilitated by establishing the concentrations of the MN in new cultivars. This method is more economic with less time consumption and enables fast screening of a large number of samples

Descriptors:Aroma. Aromatic-compounds. Cultivars. Flavour-compounds. Identification. Quantitative-analysis. Rice. Rice-bran

11. Genetic relatedness of Portuguese rice accessions from diverse origins as assessed by microsatellite markers

Source: Crop Science. 2007. 47 (2). 879-886
Author(s): Jayamani-P. Negrao-S. Martins-M. Macas-B. Oliveira-M-M
Abstract:

Simple sequence repeat (SSR) markers detect a significantly high degree of polymorphism in rice (Oryza sativa L.) and are particularly suitable for evaluating genetic diversity among closely related cultivars. A total of 176 rice accessions originating from 19 countries in the Portuguese working germplasm collection and two standard rice varieties (IR36-indica and Nipponbare-japonica) were analyzed for DNA profile using 24 SSR loci covering two loci per chromosome. A total of 184 alleles were detected. The number of alleles per locus ranged from 3 to 16, with an average of 7.7, and the PIC value ranged from 0.179 to 0.894 with an average of 0.667. All the loci were polymorphic among the accessions and clearly distinguished the indica and japonica subspecies. At 20% similarity, cluster analysis of the 178 accessions revealed three major groups, japonica, basmati, and indica (Groups I, II, and III, respectively). The japonica group contained 87% of the accessions and showed a wide range of similarity values (0.21-0.92), revealing a high degree of diversity among the accessions. Many of the accessions included in this study are morphologically similar and lack pedigree information. Hence, identification of genetic distances among the accessions should improve their use in breeding programs. As a result of this study, genetically diverse parents can be identified, increasing the usefulness of germplasm collections by broadening the genetic base of rice varieties

Descriptors:Alleles. Genetic-diversity. Genetic-markers. Genetic-polymorphism. Loci. Microsatellites. Rice. Simple-sequence-repeats

12. Performance of upland rice fitted into lowland rice-vegetable/cowpea sequence in rainfed inland valley

Source: Agronomy Journal. 2007. 99 (2). 377-383
Author(s): Adigbo-S-O. Okeleye-K-A. Adigbo-V-B
Abstract

The inland valleys (IVs) have the potential of growing three crops in sequence within a year without supplemental irrigation. Considerable opportunity exists for growing the third crop between main crop and dry season cropping. This is a niche that has not been exploited. Field experiments were conducted at the University of Agriculture, Abeokuta, Nigeria in 2000-2003 to determine the growth and yield performance of upland rice (Oryza sativa L.) in lowland rice-upland rice-fallow, lowland rice-upland rice-cowpea [Vigna unguiculata (L.)

Walp], and lowland rice-upland rice-vegetable sequences in an IV. Lowland rice-upland rice-fallow, lowland rice-upland rice-cowpea, lowland rice-upland rice-okra (Abelmoschus esculentus L.), lowland rice-upland rice-amaranth (Amaranthus cruentus), lowland rice-fallow-fallow, lowland rice-fallow-cowpea, lowland rice-fallow-okra, and lowland rice-fallow-amaranth sequences, which ran concurrently constituted a cropping cycle. The first, second, and third crops in all the cropping cycles were planted in May, October and January, respectively. The grain yields of preceding lowland rice in the various sequences with or without upland rice were similar. The preceding lowland rice variety BW 311-9 enhanced the height and grain yield performance of upland rice. The grain yields of the two upland rice varieties in the existing niche were similar in the three-crop sequence but substantially lower than the obtainable yield in an upland ecology. Upland rice crop could be grown in between the lowland rice and vegetable/cowpea without reducing the yields of lowland rice and vegetable. Inclusion of upland rice in the sequence decreased the overall benefit/cost ratio of triple cropping. Thus, two-crop sequence, which is currently being practiced by the traditional farmers, should be adhered to, until a suitable crop or technology is identified

Descriptors:Cowpeas. Crop-yield. Fallow. Growth. Okras. Plant-height. Rice. Sequential-cropping. Upland-rice. Vegetables

13. Optimization of yield and quality parameters for the Cocodrie rice variety as a function of harvest time

Source: Applied Engineering in Agriculture. 2006. 22 (1). 95-99

Author(s): Hua-N. Bengtson-R-J. Schramm-R-C. Patel-P-M. Walker-T-H. Lima-M

Abstract:

Cocodrie is a long grain rice variety commonly grown throughout the southern United States. Initial industrial scale production of this variety was largely successful, but rice harvested late in the season exhibited lower than expected yield and quality. A pilot scale rice mill was used to determine if rice milling processing parameters could be manipulated to optimize the yield and quality of early and late season Cocodrie rice. A response surface methodology was used to determine rice mill settings of roll gap (husking), feed volume - also known as flow rate - (milling), and water velocity (polishing) to achieve maximal processing outputs including yield, transparency, whiteness, wholeness, and degree of milling. Results showed that milling flow rate significantly affected whiteness and milling degree for early season Cocodrie, and whiteness, milling degree, and wholeness for late season Cocodrie. Roll gap and water velocity did not significantly affect output processing parameters. Though milling quality parameters for late season rice were lower than early season rice, optimal yields and wholeness for both batches were similar. Ridge analysis indicated that machine settings could be manipulated to optimize specific output parameters for early and late season batches of rice. A score variable was developed to determine a unique set of optimal milling settings for each batch based on the relative importance of each of the five parameters. The research presented in

this work is intended to be useful to rice processors working with the Cocodrie variety and is presented in terms of optimization

Descriptors:Crop-quality. Crop-yield. Harvesting-date. Milling. Milling-quality. Optimization. Rice

14. Genetic base and commercial utilization of rice varieties in Cuba

Source: Journal of Genetics & Breeding. 2004. 58 (4). 329-338
Author(s): Fuentes-J-L. Arteche-J. Suarez-E. Gomez-P-J. Borges-E. Cornide-M-T
Abstract:

The present work is aimed to determine the composition of the genetic base and the genetic relationship of rice cultivars released from 1972 to 2001 in Cuba, and to estimate the degree of commercial exploitation of this germplasm. The genetic relationship between all possible pair of cultivars was expressed by mean of the genetic covariance. The degree of commercial utilization of the varieties released between 1978 and 2001 was estimated for each year considering the observed field genetic uniformity. The result showed that the genetic base of this germplasm was composed by 52 ancestors, 19 of them contributing to genetic base of the cultivars during different periods, thus, it could be considered as the core group of the Cuban cultivars. This genetic base was coincident with those of rice breeding programs in Colombia and Central America, and partially coincident with the breeding program in the United States. A UPGMA dendrogram based on genetic covariance estimates separated two varietal groups and four independent varieties "IACuba-30", "Reforma", "Caribe 1" and "Perla de Cuba". An average number of 5 cultivars per year accounted for more than 99% of the rice planted area. Field genetic uniformity (rf) values varied between 0.38 to 0.82. The exploitation of a redeced number of cultivars was determinant for the high rf values observed. Optimized rf values were not reached in practice indicating that the hectarage fraction per variety was not managed adequately. The presented results are discussed to assist the traditional progeny analysis in the parental selection. Additionally, field genetic uniformity estimates are proposed as a tool to complement rice variety policies in order to minimize risks of rice crop to pest and diseases incidence

Descriptors:Coefficient-Of-Parentage; Field-Genetic-Uniformity; Oryza-Sativa; Rice-Breeding

15. Technical efficiency of rice farms under irrigated conditions of North West Himalayan Region - a non-parametric approach

Source: Indian Journal of Agricultural Economics. 2005. 60 (3). 483-493
Author(s): Kumar-L-R. Srinivas-K. Singh-S-R-K
Abstract:

This study determines the efficiency of rice cultivation under irrigated conditions in the North Western Himalayan (NWH) zone of Uttaranchal, India. It also explores the differences in technical efficiency between farms growing local varieties and those growing improved varieties. The factors associated with inefficiency are also analysed. Data for the agricultural year 2004-05 were obtained from a sample of 40 farmers in Bageswer district. It is revealed that the overall technical efficiency of farms growing improved rice varieties was higher than that of farms growing local varieties. The results also indicate that in the case of farms growing local varieties, scale inefficiency contributes more to the overall technical inefficiency. From a policy point of view, increasing the share of rice cultivation under irrigated conditions in the total farm area can bring about improvement in the overall technical efficiency. With regard to farms growing improved rice varieties, pure technical inefficiency makes the greatest contribution to the overall inefficiency

Descriptors:Crop-production. Cultivars. Economies-of-scale. Efficiency. Improved-varieties. Irrigated-farming. Production-economics. Rice

16. Rice yield constraints and production technology: perception of farmers through PRA

Source: International Rice Research Notes. 2004. 29 (1). 71-72
Author(s): Singh-S-P. Shrivastava-S-K
Abstract:

Using a participatory rural appraisal approach, 25 farmers were asked about the factors that limit rice yield in Durg district, Chhattisgarh, India. The rice varieties used by farmers were also examined. It is concluded that more promising rice varieties that can meet farmers' requirements may be introduced in the area

Descriptors:Constraints-; Crop-Production; Crop-Yield; Cultivars-; Production-Economics; Rice- South-Asia; Asia-; Developing-Countries; Commonwealth-Of-Nations; Oryza-; Poaceae-; Cyperales-; Monocotyledons-; Angiosperms-; Spermatophyta-; Plants-; India- Agricultural-Economics; Field-Crops; Plant-Production

17. Identification of heading date quantitative trait locus Hd6 and characterization of its epistatic interactions with Hd2 in rice using advanced backcross progeny

Source: Genetics. 2000. 154 (2). 885-891
Author(s): Yamamoto-T. Lin-HongXuan. Sasaki-T. Yano-M
Abstract:

A backcrossed population (BC4F2) derived from a cross between a japonica rice variety, Nipponbare, as the recurrent parent and an indica rice variety, Kasalath, as the donor parent showed a long-range variation in days to heading. Quantitative trait loci (QTL) analysis revealed that two QTL, one on chromosome 3, designated Hd6, and another on chromosome 2, designated Hd7, were involved in this variation; and Hd6 was precisely mapped as a single Mendelian factor by using progeny testing (BC4F3). The nearly isogenic line with QTL (QTL-NIL) that carries the chromosomal segment from Kasalath for the Hd6 region in Nipponbare's genetic background was developed by marker-assisted selection. In a day-length treatment test, the QTL-NIL for Hd6 prominently increased days to heading under a 13.5-h day length compared with the recurrent parent, Nipponbare, suggesting that Hd6 controls photoperiod sensitivity. QTL analysis of the F2 population derived from a cross between the QTL-NILs revealed existence of an epistatic interaction between Hd2, which is one of the photoperiod sensitivity genes detected in a previous analysis, and Hd6. The day-length treatment tests of these QTL-NILs, including the line introgressing both Hd2 and Hd6, also indicated an epistatic interaction for photoperiod sensitivity between them

Descriptors:Heading-Date. Rice. Growth-Period. Quantitative-Trait-Loci. Genes. Photoperiod. Epistasis. Gene-Mapping. Photoperiodism. Cereals

18. Plant regeneration from mature embryo-derived callus of Australian rice (Oryza sativa L.) varieties

Source: Australian Journal of Agricultural Research. 2000. 51 (2). 305-312
Author(s): Azria-D. Bhalla-P-L
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

19. Methane flux from irrigated rice fields in relation to crop growth and N-fertilization

Source: Soil Biology & Biochemistry. 1999. 31 (9). 1219-1228
Author(s): Smita-Singh. Singh-J-S. Kashyap-A-K
Abstract:

The effects of N-fertilization on rice plant growth (number of tillers, shoot and root biomass, root volume and porosity, grain yield) and their relationship with methane flux was investigated in the irrigated varieties Sarju-52, Malviya-36

and Pant Dhan-4 at Varanasi, India. The study design consisted of (a) control (unfertilized) vegetated, (b) fertilized vegetated, (c) control (unfertilized) bare, and (d) fertilized bare plots; laid down in a completely randomized block design in triplicate. Urea was applied in (b) and (d) in three split doses at a rate of 40, 30 and 30 kg N ha-1 at the time of transplanting, active tillering and grain filling stages of crop. The field was submerged before transplanting and the water depth ranged from 6.7 to 23.9 cm in response to rainfall. Every 10 d, crop growth and CH4 flux were measured from day 9 to 115 after rice transplanting. Sarju-52 and Pant Dhan-4 were similar in phenological stages but different than Malviya-36. Results showed that there were significant differences in all the growth variables measured for all the rice varieties due to growth period and fertilization. Variety x treatment, variety x growth period and treatment x growth period interactions were significant for all growth variables. Maximum CH4 flux from control (vegetated) plots was observed at the flowering stage (65 d after transplanting in Sarju-52 and Pant Dhan-4 and 76 d after transplanting in Malviya-36) and ranged from 10.79 to 14.20 mg m-2 h-1. In vegetated fertilized plots, maximum CH4 emission was observed 10 d later than in the vegetated control plots and ranged from 14.43 to 20.20 mg m-2 h-1. These values were from 7- to 12.3-fold higher than bare (unfertilized) plots. All growth variables, except mean shoot and root biomass, showed strong positive relationships with seasonal CH4 emission. It was concluded that the CH4 source strength was dependent on the rice variety under cultivation, its phenology, growth variables and soil fertilization

Descriptors: **Varietal-reactions. Rice. Biomass. Cultivation. Emission. Nitrogen-fertilizers. Filling. Flowering. Grain. Growth-period. Interactions. Methane. Phenology. Growth. Porosity. Responses. Tillering. Tillers. Transplanting. Urea. Irrigation**

20. Plant regeneration from mature embryo-derived callus of Australian rice (Oryza sativa L.) varieties

Source: Australian Journal of Agricultural Research. 2000. 51 (2). 305-312

Author(s): Azria-D. Bhalla-P-L

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**

21. The nutritive value of rice straw in relation to variety, urea treatment, location of growth and season, and its prediction from in sacco degradability

Source: Asian-Australasian Journal of Animal Sciences. 1997. 10 (2). 215-222

Author(s): Soebarinoto. Chuzaemi-S. Bruchem-J-van. Hartutik. Mashudi

Abstract:

Ten rice varieties, IR 36, Batang Pane, IR 54, IR 64, Citandui, Progo, Cisadane, Krueng Aceh, Kapuas and Tuntang, were planted at 2 locations in the province of East Java (lowland and highland), during the wet and dry seasons of different years. In vivo digestibility and voluntary intake of the straw, were estimated in groups of fat-tail sheep, supplemented with concentrate 18 g DM/kg0.75, containing 20% CP. Voluntary intake of digestible straw organic matter (DOMI) varied from 15.2 to 20.9 g/kg0.75 between straw varieties, averaged over locations, years and seasons, despite considerable variation between individual batches. This variation in the nutritive value of the straw was independent of straw and grain yield, so it would seem that there is scope for selection of rice varieties with straw of higher nutritive value. The variation in DOMI of straw among location of growth, year and season, was of a magnitude similar to the improvement brought about by urea-ammoniation. In sacco degradation characteristics and digestibility of rice straw residues were superior to those of the offered straw. This can be attributed to a preference for rice straw leaves relative to stems. Averaged over location of growth, year and season, characteristics of in sacco degradation, i.e. the rate of fermentative degradation and the truly undegradable fraction, emerged as accurate predictors of the nutritive value of rice straw

Descriptors: **Leaves. Stems. Urea. Treatment. Prediction. Degradation. In-vitro-digestibility. Rice-straw. Varieties. Nutritive-value. Estimation**

22. Varietal resistance, population dynamics and timing insecticidal application with peak oviposition by Scirpophaga incertulas (Walker) (Lepidoptera: Pyralidae) on rice

Source: Annals of Applied Biology. 1995. 127 (2). 221-228

Author(s): Harish-Kumar

Abstract:

In studies in the Philippines in April-October 1992, the flight activity of the yellow stem borer Scirpophaga incertulas (Lepidoptera: Pyralidae) peaked in the months of April-May, May-June, August-September and October. The number of egg masses and the number of adults attracted to light sources were used as indicators of S. incertulas flight activity. The rice varieties TKM6, IR22, IR60, IR66 and IR74 were infested at 7, 10, 12 and 16 weeks after the addition of 5, 10, 20 and 40 neonates of S. incertulas. All varieties except IR66 were susceptible to dead heart damage by S. incertulas. When the rice varieties TKM6, BPIRi2, BPIRi4, IR22, IR36, IR60, IR66 and IR74 were treated with carbofuran insecticide at the time of peak oviposition by S. incertulas in the field, the dead heart damage on all the varieties was significantly reduced in comparison with the untreated plots. Indiscriminate routine insecticidal treatments (fixed schedule) can be replaced by a treat-when-necessary schedule based on the population dynamics of S. incertulas

Descriptors:Varietal-resistance. Population-dynamics. Varietal-reactions. Application. Oviposition. Insect-pests. Plant-pests. Insecticides. Pest-resistance. Insect-control. Pest-control. Rice. Resistance. Carbofuran. Control. Chemical-control. Pests. Cultivars. Cereals. Biology. Agricultural-entomology

23. Hybrid rice varieties released in Maharashtra, India

Source: International Rice Research Notes. 2006. 31 (2). 27-29

Author(s): Waghmode-B-D. Ingale-B-V. Jambhale-N-D

Abstract:

Although work on hybrid rice began in 1992 at RARS Karjat, Maharashtra, India, research on heterosis breeding was intensified at this centre with the inception of the NATP-Hybrid Rice Project in 1999. Some of the promising hybrids were released for commercial cultivation in the state. Sahyadri was the first rice hybrid released from RARS in 1998 and was distributed from commercial cultivation in 2000. It is medium duration (125-130 days) and has average yield potential (6.0-6.5 t/ha), mid-tall stature (115-120 cm), slender grain, 1000-seed weight of 26.0 g, milling percentage of 67.3% and head rice recovery of 51.5%. Sahyadri-2, on the other hand, is an early duration (115-120 days) rice hybrid, which has better grain quality (long and slender), 1000-seed weight of 23.5 g, good milling percentage (70.2%) and good head rice recovery (56%). It has an average yield potential of 6.0-6.5 t/ha with multiple disease and insect pest resistance. Sahyadri-3 is a medium-duration (125-130 days), mid-tall (115-120 cm), long slender grain type, with an average grain yield potential of 6.5-7.0 t/ha. It has 5-10% higher yield than Sahyadri in farm trials, state and national coordinated trials, and farmers' fields. Sahyadri-3 has greater milling percentage (74.5%) and head rice recovery (60.2%) than Sahyadri

Descriptors:Characteristics. Disease-resistance. Hybrids. Insect-pests. Pest-resistance. Plant-diseases.

24. HUBR 2-1 (Malviya Basmati Dhan 1), a new, high-yielding basmati rice variety for cultivation in eastern India

Source: International Rice Research Notes. 2006. 31 (2). 33-34

Author(s): Singh-R-P. Jaiswal-H-K. Madhavilatha-L

Abstract:

HUBR 2-1, derived from the three-way cross HBR 92/Pusa Basmati-1//Kasturi, was named Malviya Basmati Dhan 1 and approved for general cultivation in Uttar Pradesh, India, by the State Variety Release Committee in 2004. During 1996-99 wet season varietal trials at different locations in four zones, HUBR 2-1 consistently outyielded all other recognized basmati control cultivars. Aside from having long, slender, aromatic grains, high yields, good quality and good cooking traits, HUBR 2-1 is also tolerant of blast [Magnaporthe grisea], bacterial leaf blight [Xanthomonas oryzae pv. oryzae] and stem borer

Descriptors:Characteristics. Cooking-quality. Crop-quality. Crop-yield. Disease-resistance. Insect-pests. New-cultivars. Pest-resistance. Plant-diseases. Plant-pathogenic-bacteria. Plant-pathogenic-fungi. Plant-pathogens. Plant-pests. Stem-borers

25. **Effects of amylose content, autoclaving, parboiling, extrusion, and post-cooking treatments on resistant starch content of different rice cultivars**

Source: Australian Journal of Agricultural Research. 2006. 57 (12). 1291-1296

Author(s): Kim-J-C. Mullan-B-P. Hampson-D-J. Pluske-J-R

Abstract:

Experiments were conducted to examine the effects of parboiling, extrusion, rice variety, rice:water ratio, and cooling after cooking on the resistant starch (RS) content of rice. When uncooked the medium-grain rice (Amaroo) contained less amylose (18.8 g/100 g, P=0.001), higher fast digestible starch (FDS) content (21.7 g/100 g, P<0.001), and less RS (0.1 g/100 g, P<0.001) than the long-grain rice (Doongara) (25.6, 15.9, 0.4, respectively). Parboiled rice had the highest FDS (33.9 g/100 g) and RS (0.72 g/100 g) contents, with an amylose content of 25.4 g/100 g. The effects of rice type, rice:water ratio (1:1 or 1:2 w/w), and post-cooking interventions (freshly dried or dried after cooling for 24 h at 4 deg C) on the RS content of rice cooked in an autoclave were examined. The RS contents were significantly different among the rice types (0.6, 1.4, 3.7 g/100 g for Amaroo, Doongara, and parboiled rice, respectively, P<0.001). Decreasing the rice:water ratio (1:2) and cooling (24 h at 4 deg C) after cooking significantly increased the RS content (P<0.001). Extrusion decreased the RS content in the high RS rice only (0.42-0.16 g/100 g, P=0.02). The results indicate that parboiling rice, and the use of a higher-amylose-content rice, a lower rice:water ratio, and cooling after cooking all increase RS content, whereas extrusion decreases the RS content of rice

Descriptors:Amylose. Autoclaving. Cooking. Cultivars. Extrusion. Food-analysis. Food-processing. Parboiling. Rice. Starch

26. **CSR23: a new salt-tolerant rice variety for India**

Source: International Rice Research Notes. 2006. 31 (1). 16-18

Author(s): Singh-R-K. Gregorio-G-B. Mishra-B

Abstract:

CSR23 (IET13769) is a high-yielding, salt- tolerant rice cultivar developed from a 3-way cross (IR 64//IR4630-22-2-5-1-3/IR9764-45-2-2) made at IRRI in the Philippines. In coordinated trials conducted on saline alkaline soils in India during 1994-97, CSR23 was consistently superior in grain yield to the control cultivars and qualifying cultivars. Yield increases reached 125, 90, 104, 51 and 37% over Usar 1, Vyttila 4, Jaya, Panvel 1 and CSR10, respectively. CSR23 can withstand sodicity stress of up to 10.0 pH and salinity stress of up to 8.0 dS/m (ECe). It exhibits high yield potential even on non-stressed or moderately stressed soils. Field screenings showed that this cultivar is resistant to blast [Magnaporthe grisea], neck blast, brown spot [Cochliobolus miyabeanus] and leaf folder, and moderately resistant to gall midge [Orseolia oryzae] biotype 5. CSR23 was released in 2004 for cultivation on alkaline soils in Uttar Pradesh and Haryana, and on coastal saline soils in Maharashtra, Gujarat, Tamil Nadu, Kerala and West Bengal

Descriptors:Characteristics. Crop-yield. Disease-resistance. Fungal-diseases. Insect-pests. New-cultivars. Pest-resistance. Plant-diseases. Plant-pathogenic-fungi. Plant-pathogens. Plant-pests. Rice. Saline-soils. Salinity. Salt-tolerance. Sodic-soils

27. **Antioxidative activities of bran extracts from twenty one pigmented rice cultivars**

Source: Food Chemistry. 2006. 94 (4). 613-620

Author(s): Nam-SeokHyun. Choi-SunPhil. Kang-MiYoung. Koh-HeeJong. Kozukue-N. Friedman-M

Abstract:

Ethanol-water (70:30, v/v) extracts from the bran of rice seeds from twenty one pigmented and one nonpigmented rice cultivars were evaluated for antioxidative activities using the following tests: inhibition of peroxidation of linoleic acid; inhibition of peroxidation of rabbit lipid erythrocyte membranes; reduction of potassium ferricyanide, and scavenging of superoxide anions and hydroxyl radicals. With some exceptions, extracts from the pigmented rice seeds had higher antioxidative activity than did the nonpigmented variety. The following pigmented cultivars had the highest antioxidative activities in all tests: Jumlalocal-1, Parnkhari 203, DZ78, LK1-3-6-12-1-1, and Elwee. A significant correlation was also noted between reducing power, inhibition of erythrocyte ghost membrane peroxidation, and superoxide anion and hydroxyl radical scavenging. The results suggest that: (a) ferricyanide reducing power might be a useful and simple index for large-scale evaluation of antioxidative potencies of natural products present in rice; (b) pigmented rice varieties with high antioxidative activities provide a source of antioxidants and a genetic resource to develop new health-promoting rice cultivars

Descriptors: antioxidant-properties. linoleic-acid. peroxidation. radicals. rice-bran

28. **Improving rice to meet food and nutritional needs: biotechnological approaches**

Source: Journal of Crop Production. 2002. 6 (1-2). 229-247

Author(s): Datta-S-K. Khush-G-S

Abstract:

The livelihood and calorie needs of large populations based in developing countries is dependent on rice cultivation. More than three billion people consume rice as a staple food. To meet the future demands of the human population, innovative tools such as genomics are being used to improve rice yield increase, for the incorporation of stress resistance/tolerance in rice varieties, and for the improvement of the nutritional quality of rice. These new tools include: sequencing, large-scale analysis of expressed sequence tags, high throughout microarray analysis and genetic transformation. Rice now serves as a model for a science based crop design for the agronomic, nutritional, and economic benefit of farmers. This article discusses the use of biotechnology as a tool to improve the rice plant for the benefit of mankind

Descriptors:Biotechnology. Crop-quality. Crop-yield. Genetic-transformation. Genetically-engineered-organisms. Genomics. Nucleotide-sequences. Nutrition. Plant-breeding. Rice. Transgenic-plants. Varieties

29. Governance of gene action and combining ability for certain grain quality traits in three diverse rice (Oryza sativa L.) growing ecosystems

Source: Journal of Sustainable Agriculture. 2003. 22 (4). 63-78

Author(s): Verma-O-P. Santoshi-U-S. Srivastava-H-K

Abstract:

Traditional varieties or land races from diverse rice growing ecosystems serving as repository of desirable gene pools for rice improvement including rice hybrids have been marginalized or are at the verge of perhaps total genetic erosion. Biotechnology patent systems and intellectual property rights intrinsic with genetically engineered rices weigh in at odds, competing with these good grain qualified traditional rices. Genetic analyses have been made to uncover the supremacy of gene action and combining ability for certain grain quality related physicochemical traits in seven diverse ecogeographical genotypes of indica rice using a 7x7 half-diallel cross following Griffing's Model-1, Method-2. Comparative results obtained from 7 parents + 21 F1s + 21 F2s revealed the involvement of both additive (polygenic) and non-additive (epistasis or interallelic) gene action(s) in the governance of grain quality traits. However, the ratio of sigma 2g/ sigma 2s exhibited greater importance of non-additive genes for all the traits except kernel length in F1. This suggests the plausibility of exploitation of heterosis in rice as a self-pollinated crop. Epistasis gene action (interallelic interaction) was more pronounced for all the traits. The genotypes NS 19 (for grain weight), T 21 and IR 24 (for both kernel length and L/B ratio) and Jal Lahri (for protein content) emerged as good general combiners with high gca values. The crosses Mahsuri/IR 24, NDR 359/Jal Lahri, Sarjoo 52/Jal Lahri, Mahsuri/T 21, Sarjoo 52/NS 19 and Sarjoo 52/T 21, revealed significant sca effects suggesting their role in improvizing for certain physicochemical grain quality traits. These crosses retained at least one parent with high 'gca' value and the other parent having either high, average or low 'gca' effects indicating the occurrence of both additive and non-additive genetic interactions. These findings may be of greater relevance in shuffling and combining the genes/traits between traditional and modern rice varieties (e.g. semi-dwarf, good to moderate tillering, medium maturity and good grain quality with high protein content) in almost all rice growing ecosystems

Descriptors:Chemical-composition. Combining-ability. Crop-quality. Crosses. Diallel-analysis. General-combining-ability. Genes. Genetic-analysis. Genetically-engineered-organisms. Intellectual-property-rights. Plant-composition. Protein-content. Rice. Specific-combining-ability. Transgenic-plants

30. **Managing iron toxicity in acid sulfate rice soils by integrating genetic tolerance and nutrition**

Source: International Rice Research Notes. 2005. 30 (1). 37-39

Author(s): Thampatti-K-C-M. Cherian-S. Iyer-M-S

Abstract:

A field experiment was conducted in a sandy clay loam (Entisol) during rabi season for 3 years to determine the effects of integration of genetic tolerance (by selecting varieties that vary in tolerance) with nutrition (through different levels of fertilizers and lime) on iron toxicity, and its influence on rice yield in low-lying acid sulfate soils of Kerala, India. The treatments used in the study include: 4 levels of lime - no lime (standing water 5 cm retained in the field for 3 days and thereafter drained out through surface channels), half of the lime requirement, full lime requirement, and recommended level (350 kg lime/ha as basal + 250 kg lime/ha 1 month later); 2 levels of fertilizer - 100% N:P2O5:K2O and 100% N + 150% P2O5 and K2O; and 3 rice varieties - Phalguna (tolerant), Prakash (sensitive) and Jyothi (locally preferred variety). Tabulated data are presented on the: grain and straw yield of rice and Fe content as influenced by levels of lime and fertilizer, and variety; characteristics of rice roots as influenced by variety and levels of lime and fertilizer at panicle initiation stage; and effect of liming on soil chemical properties at different growth stages of rice. The results showed that genetic tolerance and appropriate nutrients could reduce the intensity of Fe toxicity and bring about sustainable yield increases in Fe-toxic sulfate soils.

Descriptors:Acid-sulfate-soils; application-rates; crop-yield; Entisols-; induced-resistance; iron-; liming-; NPK-fertilizers; nutrient-content; rice-; rice-soils; soil-chemical-properties; soil-fertility; soil-toxicity; soil-types South-Asia; Asia-; Developing-Countries; Commonwealth-of-Nations; India-; Oryza-; Poaceae-; Cyperales-; monocotyledons-; angiosperms-; Spermatophyta-; plants- Field-Crops; Plant-Production; Soil-Chemistry-and-Mineralogy; Soil-Fertility; Fertilizers-and-other-Amendments; Genetic-Engineering-Gene-Transfer-and-Transgenics

31. **Short-duration rice varieties adaptable to sodicity**

Source: International Rice Research Notes. 2005. 30 (2). 34-35

Author(s): Geetha-S. Mohammed-S-E-N. Anthoniraj-S

Abstract:

An experiment was conducted to study the nature and magnitude of interaction of rice cultivars under sodic and normal conditions in Trichy, Tamil Nadu, India. Twenty-four rice cultivars were evaluated during the dry season

(June-September) under 3 environments: normal soil with good-quality irrigation water (E1), normal soil with poor-quality irrigation water (E2), and sodic soil irrigated with sodic water (E3). Results of ANOVA revealed significant differences in grain yield among the genotypes in all the 3 environments. The pooled ANOVA for mean data also indicated variance due to genotypes, which confirmed the variability among the genotypes. Further, the variance due to environment was also significant, indicating the effect of sodicity in soil and water on grain yield. A significant genotype x environment interaction also showed the differential response of the genotypes under different stress environments. E1 was the most favourable environment. Stability parameters showed that cultivars TRY2, IR64, ADT36, ASD16, TR2000-3 and ADT45 were the most adaptable and stable across all the environments. Some other cultivars (TKM11, IR72, TKM9 and CSR11), though adaptable to sodic soils, had low mean yield. Therefore, they could be effectively used only for hybridization programmes (pyramiding a sodicity tolerance gene).

Descriptors:Adaptability-; Crop-Yield; Cultivars-; Genetic-Variation; Genotype-Environment-Interaction; Irrigation-Water; Rice-; Sodic-Soils; Sodic-Water; Soil-Types; Stability- South-Asia; Asia-; Developing-Countries; Commonwealth-Of-Nations; Oryza-; Poaceae-; Cyperales-; Monocotyledons-; Angiosperms-; Spermatophyta-; Plants-; India- Field-Crops; Plant-Breeding-And-Genetics; Plant-Production; Soil-Water-Management-Irrigation-And-Drainage

32. Yield and water use of irrigated tropical aerobic rice systems

Source: Agricultural Water Management. 2005. 74 (2). 87-105

Author(s): Bouman-B-A-M. Peng-S. Castaneda-A-R. Visperas-R-M

Abstract:

Increasing water scarcity necessitates the development of irrigated rice systems that require less water than traditional flooded rice. In irrigated aerobic rice systems, rice grows in nonflooded and nonsaturated soil under supplemental irrigation. The development of such systems should start with the identification of promising varieties and the quantification of yield potential, water use, field water outflows, and water productivity. In this paper, we report on the results of growing different tropical upland and lowland rice varieties under irrigated aerobic conditions during six seasons in 2001-2003 at the International Rice Research Institute in the Philippines. The highest yields under aerobic conditions were realized in the dry season with the improved upland variety Apo (5.7 t ha-1) and the lowland hybrid rice Magat (6 t ha-1). These high yields were obtained in relatively wet soil with seasonal-average soil moisture tensions in the root zone of 10-12 kPa and with maximum values of around 40 kPa. On average, the mean yield of all varieties was 32% lower under aerobic conditions than under flooded conditions in the dry season and 22% lower in the wet season. Total water input was 1240-1880 mm in flooded fields and 790-1430 mm in aerobic fields. On average, aerobic fields used 190 mm less water in land preparation, and had 250-300 mm less seepage and percolation, 80 mm less evaporation, and 25 mm less transpiration than flooded fields. Without plastic sheets to prevent seepage in flooded fields, the water productivity of rice (with respect to rainfall and irrigation water input) under aerobic conditions was 32-88% higher than under flooded conditions. We conclude that the concept of aerobic rice holds promise for farmers that do not have access to enough water to grow flooded lowland rice. More research is needed into the development of improved varieties, the optimization of crop and water management, and the sustainability of aerobic rice under continuous cropping

Descriptors:Aerobic-Conditions. Crop-Yield. Cultivars. Genetic-Diversity. Genetic-Variation. Plant-Water-Relations. Rice. Transpiration. Water-Use. Water-Use-Efficiency

33. Methane emission in four rice varieties as related to sugars and organic acids of roots and root exudates and biomass yield

Source: Agriculture, Ecosystems & Environment. 2005. 108 (2). 155-163

Author(s): Kerdchoechuen-O

Abstract:

Rice (Oryza sativa L.) fields contribute to global methane (CH4) emission and warming. This study determined cultivar variations in CH4 emission in relation to sugar and organic acid composition of the roots and root exudates and shoot and root biomass at the vegetative, reproductive and ripening stages of the rice plant. Thai cultivars Supanburi 1 (SP1), Supanburi 60 (SP60), Supanburi 90 (SP90) and Chainat 1 (CN1) were used. CH4 flux rates were comparably higher in CN1 and SP1 than in SP60 and SP90. Glucose and acetic acid were the predominant sugar and organic acid, respectively. Sugar and organic acid contents of root exudate had no direct relationship with CH4 fluxes regardless of growth stage. Total sugars of root tissues did not similarly compare with CH4 flux rates. However, at the ripening stage, root glucose content was higher in CN1 while root fructose and acetic acid contents were higher in SP1. Shoot and root weights at the different growth stages were also consistently higher in SP1 and CN1 (high-CH4 emitters) than in SP60 and SP90 (low-CH4 emitters). The results demonstrate cultivar-dependent rates of CH4 production due to some compositional differences and provide fundamental basis for cultivar selection as a mitigation strategy to reduce CH4 emission from ricefields

Descriptors:Acetic-Acid. Air-Pollutants. Air-Pollution. Biomass. Crop-Growth-Stage. Cultivars. Global-Warming. Glucose. Greenhouse-Gases. Methane. Organic-Acids. Reproduction. Rice. Ripening-Stage. Root-Exudates. Roots. Shoots. Sugars. Vegetative-Period

34. Application of FAO-56 for evaluating evapotranspiration in simulation of pollutant runoff from paddy rice field in Japan

Source: Agricultural Water Management. 2005. 76 (3). 195-210

Author(s): Vu-SonHong. Watanabe-H. Takagi-K

Abstract:

Applicability of FAO-56 method in estimation of evapotranspiration for the simulation of pollutant runoff from rice paddy field in Japan was investigated.

Crop evapotranspiration and crop coefficient recommended by FAO-56 method relative to those values obtained in the field monitoring for three Japanese rice varieties, namely, Nihonbare, Mangetsumochi and Koganemochi during first three growing stages were compared. Also, the pesticide fate model, PCPF-1, which incorporates the FAO-56 method was evaluated for the applicability of the FAO-56 method towards the accurate prediction of herbicide concentration in paddy water. The estimation of cumulative ETc in paddy rice by FAO-56 method using the recommended Kc value resulted in estimation error of up to 17% from the observed values. The recommended values of Kc-ini in FAO-56 method are appropriate if reliable atmospheric data are available. However, the Kc-mid was found to be a sensitive parameter affecting ETc estimation and the careful calibration according to the regional conditions and varieties seemed to be required for the accurate prediction. Considering the effect of random errors, FAO-56 method is more reliable when calculating cumulative ETc longer than 7 days of period. Despite the relatively large error in cumulative ETc resulted from the FAO-56 method with the recommended Kc value, the maximum error expected to have on the prediction of the herbicide concentration in paddy field is 5.6%, and that of herbicide runoff loss can be 3.2%. Therefore, it can be concluded that application of FAO-56 method with the recommended Kc value is acceptable in the simulation of pesticide fate and transport

Descriptors:Evapotranspiration. Herbicide-Residues. Pollutants. Rice. Runoff. Simulation-Models. Varieties

35. Atmospheric CO2 concentration effects on N partitioning and fertilizer N recovery in field grown rice (Oryza sativa L.)

Source: Agriculture, Ecosystems & Environment. 2005. 108 (4). 342-349

Author(s): Weerakoon-W-M-W. Ingram-K-T. Moss-D-N

Abstract:

Lowland rice (Oryza sativa L.) responds positively to increased atmospheric CO2 concentration. However, the efficiency of the canopy depends on the N status of the plant, which could vary with the change in uptake and partitioning of N with increased atmospheric CO2. A field experiment was conducted at the International Rice Research Institute (IRRI) to determine changes in N requirement of the rice crop and to propose suitable management strategies to overcome tissue N dilution with increased CO2 concentration. Rice variety IR72 was grown inside open top chambers at ambient (about 350 micro mol mol-1) or elevated (700 micro mol mol-1) atmospheric CO2 in combination with three levels of applied N (0, 90, or 200 kg N ha-1). Rooting of rice was linearly related to tillering, and the relationship did not change with CO2 concentrations, but with age of the crop. When adequate N was not supplied, rice plants grown at high CO2 became inferior to plants grown at ambient CO2. N uptake and fertilizer N recovery was higher in plants grown in high CO2 until maximum tillering, but the partitioning of N towards leaves decreased by 9%. Acclimation to high CO2 by rice may, therefore, be dependent on the N uptake. Increased N uptake under high CO2 environment was related to its larger root system, which was due to increased unproductive tillering. This suggests that if

tillering is limited, rice plants at high CO2 may suffer from N limitation due to changes in both uptake and partitioning. It is concluded that management of the rice crop grown at high atmospheric CO2 should be different to that under current conditions

Descriptors:Acclimatization. Atmosphere. Carbon-Dioxide. Growth. Nitrogen. Nitrogen-Fertilizers. Rice. Rooting. Tillering. Uptake

36. Comparison of different amendments for alleviating iron toxicity in rice

Source: International Rice Research Notes. 2004. 29 (1). 50-52

Author(s): Nayak-S-C. Sahu-S-K. Mishra-G-C. Sandha-B

Abstract:

Field experiments were during 1999, 2000 and 2001 wet seasons in Orissa, India, to study the efficacy of various amendments for Fe toxicity amelioration. The treatments include application of lime (0.5 and 0.25 lime requirement), fly ash (20 and 10 tonnes/ha), K (66 kg/ha), Zn (10 and 5 kg/ha) and foliar spray of MnSO4 (0.6%). Two rice varieties, Mahsuri (tolerant of Fe toxicity) and Jajati (susceptible to Fe toxicity), were used. Symptoms of Fe toxicity such as reddish brown spots at the tips of the lower leaves with bronzing spreading over the entire leaf, appeared in the control treatment 25 days after planting the susceptible variety. Bronzing symptoms were recorded at 40 DAT. These symptoms decreased upon application of the different amendments. The application of Zn and lime at higher doses resulted in minimum toxicity. Jajati gave higher toxicity values than Mahsuri. Grain and straw yield of both varieties increased with application of the different amendments. Application of Zn showed the highest yield because of antagonism between Zn and Fe. Except for straw yield in 2001, Mahsuri produced higher yield than Jajati. Fe concentration in leaves was higher in the control treatment. A minimum concentration of Fe in leaves was observed in the Zn treatment, followed by the lime treatment. Jajati showed a higher Fe concentration in leaves than Mahsuri

Descriptors:Antagonism-; Chemical-Composition; Crop-Yield; Fly-Ash; Iron-; Leaves-; Lime-; Phytotoxicity-; Plant-Composition; Potassium-; Rice-; Rice-Straw; Soil-Amendments; Straw-; Toxicity-; Varieties-; Zinc- South-Asia; Asia-; Developing-Countries; Commonwealth-Of-Nations; India-; Oryza-; Poaceae-; Cyperales-; Monocotyledons-; Angiosperms-; Spermatophyta-; Plants- Field-Crops; Plant-Composition; Plant-Production; Plant-Toxicology; Fertilizers-And-Other-Amendments

37. In vitro selection of mature seed derived calli for increased tolerance towards Fe-toxicity in rice and their isozyme profiling

Source: Journal of Genetics & Breeding. 2003. 57 (4). 325-340

Author(s): Mandal-A-B. Roy-B

Abstract:

Fe-toxicity tolerant somaclones were developed from mature seed derived embryogenic calli of a few indica rice varieties through in vitro screening involving different concentrations of Fe. Stress was induced in alternate subculture medium, callus induction medium and callus maintenance medium individually to asses the effect of Fe on in vitro culture response, morphogenesis and isozymes. Seed germination, callus induction and plantlet regeneration decreased at higher Fe concentrations. Fe was found to be toxic to callus at 400 ppm concentration and complete necrosis was observed at the end of selection. No plantlet tolerant to 400 ppm of Fe could be developed. More plantlet regeneration was observed in C 14-8 and IR 72 than other genotypes. This indicates genotypic specificity in governing Fe-stress tolerance in rice. The in vitro developed putative plantlets tolerant to Fe toxicity were hardened and transplanted under glass house condition. Those plants could flower and mature normally. This offers ample scope to developing plants tolerant to Fe-toxicity, which bears immense importance to harness Fe-constrained soil. Somatic calli cultured with different concentrations of Fe were analyzed to pinpoint changes at isozyme level in respect of esterase, peroxidase, glucose-6-dehydrogenase, malate dehydrogenase, lactate dehydrogenase and alcohol dehydrogenase. A few bands showed gradual increase in band intensity, whereas, some displayed reduced intensity with increased concentrations of Fe. Low intensity indicates stringent regulation of the concerned locus governing translation turnover or its structural modification under increased Fe-toxicity Appearance of novel bands was also observed. Formation of new bands might be ascribed to the activation of new domain(s) in the genome or gene duplication. Some bands disappeared under stressed environment. Degradation of bands indicates their role as 'injury markers'. To the contrary, some bands were found to be unaltered across toxicity levels. This might be due to their stability under Fe-toxic condition and/or formation of isozyme from conserved domains of genome through stable mRNA synthesis. It is assumed that several potential mechanisms were operating for governing Fe-tolerance involving Fe-tolerant enzymes and elevated enzyme activities

Descriptors:Rice; Iron-Stress; Tissue-Culture; Isozyme-Analyses; In-Vitro-Selectio

38. Tensile properties of parboiled rice as affected by processing conditions

Source: Transactions of the ASAE. 2004. 47 (1). 191-197

Author(s): Saif-S-M-H. Lan-Y. Suter-D-A

Abstract:

Ultimate tensile strength (UTS) and modulus of elasticity (MOE) of two varieties of parboiled rice were measured and evaluated at different steaming durations, drying temperatures, and post-drying tempering conditions. Rice varieties of Lemont (long grain) and Rico-1 (medium grain) were used in this study. The parboiling process generally increased the UTS by four to five times that of raw rice, depending on the parboiling treatments and variety. The UTS of Lemont was higher than Rico-1 by about 25% to 50%, depending on the steaming and drying conditions. The strength of the kernel increased with the increase in steaming duration. Drying temperature greater than 40 deg C decreased the strength. Tempering of the kernels at room temperature of 21 deg C after drying increased both the UTS and the MOE of the kernels. The UTS values of Lemont were found to be in the range of 37 to 60 MPa, while the range for Rico-1 was 32 to 40 MPa, depending on the steaming and drying conditions. The range of the MOE values found for Lemont was 191 to 255 MPa and that for Rico-1 was 97 to 137 MPa

Descriptors:Drying. drying-temperature. food-processing. mechanical-properties. modulus-of-elasticity. parboiling. rice. steaming. tempering. tensile-strength

39. The effect of agronomic improvement and urea treatment on the nutritional value of Malaysian rice straw varieties

Source: Animal Feed Science and Technology. 2003. 108 (1-4). 133-146

Author(s): Vadiveloo-J

Abstract:

The objectives of the study were to estimate the effect of agronomic improvement on rice straw nutritional value and to compare the response of straw varieties to urea treatment. The agronomic characteristics (i.e. grain yield, days to maturity, culm height and morphological composition) and straw characteristics (i.e. chemical composition and in vitro dry matter digestibility (IVD)) before and after 4% urea treatment of two single-crop and six double-crop rice varieties were measured. The single-crop varieties were taller, 89 cm versus 78 cm, late maturing, 130 days versus 122 days, lower in grain yield, 1450 kg/ha versus 4382 kg/ha and contained more stem, 48% versus 28%, than the double-crop varieties. The total ash, neutral detergent fibre (NDF), insoluble ash, IVD and crude protein (CP) of the single-crop varieties averaged 18.0, 60.9, 6.2, 41.2 and 6.0%, respectively, in comparison with 17.8, 63.5, 5.2, 54.0 and 3.3%, respectively, for the double-crop varieties. Covariance-adjusted means of the single-crop varieties after urea treatment were 20.4, 64.5, 6.5, 64.4 and 11.6%, respectively, and corresponding estimates for the double-crop varieties were 19.5, 61.7, 9.2, 59.6 and 5.2%, respectively. The IVD and CP of straw, respectively, improved and declined ($P<0.05$) with improvements in agronomic characteristics. The relationship between IVD (y) and grain yield (x) was explained by the equation: $y=35.9+0.004x$ ($P<0.001$, R2=0.91). Varietal response to urea treatment was not uniform with respect to IVD and CP. The relationship between IVD after (y) and before (x) urea treatment was explained by the equation: $y=41.5+0.38x$ ($P<0.01$, R2=0.77) indicating that the single-crop varieties of lower initial IVD responded better to urea treatment. Principal component analysis ranked the single-crop varieties lower than the double-crop varieties based on their agronomic and untreated straw characteristics, but higher in their straw characteristics after urea treatment. Cluster analysis classified the single- and double-crop varieties separately. Consequently, the genetic distance between them was larger than within them. Results show that improving the agronomic qualities of rice may concurrently improve straw characteristics and that urea treatment may be suitable for improving straws of poor quality only

Descriptors:Crude-protein. Cultivars. Feed-grains. Genetic-distance. Nutritive-value. Rice. Rice-straw. Straw. Urea

40. **Basmati 2000 -- an extra long-grained aromatic rice variety in Punjab, Pakistan**
Source: International Rice Research Notes. 2003. 28 (1). 33
Author(s): Khan-MG. Akhter-M. Sabar-M
Abstract:

This paper describes the performance of an extra long-grained aromatic rice cultivar (Basmati 2000) in Punjab, India. This cultivar exhibited stiff stems, extra long grains, and excellent cooking and eating qualities

Descriptors:Cooking-quality; rice- South-Asia; Asia; Developing-Countries; Commonwealth-of-Nations; Oryza; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants Field-Crops; Plant-Breeding-and-Genetics

41. **A new, high-yielding mutant aromatic rice variety, Khushboo 95**
Source: International Rice Research Notes. 2003. 28 (1). 32
Author(s): Soomro-AM. Baloch-AW. Bughio-HR. Bughio-MS
Abstract:

Khushboo 95, a new high-yielding short-culm mutant aromatic rice cultivar derived from the line Jajai 77 is described. It has the following characteristics: reduced plant height, highly productive tillers, early maturity, increased panicle length, more grains per panicle, good grain quality and distinct aroma

Descriptors:Characteristics-; crop-yield; mutants-; rice-; yield-components Oryza; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants Field-Crops; Plant-Breeding-and-Genetics

42. **Association between physicochemical characters and cooking qualities in high-yielding rice varieties of diverse origin**
Source: International Rice Research Notes. 2003. 28 (1). 28-29
Author(s): Vanaja-T. Babu-LC
Abstract:

This paper discusses the relationships between characters such as grain length, grain breadth, L-B ratio of grain, hulling percentage and milling percentage, and their effects on cooking quality of high-yielding rice cultivars of diverse origin. Longer grain types have higher milling recovery than wider grained ones. High-amylose rice cultivars absorb more water with low gelatinization temperature and produce more cooked material

Descriptors:Amylose-; cooking-quality; crop-yield; cultivars-; genetic-variation; processing-quality; rice-; yield-components Oryza; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants Field-Crops; Plant-Breeding-and-Genetics; Crop-Produce; Food-Composition-and-Quality

43. **Efficiency and technical change in the Philippine rice sector: a Malmquist total factor productivity analysis**

Source: American Journal of Agricultural Economics. 2003. 85 (4). 943-963
Author(s): Umetsu-C. Lekprichakul-T. Chakravorty-U
Abstract:

Regional differences in total factor productivity, efficiency, and technological change in the Philippine rice sector are examined for the post-green revolution era. Malmquist productivity indices were constructed for 1971-90 and were decomposed into efficiency and technological change. The average annual Malmquist productivity growth was only slightly positive. Productivity growth was negative during the early 1970s, and was followed by a period of positive growth. Growth was negative again in the late 1980s. The period of positive growth coincided with the introduction of new rice varieties while the declines are likely to have been caused by intensification of rice production in lowland farming systems. Certain regions such as Central Luzon, Western Visayas, and Southern and Northern Mindanao had higher rates of technological change than others. It is suggested that this may be due to higher investments in infrastructure and education, increased adoption of tractors, and a better agroclimatic environment

Descriptors: **Agricultural-development. crop-production. efficiency. geographical-variation. green-revolution. production-economics. production-functions. production-structure. productivity. rice. technology**

44. Golden apple snail damage in Philippine Seed Board rice varieties
Source: International Rice Research Notes. 2002. 27 (1). 35-36
Author(s): Cruz-MS-de-la. Joshi-RC. Martin-AR. de-la-Cruz-MS
Abstract:

Thirty-two rice cultivars released by the Philippine Seed Board were evaluated for resistance to golden apple snail (GAS), Pomacea canaliculata, under no choice (field study conducted in Nueva Ecija, Philippines, during 2000 rainy season) and free-choice (greenhouse) conditions. GAS (3 per row) was released in rows planted to 21-year-old seedlings. Damage was recorded at 7 days after release as percent missing hills (% MH). Under the free-choice treatment, MH ranged from 6.7 to 80.8%, with PSBRc40 (6.7%), PSBRc36 (14.4%), and PSBRc38 (30.0%) recording the lowest MH. Under the no-choice treatment, PSBRc40 had the lowest MH (3.3%). This is thought to be the first report documenting differential GAS damage among rice cultivars in the Philippines

Descriptors: **Ccrop-damage; pest-resistance; plant-pests; rice-; varietal-resistance Oryza; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants; South-East-Asia; Asia; Developing-Countries; ASEAN-Countries; Pomacea; Ampullariidae; Gastropoda; Mollusca; invertebrates; animals Field-Crops; Plant-Breeding-and-Genetics; Plant-Pests; Host-Resistance-and-Immunity**

45. The impact of modern varieties on rice production and farmers' income in Laos

Source: International Rice Research Notes. 2002. 27 (1). 11-12
Author(s): Shrestha-S. Goeppert-K. Bell-MA. Douangsila-K
Abstract:

240 households in the main rice-producing regions (Champassak and Savannakhet provinces, Vientiane Municipality) of Laos were surveyed in April 2002 to assess the farm-level impact of improved varieties and technology packages. Both the Lao modern rice varieties (LMVs) and other modern varieties (OMVs) substantially outyielded the traditional varieties, while the LMVs outyielded the OMVs. Farmers' net income increased by 23% with the adoption of LMVs, representing an increase of $75 ha-1. With the adoption of OMVs, farmers' income increased by only $19 ha-1

Descriptors: **Crop-production; crop-yield; economic-impact; farmers'-income; improved-varieties; production-economics; rice-; surveys- Indochina; South-East-Asia; Asia; Least-Developed-Countries; Developing-Countries; ASEAN-Countries; Oryza; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants Agricultural-Economics; Income-and-Poverty; Field-Crops; Plant-Production**

46. **Pelalu Vadlu -- a fine-grained gall midge-tolerant rice variety**
Source: International Rice Research Notes. 2002. 27 (1). 33
Author(s): Rao-CP. Ganesh-M. Pradeep-T. Rao-TN. Ragaiah-B. Reddy-NN. Raju-CS. Tagore-KR. Jayaprakash-M. Rao-TS. Rao-VR. Reddy-LK. Reddy-NS. Murthy-PSS. Reddy-PR. Balram-M
Abstract:

Pelalu Vadlu (RDR8702) is a medium-duration (135-140 days) and gall midge-resistant rice cultivar derived from OBS677/IR2070-423-21-5. Released in Andhra Pradesh, India, it is suitable for cultivation in the wet season for rainfed lowland areas. Pelalu Vadlu, which is tolerant to gall midge [Orseolia oryzae], is a tall (103 cm), medium-tillering, nonlodging, erect, semicompact, photoperiod-insensitive, and fertilizer-responsive cultivar having a yield potential of 7 t/ha. Its grain yields were 4-72% higher than those of Surekha, Mahsuri, and Samba Mahsuri. The long, slender grains (kernel length of 6.44 mm and breadth of 2.26 mm) possess good cooking quality

Descriptors: **Cereal-grains; characteristics-; crop-yield; cultivars-; insect-pests; pest-resistance; plant-pests; rice- India; South-Asia; Asia; Developing-Countries; Commonwealth-of-Nations; Orseolia; Cecidomyiidae; Diptera; insects; arthropods; invertebrates; animals; Oryza; Poaceae; Cyperales; monocotyledons; angiosperms; Spermatophyta; plants Host-Resistance-and-Immunity; Crop-Produce; Food-Composition-and-Quality; Field-Crops; Plant-Breeding-and-Genetics; Plant-Pests**

47. **A single nucleotide polymorphism in the alternative oxidase gene among rice varieties differing in low temperature tolerance**
Source: FEBS Letters. 2002. 527 (1-3). 181-185

Author(s): Abe-F. Saito-K. Miura-K. Toriyama-K

Abstract:

Alternative oxidase (AOX) is encoded in a multigene family, and multiple isoforms have been observed in various plant species. We found for the first time an allelic variation in the same AOX locus. On SDS-gel blots of callus protein of rice (Oryza sativa), cultivars without the quantitative trait loci (QTL) for low temperature tolerance (Hokkai 241, Kirara 397, BT4-9-7) showed a 32-kDa AOX band, whereas those with the QTL (Silewah, Norin-PL8, Hokkai-PL5 and BT4-76-2) showed a 34-kDa band. The variation was attributed to the substitution of Lys71 for Asn71 caused by a single nucleotide polymorphism between alleles of OsAOX1a, and was tightly linked to the presence of the QTL

Descriptors:Alleles. Chromosomes. Cold-tolerance. Cultivars. Genes. Genetic-polymorphism. Genetic-variation. Nucleotides. Oxidoreductases. Quantitative-trait-loci. Rice. Temperature

48. The beneficial plant growth-promoting association of Rhizobium leguminosarum bv. trifolii with rice roots

Source: Australian Journal of Plant Physiology. 2001. 28 (9). 845-870

Author(s): Yanni-Y-G. Rizk-R-Y. El-Fattah-F-K-A. Squartini-A. Corich-V. Giacomini-A. Bruijn-F-de. Rademaker-J. Maya-Flores-J. Ostrom-P. Vega-Hernandez-M. Hollingsworth-R-I. Martinez-Molina-E. Mateos-P. Velazquez-E. Wopereis-J. Triplett-E. Umali-Garcia-M. Anarna-J-A. Rolfe-B-G. Ladha-J-K. Hill-J. Mujoo-R. Ng-P-K. Dazzo-F-B

Abstract:

This paper summarizes a multinational collaborative project to search for natural, intimate associations between rhizobia and rice (Oryza sativa), assess their impact on plant growth, and exploit those combinations that can enhance grain yield with less dependence on inputs of nitrogen (N) fertilizer. Diverse, indigenous populations of Rhizobium leguminosarum bv. trifolii (the clover root-nodule endosymbiont) intimately colonize rice roots in the Egyptian Nile delta where this cereal has been rotated successfully with berseem clover (Trifolium alexandrinum) since antiquity. Laboratory and greenhouse studies have shown with certain rhizobial strain-rice variety combinations that the association promotes root and shoot growth thereby significantly improving seedling vigour that carries over to significant increases in grain yield at maturity. Three field inoculation trials in the Nile delta indicated that a few strain-variety combinations significantly increased rice grain yield, agronomic fertilizer N-use efficiency and harvest index. The benefits of this association leading to greater production of vegetative and reproductive biomass more likely involve rhizobial modulation of the plant's root architecture for more efficient acquisition of certain soil nutrients (e.g. N, phosphorus, potassium, magnesium, calcium, zinc, sodium and molybdenum) rather than biological N2 fixation. Inoculation increased total protein quantity per hectare in field-grown grain, thereby increasing its nutritional value without altering the ratios of nutritionally important proteins. Studies using a selected rhizobial strain (E11) indicated that it produced auxin (IAA) and gibberellin (tentatively identified as gibberellin; GA7) phytohormones representing two major classes of plant growth regulators. Axenically collected rice root exudate significantly enhanced E11's production of this auxin. This strain extensively colonized the rice root surface under gnotobiotic culture conditions, producing distributions of spatial patchiness that would favour their localized erosion of the epidermal surface, colonization of small crevices at epidermal junctions as a possible portal to enter into the root, and quorum sensing of diffusible signal molecules indicating that their nearest bacterial neighbours are in close proximity in situ. Studies of selected rhizobial endophytes of rice indicated that they produced cell-bound cellulase and polygalacturonase enzymes that can hydrolyse glycosidic bonds in plant cell walls, and non-trifolitoxin bacteriocin(s) that can inhibit other strains of clover rhizobia. Strain E11 was able to endophytically colonize rice roots of varieties commonly used by Filipino peasant farmers, and also to stimulate genotype-specific growth-promotion of corn (Zea mays, maize) under field conditions. An amalgam of these results indicate some rhizobia have evolved an additional ecological niche enabling them to form a three-component life cycle including a free-living heterotrophic phase in soil, a N2-fixing endosymbiont phase within legume root nodules, and a beneficial growth-promoting endocolonizer phase within a cereal roots in the same crop rotation. Our results further indicate the potential opportunity to exploit this newly described, plant-rhizobia association by developing biofertilizer inoculants that may assist low-income farmers in increasing cereal production (especially rice) with less fertilizer N inputs, fully consistent with both sustainable agriculture and environmental safety

Descriptors:Cellulase. Chemical-composition. Crop-yield. Fertilizers. Gibberellic-acid. Harvest-index. IAA. Plant-composition. Plant-growth-regulators. Polygalacturonase. Protein-content. Rice. Use-e

49. **Assessing the sustainability of rice production growth in Bangladesh**

Source: Food Policy. 2001. 26 (5). 515-542

Author(s): Baffes-J. Gautam-M

Abstract:

This paper identifies the sources of growth in rice production in Bangladesh over the 1973-99 period. The main contributor was found to be the conversion of rice growing areas from local to modern varieties. The most important conclusion, based on simulations, is that the current level of per capita production can be sustained only through increased yields of modern rice varieties. Population control is found to have significant long-run benefits, while faster conversion of the remaining area to modern varieties has important short-run payoffs. The latter two actions, however, can only complement but not substitute efforts to increase the yields of modern varieties

Descriptors:Crop-production. Crop-yield. Population-growth. Rice. Sustainability

50. **Effect of variety and sowing date on false smut incidence in upland rice in Edo State, Nigeria**

Source: International Rice Research Notes (Pre 2002). 2000. 25 (1). 14
Author(s): Ahonsi-M-O. Adeoti-A-A. Erinle-I-D. Alegbejo-M-D. Singh-B-N. Sy-A-A
Abstract:

Two field experiments were conducted in Benin City, Edo State, Nigeria during the 1993 and 1994 wet seasons to evaluate the effect of plant variety and sowing date on incidence of false smut (Ustilaginoidea virens). In experiment 1, seven upland rice varieties (ITA 315, ITA 335, ITA 316, ITA 150, Ex-China, IRAT 170 and Agbede) were planted on 3 different dates depending on maturity period. In experiment 2, Agbede was planted on 6 dates at 2-week intervals (from 2-3 April to 16-17 June). In experiment 1, varieties reacted differently to false smut incidence. ITA150, ITA315, Agbede and ITA335 were the most susceptible to false smut (mean disease incidence (MDI) = 36.1, 40.5, 40.6 and 43.3%, respectively). ITA 316 and Ex-China showed some resistance (8.6 and 2.3%, respectively). IRAT 170 was completely free from infection. In experiment 2, rice sown with early rains between 2 April and 3 May was free from false smut or showed low incidence (MDI range = 0 to 3.1%). However, rice sown between 16 May and 3 June was highly infected (48.5 to 51.6%)

Descriptors:Cultivars. Disease-resistance. Incidence. Plant-diseases. Plant-pathogenic-fungi. Plant-pathogens. Rice. Sowing-date. Susceptibility. Upland-rice. Varietal-reactions. Varietal-resistance. Fungal-diseases

51. **Quantitative genetic analysis of biotypes of the brown planthopper Nilaparvata lugens: heritability of virulence to resistant rice varieties**
Source: Entomologia Experimentalis et Applicata. 1999. 90 (3). 279-287
Author(s): Tanaka-K
Abstract:

The virulence of N. lugens (Homoptera: Delphacidae) to a resistant variety of rice is suggested to be under polygenic control. To determine whether the virulence of N. lugens is a quantitative character that has continuous distribution or a threshold character that has a few discontinuous phenotypic forms and is determined by some underlying continuous variable, the frequency distribution of honeydew excretion that has been used as a measure of ability of attacking the rice plants, and the relationship between honeydew excretion and the oviposition rate of N. lugens females using a japonica rice line Saikai 190 which has a resistance gene Bph 1, was examined. The frequency distribution in honeydew excretion significantly differed from the normal distribution, but two distributions below and above 10 mg honeydew excretion for two days did not significantly deviate from normality, suggesting a bimodal distribution. There were significant differences in the proportion of females ovipositing and the number of eggs deposited between the female groups that excreted 0-10 mg honeydew and more than 20 mg honeydew. Within these female groups, however, the reproductive performances were not different. Thus, virulence of N. lugens can be analysed as a threshold character that has two distinct phenotypes, virulent and avirulent. The heritabilities of the virulence of N. lugens by parent-offspring regression were estimated using the percentage of virulent females in a full-sib family. The estimates of heritability were 0.41 on Saikai 190 and 0.55 on ASD7, carrying the bph 2 gene. These results showed that the N. lugens population has substantial genetic variation in virulence. The regression coefficients on female and male parents were similar, suggesting similar genetic contributions by both parents. When the parental families were examined on Saikai 190 and the progeny on ASD7, the regression coefficient approached zero. There may be a low genetic correlation between virulences to the two varieties

Descriptors:Biotypes. Genetic-analysis. Heritability. Rice. Varieties. Cultivars. Virulence. Ova. Genetic-correlation. Genetic-variation. Honeydew. Oviposition. Phenotypes. Insect-pests. Plant-pests. Cereals. Pest-resistance. Pest-control. Control. Agricultural-entomology

52. Tools for plant-based N management in different rice varieties grown in southern India

Source: International Rice Research Notes (Pre 2002). 1999. 24 (3). 23-24

Author(s): Kumar-R-M. Padmaja-K. Subbaiah-S-V

Abstract:

Three high-yielding rice cultivars, 3 hybrids and 3 scented cultivars were grown in kharif [monsoon] 1997 and rabi [winter] 1997/98 to compare different approaches to N management, assess genotypic differences in SPAD and LCC (leaf colour chart) readings, and correlate SPAD and LCC readings. N treatments were 0, 45, 90 or 135 kg N/ha applied in 2 splits, and SPAD-based N management. In kharif, mean grain yield was 4.8 t/ha with SPAD-based management compared with 4.0 and 4.4 t for fixed N rates of 90 and 135 kg N/ha, respectively, while in rabi grain yield did not differ between these 3 treatments. SPAD management gave N applications of 75 and 80 kg N/ha in kharif and rabi, respectively. Hybrids had higher grain yields than the other genotypes. Agronomic efficiency of N was highest in SPAD-based management. Mean SPAD and LCC values were positively correlated at all growth stages with mean grain yield of cultivars. Correlation coefficients between SPAD and LCC at different growth stages ranged from 0.78 to 0.90

Descriptors:Rice. varieties. cultivars. hybrid-varieties. fertilizers. nitrogen-fertilizers. application-methods. use-efficiency. fertilizer-requirement-determination

53. Response of rainfed lowland rice varieties to different N levels under two types of water management

Source: International Rice Research Notes (Pre 2002). 1999. 24 (1). 32-33

Author(s): Biswas-C-R. Mandal-A-B. Pramanik-S-C

Abstract:

In a field trial in 1994/95 to 1996/97 at Canning, West Bengal, India, 6 rice cultivars under shallow (15-25 cm) submergence and 6 different cultivars under deep (25-50 cm) submergence were given 0, 20, 40, 60, 80 or 100 kg N/ha. Yields generally increased with increasing N rate up to 80 kg, then decreased, although the increase was only significant up to 60 kg. Cv. CST7-1 gave the highest yield under shallow submergence and CSRC(D)4-3-0 gave the highest yield under deep submergence. Response to N fertilizers and N use efficiency were higher under shallow than deep submergence

Descriptors: rice. varieties. cultivars. nitrogen-fertilizers. application-rates. Submergence

54. **Grain quality characteristics of aromatic and nonaromatic rice cultivars**

Source: International Rice Research Notes (Pre 2002). 1999. 24 (2). 17-18

Author(s): Sakila-M. Ibrahim-S-M. Anandakumar-C-R. Backiyarani-S. Bastian-D

Abstract:

Twelve high-yielding rice varieties, 11 evaluation lines and scented varieties were evaluated for quality components during the wet season

Descriptors: rice. quality. cereals

55. **Genetics of tolerance for iron toxicity in rice**

Source: International Rice Research Notes (Pre 2002). 1999. 24 (1). 11

Author(s): Nipah-J-O. Safo-Kantanka-O. Jones-M-P. Singh-B-N

Abstract:

Two rice varieties tolerant to iron toxicity and two susceptible ones were crossed and 6 progeny generations evaluated at Korhogo, Cote d'Ivoire, in 1996. Most genes responsible for tolerance of iron toxicity were dominant but epistatic effects were also observed

Descriptors:Iron. Rice. Toxicity. Toxic-substances. Genetics. Inheritance. Epistasis. Cereals

56. **Genetic variability in leaf area and chlorophyll content of aromatic rice**

Source: International Rice Research Notes (Pre 2002). 1999. 24 (1). 21

Author(s): Bansal-U-K. Saini-R-G. Kaur-A

Abstract:

Some 26 aromatic rice varieties and non-aromatic high-yielding cultivars IET8585 were grown in PAU fields in kharif 1996 and evaluated for chlorophyll content, leaf area and sensory scores. Results indicated variability for all 3 traits. High chlorophyll content associated with upright foliage and delayed senescence had a positive effect on yield

Descriptors: Chlorophyll. Leaf-area. Rice. Genetic-variation. Aroma. Cereals

57. **Advanced breeding lines with resistance to rice tungro viruses**

Source: International Rice Research Notes (Pre 2002). 1998. 23 (1). 17-18

Author(s): Angeles-E-R. Cabunagan-R-C. Tiongco-E-R. Azzam-O. Teng-P-S. Khush-G-S. Chancellor-T-C-B

Abstract:

Some 139 advanced breeding lines with improved agronomic characters derived from crosses involving tungro-resistant rice varieties were evaluated for resistance to rice tungro viruses under greenhouse conditions. The crosses involved Utri Rajapan, Utri Merah, ARC11554, Habiganj DW8 and wild rices Oryza longistaminata and O. rufipogon as resistance sources, and IR1561-228-3-

3, IR24 and IR64 as recurrent parents. All of the parents, except ARC11554, O. longistaminata, IR24 and IR64 are susceptible to the virus vector green leafhopper (Nephotettix virescens). In the greenhouse studies, only 94 of the breeding lines were confirmed as resistant to tungro. Of these, only 4 showed resistance to both rice tungro bacilliform badnavirus (RTBV) and rice tungro spherical waikavirus (RTSV); the other 90 showed resistance to only RTSV. Two breeding lines from crosses involving O. rufipogon and Habiganj DW8 were resistant to both viruses. Progenies derived from O. rufipogon, Utri Merah and Utri Rajapan were among the lines that exhibited a high level of resistance to RTSV. An increase in RTBV and RTSV infection was observed in most of the breeding lines when inoculated seedlings of the test materials were transplanted in the field and further exposed to natural infection. However, breeding lines from Utri Merah and Utri Rajapan crosses showed a decrease in RTBV infection even after further exposure to natural infection

Descriptors:Rice. Interspecific-hybridization. Wild-relatives. Plant-diseases. Plant-pathogens. Disease-resistance. Varietal-reactions. Cereals. Plant-genetic-resources. Plant-pathology

58. The effect of Trichoderma and antifungal agents on rice germination

Source: International Rice Research Notes (Pre 2002). 1998. 23 (2). 43-44

Author(s): Duncan-K. Su-YouXan

Abstract:

An antifungal seed-raising mixture was made by cultivating Trichoderma viride in nutrient-supplemented sawdust from Pinus radiata wood. When sown in the antifungal seed-raising mixture, carrots, radishes, lettuces and tomatoes germinated and grew well, with no disease mortality. However, when 4 rice varieties were tested, the germination rate was 0-2% and growth of those seeds that did germinate was extremely poor. Results are discussed of tests conducted to determine whether T. viride is toxic to rice or if rice might have a specific requirement for a symbiont that is killed by T. viride. Germination and growth were enhanced when rice was germinated in the presence of Spirulina platensis

Descriptors:Antifungal-agents. Rice. Carrots. Radishes. Lettuces. Tomatoes. Seed-germination. Seedling-growth. Phytotoxicity. Biological-control-agents. Plant-pathogens. Plant-pathogenic-fungi. Plant-diseases. Plant-disease-control. Plant-pathology

59. Satyam and Kishori, two high-yielding varieties developed for the rainfed lowlands of Bihar, India

Source: International Rice Research Notes (Pre 2002). 1998. 23 (3). 20-21

Author(s): Thakur-R. Singh-A-K. Singh-R-S. Mishra-S-B. Singh-N-K. Rai-J-N

Abstract:

Many high yielding rice varieties are unsuitable for planting when the monsoon is delayed as flowering starts when temperatures are low, causing non-uniform flowering and poor seed set. Several genotypes derived from IR8/Barogar and RD19/Desaria were tested under normal and delayed monsoon conditions in regional trials and, subsequently, in multilocational trials. In trials conducted during 1993-96, RAU1119-13-3-1 (Kishori), derived from IR8/Barogar, and RAU3025-2-1B-2-1 (Satyam), derived from RD19/Desaria, were both superior to standard checks Radha and Pankaj. Satyam had a 10.8% and 13.8% yield advantage over Radha and Pankaj, respectively, whereas Kishori yielded 13.5% and 16.6% more than these checks, respectively. Both new varieties were released for general cultivation in rainfed lowlands. Satyam and Kishori both have intermediate heights (120-125 cm), a compact erect habit and a 145-150 day growth period. Satyam has long fine grains while Kishori has long bold grains. Both are resistant to bacterial blight (Xanthomonas oryzae), are tolerant of brown spot (Cochliobolus miyabeanus), and of Zn and Fe deficiencies

Descriptors: **Varieties. Cultivars. Rice. Growth-period. Crop-yield. Planting-date. Plant-pathogens. Plant-pathogenic-fungi. Plant-diseases. Disease-resistance. Varietal-reactions. Plant-pathogenic-bacteria. Zinc. Iron. Deficiency. Mineral-nutrition. High-yielding-varieties. Cereals**

60. Green leafhopper-susceptible advanced lines resistant to rice tungro viruses

Source: International Rice Research Notes (Pre 2002). 1998. 23 (3). 16-17

Author(s): Tiongco-E-R. Martin-H-C. Abdula-S-E. Truong-X-A. Villanueva-A-E. Sebastian-L-S. Angeles-E-R. Khush-G-S

Abstract:

Eight rice varieties and lines susceptible to green leafhoppers (Nephotettix cincticeps) were tested in field plots at two sites Munoz, Nueva Ecija and Midsayap, North Cotabato, for their reactions to tungro viruses during 3 cropping seasons in 1996-97. Visual assessment for disease incidence was made 30 and 60 days after transplanting. ELISA was used to determine the presence of rice tungro bacilliform badnavirus (RTBV) and rice tungro spherical waikavirus (RTSV) in leaf tissue. The results showed that yields of test varieties is similar to those of high yielding varieties when grown in an area with low tungro disease incidence

Descriptors: **Rice. Screening. ELISA. Plant-pathogens. Plant-diseases. Disease-resistance. Varietal-reactions. Insect-pests. Disease-vectors. Cereals. Pest-resistance. Pest-control. Control. Plant-pathology. Agricultural-entomology**

61. Growth and yield response of improved and traditional rice varieties to N fertilization at various growth stages

Source: International Rice Research Notes (Pre 2002). 1998. 23 (3). 23-24

Author(s): Singh-S

Abstract:

A pot experiment compared the N response of traditional rice cv. C14-8 (tall, lodging-susceptible) and improved cv. Mansarover (semitall). Mansarover responded most when N was applied during active tillering, followed by N applied at panicle initiation, but did not respond to N applied at flowering. C14-8 was most responsive at panicle initiation, followed by N applied at flowering, and did not respond to N applied during active tillering. Response to N was associated with increases in leaf area, panicles/plant and grains/panicle. N reduced harvest index in C14-8 but not in Mansarover

Descriptors:Growth-stages. responses. rice. varieties. cultivars. fertilizers. nitrogen-fertilizers. crop-growth-stage. application-date

62. **The relationship between the morphological fertility of pollen and marker gene Est9**

Source: International Rice Research Notes (Pre 2002). 1997. 22 (2). 6-7

Author(s): Lu-ChuanGen

Abstract:

F2s from the three-way crosses of rice varieties Akihikari x IR36 x Calotoc (AIC) and Ketan Nangka x IR36 x Kamairazu (KIK) were analysed for the Est9 (esterase) isoenzyme marker on chromosome 7. Morphological fertility of pollen was determined by staining grains with 1% I2KI solution. In the F2s of both three-way crosses, morphological fertility was reflected by marker genotypes Est9-12 and Est9-11, derived from the 2 individual crosses, respectively. This indicates the existence of a locus for determining pollen fertility, which may be located near Est9. It is suggested that the locus for pollen fertility is identical to ga11, a gamete abortion gene

Descriptors:Wide-hybridization. rice. isoenzymes. genetic-markers. pollen. genes. fertility. cereals. biotechnology

63. **Control of insect pests on rice crop using tillage practices**

Source: AMA, Agricultural Mechanization in Asia, Africa and Latin America. 1997. 28 (1). 29-30

Author(s): Abdul-Razzaq. Sabir-B-A. Zafar-M-A

Abstract:

Fine rice varieties are severely attacked by insect pests such as the stem borer, Tryporyza [Scirpophaga] and Sesamia species in Pakistan. Rice stubble, if not properly destroyed after harvesting, acts as the main host for the hibernation of stem borer larvae during winter. The effect of various tillage practices on the destruction of stubble and hibernating rice stem borer larvae was assessed. The effect of no-tillage, for wheat production after rice cropping, on stem borer infestation was also evaluated. Stubble intensity and infestation was highest in untilled fields. Rotovation caused the complete destruction of stubble and left no hibernating larvae. The cultivator and plank with fewer passes was not so effective for stubble destruction or killing stem borer larvae, although the effectiveness increased with the number of cultivator and plank passes

Descriptors:Stem-borers. Hibernation. Larvae. Stubble. Rice. Insect-control. Tillage. Plant-pests. Insect-pests. Cultural-control. Control. Pests. Cereals. Pest-control. Agricultural-entomology

64. **Genetic resources, international organizations, and improvement in rice varieties**

Source: Economic Development and Cultural Change. 1997. 45 (3). 471-500

Author(s): Evenson-R-E. Gollin-D

Abstract:

The economic role of IRRI's international programmes for rice improvement, International Network for the Genetic Evaluation of Rice (INGER), International Rice Germplasm Centre (IRGC) and its own plant breeding programme (IRPB) are assessed for the period 1965-1990. Section I of this paper contains a brief discussion of rice breeding methods and the role of genetic resources. Section II has reports on released varieties and their origins, and in Section III, the route taken by varieties to release is analysed. Section IV has an economic analysis of IRRI's programmes on the number and characteristics of released varieties

Descriptors:Cultivars. Plant-breeding. Plant-genetic-resources. International-organizations. Rice. Varieties. Germplasm. Economic-evaluation. Breeding. Genetic-resources. Economics. Gene-banks. Organizations. Irri. Cereals

65. **Performance of rice mutants in different seasons**

Source: International Rice Research Notes (Pre 2002). 1997. 22 (1). 7

Author(s): Kulkarni-N. Gangaram-A. Kashikar-M

Abstract:

During 1994-95, 12 M5, M6 and M7 early (120-140 days) mutants of rice variety Samba Mahsuri were evaluated for days to flowering. Flowering of the mutants during the winter season was delayed by 5.0-30.5 days compared to the monsoon season, with M12 and M41 showing the least delay (5.0-11.5 days, respectively). However, due to the dry weather and prolonged growing season, winter yields were significantly higher than monsoon yields. M34, M41 and M47 were recommended for cultivation during the monsoon season, M9 for the winter season and M16 and M22 for both seasons

Descriptors: mutants. rice. flowering. seasonal-variation. mutations. yields. cereals

66. **Transgenic rice plants expressing rice yellow mottle virus coat protein gene**

Source: International Rice Research Notes (Pre 2002). 1997. 22 (1). 14-15

Author(s): Kouassi-N. Brugidou-C. Chen-L. Ngon-M. Yassi-A. Beachy-R-N. Fauquet-C-

Abstract:

Four different constructs containing the cDNA sequence of the rice yellow mottle sobemovirus (RYMV) coat protein (CP) inserted into the ubiquitin promoter-Nos terminator cassette and plasmid pMON410 carrying the hygromycin resistance gene, were introduced into embryogenic calli of japonica rice variety Taipei 309. After several rounds of selection on hygromycin, plantlets were transferred to soil. About 62% of transformed lines carried the ubiquitin-Nos cassette as determined by PCR and Southern blotting. Accumulation of mRNA and coat protein were detected by Northern and Western blotting, respectively. Several levels of resistance to RYMV were observed in transgenic lines

Descriptors:Plant-diseases. disease-resistance. coat-proteins. rice. plasmid-vectors. genetic-transformation. polymerase-chain-reaction. southern-blotting. northern-blotting. western-blotting. gene-expression. transgenic-plants. ubiquitin. embryo-culture. cereals. biotechnology. plant-pathology

67. **Variability and quality indices in aromatic rice germplasm**
Source: International Rice Research Notes (Pre 2002). 1997. 22 (1). 22-23
Author(s): Singh-V-P. Khush-G-S. Cruz-N-dela
Abstract:

Some 356 traditional aromatic rice varieties were evaluated for 8 grain and cooking traits to identify basmati types. Highest variation was found for gel consistency followed by 1000-grain weight (WT) and amylose content (AC). AC was significantly and negatively correlated with all other traits. WT was negatively correlated with AC and grain elongation after cooking (KE), indicating that lower grain weight types must be selected to identify basmati types. Based on grain shape and elongation, 39 varieties were identified as basmati type

Descriptors: Rice. cooking-quality. correlation-analysis. amylose. cereals

68. **Effect of blast disease on rice yield**
Source: International Rice Research Notes (Pre 2002). 1997. 22 (1). 25-26
Author(s): Surek-H. Beser-N
Abstract:

The effect of blast disease, caused by Magnaporthe grisea, on 12 rice varieties and lines was studied in field experiments at Edirne and Uzunkopru, Turkey, in 1995. Rice yield, total rice recovery, head rice and 1000-grain weight were determined. Significant differences in all characters studied were recorded for the 2 locations, with all being less for rice grown in Uzunkopru. The varieties with moderate susceptibility to node and neck blast (Ribe, TR-427, TR-475, TR-489 and TR-765) differed less for yield and yield components between the 2 sites than the susceptible and highly susceptible varieties (Ergene, Serhat-92, Ana/Mar, Lap/PG, TR-648, Ipsala and Surek-95). Blast infection in conjunction with environmental factors accounted for the smaller yields at Uzunkopru. Node and neck blast caused more damage to the varieties than did leaf blast because none of the varieties were even moderately resistant to it

Descriptors: Plant-diseases. Plant-pathogens. Plant-pathogenic-fungi. Rice. Disease-resistance. Resistance. Screening. Varieties. Varietal-reactions. Yields. Yield-losses. Crop-losses. Grain. Environmental-factors. Spatial-variation. Cereals. Plant-pathology

69. **RFLP variation among commercial rice germplasms in China**
Source: Journal of Genetics & Breeding. 1997. 51 (4). 263-268
Author(s): Zhuang-J-Y. Qian-H-R. Lu-J. Lin-H-X. Zheng-K-L
Abstract:

Some 74 rice varieties used in China were selected for RFLP analysis using 90 probes covering 12 chromosomes of rice. Polymorphism between varieties was detected by 56 probes, generating 161 polymorphic fragments based on a single restriction endonuclease. Cluster analysis clearly distinguished indica and japonica varieties. However, within the indica and japonica groups, there was only little genetic variation

Descriptors:Restriction-fragment-length-polymorphism. Cluster-analysis. Rice. Genetic-variation

70. **New varieties of rainfed rice for Vietnam**

Source: Agriculture et Developpement. 1997. (15). 155-161

Author(s): Godon-P. Nguyen-Gia-Quoc. Nguyen-Thanh-Thuy

Abstract:

Agronomic traits and yield performances are presented of 7 medium and early maturing rainfed rice varieties selected from national and international collections for their suitability in temporary intercropping systems with tree crops. Rainfed rice can be grown in systems where inputs are available, before cashews, rubber or coffee come into production. In trials during 1992-96 throughout Vietnam, conclusive results were obtained from propagation carried out by smallholders. LC88.66 is noted for good yield stability in northern, central and southern provinces and may be cultivated in semi-flooded conditions. LC90.5 is well adapted to northern, mountainous regions and has good cooking quality characteristics. Seven varieties are currently being distributed by agricultural extension services

Descriptors:Yields. Intercropping. Earliness. Rice. Cropping-systems. Stability. Cultivars. Varieties. Cereals

71. **Embryogenic cell suspensions established from a high-protein purple black rice**

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 40-41

Author(s): Fu-HuiHua. Tian-TingLiang. Zhu-YingGuo

Abstract:

The effects of explants, media, hormones and culture procedures on callus induction and cell suspension were investigated in indica rice variety Hua Hei 01. The lowest callus induction (0.4%) occurred using anthers, whereas young panicles and mature seeds gave high callus induction (24.6 and 21.3%, respectively). Hormones significantly affected induction frequency and callus quality, and these effects are discussed

Descriptors:Rice. Anther-culture. In-vitro-culture. Plant-growth-regulators. Callus. Culture-media. Explants. Tissue-culture. Cereals

72. **Fingerprinting rice germplasm using ALP and PCR-based RFLP**

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 10-12

Author(s): Ghareyazie-B. Huang-N. Second-G. Bennett-J. Khush-G-S

Abstract:

Converting mapped RFLP markers to PCR-based markers such as amplicon length polymorphism (ALP) was evaluated for classifying DNA of 35 Iranian rice varieties, and 3 indica and 2 japonica varieties. A dendrogram was constructed based on genetic distances obtained from pooled ALP and PCR data of 13 loci. Three groups were distinguished among the 35 Iranian varieties: indica, japonica and those distinct from the 2 types. Sadri varieties were genetically closer to japonica than to indica varieties, despite their typical indica morphology. PCR-based RFLP was faster, easier and cheaper than Southern-based RFLP

Descriptors:Rice. Molecular-genetics. DNA-fingerprinting. Techniques. Cereals

73. **Molecular mapping of genes for F1 pollen sterility in rice**

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 20-21

Author(s): Zhuang-ChuXiong. Zhang-GuiQuan. Mei-ManTong. Lu-YongGen

Abstract:

Rice variety Taichung 65 (E1) and its isogenic F1 pollen sterile line (E5) were used as parents to map S-c (an F1 pollen sterility gene). RFLP markers were used to investigate polymorphism between E1 and E5. The 3 positive markers (RG227, RG166 and RG369A) were closely linked and were mapped to chromosome 3. Polymorphism was low between E1 and E5. The genetic distances between the S-c locus and markers RG227 and RG369 were 0.5 and 2.5 cM, respectively

Descriptors:Rice. Genes. Molecular-genetics. Restriction-fragment-length-polymorphism. Genetic-markers. Cytoplasmic-male-sterility. Gene-mapping. Cereals

74. **Principal component analysis and variety classification in relation to rice seedling salinity tolerance**

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 55-56

Author(s): Gonzales-L-M

Abstract:

The salinity tolerance of 19 rice varieties was investigated. Principal component analysis was conducted using the characteristics seedling height, root length, seedling fresh weight and seedling dry weight. More than 83% of the total variability between varieties was accumulated in the first 2 components. Varieties were placed in 4 groups according to the first 2 components. Group I, containing Caribe 1, IA Cuba-26, 2196, Ecia 22-8, J112, 2006, IR42 and IR5931, gave the highest salinity tolerance index values and was the most salt-tolerant group

Descriptors:Salt-tolerance. Rice. Principal-component-analysis. Salinity. Seedlings. Stress. Cereals

75. **Influence of rice plant morphology on leaffolder incidence**

Source: International Rice Research Notes (Pre 2002). 1996. 21 (1). 31

Author(s): Islam-Z. Karim-A-N-M-R

Abstract:

Sixteen rice varieties and breeding lines were evaluated for the influence of 4 morphological traits on leaf folder (Cnaphalocrocis medinalis, Marasmia patnalis and M. exigua) incidence during summer 1993 in Gazipur, Bangladesh. On average, leaf folders had folded 5.3% of the leaves of plants between the booting and dough-ripeness stages of development. Leaf folder resistant variety TKM6, with narrow and long leaves, had the lowest level of folded leaves (0.9%), while Purbachi, with wide and short leaves, had the highest level (14.1%). The incidence of folded leaves was negatively correlated with leaf blade length and positively correlated with leaf blade width. There was no correlation between folded leaves and plant height or green leaf number

Descriptors:Rice. Pest-resistance. Insect-pests. Leaves. Plant-morphology. Morphology. Pests. Varietal-resistance. Cultivars. Resistance. Cereals. Pest-control. Control. Agricultural-entomology

76. Histological observation of callus morphology in rice

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 39

Author(s): Narciso-J-O. Hattori-K

Abstract:

Callus morphology was investigated, with the emphasis on cell composition, in 5 indica (IR54, Rc2, Toboshi 2757 and 2764), 2 japonica (Nipponbare and Tsutsu) and 2 javanica (Lemonte and Rinatte) rice varieties on 2 induction media. IR54, Toboshi, Nipponbare, Tsutsu and Rinatte showed good callus growth. Callus morphologies differed between the varieties and are described

Descriptors: In-vitro-culture. Rice. Callus. Cereals

77. Effect of organic and inorganic source of nitrogen on the nutrients in soil and soil solution and growth of rice

Source: Journal of the Indian Society of Soil Science. 1996. 44 (2). 263-266

Author(s): Medhi-B-D. Barthakur-H-P. Barthakur-S-N

Abstract:

A greenhouse experiment was conducted to study the changes on the nutrients in soil and soil solution and growth of rice treated with organic manures (farmyard manure, Sesbania rostrata, and Sesbania aculeata), and prilled urea (PU). The nitrogen was applied at 60 kg N/ha and rice variety 'Ratna' was used as the test crop. Incorporation of organic and inorganic sources of N increased soil and soil solution NH_4^+-N to a peak and then declined to a very low level. Prilled urea gave higher NH_4^+-N than did organic sources at 2 weeks after flooding (WAF) whereas the reverse trend was obtained at 6 WAF indicating slow release of N from organic manures. The concentration of P, K^+, Fe^{2+} and Mn^{2+} in the soil and soil solution were higher with PU and organic sources than control. Addition of N, regardless of sources, increased grain yield significantly. Nitrogen and Mn uptake by grain also increased significantly with the addition of N

Descriptors: Green-manures. Nutrient-uptake. Soil-solution. Nitrogen. Nutrients. Soil. Growth. Rice. Amendments. Farmyard-manure. Nitrogen-fertilizers. Urea. Organic-amendments. Fertilizers

78. **Variability, heritability, correlation, path analysis, and genetic divergence studies in M2 generation of gamma-irradiated upland rice**
Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 56-58
Author(s): Mehetre-S-S. Mahajan-C-R. Patil-P-A. Dhumal-P-M

Abstract:

Information on heritability, yield correlations and genetic variability is derived from data on 8 characters in the M2 generation of 8 upland rice varieties treated with gamma radiation (10, 20, 30, 40 or 50 kR). Significant differences occurred among genotypes for all characters. Estimates of heritability ranged from 91.2 (plant height) to 35.6% (sterility). Expected genetic advance ranged from 6.9 (panicle length) to 54.9% (grain yield/plant). Correlation and path analyses showed that filled grains/panicle, plant height and panicle length are important characters for selection in breeding programmes. Multivariate analysis showed that the 75 M2 families had formed 14 genetically diverse groups

Descriptors: Rice. Path-analysis. Correlation-analysis. Yields. Gamma-radiation. Yield-correlations. Yield-components. Heritability. Multivariate-analysis. Induced-mutations. Cereals

79. **Genetic analysis of plant regeneration ability from cell suspension cultures of rice**
Source: International Rice Research Notes (Pre 2002). 1996. 21 (1). 14-15
Author(s): Tsukahara-M. Hirosawa-T. Nagai-E. Kato-H. Ikeda-R. Maruyama-K
Abstract:

Regenerative ability was studied in cell suspension cultures from 14 rice varieties and their 164 F1 hybrids. Among the parent varieties, the number of regenerated plantlets varied from 108.3 (Kele) to 0 (Lemont, CP231, Nan Jing 11 and Qing Er Ai). The number of regenerated plantlets for the F1 was widely distributed from 164 (Kele x Banten) to 0. Eight F1 hybrids which did not regenerate, each had a parent, usually the female, which also did not regenerate. Five of the 7 F1 hybrids with both parent varieties unable to regenerate, did regenerate. It is suggested that 2 or more genes with complementary gene action control regenerative ability. Both additive and dominant gene effects were significant, as were reciprocal effects. Heterosis for regenerative ability in japonica x indica, javanica x indica and their respective reciprocal crosses was higher than in japonica x japonica, japonica x javanica and javanica x japonica crosses

Descriptors:Rice. Regeneration. Cell-culture. Heterosis. Genetics. Regenerative-ability. In-vitro-culture. Cereals

80. **Maintainers and restorers identified in some rice cultivars of Pakistan**
Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 31
Author(s): Ali-S-S. Khan-M-G
Abstract:

Local rice varieties and lines (38) were crossed with IR58025A and IR62829A wild-abortive (WA) cytoplasmic male sterile (CMS) lines in Lahore, Pakistan, in 1994. Male parents of the hybrids with 100% pollen and spikelet sterility were classified as potential maintainers, those of hybrids with 80-100% fertility were classified as restorers and the rest were classified as partial restorers. Lines 1021-8 and KS282 were the only potential restorers for both CMS lines, and Basmati 385 restored fertility in IR58025A

Descriptors:Rice. Sterility. Fertility. Cereals

81. **Heritable chilling tolerance improvement in rice through somaclonal variation and cell line selection**

Source: Australian Journal of Botany. 1996. 44 (1). 91-105

Author(s): Bertin-P. Kinet-J-M. Bouharmont-J

Abstract:

Four rice varieties were used in this study: the japonica cv. Kirundo 3 and the indica cv. Kirundo 9, derived from off-types of cv. Yunnan 3, and the indica cultivars Facagro 57 and Facagro 76. In preliminary studies, Kirundo 3 was classified as the most chilling tolerant, followed by Kirundo 9, and finally Facagro 57 and Facagro 76 which were indistinguishable for this trait. Embryo-derived calluses of these varieties were submitted to different continuous or discontinuous periods of chilling stress at 4 deg C, with a total length varying from 2 to 6 weeks. Other calluses were cultivated without cold stress. The reduction of plant regeneration percentages induced by low temperature was more pronounced in the more cold-sensitive varieties. Regenerated plants and their descendants in the R1, R2 and R3 generations were cold-screened together with control plants. A mass selection was applied to the control plants during three successive generations. In all varieties, significantly higher chilling survival rates were obtained in R3 progeny compared with control plants. Higher plant survival rates were obtained from the more chilling-sensitive varieties when a short discontinuous chilling treatment or no treatment was applied, from the intermediate variety under short or intermediate treatments, and from the more cold-tolerant variety under longer, continuous treatments. The relative importance of pre-existing versus in vitro-induced variation and of epigenetic versus heritable variation are discussed, together with the significance of such cold tolerance improvement for breeding purposes

Descriptors:Somaclonal-variation. Chilling. Tolerance. Improvement. Rice. Selection. In-vitro-selection. Cold-resistance. Breeding. Cereals. Biotechnology

82. **Utilisation of anther culture in rice (Oryza sativa L.) breeding in Italy**

Source: Australian Journal of Experimental Agriculture. 1994. 34 (7). 911-915

Author(s): Callegarin A M. Perfanov K. Dorotea G. Baldi G

Abstract:

Increasing market demand has led to efforts to select for non-sticky, long-grain rice varieties suited to the Italian environment. The variability of recombinant populations derived from crosses between Italian and USA genotypes was exploited. Together with the conventional breeding methods, in vitro anther culture was used to obtain homozygous lines from crosses more quickly. Moreover, hybrid lines were obtained from crosses otherwise impossible to exploit owing to sterility in the F1 generation (namely those resulting from crosses involving semi-dwarf USA varieties). Plant regeneration was obtained from 6 F1 hybrids whose parents were chosen for grain quality or suitability to the Italian environment. About 5500 plantlets were regenerated. Of these, 1000 were albino, and about 50% of the green ones died after transplanting into soil; 65% of the surviving plants were sterile, so about 1000 progeny were obtained (30-445 for each cross). Progeny with desirable characteristics were evaluated for agronomic traits. On the basis of these results, limits and possibilities of anther-culture breeding in rice are discussed

Descriptors:Rice. Plant-breeding. Anther-culture. In-vitro-culture. Breeding. Cereals

83. Effects of combine operating parameters on harvest loss and quality in rice

Source: Transactions of the ASAE. 1993. 36 (6). 1599-1607

Author(s): Andrews S B. Siebenmorgen T J. Vories E D. Loewer D H. Mauromoustakos

Abstract:

Combine tests were conducted in commercial rice fields near Keiser, Arkansas, USA. Data was collected and analysed for 2 long-grain rice varieties, 'Newbonnet' and 'Lemont', over a period of 2 harvest seasons. The test system used allowed for the collection of the clean grain auger discharge, shoe discharge, and rotor discharge separately and simultaneously. Independent variables tested were field speed (feed rate), material-other-than-grain to grain (MOG/G) ratio, m.c., rotor speed, and concave clearance. Feed rate was the most important factor affecting combine harvest loss. MOG/G ratio was the second most important factor affecting loss rates. The m.c., by itself, was significant only in the 'Newbonnet' variety but affected loss rate in the 'Lemont' variety by influencing feed rate and MOG/G ratio. Rotor speed also influenced loss rates but affected each of the varieties differently. Concave setting was significant in both varieties but to a lesser degree in 'Newbonnet'. Head rice yields from combine-harvested samples and hand-harvested samples followed similar trends. Less than 2% reduction in head rice yield was found in the combine-harvested samples when compared to hand-harvested samples

Descriptors: Rice. Harvesting-losses. Combine-harvesters. Losses. Harvesters. Farm-machinery. Harvesting. Equipment

84. Virus detection in varieties resistant to tungro (RTD)

Source: International Rice Research Notes (Pre 2002). 1993. 18 (1). 22-23

Author(s): Cabunagan R C. Flores Z M. Coloquio E C. Koganezawa H

Abstract:

The infection of rice plants inoculated with rice tungro bacilliform badnavirus (RTBV) was traced by ELISA for 5 weeks. RTBV was detectable in rice varieties TKM6, Gam Pai 30-12-15 and TN1 throughout the test. Varieties Utri Merah and Balimau Putih had relatively high RTBV infection 1 week after inoculation but the virus concn in these varieties decreased over time to below the level of detection and it is suggested that this is the reason why past tests, done at 3-4 weeks after inoculation, show low RTBV infection rates

Descriptors:Rice. Varietal-reactions. Detection. Techniques. Diseases. Varietal-resistance. Cultivars. Disease-resistance. ELISA. Cereals. Plant-pathology

85. Bogabordhan: a stable, high-yielding, low-input traditional variety of Assam, India

Source: International Rice Research Notes (Pre 2002). 1993. 18 (3). 22

Author(s): Kalita U C. Baruah D K. Upadhaya L P

Abstract:

Twenty local rice varieties selected from sali (wet season) stock and 2 widely grown controls (Manoharsali and Jaya) were evaluated for 12 agronomic traits and disease reaction under rainfed lowland conditions during the 1989-90 wet season. Jaya is photoperiod insensitive whilst Manoharsali and Jaya are sensitive. Bogabordhan outyielded both controls (4.9 versus 4.8 and 3.4 t/ha, respectively) and was also superior for filled spikelet percentage (96%) and 1000-grain weight (30 g). Its field resistance to sheath rot [Sarocladium oryzae], bacterial blight [Xanthomonas oryzae], sheath blight [Rhizoctonia solani] and false smut [Ustilaginoidea virens] is adequate to moderate and better than Jaya. Lack of significance in regression of yield across the years, indicated the good stability of this new cultivar, which is needed by resource-poor farmers

Descriptors:Stability. Varieties. Cultivars. Rice. Disease-resistance. Yields. Yield-components. Photoperiodism. Cereals

86. Combining ability and heterosis in U.S. southern long-grain rice

Source: Crop Science. 1993. 33 (1). 83-86

Author(s): Gravois K A. McNew R W

Abstract:

Combining ability and heterosis estimates are excellent statistics to help discern breeding programme goals and direction. Currently, combining ability and heterosis estimates for US southern long-grain rice are lacking; thus, studies were conducted to estimate these parameters for rice yield, plant height, panicle number, panicle length, panicle weight, and primary branch number. In 1989, two 4 x 4 crossing factorials were completed, and the 32 F1 hybrids and their 16 parents were evaluated in 1990 at two Arkansas locations: the Rice Research and Extension Center near Stuttgart and the Cotton Branch Experiment Station near Marianna. The 16 parents constituted a representative sample of elite US southern long-grain rice germplasm available to rice breeders. Hill plots consisting of single plants were planted 61 cm apart in a square grid pattern. GCA was more important than SCA, accounting for 70% of the variation for yield, 89% for plant height, 84% for panicle number, 60% for panicle length, 69% for panicle weight, and 85% for primary branches. SCA was significant for all traits except panicle number, indicating that non-additive gene action was important as well. When crossing combinations are being decided, the sole use of midparent means would not adequately predict progeny mean performance. High parent heterosis for yield ranged from -16 to 68%. Heterosis for yield was due primarily to heterosis for panicle weight rather than panicle number. US southern long-grain rice yields could be improved through the use of hybrid rice varieties

Descriptors: Rice. Combining-ability. Yield-components. Heterosis. Genetics. Cereals

87. **TRY(R)2: a short-duration, salt-tolerant rice variety**

Source: International Rice Research Notes. 2004. 29 (1). 27

Author(s): Rajagopalan-R. Robin-S. Sivasubramanian-P. Mohammad-S-E-N. Ali-A-J. Kandasamy-M. Sivanantham-M

Abstract:

Trichy(Rice)2 (TRY(R)2), developed from the cross IET6238/IR36, is a new short-duration salt-tolerant rice cultivar released for cultivation in Tamil Nadu, India, during 2002. TRY(R)2 has an average productivity of 5.4 t/ha and a 1000-grain weight of 22.84 g, and is capable of producing 19.7 and 11.9% higher yield than the control cultivars ADT36 and ADT16, respectively

Descriptors: Characteristics-; crop-yield; rice-; salt-tolerance South-Asia; Asia-; Developing-Countries; Commonwealth-of-Nations; Oryza-; Poaceae-; Cyperales-; monocotyledons-; angiosperms-; Spermatophyta-; plants-; India- Field-Crops; Plant-Breeding-and-Genetics; Environmental-Tolerance-of-Plants

88. **Rajendra Mahsuri 1, a potentially high-yielding rice variety for medium and shallow lowland ecosystems of Bihar, India**

Source: International Rice Research Notes. 2004. 29 (1). 25

Author(s): Sahai-V-N. Ghosh-S. Chaudhary-R-C

Abstract:

Rajendra Mahsuri 1 (designated RAU83-500), developed from the cross BR51-46/Mahsuri, is a new rice cultivar released in 2003 for commercial cultivation. It is resistant to brown planthoppers [Nilaparvata lugens] and leaffolders [Cnaphalocrocis medinalis], and is moderately-resistant to sheath blight [Rhizoctonia solani] and bacterial leaf blight [Xanthomonas oryzae pv. oryzae]. In yield trials and on-farm trials, Rajendra Mahsuri 1 showed yield consistency and wide adaptability. Under medium land conditions, it gave higher yield (5.0 t/ha) than Sita (4.2 t/ha) and Kanak (4.4 t/ha). Under shallow lowland conditions, it also had higher yield (4.9 t/ha) than Radha (4.0 t/ha) and Satyam (4.1 t/ha)

Descriptors: Characteristics-; crop-yield; disease-resistance; fungal-diseases; high-yielding-varieties; insect-pests; pest-resistance; plant-diseases; plant-pathogenic-bacteria; plant-pathogenic-fungi; plant-pathogens; plant-pests; rice-; varietal-resistance; variety-trials India-; South-Asia; Asia-; Developing-Countries; Commonwealth-of-Nations; Cnaphalocrocis-; Pyralidae-; Lepidoptera-; insects-; arthropods-; invertebrates-; animals-;

Nilaparvata-; Delphacidae-; Fulgoroidea-; Auchenorrhyncha-; Homoptera-; Hemiptera-; Oryza

89. **Farmers' participatory evaluation of rice varieties and herbicidal technologies in the Godavari Delta**

Source: International Rice Research Notes. 2004. 29 (1). 76-77

Author(s): Raju-R-A. Reddy-M-D

Abstract:

In 2000-02, ten villages were selected in West Godavari, Andhra Pradesh, India, and 20 respondents from each village were obtained randomly for a participatory rural appraisal technique to compare the performance of rice cultivars Vijentha, Samba Masuri, Chaitanya and Swarna, and to evaluate the adoption of herbicidal technology in rice from the farmers' perspective. a majority of the farmers preferred Samba Masuri and Swarna despite their higher susceptibility to pests and diseases. Based on the attitude towards weed management practices in rice, a majority of the respondents had more than 60% knowledge about summer ploughing, suboptimal plant population and unskilled labour leading to ineffective weed control. None of the farmers used manual weeding or herbicide alone. Many adopted integrated weed management practices. Farmers reported the highest gap with respect to dose and time of herbicide application. There was zero adoption of barnyardgrass control in the rice nursery, although farmers knew about it. The herbicide sales representative had maximum contact with farmers, while the agricultural department officers were the least consulted on herbicidal technology. Friends and mass media (radio and television) were the most often used sources of information on weed management. Farmers preferred broad-spectrum-based chemicals with no toxic effects on fish

Descriptors: Cultivars-; farmers'-attitudes; farming-systems-research; herbicides-; integrated-control; manual-weed-control; rice-; weed-control; weeds- India-; South-Asia; Asia-; Developing-Countries; Commonwealth-of-Nations; Echinochloa-; Poaceae-; Cyperales-; monocotyledons-; angiosperms-; Spermatophyta-; plants-; Oryza- Extension-and-Advisory-Work; Field-Crops; Plant-Breeding-and-Genetics; Weeds-and-Noxious-Plants; Environmental-Pest-Management; Integrated-Pest-Management; Pesticides-and-Drugs-Control

90. **Two outstanding rice varieties developed through selection from naturally occurring genetic variation in Sri Lanka**

Source: International Rice Research Notes. 2004. 29 (2). 22-23

Author(s): Abeysiriwardena-D-S-de-Z

Abstract:

Two outstanding rice cultivars were developed through selection from naturally occurring genetic variation in Sri Lanka. 'Lanka Samurdhi' is a semi-dwarf cultivar with Basmati-type grain quality traits and high yield potential. This cultivar has been officially released in Sri Lanka. 'Bg 250' is an ultra-short-duration, nonlodging, short-plant type cultivar with high yielding ability, acceptable grain quality and resistance to leaf blast [Magnaporthe grisea], bacterial leaf blight [Xanthomonas oryzae pv. oryzae], thrips and brown planthopper [Nilaparvata lugens]. This cultivar is also tolerant of drought (if planted early) and flooding conditions (if planted after the flood has receded). This cultivar is expected to be officially released in Sri Lanka before the end of 2004

Descriptors: Characteristics-; crop-quality; crop-yield; drought-resistance; flooding-tolerance; fungal-diseases; insect-pests; pest-resistance; plant-diseases; plant-pathogenic-bacteria; plant-pathogenic-fungi; plant-pathogens; plant-pests; rice-Magnaporthe-; Polystigmatales-; Ascomycotina-; Eumycota-; fungi-; Nilaparvata-; Delphacidae-; Fulgoroidea-; Auchenorrhyncha-; Homoptera-; Hemiptera-; insects-; arthropods-; invertebrates-; animals-; Oryza-; Poaceae-; Cyperales-; monocotyledons-; angiosperms-; Spermatophyta-; plants-; South-Asia; Asia-; Developing-Countries; Commonwealth-of-Nations; Xanthomonas-oryzae; Xanthomonas-; Xanthomonadaceae-; Gracilicutes-; bacteria-; prokaryotes- Field-Crops; Plant-Breeding-and-Genetics; Plant-Production; Plant-Pests; Environmental-Tolerance-of-Plants; Host-Resistance-and-Immunity

91. **Variability in bioavailable iron in hand-pounded traditional rice varieties from a highland village in northern Thailand**

Source: International Rice Research Notes. 2004. 29 (1). 46-47

Author(s): Prom-u-thai-C. Rerkasem-B

Abstract:

An experiment was conducted to determine the bioavailability of Fe in hand-pounded rice (cultivars Bue Po Lo, Bue Kee (B), Bue Kaset, Bue Tolae, Bue Goa, Bue Kee (F) and Bue Bang) from Tee Cha village, Thailand. The grain Fe concentration of hand-pounded rice from Tee Cha was highly variable. The hand-pounded cultivars with grain Fe concentration of >10 mg/g were Bue Po Lo, Bue Kee (B), Bue Tolae and Bue Kee (F). Furthermore, phytate concentration of hand-pounded rice was also highly variable. It was highest in Bue Po Lo, Bue Tolae and Bue Kee (F). However, there was no correlation between grain Fe and phytate concentration in all hand-pounded rice cultivars. Bioavailability of rice grain Fe in the village varied among different cultivars. Bue Po Lo, Bue Tolae and Bue Goa had a higher Fe bioavailability than the standard Nishiki. It was highest in Bue Po Lo, lowest in Bue Goa and intermediate in Bue Tolae. There was no correlation between bioavailability of Fe and grain Fe, and phytate concentration in rice grain

Descriptors:Bioavailability-; correlation-analysis; crop-quality; cultivars-; iron-; nutritive-value; phytates-; rice- Oryza-; Poaceae-; Cyperales-; monocotyledons-; angiosperms-; Spermatophyta-; plants-; South-East-Asia; Asia-; Developing-Countries; ASEAN-

Countries Field-Crops; Plant-Breeding-and-Genetics; Crop-Produce; Food-Composition-and-Quality

92. Reactions to an inferred resistance of Indian and Bangladesh rice varieties to bacterial blight

Source: International Rice Research Notes (Pre 2002). 2000. 25 (1). 12-13

Author(s): Lee-K-S. Angeles-E-R. Khush-G-S

Abstract:

The reaction of 170 cultivars obtained from the International Rice Germplasm Center (IRGC) to 6 Philippine races of Xanthomonas oryzae pv. oryzae (Xoo), the causal agent of bacterial blight, was evaluated. Based on their pattern of resistance, the cultivars were classified as belonging to one of 3 groups. The DZ192 group (39 cultivars, 23%) were resistant to races 1, 2, 3 and 5, moderately susceptible to race 4 and susceptible to race 6. The BJ1 group (62 cultivars, 36%) was resistant to all 6 races, while the remaining 61 (41%) cultivars (Makhmal Mehi (MM), group) showed resistance to races 1, 2, 3, 4 and 5 and susceptibility to race 6. The resistance of DZ192, BJ1 and MM cultivars to races 1, 2, 3 and 5 was governed by the xa5 gene, resistance of BJ1 cultivars to race 6 by xa13 and resistance of MM cultivars to race 4 by xa4. Resistance of BJ1 cultivars to race 4 was due to complementary action of xa13 and xa5. DZ192 cultivars originated from Bangladesh while BJ1 and MM cultivars came from India and Bangladesh

Descriptors: Cultivars. Disease-resistance. Plant-diseases. Plant-pathogenic-bacteria. Plant-pathogens. Rice. Susceptibility. Varietal-resistance. Varietal-reactions. Genetics. Genes

93. Differentiation of rice varieties cultivated in Yunnan, China, using PCR markers corresponding to conserved motifs of disease resistance genes

Source: International Rice Research Notes (Pre 2002). 2000. 25 (2). 11-12

Author(s): Wang-Z-H. Borromeo-E-S. Teng-P. Leung-H. Zhu-Y-Y

Abstract:

Using the polymerase chain reaction (PCR), primers can be designed to amplify sequences that correspond to conserved motifs of disease resistance genes. These PCR markers, known as resistance gene analogue (RGA) markers, can be used to characterize germplasm and breeding lines. This approach was used to evaluate the genetic diversity of a set of 41 landraces and modern varieties of rice from Yunnan Province. RGA banding patterns produced by each of 5 primer pairs revealed a high degree of intervarietal polymorphism, and a consensus dendrogram based on the markers was developed

Descriptors: Rice. Cultivars. Landraces. Polymerase-chain-reaction. Genetic-markers. Genetic-diversity. Polymorphism. Genetic-distance. Plant-diseases. Disease-resistance. Molecular-genetics. Plant-genetic-resources

94. A study of head rice yield reduction of long- and medium-grain rice varieties in relation to various harvest and drying conditions

Source: Transactions of the ASAE. 2000. 43 (6). 1709-1714

Author(s): Fan-J. Siebenmorgen-T-J. Yang-W

Abstract:

In this research, the effects of harvest moisture content (HMC), harvest location, variety difference, and heated-air drying conditions on head rice yield reduction (HRYR) of long-grain (Kaybonnet and Cypress) and medium-grain (Bengal) varieties were investigated. The rice was harvested at moisture contents (MCs) of approximately 16 to 26% from two locations (Stuttgart and Keiser, Arkansas, USA). The rough rice was dried under three conditions: 43.5 deg C, 38% relative humidity (RH), 9.5% equilibrium moisture content (EMC); 51.7 deg C, 25% RH, 7.3% EMC; and 60 deg C, 17% RH, 5.8% EMC. The results indicated that variety, HMC, drying condition, and drying duration had significant interactive effects on the HRYR during drying. Medium-grain Bengal rice exhibited more HRYR than did long-grain Cypress or Kaybonnet rice under a given drying condition. The results further indicated that a decrease in MC of rice at the early drying stages did not substantially affect the HRY until a certain MC level was reached. It appeared in this study that the amount of moisture that could be removed without affecting HRY increased as harvest MC increased

Descriptors: Crop-yield. Drying. Drying-methods. Grain-drying. Postharvest-systems. Processing. Rice. Technology. Water-content

95. **Modelling the spatio-temporal deployment of resistant varieties to reduce the incidence of rice tungro disease in a dynamic cropping system**

Source: Plant Pathology. 1999. 48 (4). 453-461

Author(s): Holt-J. Chancellor-T-C-B

Abstract:

A dynamic cropping system was represented by a square lattice of fields in which crops were successively harvested and replanted. A spectrum of crop ages existed at any one time and the virus disease persisted by spread of inoculum between crops. Such a situation is typical of many areas of tropical irrigated rice cultivation in which rice tungro virus disease (RTVD) occurs. Using a mathematical model of the epidemiology of RTVD in the cropping system, the deployment of fields of a genotype expressing some resistance to the disease was investigated. Previous studies on the effect of genotype mixtures on disease progress within a single crop have shown that both the rate of disease increase and the rate of focus expansion were proportional to the logarithm of the fraction of susceptible plants in the mixture. In this study, looking at long-term disease incidence in a dynamic cropping system, it was found that this same 'logarithmic rule' applied, provided that resistant crop deployment was spatially random. A relatively large proportion of fields had to be planted with resistant varieties in order to have sufficient area-wide impact on inoculum to reduce disease incidence in fields of susceptible varieties. In many rice cropping systems there are two growing seasons per year and the modelling indicated that the best strategy was to concentrate deployment of resistant varieties in the season of greatest disease spread. Attempts to minimize inoculum carry-over to the 'high spread' season by concentrating resistant varieties in the previous season had little effect over a range of simulated conditions. In considering recommendations for the management of RTVD, a conflict existed between the reduction of disease incidence strategically and in the individual fields of a newly deployed variety. To maximize area-wide strategic impact, small genotype units and random patterns were best, but to protect individual fields, large units and concentrated deployment were best

Descriptors: Rice. Varieties. Cultivars. Cropping-systems. Genotypes. Genotype-mixtures. Mathematical-models. Models. Plant-pathogens. Epidemiology. Plant-disease-control. Plant-diseases. Disease-resistance. Cereals. Plant-pathology

96. **Jaymati, a high-yielding summer rice variety with good grain quality for Assam**

Source: International Rice Research Notes (Pre 2002). 1998. 23 (2). 20

Author(s): Ahmed-T. Sarma-K-C. Pathak-A-K. Borah-H. Sharma-K. Hussain-S. Ali-S

Abstract:

Derived from the cross Jaya x Mahsuri, Jaymati is recommended for summer cropping in the central and Brahmaputra Valley zone of Assam. It is medium-tall (130 cm), photoperiod-insensitive, suitable for transplanting in summer and autumn, and has well exserted panicles and a brownish husk. The 1000-grain weight is 20.2 g, and the kernels are white with a nonglutinous endosperm. Milling recovery is 66.5%. Duration of Jaymati from sowing to seed is 170 days for summer, and 130 days for autumn and winter rice

Descriptors: Rice. Cultivars. Hybrid-varieties. Summer. Characteristics. Cereals

97. **Zhenong 921: a new indica rice variety with high yield and blast resistance**

Source: International Rice Research Notes (Pre 2002). 1998. 23 (2). 7-8

Author(s): Shi-ChunChai. Chen-WenGuang. Chen-GuoLin. Zhang-GenXian. Shen-ZongTan. Wu-JianGuo

Abstract:

This new semidwarf indica variety is derived from the cross Zhongzhe 1 x K125-34 and is suitable for the double-cropped area of southern China. It was registered by Zhejiang Province in 1997 as an early variety. Zhenong 921 has a high, stable yield potential under normal fertilization, yielding 6.7-7.5 t/ha in yield trials, and its highest yield of 8.1 t/ha was 9.5% more than that of the control in 1994. It is resistant to leaf and neck blast [Magnaporthe grisea], and has good cold resistance and the seedling stage and good lodging resistance. Zhenong 921 has 83.9% brown rice recovery, 75.5% milled rice recovery, 43.9% head milled rice recovery, 26.3% amylose content, 50 mm gel consistency, an alkali spreading value of 3, and acceptable cooking quality

Descriptors: Rice. Cultivars. Hybrid-varieties. Characteristics. Cereals

98. **Chinoor: a promising spontaneous mutant and high-quality rice variety of Madhya Pradesh, India**

Source: International Rice Research Notes (Pre 2002). 1998. 23 (2). 12
Author(s): Sharma-D. Janoria-M-P
Abstract:

In an effort to reduce the duration and plant height of rice cv. Chinoor, farmers' fields were surveyed in 1995 to collect possible spontaneous mutants. Progenies of 25 single-plant selections made were transplanted along with Chinoor for observation. One of the progenies flowered 31 days earlier and was 28 cm shorter than Chinoor. Compared to Chinoor, the mutant had similar kernel aroma and translucency, but recorded 80% higher grain yield/plant. This high yield advantage resulted largely from its 30% more panicles/plant and 20% higher grain weight/panicle. It is suggested that this mutant of Chinoor has the potential to not only replace Chinoor, but also to be extended to new rice areas

Descriptors: Rice. Plant-height. Growth-period. Mutants. Mutations. Crop-quality. Crop-yield. Cereals

99. **Inheritance of resistance to bacterial leaf blight in differential rice variety Asominori**

Source: International Rice Research Notes (Pre 2002). 1998. 23 (3). 13-14
Author(s): Ise-K. Li-C-Y. Sun-Y-Q. Ye-C-R
Abstract:

To test the association between phenol reaction of grains and resistance to bacterial leaf blight (BLB; Xanthomonas oryzae pv. oryzae), 16 lines in the pedigree of Asominori were screened. Only Saikai 85 displayed a positive phenol reaction and resistance to BLB isolates. In a second study, BLB field resistance of these lines, and their F1s and F2s, was assessed using clip inoculation at heading. All F1 plants were resistant to BLB isolates T7174 (race I), H9153 (race II-2) and H75304 (race V) which were collected in Japan. Segregation ratios suggested that BLB resistance in Asominori was controlled by a single dominant gene (allele at Xa1 locus) closely linked to the Ph gene (2.4% recombination value)

Descriptors: Inheritance. Rice. Plant-pathogens. Plant-pathogenic-bacteria. Plant-diseases. Disease-resistance. Varietal-reactions. Genetics. Genes. Cereals

100. **On-farm characterization of upland rice varieties in north Thailand**

Source: International Rice Research Notes (Pre 2002). 1998. 23 (3). 21-22
Author(s): Keer-K-van. Trebuil-G. Courtois-B. Vejpas-C
Abstract:

An on-farm diagnostic survey on the extent and causes of variability of upland rice yields was carried out in 1993-96 in Chiang Mai Province, N. Thailand, at 600-700 m altitude. Farmers' cultivars were characterized from physiological, agronomic and genetic viewpoints

Descriptors: Characterization. Rice. Cultivars. Variety-classification. Genotypes

101. Influence of planting dates on productivity of traditional scented rice varieties

Source: International Rice Research Notes (Pre 2002). 1997. 22 (1). 42

Author(s): Gangwar-K-S. Sharma-S-K

Abstract:

In a field trial in western Uttar Pradesh, in the 1993-94 wet seasons, rice cv. Basmati 370, Ranveer Basmati and Taraori Basmati were transplanted on 1, 16 or 31 July or 16 August. Yield was not significantly different between the cultivars, but decreased from 4.1 t/ha with the earliest planting date to 2.5 t when planted in August

Descriptors: rice. Transplanting. Date. Cultivars

102. Genetic diversity among upland rice varieties from India and Bangladesh

Source: International Rice Research Notes (Pre 2002). 1997. 22 (3). 8-9

Author(s): Courtois-B. Sinha-P-K. Prasad-K. Carandang-S

Abstract:

Isoenzyme variation was analysed at 14 loci in 64 upland varieties. Five of the loci proved to be monomorphic. When the 64 varieties were classified using an algorithm bases on alleles present at 5 polymorphic loci, 35 were classed as indica and 22 as aus. A dendrogram clustering 62 of the varieties was established; this also showed clear-cut differentiation into the 2 varietal groups

Descriptors: Rice. Genetic-variation. Isoenzymes. Variety-classification. Genetics. Cereals. Plant-genetic-resources

103. Performance of midland rice varieties in a blast hot spot

Source: International Rice Research Notes (Pre 2002). 1997. 22 (3). 15

Author(s): Ramappa-H-K. Shivakumar-N. Poonachha-N-M. Anilkumar-T-B

Abstract:

Thirteen varieties from the midlands of Karnataka and the local standard Intan were grown during 1992-94 at Ponnampet, a blast (Pyricularia oryzae [Magnaporthe grisea]) hot spot. Mean neck blast incidence was highest in Intan (69.37%) and lowest in IYT(SHW)91/10609 (5.69%). Mean grain yields were highest in IRLON90/18 (3.9 t/ha) and lowest in Intan (1.0 t/ha)

Descriptors:Rrice. disease-resistance. plant-diseases. plant-pathogenic-fungi. cultivars. cereals. plant-pathology

104. Cilosari: a new rice variety released in Indonesia through cross hybridization of the mutant line with IR36

Source: International Rice Research Notes (Pre 2002). 1997. 22 (3). 21

Author(s): Mugiono

Abstract:

Seed of rice cv. Seratus Malam was gamma irradiated in 1983, and 130 semidwarf mutants were selected in the M2. One of these mutants, SM268/PsJ, selected from the 20 krad treatment, was crossed with cv. IR36. An early maturing line, Obs1647/PsJ, was selected in the F3 and advanced to the F10. In trials at 27 sites in Indonesia in 1992-95, Obs1647/PsJ exceeded IR64 in yield. Released in 1996, the line was renamed Cilosari. It is 110-125 cm tall, gives an average yield of 5-6.5 t/ha, has good cooking and eating quality, and is resistant to brown planthopper [Nilaparvata lugens] biotypes 1 and 2 and bacterial blight [Xanthomonas oryzae]

Descriptors:Rice. Cultivars. Characteristics. Plant-height. Dwarfing. Gamma-radiation. Induced-mutations. Cereals

105. Ranjini (MO12): a high-yielding rice variety with blast and brown planthopper resistance

Source: International Rice Research Notes (Pre 2002). 1997. 22 (2). 29-30

Author(s): Devika-R. Remabai-N. Regina-A. Kumari-S-L

Abstract:

Ranjini was derived from the cross MO5 x Improved Sona and released for use in Kerala in 1966. It is a short-duration, dwarf variety with red medium-bold grains and resistance to blast [Magnaporthe grisea] and brown planthopper [Nilaparvata lugens]. It is also tolerant of gall midge [Orseolia oryzae], sheath blight [Rhizoctonia solani] and sheath rot [Sarocladium oryzae]

Descriptors:Rice. Plant-pathogenic-fungi. Plant-diseases. Plant-pathogens. Disease-resistance. Plant-pests. Pest-resistance. Cultivars. Cereals

106. Estimation of elongation efficiency in deepwater rice varieties

Source: International Rice Research Notes (Pre 2002). 1997. 22 (2). 33

Author(s): Mohapatra-P-M. Panda-A-R

Abstract:

During the wet season 1996, 15 deep water varieties of rice were evaluated for elongation efficiency under submerged conditions at Cuttack. Jalamagna had the highest elongation efficiency index (EEI) (0.70), followed by NDGR410 (0.69), TCA4 (0.65) and Karawa (0.59). Most varieties reached their maximum elongation rate after 6 days of submergence. Varieties with EEI > 0.44 managed to penetrate the water surface while those with EEI < 0.44 remained submerged

Descriptors: Plant-development. Rice. Flooding. Submergence. Deep-water-rice. Growth. Stems. Cereals

107. Rice varieties of Kerala as restorers and maintainers for wild abortive cytoplasmic male sterile lines

Source: International Rice Research Notes (Pre 2002). 1997. 22 (2). 11-12

Author(s): Kumari-S-L. Valarmathi-G. Joseph-T. Kanakamany-M-T. Nayar-N-K

Abstract:

During the 1994 wet season, 3 exotic cytoplasmically male sterile (CMS) lines of wild abortive (WA) origin were crossed with 43 male parents from the source germplasm, including 26 locally released varieties and 17 elite varieties, and hybrids and parents were evaluated for fertility. Of the 43 parent varieties, 18 were identified as effective maintainers, 7 as effective restorers and 16 as partial restorers. Hybrids of red-grain Kerala varieties were either sterile or partially fertile. Sterile hybrids were backcrossed to some of the identified maintainers to develop locally adaptable CMS lines with red grains for use in breeding

Descriptors: hybrids. Rice. Cytoplasmic-male-sterility. Fertility. Seeds. Colour. Cereals

108. Machhapuchhre 3 (MP3), the first rice variety developed through a participatory plant breeding approach released for mid to high altitudes of Nepal

Source: International Rice Research Notes (Pre 2002). 1997. 22 (2). 12

Author(s): Joshi-K-D. Sthapit-B-R. Gurung-R-B. Gurung-M-B. Witcombe-J-R

Abstract:

MP3 was released for altitudes of 1400-2000 m in western Nepal in 1996. It was selected by farmers as a result of field trials of 7 F5s of 3 crosses. Farmers evaluated the entries for yield and quality at different sites and compared them to their local varieties. It was concluded that participatory plant breeding is a cost-effective method for developing crop varieties based on farmers' needs

Descriptors:Rice. farming-systems-research. yields. quality. variety-trials. cereals

109. Flowering behavior of rainfed lowland rice varieties during dry season in West Bengal, India

Source: International Rice Research Notes (Pre 2002). 1997. 22 (1). 28-29

Author(s): Sinha-S-K. Chatterjee-S-D

Abstract:

During the dry seasons of 1992-94, the flowering behaviour of 5 popular rainfed lowland rice cultivars was compared to that of 2 photoperiod-insensitive boro controls. Seeds were sown on 3 dates during November to January and dates to 50 and 100% flowering and grain yields were recorded. Lowland varieties sown after November exhibited significant variety x sowing date interaction for flowering. Time to flowering decreased in successive sowings for IR42, Jaya and IR36. IR42 retained flowering synchrony under all 3 sowing dates

Descriptors: Genotype-environment-interaction. Rice. Sowing-date. Flowering. Yields. Cereals

110. Vijetha: a high-yielding, short duration rice variety for Andhra Pradesh, India

Source: International Rice Research Notes (Pre 2002). 1997. 22 (1). 29

Author(s): Suryanarayana-Y. Rao-P-S. Reddi-N-S-R. Murthy-K-R-K. Murthy-P-S-S

Abstract:

Vijetha was developed from a cross between MTU5249 and MTU7014 at ARS. In trials during 1991-94 dry seasons it yielded on average 7.5 t/ha which is 22.8% more than that of control variety IR64. It is resistant to brown planthopper [Nilaparvata lugens], moderately resistant to gall midge [Orseolia oryzae], whiteback planthopper [Sogatella furcifera], stemborer [Pyralidae], leaffolder

[Cnaphalocrocis medinalis] and blast [Magnaporthe grisea]. Vijetha is semi-dwarf with dark green foliage and 8-10 productive tillers. It was released by the State Seed Subcommittee in 1995

Descriptors: Rice. Plant-pests. Pest-resistance. Plant-pathogenic-fungi. Plant-diseases. Plant-pathogens. Disease-resistance. Insect-pests. Cultivars. Cereals

111. Saraswati and Jalaprabha: two new deepwater rice varieties for eastern India

Source: International Rice Research Notes (Pre 2002). 1997. 22 (3). 25-26

Author(s): Mallik-S. Mandal-B-K. Kundu-C. Roy-S-K-B. Banerjee-B. Dutta-S-K. Chatterjee-S-

Abstract:

Released in 1996, Saraswati was developed from the cross Pankaj x Patnai 23, and Jalaprabha was developed by pedigree selection in a composite cross from IRRI. Both are tall and photoperiod sensitive. Their submergence tolerance is mainly due to elongation, and both have very good kneeing ability. Grains are short, bold and golden coloured. They are resistant to the main pests and diseases. In national trials during 1989-94 Saraswati, with a yield potential of 4.6 t/ha, gave a mean yield of 2.7 t/ha, 50% above that of the national standard Utkal Prabha, while Jalaprabha yielded 73% more than the standard Jalamagna and had a yield potential of 4.1 t/ha

Descriptors: R**ice. Cultivars. Characteristics. Flooding. Cereals**

112. FARO 45 to FARO 49: two early-maturing and three medium-maturing upland rice varieties released in Nigeria

Source: International Rice Research Notes (Pre 2002). 1997. 22 (3). 24-25

Author(s): Imolehin-E-D. Ukwungwu-M-N. Kehinde-J-K. Maji-A-T. Akinremi-J-A. Singh-B-N. Oladimeji-O

Abstract:

FARO 45 is an F4 selection from the cross IRAT13/Dourado Precoce/TOX490-1 made in 1979. It is early maturing (70 days to 50% flowering), is 100 cm tall and has an average grain yield of 2 t/ha. It is recommended for northwestern and northeastern regions of Nigeria. FARO 46 is an F5 selection from a complex cross involving parents such as 63-83, ROK1 and Dourado Precoce made in 1975. It is early maturing (75 days to 50% flowering), is 110 cm tall and has an average grain yield of 2 t/ha. It is recommended for cultivation throughout Nigeria. FARO 47 is an F5 selection from the cross 13A-18-3-1-3/1529-430-3/TOX7-4-2-5-2 made in 1975. It is midseason maturing (85 days to 50% flowering), is 105 cm tall and has an average grain yield of 2.5 t/ha. It is recommended for the southeastern zone of Nigeria. FARO 48 is an F8 selection from the cross IRAT13/Dourado Precoce//Padipayak made in 1978. It is midseason maturing (98 days to 50% flowering), is 100 cm tall and has an average grain yield of 2.5 t/ha. It is recommended for the major river valleys of central Nigeria and upland areas of the southwest. FARO 49 is an F6 selection from the cross IR1529-430-3/Iguape Cateto made in 1979. It is midseason maturing (90 days to 50% flowering), is 100 cm tall and has an average grain yield of 2 t/ha. It is recommended for the same areas as FARO 48. All 5 varieties are resistant to leaf blast [Magnaporthe grisea]

Descriptors: Cultivars. characteristics. rice. cereals

113. Cibodas, a high-yielding variety with good grain quality

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 43

Author(s): Partoatmodjo-A. Allidawati. Harahap-Z

Abstract:

B9775b-Mr-8-1-1, derived from a cross between B7004d-Mr-10-1 and B6992f-Mr-262, is a high-yielding rice line with good grain quality. Released as Cibodas for irrigated rice systems in September 1995, the variety is resistant to brown planthopper [Nilaparvata lugens] biotype 1 and bacterial blight [Xanthomonas oryzae] strain III. It yields c. 30% more than IR64 and Cisadane at 200-500 m above sea level, and is particularly suitable for cropping at intermediate elevation (c. 400 m). The grains are large with a 1000-grain weight of 34 g compared with 25 and 28 g for IR64 and Cisadane, respectively. Grain quality characteristics for Cibodas, IR64 and Cisadane were compared and are tabulated. Cibodas matures in 123 days, and has a head rice recovery of 80%, intermediate amylose content and tender cooking quality

Descriptors: Rice. Variety-trials. Yields. Yield-components. Varieties. Quality. Insect-pests. Plant-pests. Pest-resistance. Plant-diseases. Plant-pathogens. Plant-pathogenic-bacteria. Disease-resistance. Cultivars. Cereals

114. Shakuntla: a rice variety for rainfed lowlands in Bihar, India

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 61

Author(s): Sahai-V-N. Singh-B-K. Saran-S. Chaudhary-R-C

Abstract:

Derived from the cross Panka/Br8, Shakuntla (RAU73-16-1-40) was released for cultivation in rainfed lowland areas of Bihar in 1995. Shakuntla is weakly photoperiod-sensitive, of long duration (140-145 days), of medium height and has long, slender grains. In 1990-94 field trials, Shakuntla outyielded the variety Mahsuri, with averages of 3.5 and 2.6 t/ha, respectively

Descriptors: Rice. yields. varieties. characteristics. growth-period. cultivars. Cereals

115. KK15-36-C: a modern high-yielding rice variety for irrigated lowlands in Papua New Guinea

Source: International Rice Research Notes (Pre 2002). 1996. 21 (2-3). 60

Author(s): Sajjad-M-S

Abstract:

Of 122 rice genotypes evaluated in Papua New Guinea during 1991, KK15-36-C performed the best. High yielding KK15-36-C, derived from the cross

IR5657-33-2 x BKNDR1031-7, is semi-dwarf (<110 cm) with medium-tillering ability and remains green up to late maturity. It has long (>25 cm) fully filled panicles with >100 grains/panicle and a 1000-grain weight of 30 g. The grains are long, medium bold, awned and translucent. KK15-36-C is particularly well suited for general cultivation in the irrigated lowland fields of Papua New Guinea

Descriptors: Rice. yields. quality. varieties. characteristics. cultivars. Cereals

116. Fissure resistance of rice varieties

Source: Applied Engineering in Agriculture. 1996. 12 (3). 365-368

Author(s): Lan-YuBin. Kunze-O-R

Abstract:

Fourteen varieties of high moisture rice were harvested from border rows of breeding plots at Beaumont and Eagle Lake, Texas (USA) in August of 1989, 1990 and 1991. Samples of the rough rice were dried in an environmentally controlled laboratory at 21 deg C and 54% RH. Grains were then randomly selected from given lots and exposed to 100% RH at 24 deg C for 30 h. Fissured grains were counted and varieties were aligned according to their potential to fissure on a scale of 0 to 100. GuiChow, a medium grain variety, was the most susceptible to fissuring (100%) and Rexmont, a long grain variety, was the least susceptible (28.6%)

Descriptors: Rice. adsorption. humidity. seed-moisture. cracking. moisture-content. varietal-reactions. seeds. quality. physical-properties. grain. cultivars. Cereals

117. Performance of lowland transplanted sali (winter) rice varieties under late planting in Assam, India

Source: International Rice Research Notes (Pre 2002). 1994. 19 (3). 20

Author(s): Choudhary J K. Kurmi K. Baruah R K S M. Das G R

Abstract:

The performance of 3 photoperiod insensitive semi-dwarf varieties, IET10334, IET97574 and IET7251; 2 photosensitive semi-dwarfs, Biraj and Kmj1-52-3; and 2 photoperiod sensitive tall cultivars, Andrewsali and Monoharsali, was compared under normal and late transplanting date (TPD) conditions. The mean yield was greater in 1991-92 than 1990-91, perhaps because of more favourable cessation of the wet season. Also, rainfall during November-December was greater in 1991 (120.7 mm) than in 1990 (71.8 mm). Andrewsali had the greatest mean yield (2.4 t/ha in 1990-91 and 4.1 t/ha in 1991-92) and the IET cultivars the smallest (1.8 t/ha in 1990-91 and 2.3 t/ha in 1991-92). Grain yield decreased significantly with delay in transplanting, this decrease being greater in photoperiod insensitive cultivars than in photoperiod sensitive cultivars. In flood prone areas of Assam, tall photoperiod insensitive cultivars, such as Andrewsali, are favoured. If floods delay transplanting, such cultivars are less susceptible to delay in flowering and the likely reduction in grain yield due to terminal drought stress

Descriptors: Rice. water-stress. yields. photoperiodism. transplanting. planting-date. date. cultivars

118. **Reactions of advanced IET rice varieties to major pests in Raipur, India**

Source: International Rice Research Notes (Pre 2002). 1994. 19 (3). 10-11

Author(s): Rana D K. Pophaly D J. Kotasthane A S. Kaushik U K

Abstract:

A collection of 58 IET rice genotypes were studied for resistance to rice gall midge (GM; Orseolia oryzae), brown planthopper (BPH; Nilaparvata lugens) and bacterial leaf blight (BLB; caused by Xanthomonas oryzae pv. oryzae) during 1988-92 under field and laboratory conditions. During the 1989-90 kharif (June to October) seasons, entries were inoculated with X. oryzae pv. oryzae, and those entries exhibiting low plant damage were tested for resistance to BPH using the standard evaluation techniques in a glasshouse experiment. BPH resistant varieties were grown in the field during kharif 1990-91, to record GM infestation. The varieties which were resistant to GM were exposed to emerging grain moths [Sitotroga cerealella]. Fifty-six of the varieties were resistant to BPH, 13 to GM and 12 to BLB. Only 8 varieties exhibited strong resistance to grain moth, with infestation restricted to only 0.8% of grains. R650-1820 was the only variety resistant to BLB, BPH, GM and grain moth infestation

Descriptors: Rice. insect-pests. pest-resistance. disease-resistance. plant-diseases. plant-pathogens. plant-pathogenic-bacteria. varietal-reactions. cereals. cultivars. pests. varietal-resistance. diseases. plant-pests. resistance. pest-control. control. plant-pathology. agricultural-entomology

119. **Analysis of bacterial blight resistance genes in three japonica rice varieties**

Source: International Rice Research Notes (Pre 2002). 1994. 19 (3). 11

Author(s): Xu J L. Lin Y Z. Xi Y G

Abstract:

Japonica varieties Ning 67, Tai 202 and Bing 814 were crossed with Shennong 1033, which is susceptible to bacterial blight [Xanthomonas oryzae] strains W1, P1 and T1. CBB3, CBB4 and CBB12, near isogenic lines with resistance genes Xa3, Xa4 and Xa12, respectively, are resistant to these isolates. Crosses were also made between these resistant varieties and the japonica cultivars. A total of 12 crosses were made, including resistant/susceptible and resistant/resistant crosses. A single dominant gene controls the resistance of Ning 67 and Tai 202 to the 3 isolates and 2 dominant duplicate genes condition resistance in Bing 814. Allelism tests indicated that the genes of Ning 67 and Tai 202 were allelic to Xa3, as was one of the 2 genes in Bing 814

Descriptors:Rice. disease-resistance. genes. genetics. plant-pathogenic-bacteria. plant-diseases. plant-pathogens. cereals. diseases. varietal-resistance. plant-pathology

120. Effect of rice variety on methane emission from Louisiana rice

Source: Agriculture, Ecosystems & Environment. 1995. 54 (1-2). 109-114

Author(s): Lindau-C-W. Bollich-P-K. DeLaune-R-D

Abstract:

In a field experiment in 1993 at Crowley, Louisiana, USA, 6 local cultivars (3 semidwarf, 1 not a true semidwarf and 2 tall) were drill-seeded into a Crowley silt loam (Typic Albaqualf) and methane fluxes were measured twice a week over the first and ratoon cropping seasons. Semidwarf cultivars produced significantly less methane over both growing seasons. Over the main cropping season, semidwarfs emitted on average 185 kg CH4 ha-1 to the atmosphere compared with 300 kg ha-1 for the tall cultivars. During the ratoon sampling season, semidwarf and tall cultivars produced 540 and 830 kg CH4 ha-1, respectively. Compared with tall cultivars, semidwarfs produced 36% less methane over both seasons

Descriptors: S**ilt-loam-soils. alfisols. varieties. emission. rice. metabolism. methane. cultivars. height. stems. leaves. cereals**

121. Resistance to green leafhopper in rice varieties with different resistance genes

Source: International Rice Research Notes (Pre 2002). 1994. 19 (3). 15-16

Author(s): Velusamy R. Kumar M G. Edward Y S J T. Babu P C S

Abstract:

Differences in levels of resistance to green leafhopper (GLH), Nephotettix virescens, among varieties identified as resistant at IRRI were observed. Varieties with known resistance gene or genes and varieties with unknown dominant resistance genes were evaluated for damage and effect on the Tamil Nadu GLH population. Of 18 varieties tested, 13 were rated resistant. Pankhari 203 with gene Glh1 gene, Hashikalmi, Ghaiya and ARC10313 with a dominant gene, were rated as susceptible. GLH population increase was significantly higher on these varieties. Glh1 and a dominant gene in Hashikalmi, Ghaiya and ARC10313 do not confer resistance to the GLH population of Tamil Nadu. Varieties with Glh2, Glh3, glh4, Glh5, Glh6, Glh7, Glh1+Glh2 or Glh3+Glh5 are resistant

Descriptors: Rice. pest-resistance. insect-pests. genes. cultivars. genetics. pests. varietal-resistance. plant-pests. resistance. cereals. pest-control. control. agricultural-entomology

122. Resistance to thrips in traditional rice varieties

Source: International Rice Research Notes (Pre 2002). 1994. 19 (2). 13-14

Author(s): Velusamy R. Kumar M G. Edward Y S J T. Babu P C S

Abstract:

A preliminary field evaluation during October 1993 of 100 varieties for resistance to Stenchaetothrips biformis, by interspersing test cultivars between rows of resistant cv. Ptb 21 and susceptible cv. TN1 as controls, identified 18 entries with a high level of resistance. These were retested with control cultivars randomly sown among them. The cultivars were scored when TN1 showed >50% dead or wilted plants at 20 days after sowing (DAS). All 18 selections had a low thrip population at 20 DAS and all, except Vali, showed high resistance to damage

Descriptors:Rice. genetic-variation. insect-pests. pest-resistance. varietal-reactions. resistance. pests. varietal-resistance. cultivars. cereals. pest-control. control. agricultural-entomology

123. Quantitative assessment of improved rice variety adoption: the farmer's perspective

Source: Agricultural Systems. 2000. 66 (2). 129-144

Author(s): Sall-S. Norman-D. Featherstone-A-M

Abstract:

Using data collected from 400 farming households in the Casamance area of Senegal, the paper demonstrates that not only farm and farmers' characteristics, but also farmers' perceptions of technology-specific characteristics, significantly influence adoption decisions relating to improved rice varieties. Farmers' perceptions about improved rice varieties were quantified using a quasi-arbitrary ordinal weighting system, based on a methodology first used in industry. The results of Tobit regression analysis including variables representing both farmers' perceptions, as well as farm and farmer characteristics, were found to be important in determining the decision to adopt and the intensity of adoption of the improved rice varieties. It is concluded that it is important for farmers, with the help of on-farm interdisciplinary farming systems teams, to provide an input into the rice breeding programme of the Senegal Agricultural Research Institute during the process of rice variety development, rather than only having an opportunity to evaluate the varieties at the end of the research cycle. It is argued that quantifying farmers' perceptions in the manner suggested in the paper potentially makes them more palatable to station-based researchers used to cardinal types of analysis. The findings also provide support for the farmer participatory crop breeding programmes that have become popular in recent years in both international and national research systems

Descriptors:Rice. Varieties. Innovation-adoption. Farmers'-attitudes. Decision-making. Research. Plant-breeding. Farmers. Participation

124. Improved rice variety adoption and its welfare impact on rural farming households in Akwa Ibom State of Nigeria

Source: Journal of New Seeds. 2008. 9 (2). 156-173

Author(s): Udoh-E-S. Omonona-B-T

Abstract:

In this study cross-sectional data from 200 rice farmers were used to examine the various factors that influence the adoption of improved rice varieties distributed by the State Agricultural Development Programme (AKADEP) and its welfare impact on the farmers. The Foster, Greer and Thorbecke (FGT) class of measures was used to determine the incidence, the depth and severity of poverty among rice farming households who are adopters and non-adopters of improved rice varieties. The incidence, depth, and severity of poverty were higher among households who were non-adopters of improved rice varieties. The Tobit regression model was used to determine the factors that affect adoption and poverty. Educational attainment, access to extension agents, access to credit, access to augmented inputs, farm size, and crop yield were significant determinants of adoption of improved rice varieties. The results of the determinants of household poverty revealed that age, educational attainment, extent of commercialization and probability of adoption negatively influenced household poverty, whereas household size exerted a positive impact on the household poverty levels. The negative impact of adoption of improved rice varieties on household poverty implicitly showed improvement in households' welfare that had adopted improved rice varieties. These results generally suggest the relevance of adoption of improved rice varieties in improving the welfare of rice farming households. It also suggests relevance of human capital indices like education and extension services as drivers of poverty alleviation and dissemination of new innovations to farming households

Descriptors: **Academic-achievement. Age. Commercialization. Crop-yield. Cultivars. Extension. Farm-inputs. Farm-size. Genetic-improvement. Households. Innovation-adoption. Poverty. Rice. Rural-communities. Welfare-economics**

125. Isolation and 16S rRNA sequence analysis of the beneficial bacteria from the rhizosphere of rice

Source: Canadian Journal of Microbiology. 2001. 47 (2). 110-117

Author(s): Mehnaz-Samina. Mirza-M-Sajjad. Haurat-Jacqueline. Bally-Rene. Normand-Philippe. Bano-Asghari. Malik-Kauser-A

Abstract:

The present study deals with the isolation of plant growth promoting rhizobacteria (PGPR) from rice (variety NIAB IRRI-9) and the beneficial effects of these inoculants on two Basmati rice varieties. Nitrogen-fixing activity (acetylene-reduction activity) was detected in the roots and submerged shoots of field-grown rice variety NIAB IRRI-9. Estimation of the population size of diazotrophic bacteria by ARA-based MPN (acetylene reduction assay- based most probable number) in roots and shoots indicated about 105- 106 counts/g dry weight at panicle initiation and grain filling stages. Four bacterial isolates from rice roots and shoots were obtained in pure culture which produced phytohormone indoleacetic acid (IAA) in the growth medium. Among these, three isolates S1, S4, and R3 reduced acetylene to ethylene in nitrogen-free semi- solid medium. Morphological and physiological characteristics of the isolates indicated that three nitrogen-fixing isolates S1, S4, and R3 belonged to the genus Enterobacter, while the non-fixing isolate R8 belonged to the genus Aeromonas. 16S rRNA sequence of one isolate from root (R8) and one isolate from shoot (S1) was obtained which confirmed identification of the isolates as Aeromonas veronii and Enterobacter cloacae, respectively. The 1517- nucleotide-long sequence of the isolate R8 showed 99% similarity with Aeromonas veronii (accession No. AF099023) while partial 16S rRNA sequence (two stretches of total 1271 nucleotide length) of S1 showed 97% similarity with the sequence of Enterobacter cloacae (accession No. AJ251469). The seedlings of two rice varieties Basmati 385 and Super Basmati were inoculated with the four bacterial isolates from rice and one Azospirillum brasilense strain Wb3, which was isolated from wheat. In the rice variety Basmati 385, maximum increase in root area and plant biomass was obtained in plants inoculated with Enterobacter S1 and Azospirillum Wb3, whereas in the rice variety Super Basmati, inoculation with Enterobacter R3 resulted in maximum increase of root area and plant biomass. Nitrogen fixation was quantified by using 15N isotopic dilution method. Maximum fixation was observed in Basmati 385 with the inoculants Azospirillum Wb3 and Enterobacter S1 where nearly 46% and 41% of the nitrogen was derived from atmosphere (%Ndfa), respectively. In general, higher nitrogen fixation was observed in variety Basmati 385 than in Super Basmati, and different bacterial strains were found more effective as inoculants for the rice varieties Basmati 385 and Super Basmati

Descriptors:Bacterial populations; nitrogen fixation; plant biomass; soil microbiology; soils. Molecular Genetics (Biochemistry and Molecular Biophysics); Microbiology; Soil Science. Phytohormones; rrna [ribosomal RNA]: sequencing

126. Major gene, nonallelic sheath blight resistance from the rice cultivars Jasmine 85 and Teqing

Source: Crop Science. 1999. 39 (2). 338-346

Author(s): Pan-X-B. Rush-M-C. Sha-X-Y. Xie-Q-J. Linscombe-S-D. Stetina-S-R. Oard-

Abstract:

Only partial resistance is available for sheath blight (Rhizoctonia solani), the second most important disease of rice (Oryza sativa) worldwide. This partial resistance has been considered to be polygenic. The partial resistance of the cultivars Jasmine 85 and Teqing was studied by evaluating the resistance of F1, F2, F3, F4 and backcross F1 generations of crosses between the resistant parents and the susceptible cultivars Maybelle and Cypress. F1 plants from the crosses were resistant. Segregating F2 populations from both crosses showed ratios of 3:1 resistant/susceptible plants. Segregating backcross F1 populations showed a ratio of 1:1 resistant/susceptible plants when the F1 was crossed to a susceptible parent and no segregation occurred when the F1 was crossed to a resistant parent. These results were consistent with the partial resistance from the two resistant cultivars being controlled by single dominant genes. When the resistant cultivars were crossed, the segregating F2 population showed a 15:1 resistant/susceptible ratio, suggesting that the two resistant parents each possessed a nonallelic dominant major resistance gene that segregated independently. Some of the F4 lines from this cross appeared to have both resistance genes and a higher level of resistance than either resistant parent. This suggests that major genes conferring high levels of partial resistance to sheath blight may be incorporated together into lines to give near complete resistance. This makes the identification of major genes for partial resistance to sheath blight critically important to rice breeding programmes

Descriptors:Rice. Genes. Plant-pathogens. Plant-diseases. Disease-resistance. Plant- pathogenic-fungi. Segregation. Genetics. Cereals

127. Agrobacterium tumefaciens-mediated transformation of rice (Oryza sativa L. ssp. japonica) Italian cultivars. 1. Interaction among Agrobacterium strains and rice genotypes in embryogenic callus of somatic and gametic origin

Source: Journal of Genetics & Breeding. 1998. 52 (4). 313-323

Author(s): Balconi-C. Perugini-I. Castelletti-S. Reali-A. Russo-S. Chan-M-T.

Abstract:

The purpose of the present research was to establish a routine procedure for Agrobacterium tumefaciens-mediated transformation of important Italian rice cultivars (Oryza sativa ssp. japonica). A detailed investigation on in vitro culture, plant regeneration and susceptibility to infection from various strains of Agrobacterium tumefaciens was performed. Twenty-six genetically differentiated rice cultivars, chosen for outstanding grain quality and agronomical characters, were established as tissue cultures from somatic and gametic cells. Regenerative callus cultures were obtained from both mature and immature embryos, and from microspores through anther culture. Highly responsive varieties to tissue culture and plant regeneration were identified. Several genotypes showed high embryogenic callus induction frequency which was genetically determined. The interaction between the callus systems and different Agrobacterium tumefaciens strains characterized by different chromosomal background and Ti-plasmid content was subsequently investigated. Five Agrobacterium tumefaciens strains, all carrying the marker cassette -INTGUS- for early detection of transformation, were co-cultivated with rice tissues in the presence of acetosyringone according to standard procedures. The tissues were histochemically stained for GUS activity and evaluated using a visual scoring scale. In all cases a good combination Agrobacterium x rice genotype was identified, and the interaction was genotype-dependent. In some cases the combination explored gave a very high rating of transient expression, thus confirming the reliability of the system for transformation of the genotypes considered. Good combination Agrobacterium x rice genotypes were found for both somatic and gametic systems and, in several cases, the combination efficiency for an Agrobacterium strain was different depending on the cell system. In most cases, the infection process did not hamper the subsequent capability of the rice cultures to promote plant regeneration. These indications are of major interest for the identification of key parameters in the establishment of efficient routine procedures for Agrobacterium tumefaciens-mediated genetic transformation of Italian rice cultivars

DURIAN

1. **Durian: a key fruit in Southeast Asia**
   Source: Fruits. 1997. 52 (1). 47-57
   Author(s): Vilcosqui-L. Dury-S
   Abstract:
   In Southeast Asia, durians are grown traditionally in monospecific orchards of improved cultivars. Sexually-propagated plants have a wide range of qualities; they can be multiplied by grafting and suckering. Wild species should be added to current collections, for potential hybridizations, as rootstocks, and to establish a pool of resistance genes. Germination is quick and easy. Depending on cultivar, the juvenile phase lasts 5-13 years. Trees yield fruits for 30 (improved cultivars) to 150 years (traditional cultivars). Fruits are harvested 95-130 days after flowering. Durian trees are attacked by a root fungus (Phytophthora palmivora), a larval parasite that lives between the bark and wood, and by some fruit predators. Durian trees are biennial bearing. Ripe-picked fruits can be stored in ambient temperature for 4 days, and for 3 weeks at 15 deg C. In 1990, Indonesia was the second-ranking world durian producer after Thailand. Since 1993, Indonesia has reduced its exports and quadrupled its imports. To fulfil domestic demand, efficient cultivars should be cropped using advanced techniques
   Descriptors:Production. Fruits. Durians. Cultural-methods. Cultivars. Genetic-resources. Plant-breeding. Rootstocks. Seed-germination. Growth. Plant-development. Harvesting. Flowering. Plant-pests. Plant-diseases. Insect-pests. Plant-pathogens. Bark. Wood. Ripening. Storage. Multipurpose-trees. Tropical-crops. Fruit-crops. Agricultural-entomology

2. **Characterisation of Malaysian durian (Durio zibethinus Murr.) cultivars: relationship of physicochemical and flavour properties with sensory properties**
   Source: Food Chemistry. 2007. 103 (4). 1217-1227
   Author(s): Voon-Y-Y. Abdul-Hamid-N-S. Rusul-G. Osman-A. Quek-S-Y
   Abstract:
   The physicochemical (pH, soluble solids, titratable acidity, sugars and organic acids), flavour and sensory properties of five Malaysian durian cultivars (D2, D24, MDUR78, D101 and Chuk) were studied. There were significant differences ($P<0.05$) among the five cultivars in terms of all physicochemical characteristics tested with the exception for D2 and MDUR 78, which had similar physicochemical characteristics. Twenty two esters, 14 sulphur compounds, 7 alcohols, 3 aldehydes and 1 ketone were detected in the durian pulp of the five different cultivars using solid-phase microextraction coupled to gas chromatography-time of flight mass spectrometry. Diethyl disulphide, ethyl-n-propyl disulphide, diethyl trisulphide and ethanethiol were the predominant sulphur-containing compounds in all the cultivars. The major esters present in durian were either ethyl propanoate, ethyl-2-methyl butanoate, or propyl-2-methylbutanoate and their levels varied within cultivars. Principal component

analysis applied to the data differentiated all cultivars based on 29 volatile flavour compounds exhibiting significant differences ($P<0.05$) between cultivars. Principal components 1 and 2 explained 89% of the total variance. A strong correlation was observed between sensory properties with flavour compound and physicochemical characteristics of the fruit

Descriptors:Aldehydes. Cultivars. Durians. Flavour. Ketones. Organic-acids. Organoleptic-traits. Ph. Physicochemical-properties. Sugars. Sulfur. Titratable-acidity

3. **Durian flowering, pollination and incompatibility studies**

Source: Annals of Applied Biology. 1998. 132 (1). 151-165

Author(s): Lim-T-K. Luders-L

Abstract

Seasonal fluctuations in weather conditions influenced flowering and fruiting and reproduction of durians grown in Darwin, Australia. Manually assisted cross-pollination resulted in fruit set of 31%, compared with <10% obtained by selfing. This resulted in higher yields and better quality fruits. Self-pollination resulted in greater fruit abortion and misshaped fruits, with lower numbers of arils/locule and arils/fruit, and lower numbers of seeds which were usually shrunken and dysfunctional. It is suggested that the self-incompatibility system in durians is gametophytically controlled, and that cultivars could be totally self-incompatible, partially self-incompatible or totally compatible. Durian pollen exerted metaxenic effects influencing fruit characteristics, and exerted xenic effects on seeds

Descriptors:Pollination. Xenia. Flowering. Pollen. Incompatibility. Self-pollination. Fruits. Yields. Durians. Flowers. Set. Seeds. Quality. Fruit-set. Tropical-crops. Fruit-crops

4. **Patch canker of Durio zibethinus caused by Phytophthora palmivora in Brunei Darussalam**

Source: Plant Disease. 1997. 81 (1). 113

Author(s): Sivapalan-A. Hamdan-F-H. Junaidy-M-A-H-M

Abstract:

A stem canker was found on many durian (D. zibethinus) trees in an orchard in Sungai Liang, Brunei Darussalam. This disease, commonly known as patch canker, is widespread in other countries in Southeast Asia. Disease symptoms of the trunk, branches and tree canopy are described. Cultures of a single fungus derived from infected bark and canker margins were grown on potato dextrose agar and tap water agar. The fungus was identified as P. palmivora. This is the first published report of patch canker of durian caused by P. palmivora in Brunei Darussalam

Descriptors:Plant-diseases. Plant-pathogens. Plant-pathogenic-fungi. Durians. Multipurpose-trees. Cankers. Fungal-diseases. Fruit-crops. Plant-pathology

KENTANG

1. **Specific detection of the Andean strain of potato virus S by monoclonal antibodies**

   Source: Annals of Applied Biology. 1995. 127 (1). 87-93

   Author(s): Cerovska-N. Filigarova-M

   Abstract:

   Four mouse monoclonal antibodies (MAbs) specific for the Andean strain of potato S carlavirus (PVSA) were produced. The MAbs reacted with 4 isolates of PVSA but did not react with 4 isolates of ordinary strain of PVS (PVSO). The MAbs did not react with 6 other members of the carlavirus group including potato M carlavirus. A MAb-based ELISA, using MAbs (IEB-1 and IEB-4-AP), was devised and shown to specifically detect PVSA

   Descriptors:Plant-diseases. Plant-pathogens. Monoclonal-antibodies. Potatoes. Detection. Techniques. Immunodiagnosis. Diseases. Root-crops. Plant-pathology

2. **Comparison of resistance to potyviruses within Solanaceae: infection of potatoes with tobacco etch potyvirus and peppers with potato A and Y potyviruses**

   Source: Annals of Applied Biology. 1996. 129 (1). 25-38

   Author(s): Valkonen-J-P-T. Kyle-M-M. Slack-S-A

   Abstract:

   The reaction of several cultivated potato varieties to 3 strains of tobacco etch potyvirus (TEV-F, TEV-Mex21 and TEV-ATCC) and the reaction of several Capsicum lines (C. annuum and C. chinense) to 2 strains of potato Y potyvirus (PYVO and PYVN) and 1 strain of potato A potyvirus (PAV-M) was tested. The potato varieties included in this study carried resistance genes against PYV, PAV and potato V potyvirus, but all were susceptible to TEV and developed mottle and mosaic symptoms. TEV was readily transmitted by mechanical inoculation from tobacco and potato to potato, whereas transmission from Capsicum to potato rarely occurred. TEV was transmitted through potato tubers and from Capsicum to potato plants by aphids. Lack of detectable systemic infection following graft-inoculation indicated extreme resistance to PYVO and PAV in several Capsicum lines. No Capsicum line was systemically infected with PYVN following mechanical inoculation (graft-inoculation was not carried out with PYVN). The development of necrotic lesions following mechanical and graft inoculation suggested a hypersensitive response to PYVO in several Capsicum lines which resembled the resistance responses to these potyvirus strains in potato. It is suggested that C. annuum cv. Avelar is resistant to 4 potyviruses (PYV, PAV, pepper mottle potyvirus (PepMoV) and some isolates of TEV); C. annuum cv. Criollo de Morelos and C. chinense PI 152225 and PI 159236 were resistant to 3 potyviruses (PYV, PepMoV and PAV; and PYV, PepMoV and TEV, respectively); C. annuum 9093-1 and 92016-1 were resistant to PYV and PepMoV; and C. annuum cv. Jupiter and C. annuum cv. RNaky were resistant to PYVN and PAV

Descriptors: Plant-diseases. Plant-pathogens. Plant-disease-control. Disease-resistance. Disease-transmission. Varietal-reactions. Potatoes. Transmission. Diseases. Cultivars. Root-crops. Vegetables. Plant-pathology

3. **The occurrence of PVYO, PVYN, and PVYN:O strains of Potato virus Y in certified potato seed lot trials in Washington and Oregon**

   Source: Plant Disease. 2006. 90 (8). 1102-1105

   Author(s): Crosslin-J-M. Hamm-P-B. Hane-D-C. Jaeger-J. Brown-C-R. Shiel-P-J. Berger-P-H. Thornton-R-E

   Abstract:

   Totals of 960 and 286 certified potato seed lots from locations across North America were planted in trials in Washington and Oregon, respectively, in 2001 to 2003 and tested for strains of Potato virus Y (PVY). The incidence of PVYO-infected lots averaged 16.4 and 25.9% in the Washington and Oregon trials, respectively. There was a general trend of increasing incidence of the PVYO, PVYN:O, and PVYN strains during this period, as evidenced by more infected cultivars, sites of seed origin, and number of seed growers providing infected seed lots. In particular, there was a dramatic increase in seed lots with the PVYN:O strain from 2002 to 2003. PVYN:O, in contrast to PVYO, which only causes yield reduction, also causes internal and external damage to tubers, making them unmarketable. In 2003, PVYN:O occurred in seed lots originating in eight states and three Canadian provinces. The increased incidence of PVYN:O was likely due to the difficulty in differentiating this strain from PVYO. The prevalence of PVY in potato seed lots documented herein poses a threat to potato production in the United States and suggests that current measures to reduce the incidence of this virus are inadequate

   Descriptors: Crop-yield. Plant-diseases. Plant-pathogens. Plant-viruses. Potatoes

   Countries

4. **Marker-assisted selection for the broad-spectrum potato late blight resistance conferred by gene RB derived from a wild potato species**

   Source: Crop Science. 2006. 46 (2). 589-594

   Author(s): Colton-L-M. Groza-H-I. Wielgus-S-M. Jiang-J-M

   Abstract:

   Potato (Solanum tuberosum L.) late blight, caused by Phytophthora infestans (Mont.) de Bary, is one of the most damaging diseases in any crop. Deployment of resistant varieties is the most effective way to control this disease. However, breeding for late blight resistance has been a challenge because the race-specific resistance genes introgressed from wild potato S. demissum Lindl. have been short lived and breeding for "horizontal" or durable resistance has achieved only moderate successes. We previously demonstrated that the high-level late blight resistance in a wild potato relative, S. bulbocastanum Dunal subsp. bulbocastanum, is mainly controlled by a single resistance gene RB. Transgenic potato lines containing the RB gene have showed strong late blight resistance, comparable to the backcrossed progenies derived from the somatic hybrids between potato and S. bulbocastanum. Here we report the development of a polymerase chain reaction-based DNA marker for tracking the RB gene in breeding populations derived from the potato x S. bulbocastanum somatic hybrids. Several marker-positive breeding lines showed the expected late blight resistance in greenhouse evaluations. Our results demonstrate that marker-based selection will allow us to effectively transfer the RB gene into potato using traditional breeding methods, an alternative to deploying the RB gene through genetic transformation

Descriptors: artificial-selection. disease-resistance. fungal-diseases. gene-transfer. genes. genetic-markers. plant-diseases. plant-pathogenic-fungi. plant-pathogens. polymerase-chain-reaction. potatoes. somatic-hybridization. wild-relatives

5. **Recruitment of adult Colorado potato beetles in Bt-transgenic potato fields**

Source: American Journal of Potato Research. 2005. 82 (5). 379-387

Author(s): Boiteau-G

Abstract:

A refuge of conventional potato plants adjacent to Colorado potato beetle (CPB), Leptinotarsa decemlineata (Say)-resistant, Bt-potato (transgenic) plants may reduce opportunity for the development of tolerance to the resistant plants. The refuge strategy was developed on the basis of data available for CPB recruitment in conventional potato fields. This study was undertaken to provide information on CPB recruitment in Bt-transgenic potato fields. A marking experiment was conducted over the 2000 and 2001 crop seasons to determine the relative contributions of beetle populations from fields 10 m, 175 to 300 m, and 1200 to 1280 m distant to the pattern of CPB recruitment (immigration) in a Bt-potato field. Season-long CPB recruitment in the Bt-potato field decreased with source distance in a manner similar to that previously reported in conventional potato fields. Although marked beetles from the 10-m field plot contributed more to the recruitment than the more distant fields, they contributed only 3.3%, and 6.6% of the total beetle sightings in the Bt-potato field. Therefore, results suggest that a larger acreage of conventional potato fields at some distance from the resistant crop could replace the adjacent designated refuge. Seasonally, beetles from the overwintering sites provided the first recruits to the resistant field. As their contribution declined, the overwintered beetles from the refuge were recruited until the beginning of the summer population. These results suggest that locating the resistant fields close to active overwintering sites will improve the probability that the refuge strategy will be effective by ensuring the presence of recruits at the very beginning of the crop season. The substantially lower recruitment level obtained for summer than for over-wintered CPB in resistant and conventional potato fields highlights the need to reconsider the applicability of the refuge strategy for the summer population

Descriptors: insect-pests. migration. plant-pests. population-dynamics. potatoes. transgenic-plants

6. **Transgenic potato expressing A beta reduce A beta burden in Alzheimer's disease mouse model**

Source: FEBS Letters. 2005. 579 (30). 6737-6744

Author(s): Youm-JungWon. Kim-Hee. Han-J-H-L. Jang-ChangHwan. Ha-HeeJin. Mook-Jung-InHee. Jeon-JaeHeung. Choi-CheolYong. Kim-YoungHo. Kim-HyunSoon. Joung-Hyouk

Abstract:

Beta amyloid (A beta) is believed one of the major pathogens of Alzheimer's disease (AD), and the reduction of A beta is considered a primary therapeutic target. Immunization with A beta can reduce A beta burden and pathological features in transgenic AD model mice. Transgenic potato plants were made using genes encoding 5 tandem repeats of A beta 1-42 peptides with an ER retention signal. Amyloid precursor protein transgenic mice (Tg2576) fed with transgenic potato tubers with adjuvant showed a primary immune response and a partial reduction of A beta burden in the brain. Thus, A beta tandem repeats can be expressed in transgenic potato plants to form immunologically functional A beta, and these potatoes has a potential to be used for the prevention and treatment of AD

Descriptors:

7. **Performance of transgenic potato containing the late blight resistance gene RB**

Source: Plant Disease. 2008. 92 (3). 339-343

Author(s): Halterman-D-A. Kramer-L-C. Wielgus-S. Jiang-J-M

Abstract:

Late blight of potato, caused by Phytophthora infestans, is one of the most devastating diseases of potato. A major late blight resistance gene, called RB, previously was identified in the wild potato species Solanum bulbocastanum through map-based cloning. The full-length gene coding sequence, including the open reading frame and promoter, has been integrated into cultivated potato (S. tuberosum) using Agrobacterium-mediated transformation. RB-containing transgenic plants were challenged with P. infestans under optimal late blight conditions in greenhouse experiments. All transgenic lines containing RB exhibited strong foliar resistance. Field-grown transgenic tubers also were tested for resistance to P. infestans. In contrast to the foliar resistance phenotype, RB-containing tubers did not exhibit increased resistance. Two years of field trials were used to ascertain whether the presence of RB had any effect on tuber yield. We were unable to detect any significant effect on tuber size or yield after addition of the resistance gene to several S. tuberosum cultivars

Descriptors: **DNA-cloning. fungal-diseases. genes. genetic-mapping. genetic-resistance. genetic-transformation. open-reading-frames. phenotypes. plant-diseases. plant-pathogenic-fungi. plant-pathogens. potatoes. transgenic-plants. wild-relatives**

KENTANG TRANSGENIK

8. **Age-specific bioassays and fecundity of Phthorimaea operculella (Lepidoptera: Gelechiidae) reared on cry1Ac -transgenic potato plants**

   Source: Annals of Applied Biology. 2005. 146 (4). 493-499

   Author(s): Davidson-M-M. Butler-R-C. Wratten-S-D. Conner-A-J

   Abstract:

   Variation in the susceptibility of lepidopterous pest larvae of different ages to transgenic crops and the potential for survivors to reproduce could have important consequences for the development of resistance in such pests. Experiments were undertaken in the laboratory to determine if larvae of the potato tuber moth, Phthorimaea operculella, of different ages (0 (<1 day old), 3, 5, 7 days) varied in their susceptibility to cry1Ac9-transgenic potato (Solanum tuberosum) foliage grown in the glasshouse or field. The survival and fecundity of larvae reared on transgenic tubers was also determined in the laboratory. There were no apparent differences in susceptibility of larvae of different ages to transgenic foliage. Larvae fed glasshouse or field-grown non-transgenic foliage had significantly larger relative growth indices and more larvae pupated, than those fed transgenic foliage, regardless of larval age. Eggs from a laboratory colony were placed on transgenic or non-transgenic tubers to measure survival and fecundity. Between 6% and 15% of eggs placed on transgenic tubers developed into pupae for three of the four transgenic potato lines tested. On one transgenic line, only six adults emerged from 1300 eggs. In contrast, between 71% and 97% of the eggs placed on non-transgenic tubers developed into pupae. Male and female pupae from transgenic lines weighed less than those from non-transgenic lines. The fecundity of females from two of four transgenic lines was lower than from the non-transgenic parent cultivar. Although larvae of different ages did not exhibit any overall age-dependent pattern of increasing or decreasing susceptibility to transgenic foliage of glasshouse or field-grown plants, the ability of larvae to survive and reproduce on transgenic tubers suggests this pest has the ability to evolve resistance to the transgenic plants used in the present study

   Descriptors: **age. Eclosion. Fecundity. Genetic-resistance. Insect-pests. Pest-resistance. Plant-pests. Potatoes. Survival. Susceptibility. Transgenic-plants**

9. **Resistance of potatoes transgenic for a cry1Ac9 gene, to Phthorimaea operculella (Lepidoptera: Gelechiidae) over field seasons and between plant organs**

   Source: Annals of Applied Biology. 2004. 145 (3). 271-277

   Author(s): Davidson-M-M. Butler-R-C. Wratten-S-D. Conner-A-J

Abstract:

Stable performance of insect-resistant transgenic plants across field seasons and between plant organs damaged by the insect pest is critical for management of this resistance in the field. To evaluate this, potato (Solanum tuberosum) lines transgenic for a cry1Ac9 gene with resistance to potato tuber moth (Phthorimaea operculella) were established in the field during the southern hemisphere summers of 1997/98, 1998/99 and 1999/00 as small field plots, each of 10 plants. Replicate plots of the non-transgenic parent cultivars (at least one for every three independently derived transgenic lines) were planted randomly throughout the trials. Field-grown foliage was challenged with larvae in the laboratory and a growth index (GI) was calculated for recovered larvae from each transgenic and non-transgenic potato line. Larval growth on young and mature leaves, and on newly harvested or stored tubers was also measured in the laboratory. Foliage from the transgenic lines inhibited larval growth in all seasons tested. For both control and transgenic lines, larvae had slightly lower GIs when reared on mature leaves compared with young leaves, although the correlation between mean GI for young and mature transgenic leaves was high (r=0.97). The correlation between the mean GIs of larvae on newly harvested tubers and on those stored for 5 months was also high (r=1.0). However, the GIs of larvae on newly harvested transgenic tubers were larger than on transgenic tubers stored for 5 months. The relative growth indices (RGI=mean GI/number days before final weighing) of larvae reared on newly harvested tubers from transgenic lines were generally higher than those from young transgenic foliage, while the RGIs of larvae reared on non-transgenic tubers were slightly lower than those fed non-transgenic foliage. The correlation between mean RGIs of larvae fed tubers or foliage was 0.62. The transgenic potato lines exhibited stable resistance to larvae across field seasons, between affected plant organs, and between plant organs of different ages

Descriptors:Growth. Insect-pests. Larvae. Pest-resistance. Plant-organs. Plant-pests. Potatoes. Seasons. Transgenic-plants

10. Recruitment of adult Colorado potato beetles in Bt-transgenic potato fields

Source: American Journal of Potato Research. 2005. 82 (5). 379-387

Author(s): Boiteau-G

Abstract:

A refuge of conventional potato plants adjacent to Colorado potato beetle (CPB), Leptinotarsa decemlineata (Say)-resistant, Bt-potato (transgenic) plants may reduce opportunity for the development of tolerance to the resistant plants. The refuge strategy was developed on the basis of data available for CPB recruitment in conventional potato fields. This study was undertaken to provide information on CPB recruitment in Bt-transgenic potato fields. A marking experiment was conducted over the 2000 and 2001 crop seasons to determine the relative contributions of beetle populations from fields 10 m, 175 to 300 m, and 1200 to 1280 m distant to the pattern of CPB recruitment (immigration) in a Bt-potato field. Season-long CPB recruitment in the Bt-potato field decreased with source distance in a manner similar to that previously reported in conventional potato fields. Although marked beetles from the 10-m field plot contributed more to the recruitment than the more distant fields, they contributed only 3.3%, and 6.6% of the total beetle sightings in the Bt-potato field. Therefore, results suggest that a larger acreage of conventional potato fields at some distance from the resistant crop could replace the adjacent designated refuge. Seasonally, beetles from the overwintering sites provided the first recruits to the resistant field. As their contribution declined, the overwintered beetles from the refuge were recruited until the beginning of the summer population. These results suggest that locating the resistant fields close to active overwintering sites will improve the probability that the refuge strategy will be effective by ensuring the presence of recruits at the very beginning of the crop season. The substantially lower recruitment level obtained for summer than for over-wintered CPB in resistant and conventional potato fields highlights the need to reconsider the applicability of the refuge strategy for the summer population

Descriptors:Iinsect-pests. Migration. Plant-pests. Population-dynamics. Potatoes. Transgenic-plants

11. **Feeding behaviour and reproductive biology of Colorado potato beetle adults fed transgenic potatoes expressing the Bacillus thuringiensis Cry3B endotoxin**

Source: Entomologia Experimentalis et Applicata. 2000. 95 (1). 31-37

Author(s): Arpaia-S. Marzo-L-de. Leo-G-M-di. Santoro-M-E. Mennella-G. Loon-J-J-A-

Abstract:

Colorado potato beetle (Leptinotarsa decemlineata Say) adult longevity and fecundity were studied on transgenic potato clones expressing a Cry3B endotoxin of Bacillus thuringiensis (Bt). Adult longevity and fitness were studied for the first 3 weeks after emergence. Beetle reproductive biology on highly resistant clones, intermediary resistant clones and control potato plants was monitored by dissecting females after 7-15 days of feeding and also by analysing haemolymph protein content after 3 days of feeding. Feeding behaviour on transgenic plants expressing high toxin concentrations and on control plants was monitored individually for 36 newly emerged adult beetles feeding on leaf disks during the first two meals. Lethal Time50 for adult beetles feeding on transgenic clones as the sole source of food was not significantly shorter than for beetles on control clones reared in a growth chamber. Differences tended to be larger when the experiment was conducted in a greenhouse with a less optimal temperature range (LT50=9.52 and 10.45 days for two transgenic clones and 13.86 for control). In contrast, female egg production on transgenic plants was almost totally inhibited. Dissection studies indicated that adult males living on high-level Bt-expressing transgenic potatoes were still able to mate and produce mobile sperm, but the females were impaired in their reproductive ability since their ovaries were generally not fully developed. An examination of the haemolymph revealed the protein concentration in females living on transgenic plants to be dramatically reduced (approx equal to 50%), and electrophoresis showed a reduced content of vitellogenin in these samples. Feeding behaviour of adult

Colorado potato beetles was not affected by the different food plants; this indicates that transgenic potato plants were readily accepted as host plants by beetles. The effects of these findings on the use of transgenic plants as a means of L. decemlineata control are discussed

Descriptors: **Endotoxins. potatoes. transgenics. clones. electrophoresis. fecundity. feeding. feeding-behaviour. fitness. food-plants. host-plants. longevity. toxins. transgenic-plants. gene-expression. animal-behaviour. agricultural-entomology**

12. Transgenic Bt potato and conventional insecticides for Colorado potato beetle management: comparative efficacy and non-target impacts

Source: Entomologia Experimentalis et Applicata. 2001. 100 (1). 89-100

Author(s): Reed-G-L. Jensen-A-S. Riebe-J. Head-G. Duan-J-J

Abstract:

Field studies were conducted in 1992 and 1993 in Hermiston, Oregon, USA, to evaluate the efficacy of transgenic Bt potato (Newleaf, which expresses the insecticidal protein Cry3Aa) and conventional insecticide spray programmes against the important potato pest, Leptinotarsa decemlineata (Say), Colorado potato beetle (CPB), and their relative impact on non-target arthropods in potato ecosystems. Results from the two years of field trials demonstrated that Newleaf potato plants were highly effective in suppressing populations of CPB, and provided better CPB control than weekly sprays of a microbial Bt-based formulation containing Cry3Aa, bi-weekly applications of permethrin, or early- and mid-season applications of systemic insecticides (phorate and disulfoton). When compared with conventional potato plants not treated with any insecticides, the effective control of CPB by Newleaf potato plants or weekly sprays of a Bt-based formulation did not significantly impact the abundance of beneficial predators or secondary potato pests. In contrast to Newleaf potato plants or microbial Bt formulations, however, bi-weekly applications of permethrin significantly reduced the abundance of several major generalist predators such as spiders (Araneae), big-eyed bugs (Geocorus sp.), damsel bugs (Nabid sp.), and minute pirate bugs (Orius sp.), and resulted in significant increases in the abundance of green peach aphid (GPA), Myzus persicae - vector of viral diseases, on the treated potato plots. While systemic insecticides appeared to have reduced the abundance of some plant sap-feeding insects such as GPA, lygus bugs, and leafhoppers, early and mid-season applications of these insecticides had no significant impact on populations of the major beneficial predators. Thus, transgenic Bt potato, Bt-based microbial formulations and systemic insecticides appeared to be compatible with the development of integrated pest management (IPM) against other potato pests such as GPA because these CPB control measures have little impact on major natural enemies. In contrast, the broad-spectrum pyrethroid insecticide (permethrin) is less compatible with IPM programmes against GPA and the potato leafroll viral disease

Descriptors: **Bacterial-insecticides. Beneficial-organisms. Biological-control-agents. Chemical-control. Disease-vectors. Disulfoton.**

Genetic-control. Insect-control. Insect-pests. Integrated-control. Natural-enemies. Nontarget-effects. Nontarget-organisms. Pathogens. Permethrin. Pest-control. Phorate. Plant-pests. Potatoes. Predators. Transgenic-plants

13. **Modifications in dispersal and oviposition of Bt-resistant and Bt-susceptible Colorado potato beetles as a result of exposure to Bacillus thuringiensis subsp. tenebrionis Cry3A toxin**

Source: Entomologia Experimentalis et Applicata. 1999. 90 (1). 93-101

Author(s): Alyokhin-A-V. Ferro-D-N

Abstract:

Laboratory strains of Colorado potato beetle, Leptinotarsa decemlineata, physiologically resistant and susceptible to Bacillus thuringiensis subsp. tenebrionis Cry3A toxin were reared to adults on caged potato plants. Influence of three different diets (transgenic potatoes, regular potatoes, and regular potatoes followed by the transgenic potatoes) on beetle mortality, fecundity, and flight behaviour were tested under laboratory conditions. A computer-linked flight mill system was used to quantify beetle flight, and dissections were performed to determine the level of flight muscle development. Susceptible beetles continuously fed on transgenic foliage suffered heavy mortality, did not develop flight muscles, and did not produce any eggs. Resistant beetles continuously fed on transgenic foliage were capable of flight and reproduction; however, it took them longer to initiate flight behaviour, and their fecundity was lower than fecundity of other treatments. In both strains, detrimental effects became significantly less severe when the beetles were allowed to feed on regular foliage prior to toxin ingestion. In the resistant strain, ingestion of Cry3A toxin significantly increased flight activity, indicating that physiological resistance was probably reinforced by the behavioural escape from toxic environments. No such response was observed for susceptible beetles. When fed on regular foliage, resistant Colorado potato beetles engaged in significantly fewer flights than susceptible beetles. Behavioural differences between resistant and susceptible beetles observed in the present study are likely to affect gene flow between transgenic crops and adjacent refugia, and should be taken in consideration when designing resistance management plans for transgenic potato crops

Descriptors:P**otatoes. Flight. Mortality. Fecundity. Plant-pests. Insect-pests. Entomopathogenic-bacteria. Bacterial-toxins. Transgenic-plants. Pest-resistance. Bacterial-insecticides. Insecticide-resistance. Oviposition. Dispersal. Root-crops. Biology. Pest-control. Control. Agricultural-entomology**

14. **High-level expression of apple PGIP1 is not sufficient to protect transgenic potato against Verticillium dahliae**

Source: Physiological and Molecular Plant Pathology. 2004. 65 (3). 145-155

Author(s): Gazendam-I. Oelofse-D. Berger-D-K

Abstract:

Polygalacturonase-inhibiting proteins (PGIPs) are plant proteins believed to play a role in the defence against pathogenic fungi. Purified apple PGIP1 inhibited polygalacturonases (PGs) secreted by Verticillium dahliae grown on potato root cell walls and pectin. We therefore hypothesised that apple PGIP1 could be used to confer resistance against Verticillium-wilt, a major disease of potato caused by the fungus V. dahliae. Transgenic lines containing the apple pgip1 gene under control of the enhanced CaMV 35S (e35S) promoter were generated. Stable integration of the apple pgip1 transgene into the potato genome was shown by the polymerase chain reaction (PCR) and Southern blot. Cross hybridisation with potato pgip(s) was not observed. High-level expression of the apple PGIP1 in several independent transgenic potato events was verified by silver staining of SDS-PAGE separated proteins and Western blot. All but one of the PGIP1 extracts prepared from the transgenic potato lines were successful in inhibiting V. dahliae PGs. Active PGIP1 was expressed in the leaves as well as the roots of the transgenic plants. The apoplastic localisation of PGIP activity in the pgip-transgenic potato plants was demonstrated by a vacuum infiltration-extraction experiment. A glasshouse trial indicated that six transgenic lines (A10, B10, B13, A3, A14 and B16) had significantly reduced disease symptoms compared to the untransformed control and other lines when grown in the inoculated soil, but five of them also showed significantly slower senescence symptoms when grown in the control soil. It is proposed that an extended juvenile phase in the transgenic lines resulted in the apparent increased disease resistance, and this could not be attributed to inhibition of V. dahliae PGs, despite high-level expression of the apple PGIP1

15. **Genetic engineering of potato starch composition: inhibition of amylose biosynthesis in tubers from transgenic potato lines by the expression of antisense sequences of the gene for granule-bound starch synthase**

Source: Journal of Genetics & Breeding. 1995. 49 (1). 69-76

Author(s): Kull-B. Salamini-F. Rohde-W

Abstract:

The Solanum tuberosum waxy (Wx) gene encodes granule-bound starch synthase (GBSS), the enzyme catalysing the biosynthesis of the starch component amylose. Two subgenomic fragments of 130 and 640 bp, respectively, of the potato GBSS gene were used for the production of transgenic potato lines which expressed these fragments in antisense orientation under the control of the CaMV 35S promoter and terminator. Antisense RNAs from both fragments, which represent the 5' terminal part of the coding region, were effective in inhibiting amylose biosynthesis in tubers of transgenic potato lines. The waxy phenotype was stable during vegetative propagation in two out of ten independent transgenic lines. Stable transformation with the heterologous Wx cDNA from barley did not result in amylose-free potato. Moreover, for three ribozymes designed to cleave potato Wx RNA transcripts at GUC triplets in exon 2 and intron 2, respectively, transgenic, amylose-free potato lines were not obtained after regeneration of transgenic calli, although in vitro one of the ribozymes cleaved Wx RNA with high efficiency under mild cleavage conditions

Descriptors: **Antisense-RNA. genetic-engineering. potato-starch. composition. inhibition. amylose. biosynthesis. tubers. lines. sequences. starch. potatoes. barley. introns. exons. quality. genes. genetic-transformation. gene-expression. enzymes. root-crops. biotechnology**

16. Fulfilling the promise of Bt potato in developing countries

Source: Journal of New Seeds. 2003. 5 (2-3). 93-113

Author(s): Ghislain-M. Lagnaoui-A. Walker-T

Abstract:

Potato production is expanding rapidly in developing countries, particularly in Asia. For many poor farmers, potatoes represent a staple food and an important cash crop. Potato insect pests have a substantial negative impact on the livelihood of farmers. Bt-potatoes have been effective on a commercial scale in controlling Colorado potato beetle (Leptinotarsa decemlineata) in North America. Small-scale tests have demonstrated Bt's efficacy in controlling potato tuber moth. Reliance on chemical pesticides can be reduced and/or replaced by pest-protected potato, genetically engineered to express genes from the bacterium Bacillus thuringiensis (Bt). Reductions in insecticide use would provide significant economic, health and environmental benefits. Unintentional Bt gene escape into wild relatives of cultivated potato should be rare and unlikely to persist. However, a monitoring system should be in place in areas where sexually compatible relatives of potato occur. The potential of Bt varieties to displace land races or reduce crop genetic diversity should be addressed by the creation of sanctuaries or germplasm banks. Because farmers in developing countries exchange their seeds and mandatory labelling would likely exclude small-scale farmers, Bt genes should be introduced only into varieties handled through the formal seed systems, providing the basis for a variety-based system for segregating genetically engineered (GE) and non-GE produce. We conclude that properly managed Bt-potato technology offers substantial benefits for developing countries

Descriptors: B**iosafety. genetic-transformation. genetically-engineered-organisms. insect-pests.**

17. Tissue culture methods for the screening and analysis of putative virus-resistant transgenic potato plants

Source: Phytopathology. 1998. 88 (5). 437-441

Author(s): Russo-P. Slack-S-A

Abstract:

Following regeneration, putative virus-resistant transgenic plants are usually transferred from tissue culture to a greenhouse or growth chamber to screen for resistance to infection and disease development using mechanical, graft, or insect vector inoculation methods. To reduce initial screening costs and time, mechanical and graft inoculation methods suitable for tissue culture use were developed. The in vitro methods were validated by comparing them with similar greenhouse screens using putative potato virus Y strain o (PVY deg) replicase-mediated resistant regenerants of the potato cultivar Atlantic. Five transgenic lines were tested, with similar results obtained from in vitro and greenhouse experiments. Two of the transgenic lines, A1 and A3, showed the greatest resistance to PVY deg infection, as indicated by low enzyme-linked immunosorbent assay values and infection rates. In vitro mechanical inoculation methods were also used to infect wild-type tomato and tobacco plants with cucumber mosaic virus and potato virus Y. Potato plants were also infected with the phloem-restricted potato leafroll virus, a low-titre virus, using in vitro graft inoculation methods. These results suggest the potential usefulness of these simple, effective, and economical techniques for screening large numbers of putative virus-resistant plants

Descriptors:Screening. transgenics. ELISA. disease-resistance. techniques. tissue-culture. tobacco. transgenic-plants. plant-diseases. plant-pathogens. potatoes. genetic-transformation. molecular-genetics

18. Transgenic potato expressing A beta reduce A beta burden in Alzheimer's disease mouse model

Source: FEBS Letters. 2005. 579 (30). 6737-6744

Author(s): Youm-JungWon. Kim-Hee. Han-J-H-L. Jang-ChangHwan. Ha-HeeJin. Mook-Jung-InHee. Jeon-JaeHeung. Choi-CheolYong. Kim-YoungHo. Kim-HyunSoon. Joung-Hyouk

Abstract:

Beta amyloid (A beta) is believed one of the major pathogens of Alzheimer's disease (AD), and the reduction of A beta is considered a primary therapeutic target. Immunization with A beta can reduce A beta burden and pathological features in transgenic AD model mice. Transgenic potato plants were made using genes encoding 5 tandem repeats of A beta 1-42 peptides with an ER retention signal. Amyloid precursor protein transgenic mice (Tg2576) fed with transgenic potato tubers with adjuvant showed a primary immune response and a partial reduction of A beta burden in the brain. Thus, A beta tandem repeats can be expressed in transgenic potato plants to form immunologically functional A beta, and these potatoes has a potential to be used for the prevention and treatment of AD

Descriptors: Alzheimer's-disease. amyloid. animal-models. brain. disease-models. potatoes. transgenic-plants

19. Monitoring changes in anthocyanin and steroid alkaloid glycoside content in lines of transgenic potato plants using liquid chromatography/mass spectrometry

Source: Phytochemistry. 2003. 62 (6). 959-969

Author(s): Stobiecki-M. Matysiak-Kata-I. Franski-R. Skala-J. Szopa-J

Abstract:

Transgenic potato plants overexpressing and repressing enzymes of flavonoids biosynthesis were created and analysed. The selected plants clearly showed the expected changes in anthocyanins synthesis level. Overexpression of a DNA encoding dihydroflavonol 4-reductase (DFR) in sense orientation resulted in an increase in tuber anthocyanins, a 4-fold increase in petunidin and pelargonidin derivatives. A significant decrease in anthocyanin level was observed when the plant was transformed with a corresponding antisense construct. The transformation of potato plants was also accompanied by significant changes in steroid alkaloid glycosides (SAG) level in transgenic potato tuber. The changes in SAGs content was not dependent on flavonoid composition in transgenic potato. However, in an extreme situation where the highest (DFR11) or the lowest (DFRa3) anthocyanin level was detected the positive correlation with steroid alkaloid content was clearly visible. It is suggested that the changes in SAGs content resulted from chromatin stressed upon transformation. A liquid chromatography/mass spectrometry (LC/MS) system with electrospray ionization was applied for profiling qualitative and quantitative changes of steroid alkaloid glycosides in tubers of twelve lines of transgenic potato plants. Except alpha -chaconine and alpha -solanine, in the extracts from dried tuber skin alpha -solamargine and alpha -solasonine, triglycosides of solasonine, were identified in minor amounts, triglycosides of solanidine dehydrodimers were also recognized

Descriptors:Alkaloids. anthocyanins. biosynthesis. chromatin. enzymes. genetic-transformation. glycosides. pelargonidin. potatoes. solanine. steroids. transgenic-plants

20. **Effects of potato plants expressing the nptII-gus fusion marker genes on reproduction, longevity, and host-finding of the peach-potato aphid, Myzus persicae**

Source: Entomologia Experimentalis et Applicata. 2003. 106 (2). 95-102

Author(s): Alla-S. Cherqui-A. Kaiser-L. Azzouz-H. Sangwann-Norreel-B-S. Giordanengo-P

Abstract:

Transgenesis developed in the last 20 years offers new possibilities for crop protection. The transgenic process, however, requires the use of marker fusion genes to select and visualize the transformed tissues. Although the expression products of these marker genes are stably expressed in crops, little attention has been given to assess the eventual risks of these recombinant proteins on phytophage populations. Three independent transgenic potato (Solanum tuberosum) clones from the cultivar Desiree (DG5, DG18, and DG20) carrying the commonly used nptII-gus gene construct and exhibiting different beta -glucuronidase activity (0.843 plus or minus 0.011, 0.576 plus or minus 0.096, and 0.002 plus or minus 0.000 pmol min-1.mg-1, respectively) were evaluated to determine the impact of the encoded proteins on the behaviour, development, reproduction, and demography of the peach-potato aphid, Myzus persicae, under laboratory-controlled light and temperature. Our results revealed that the transgenic event can alter aphid physiology or behaviour. Experiments showed a probiotic effect of one transgenic line, the DG5, resulting in reduced prereproductive period and mortality, and enhanced daily fecundity, which was expressed in a greater population growth potential (rm=0.205 vs. rm=0.174 of the control). In contrast, aphids fed with the DG18 line exhibited reduced adult survival and reproductive period but no alteration of their demographic parameters (rm=0.176). Finally, no physiological alteration was induced in aphids fed on a DG20 diet (rm=0.170). Behavioural experiments conducted in a 4-choice olfactometer demonstrated that insects were significantly more attracted by the odour of transgenic DG18 potato plant than that of Desiree non-transformed plant, spending twice as much time in the DG18 plant odour. The two other transformed clones (DG5 and DG20) were as attractive as the non-transformed cultivar. It is concluded that the beta -glucuronidase expression in potato plants might be responsible for the probiotic effect measured on the feeding aphids, whereas alteration of the foliage odour would result from a pleiotropic effect

Descriptors:Beta-glucuronidase. clones. demography. enzyme-activity. foliage. gene-expression. genetic-engineering. growth. host-seeking-behaviour. insect-pests. lines. longevity. marker-genes. mortality. odours. plant-pests. potatoes. recombinant-proteins. reproduction. transgenic-plants

21. Photosynthesis, carbohydrate metabolism, and yield of phytochrome-B-overexpressing potatoes under different light regimes

Source: Crop Science. 2004. 44 (1). 131-143

Author(s): Schittenhelm-S. Menge-Hartmann-U. Oldenburg-E

Abstract:

Transgenic potatoes (Solanum tuberosum L.) overexpressing Arabidopsis thaliana (L.) Heynh. phytochrome B (phyB) have been reported to exhibit a substantially modified plant architecture, increased photosynthetic performance, reduced photoinhibition, delayed leaf senescence, and increased tuber yield. A greenhouse and a growth chamber experiment were conducted at Braunschweig, Germany, to elucidate the crop physiological basis for the yield differences between moderately phyB-overexpressing transgenic (Dara-5) and wild-type potato plants. In the greenhouse experiment, Dara-5 leaves showed a 23% greater leaf carbon exchange rate (CER) at light saturation, 32% greater leaf conductance, and 21% longer green leaf area duration (GLAD) than the wild-type plants. The transgenic plants partitioned a considerably greater portion of their biomass to stems and roots, but tuber and total biomass yield did not significantly differ among genotypes. The leaves and stems of the transgenic plants had lower starch and soluble sugar concentrations but consistently higher N concentration than those of the nontransgenic plants. Light response curves showed increasing CER superiority of Dara-5 leaves with increasing photosynthetic photon flux (PPF), suggesting higher productivity of the transgenic plants in high-radiation environments. Therefore, the two genotypes were compared in growth chambers at low, medium, and high light levels of 300, 600, and 900 micro mol m-2 s-1 PPF. Leaf CER of the transgenic plants reached 123, 115, and 120% of the wild-type plants at low, medium, and high PPF, but only at low PPF did the transgenic plants produce significantly greater (+8%) tuber yield than the nontransgenic plants. It is supposed that enhanced C loss from respiration is responsible for the lack of consistent transgenic yield superiority

Descriptors: Biomass. carbohydrate-metabolism. crop-yield. gene-expression. genes. genotypes. irradiation. leaf-area. leaf-conductance. leaves. light-regime. light-relations. photoinhibition. photosynthesis. phytochrome. potatoes. respiration. roots. senescence. stems. transgenic-plants. tubers

22. Characterization of acquired resistance in lesion-mimic transgenic potato expressing bacterio-opsin

Source: Molecular Plant Microbe Interactions. 1997. 10 (5). 635-645

Author(s): Abad-M-S. Hakimi-S-M. Kaniewski-W-K. Rommens-C-M-T. Shulaev-V. Lam-E. Shah-D-M

Abstract:

A lesion-mimic phenotype in transgenic Russet Burbank potato plants has been engineered through constitutive expression of a bacterio-opsin (bO) proton pump derived from Halobacterium halobium. Transgenic potato plants exhibiting a lesion-mimic phenotype had increased levels of salicylic acid and overexpressed several pathogenesis-related messenger RNAs, all hallmarks of systemic acquired resistance (SAR). The lesion-mimic plants also displayed enhanced resistance to the US1 isolate (A1 mating type) of Phytophthora infestans. In contrast, little resistance was observed against the US8 isolate (A2 mating type) of this pathogen. Furthermore, a majority of the transgenic plants displaying the lesion-mimic phenotype had increased susceptibility to potato X potexvirus. The tubers of these plants were not resistant to Erwinia carotovora. These results indicated that expression of bO can result in the activation of defence responses in transgenic potato plants and show for the first time that bO expression can confer resistance to a pathogenic fungus. However, these results also demonstrated that like SAR, this "engineered" resistance is likely to be limited to certain pathogens and particular cultivars

Descriptors:Disease-resistance. plant-pathogenic-fungi. plant-pathogenic-bacteria. plant-pathogens. potatoes. transgenic-plants. genetic-engineering. root-crops. plant-pathology

23. Transgenic tobacco plants expressing the Potato virus X open reading frame 3 gene develop specific resistance and necrotic ring symptoms after infection with the homologous virus

Source: Molecular Plant Microbe Interactions. 2001. 14 (11). 1274-1285

Author(s): Kobayashi-K. Cabral-S. Calamante-G. Maldonado-S. Mentaberry-A

Abstract:

Tobacco cv. Xanthi D8 NN plants were transformed with the open reading frame 3 gene from potato virus X (PVX) coding for the p12 protein. Although the transgenic plants exhibited a normal morphological aspect, microscopic examination revealed extensive alterations in leaf tissue structure. After being challenged with PVX, the transgenic plants showed resistance to PVX infection and formation of specific leaf symptoms consisting of concentric rings encircled by necrotic borders. These novel symptoms were accompanied by biochemical changes normally associated with the hypersensitive response (HR), and were absent in non-infected transgenic plants or in PVX-infected non-transgenic plants. No equivalent virus resistance was observed after inoculation with tobacco mosaic virus or potato virus Y, suggesting the presence of a specific resistance mechanism. Despite development of HR-like symptoms, systemic-acquired resistance was not induced in PVX-infected p12 transgenic plants. No evidence of an RNA-mediated resistance mechanism was found

Descriptors:Disease-resistance. open-reading-frames. plant-pathogens. tobacco. transgenic-plants

24. **Antioxidant enzymes in Nicotiana cells containing an Ipomoea peroxidase gene**

Source: Phytochemistry. 1998. 48 (8). 1287-1290

Author(s): Yun-ByungWook. Huh-GyungHye. Kwon-SukYoon. Lee-HaengSoon. Jo-JinKi. Kwak-SangSoo

Abstract:

The levels of the antioxidant enzymes, peroxidase (POD), superoxide dismutase (SOD), catalase (CAT) and glutathione reductase (GR), were investigated in seven cell lines (referred to as transgenic tobacco cell lines) derived from transgenic tobacco (Nicotiana tabacum) plants carrying a sweet potato (Ipomoea batatas) anionic POD cDNA (swpa1). Transgenic tobacco cell lines were induced from the leaf tissues of transgenic plants on MS medium supplemented with 1 mg 2,4-D/litre. A novel isoenzyme encoded by the swpa1 cDNA was detected on the native-PAGE in all transgenic tobacco cell lines. Average POD activity in transgenic cell lines was approx equal to 1.3 times higher than that of control cell lines, whereas the other three antioxidant enzymes showed a slightly lower level in transgenic cell lines. The POD specific activity in each transgenic cell line had a high correlation with that of leaves in the original transgenic plants (r = 0.63). The ratio of in vitro cell lines to plant leaves in specific activities of four antioxidant enzymes showed a considerable difference: 2.5 in POD activity, 2.1 in SOD activity, 0.05 in CAT activity and 0.9 in GR activity. These results suggest that the antioxidative mechanism between in vitro cultured cells and intact plants may be differently regulated

Descriptors:Transgenic-plants. peroxidases. superoxide-dismutase. catalase. enzymes. enzyme-activity. peroxidase. 2,4-D. complementary-DNA. cell-lines. glutathione. sweet-potatoes. tobacco. transgenics. PAGE. gene-expression. genetic-transformation. genetic-engineering. root-crops. biotechnology. stimulant-plants

25. **Systemic Potato virus YNTN infection and levels of salicylic and gentisic acids in different potato genotypes**

Source: Plant Pathology. 2005. 54 (4). 441-447

Author(s): Krecic-Stres-H. Vucak-C. Ravnikar-M. Kovac-M

Abstract:

Endogenous levels of free and conjugated salicylic (SA) and gentisic (GA) acids, both putative signal molecules in plant defence, were analysed in order to investigate their involvement in the resistance of four potato (Solanum tuberosum) genotypes with different susceptibilities to Potato virus YNTN (PVYNTN) infection: the highly susceptible cv. Igor and its extremely resistant transgenic line, the extremely resistant cv. Sante and the tolerant cv. Pentland Squire. The lowest levels of free and conjugated SA were observed in the extremely resistant cv. Sante, while free GA, which was detected in all the other varieties, was absent. The extremely resistant transgenic cv. Igor contained the highest basal total SA level and the lowest level of total GA of all four cultivars. In susceptible cv. Igor, but not in resistant transgenic cv. Igor, a systemic increase of free SA was measured 1 day postinfection (dpi). Even more significant increases of free and conjugated SA and GA were detected 11 dpi when systemic symptoms appeared. In inoculated but not in upper noninoculated leaves of resistant transgenic cv. Igor, significant increase of SA conjugates occurred, but not before 11 dpi. The increase of SA and GA in susceptible cv. Igor could contribute to the general elevated levels of phenolic compounds as a response to stress caused by virus infection. It appears that basal levels of SA and GA do not correlate with resistance to PVYNTN in potato plants

Descriptors:Benzoic-acids. cultivars. defence-mechanisms. disease-resistance. genetic-engineering. genetic-transformation. genotypes. leaves. lines. plant-pathogens. potatoes. salicylic-acid. transgenic-plants

26. **Strong resistance to potato tuber necrotic ringspot disease in potato induced by transformation with coat protein gene sequences from an NTN isolate of Potato virus Y**

Source: Annals of Applied Biology. 2001. 139 (2). 269-275

Author(s): Racman-D-S. McGeachy-K. Reavy-B. Strukelj-B. Zel-J. Barker-H

Abstract:

Potato cv. Igor is susceptible to infection with potato virus Y (PVY) and, in Slovenia, it has been so severely affected with NTN isolates of PVY causing potato tuber necrotic ringspot disease (PTNRD) that its cultivation has ceased. Plants of potato cv. Igor were transformed with two transgenes that contained coat protein gene sequence of PVYNTN. Both transgenes used PVY sequence in a sense (+) orientation, one in native translational context (N-CP), and one with a frame-shift mutation (FS-CP). Although most transgenic lines were susceptible to infection with PVYNTN and PVYO, several lines showed resistance that could be classified into two types. Following manual or graft inoculation, plants of partially resistant lines developed some symptoms in foliage and tubers, and virus titre in the foliage, estimated by ELISA, was low or undetectable. In highly resistant (R) lines, symptoms did not develop in foliage and on tubers, and virus could not be detected in foliage by ELISA or infectivity assay. Four lines from 34 tested (two N-CP and two FS-CP) were R to PVYNTN and PVYO and one additional line was R to PVYO. When potato cv. Spey was

transformed with the same constructs, they did not confer strong resistance to PVYO

Descriptors:Coat-proteins. disease-resistance. genetic-transformation. leaves. nucleotide-sequences. plant-diseases. plant-pathogens. potatoes. susceptibility. transgenic-plants. tubers

27. **Herbicide metabolism and cross-tolerance in transgenic potato plants expressing human CYP1A1**

Source: Pesticide Biochemistry and Physiology. 1999. 64 (1). 33-46

Author(s): Inui-Hideyuki. Ueyama-Yukiko. Shiota-Noriaki. Ohkawa-Yasunobu. Ohkawa-Hideo

Abstract:

Transgenic potato plants expressing human CYP1A1 and human CYP1A1/yeast NADPH-cytochrome P450 reductase (YR) fused enzyme were generated from microtubers by the use of an Agrobacterium transformation system. The transgenic plants S1384 expressing human CYP1A1 and both F1386 and F1515 expressing the fused enzyme were selected by kanamycin resistance, PCR analysis, chlortoluron (CT) resistance, and Western blot analysis. The integration and transcription of the corresponding CYP1A1 genes were confirmed in these selected transgenic plants by Southern and Northern blot analyses. CYP1A1 and its fused proteins were found to be produced in the transgenic plants S1384 and F1515, respectively. The P450- dependent monooxygenase activity of the transgenic plants S1384, S1386, and F1515 was 3.5, 4.2, and 3.8 times higher in 7- ethoxycoumarin O-deethylation in vitro and 6.4, 5.8, and 5.3 times higher in (14C)CT metabolism in vivo than those of the control plants, respectively. In the metabolism of (14C)atrazine (AT), four metabolites were found in both control and transgenic plants. The diesopropylated deethylated metabolite DIDE, which is nonphytotoxic, was produced to a higher extent in S1384 and F1515 compared with the control. With herbicide tolerance tests, S1384 showed tolerance toward both AT and pyriminobacmethyl (PM), and F1386 and F1515 were tolerant toward PM, while the control died by treatment with both herbicides. Thus, it was found that the transgenic potato plants expressing human CYP1A1 metabolized the herbicides CT and AT with different structures and herbicide modes of action and resulted in cross-tolerance to both herbicides as well as PM

Descriptors:Molecular Genetics (Biochemistry and Molecular Biophysics); Pesticides. chlortoluron: cross-tolerance, herbicide, metabolism; human CYP1A1 gene (Hominidae)

28. **Marker-assisted selection for the broad-spectrum potato late blight resistance conferred by gene RB derived from a wild potato species**

Source: Crop Science. 2006. 46 (2). 589-594

Author(s): Colton-L-M. Groza-H-I. Wielgus-S-M. Jiang-J-M

Abstract:

Potato (Solanum tuberosum L.) late blight, caused by Phytophthora infestans (Mont.) de Bary, is one of the most damaging diseases in any crop.

Deployment of resistant varieties is the most effective way to control this disease. However, breeding for late blight resistance has been a challenge because the race-specific resistance genes introgressed from wild potato S. demissum Lindl. have been short lived and breeding for "horizontal" or durable resistance has achieved only moderate successes. We previously demonstrated that the high-level late blight resistance in a wild potato relative, S. bulbocastanum Dunal subsp. bulbocastanum, is mainly controlled by a single resistance gene RB. Transgenic potato lines containing the RB gene have showed strong late blight resistance, comparable to the backcrossed progenies derived from the somatic hybrids between potato and S. bulbocastanum. Here we report the development of a polymerase chain reaction-based DNA marker for tracking the RB gene in breeding populations derived from the potato x S. bulbocastanum somatic hybrids. Several marker-positive breeding lines showed the expected late blight resistance in greenhouse evaluations. Our results demonstrate that marker-based selection will allow us to effectively transfer the RB gene into potato using traditional breeding methods, an alternative to deploying the RB gene through genetic transformation

Descriptors:Artificial-selection. disease-resistance. fungal-diseases. gene-transfer. genes. genetic-markers. plant-diseases. plant-pathogenic-fungi. plant-pathogens. polymerase-chain-reaction. potatoes. somatic-hybridization. wild-relatives

29. Reduced field spread of potato leafroll virus in potatoes transformed with the potato leafroll virus coat protein gene

Source: Plant Disease. 1997. 81 (12). 1447-1453

Author(s): Thomas-P-E. Kaniewski-W-K. Lawson-E-C

Abstract:

Potato cv. Russet Burbank was transformed with plant expression vectors containing the potato leaf roll luteovirus (PLRV) coat protein (CP) gene. Transgenic potato lines contained a gene expression cassette with 2 copies of a PLRV CP gene in which the nucleotide sequence was modified to improve expression of the gene. In addition, the 2 copies of the PLRV CP gene were each driven by a different promoter. Field test screening for PLRV resistance identified 15 lines which showed moderate resistance to PLRV infection and virus titre build-up, and a longer incubation period for systemic infection. By conducting field resistance assays during a period when the vector of PLRV (Myzus persicae) was not present, it was possible to test whether the observed resistance was sufficient to restrict aphid transmission of PLRV in a field test. Two years of field testing showed that PLRV-spread from an infected plant to adjacent healthy plants of the same line was severely restricted in nearly all the transgenic lines in the field. It is suggested that these lines have useful resistance to PLRV and could aid in managing PLRV disease in Russet Burbank potato

Descriptors:Genetic-engineering. spread. potatoes. plant-diseases. plant-pathogens. molecular-genetics. transgenic-plants. genes. coat-

proteins. disease-resistance. transmission. genetic-transformation. root-crops. biotechnology. plant-pathology

30. **Expression of the potato leafroll virus ORF0 induces viral-disease-like symptoms in transgenic potato plants**

    Source: Molecular Plant Microbe Interactions. 1997. 10 (2). 153-159

    Author(s): Wilk-F-van-der. Houterman-P. Molthoff-J. Hans-F. Dekker-B. Heuvel-J-van-den. Huttinga-H. Goldbach-R

    Abstract:

    To investigate the function of the potato leaf roll luteovirus (PLRV) p28 protein, transgenic potato plants were produced containing the ORF0. In the lines in which the ORF0 transcripts could be detected by Northern (RNA) analysis, the plants displayed an altered phenotype resembling virus infected plants. A positive correlation was observed between levels of accumulation of the transgenic transcripts and severity of the phenotypic aberrations observed. In contrast, potato plants transformed with a modified, untranslatable ORF0 sequence were phenotypically indistinguishable from wild-type control plants. These results suggested that the p28 protein is involved in viral symptom expression. Southern blot analysis showed that the transgenic plants that accumulated low levels of ORF0 transcripts detectable only by RT-PCR, contained methylated ORF0 DNA sequences, indicating down-regulation of the transgene provoked by the putatively unfavourable effects p28 caused in the plant cell

    Descriptors:Plant-pathogens. transgenic-plants. proteins. plant-diseases. molecular-genetics. gene-expression. symptoms. potatoes. root-crops. plant-pathology

31. **Survival of two strains of Phthorimaea operculella (Lepidoptera: Gelechiidae) reared on transgenic potatoes expressing a Bacillus thuringiensis crystal protein**

    Source: Agronomie. 1998. 18 (2). 151-155

    Author(s): Rico-E. Ballester-V. Mensua-J-L

    Abstract:

    Two populations of Phthorimaea operculella, one of them presumed to be resistant to Dipel (a commercial preparation of Bacillus thuringiensis delta-endotoxins), and the other susceptible, were grown on four cultivars of potatoes, two of them a first generation of transgenic plants, expressing the Bacillus thuringiensis Cry1Ab delta endotoxin protein, and the other two untransformed. The moth population which was reported to be resistant, proved to have less mortality than the susceptible one, but it was not really resistant to Cry1Ab. The transgenic potatoes were partially protected against the attack of the moth. The adult survival of the two strains of Phthorimaea operculella reared on transgenic potatoes was less than half their survival on untransformed potatoes, so that Cry1Ab expressing potato tubers proved to protect partially against attack of the moth

Descriptors:Strains. pathogens. microbial-pesticides. potatoes. protein. transgenics. transgenic-plants. endotoxins. root-crops. agricultural-entomology

32. Ecological risk of growing transgenic potatoes in the United States and Canada

Source: American Potato Journal. 1994. 71 (10). 647-658

Author(s): Love S L

Abstract:

Concerns are outlined which should be addressed before transgenic potatoes can be commercialized and grown in production agriculture. Using available literature, a risk assessment was made of the possible escape and proliferation of transgenic cultivated potatoes and subsequent introgression of transgenes into wild species growing within the geographical borders of the USA and Canada. It was concluded that escape and proliferation of domestic transgenic varieties is not of concern because potatoes are not competitive outside of cultivated areas. Potatoes will not hybridize with the non-tuberous Solanum weed species common to potato production sites. The presence of three tuber-bearing Solanum species (S. fendleri, S. jamesii and S. pinnatisectum) in the southwestern USA suggests a conceivable avenue for transgene escape. However, a number of barriers exist to prevent natural hybridization and introgression, including geographical isolation, endosperm imbalances, multiple ploidy levels and incompatibility. The number and magnitude of these barriers makes natural hybridization highly unlikely and transgene introgression impossible or at least highly improbable

Descriptors:Potatoes. Transgenic-plants. Introgression. Wild-relatives. Interspecific-hybridization. Incompatibility. Weeds. Endosperm. Ploidy. Gene-flow. Outcrossing. Biosafety. Release. Genetic-transformation. Root-crops. Biotechnology

33. Performance of transgenic potato containing the late blight resistance gene RB

Source: Plant Disease. 2008. 92 (3). 339-343

Author(s): Halterman-D-A. Kramer-L-C. Wielgus-S. Jiang-J-M

Abstract:

Late blight of potato, caused by Phytophthora infestans, is one of the most devastating diseases of potato. A major late blight resistance gene, called RB, previously was identified in the wild potato species Solanum bulbocastanum through map-based cloning. The full-length gene coding sequence, including the open reading frame and promoter, has been integrated into cultivated potato (S. tuberosum) using Agrobacterium-mediated transformation. RB-containing transgenic plants were challenged with P. infestans under optimal late blight conditions in greenhouse experiments. All transgenic lines containing RB exhibited strong foliar resistance. Field-grown transgenic tubers also were tested for resistance to P. infestans. In contrast to the foliar resistance phenotype, RB-containing tubers did not exhibit increased resistance. Two years of field trials were used to ascertain whether the presence of RB had any effect on tuber yield. We were unable to detect any significant effect on tuber size or yield after addition of the resistance gene to several S. tuberosum cultivars

Descriptors: DNA-cloning. fungal-diseases. genes. genetic-mapping. genetic-resistance. genetic-transformation. open-reading-frames. phenotypes. plant-diseases. plant-pathogenic-fungi. plant-pathogens. potatoes. transgenic-plants. wild-relatives

34. Potato gene Y-1 is an N gene homolog that confers cell death upon infection with potato virus Y

Source: Molecular Plant Microbe Interactions. 2002. 15 (7). 717-727

Author(s): Vidal-S. Cabrera-H. Andersson-R-A. Fredriksson-A. Valkonen-J-P-T

Abstract:

ADG2 is a DNA sequence mapped to a resistance (R) gene-rich region at the distal end of chromosome XI in potato (Solanum tuberosum subsp. andigena). The gene, in which ADG2 represents the predicted nucleotide-binding domain (NBS), was cloned and characterized. The coding region of the gene (designated as Y-1) is 6187-bp long and structurally similar to gene N that confers hypersensitive resistance to tobacco mosaic virus in Nicotiana spp. Both belong to the TIR-NBS-LRR class of genes and show 57% identity at the amino acid sequence level. The introns of Y-1 were spliced as predicted from the sequence. Y-1 cosegregated with Ryadg, a gene for extreme resistance to potato virus Y (PVY) on chromosome XI, as tested in a potato-mapping population and with independent potato cultivars. Leaves of the transgenic potato plants expressing Y-1 under the control of cauliflower mosaic virus 35S promoter developed necrotic lesions upon infection with PVY, but no significant resistance was observed, and plants were systemically infected with PVY

Descriptors:Chromosomes. disease-resistance. gene-expression. genes. introns. nucleotide-sequences. plant-pathogens. potatoes. transgenic-plants

35. Transgenic potato plants can be used to evaluate stability of foreign genes: reversions and chimeras in multiple copies of rolC harboring clones

Source: Agronomie. 1996. 16 (2). 113-121

Author(s): Fladung-M

Abstract:

35S-rolC and rbcS-rolC transgenic potato plants were used to evaluate the stability of the phenotypic marker gene rolC during the life cycle of transgenic potato plants and in subsequent vegetative generations. Transgenics carrying one or two copies of the gene revealed a high stability of the gene during growth and vegetative propagation. Two 35S-rolC transgenic plants harbouring four and five copies of the rolC gene showed a strong phenotypic rolC expression and were viable only when grown in vitro. Under these conditions, spontaneous reversions were observed to a less expressed rolC phenotype. In Southern experiments, these transgenics still carried four and five copies of the rolC gene, whereas the northern blot signals were comparable to those of transgenics carrying a lower copy number of rolC. From the same two clones, chimaeric shoots were observed during vegetative growth in a greenhouse that showed light and dark green normal sectors on the same leaf. The presence of four or five copies of rolC was confirmed in the dark green normal sectors, although no signal was obtained in northern blots for this phenotypically normal tissue. The results are discussed with respect to possible gene inactivation

Descriptors:Potatoes. reporter-genes. genetic-markers. chimaeras. gene-expression. transgenic-plants. genetic-transformation. root-crops. biotechnology

36. Expression of a Fibrobacter succinogenes 1,3-1,4- beta -glucanase in potato (Solanum tuberosum)

Source: American Journal of Potato Research. 2002. 79 (1). 39-48

Author(s): Armstrong-J-D. Inglis-G-D. Kawchuk-L-M. McAllister-T-A. Leggett-F. Lynch-D-R. Selinger-L-B. Cheng-K-J

Abstract:

The potential development of potato (S. tuberosum) as a low-cost eukaryotic system for the production of a commercially valuable enzyme feed supplement was examined. A F. succinogenes 1,3-1,4- beta -glucanase [1,3-1,4-beta -D-glucan 4-glucanohydrolase] gene under the control of the constitutive cauliflower mosaic virus 35S promoter was transferred into the potato cultivar, Desiree. The presence of the beta -glucanase cDNA in the plant genome of independent transgenic potato lines was confirmed by PCR and Southern analysis. Northern analysis identified the presence of the beta -glucanase mRNA in the leaf tissue of transgenic plants. Furthermore, western analysis showed F. succinogenes beta -glucanase accumulations of 0.1% and 0.05% of total soluble protein in the leaves and tubers, respectively. Specific activities of the enzyme in leaves (1693 units/mg beta -glucanase) and tubers (2978 units/mg beta -glucanase) were comparable to that previously reported for the enzyme produced in bacteria. Lyophilization of leaves had no effect on the specific activity of beta -glucanase, and only marginally influenced the specific activity of the enzyme expressed in tubers. Relative to the control line (cv. Desiree), tuber yields were significantly reduced by 28-72% in all lines expressing the F. succinogenes beta -glucanase, and microscopy showed that the expression of the beta -glucanase caused changes in cell wall structure. The results of this study demonstrate that a 1,3-1,4- beta -glucanase can be expressed in potato tissues, and that potato plants have the potential to be used for the commercial production of heterologous enzymes

Descriptors:Beta-glucanase. Complementary-dna. Crop-yield. Enzyme-activity. Enzymes. Gene-expression. Genes. Leaves. Messenger-rna. Potatoes. Transgenic-plants

37. Assessing compensation for insect damage in mixed plantings of resistant and susceptible potatoes

Source: American Potato Journal. 1995. 72 (3). 157-176

Author(s): Nault-B-A. Follett-P-A. Gould-F. Kennedy-G-G

Abstract:

Plant mixtures have been proposed for pesticidal transgenic potatoes as a means to reduce selection intensity favouring resistant insect genotypes. Defoliation by Leptinotarsa decemlineata was simulated in mixed plantings of susceptible and resistant potato 'mimics' to evaluate yield compensation. Various mixtures of susceptible and resistant potato were planted at two densities and two locations in eastern North Carolina. Resistant plants were undamaged throughout the season whereas susceptible plants were completely defoliated by hand either during early or late bloom. The ability of non-defoliated plants to compensate for neighbouring defoliated plants was investigated through single-plant and small-plot field experiments for 2 years. Yield compensation for defoliated plants by neighbouring non-defoliated plants was not evident in the studies. The yield of 2 potato plants, positioned on either side of a defoliated plant, was not different from yield of 2 potato plants positioned on either side of a non-defoliated potato plant. Compensation in mixtures of resistant and susceptible potato was not evident using several non-linear regression analyses. A negative linear relationship existed between yield and an increasing percentage of susceptible plants in the mixture for all planting densities, at each location, every year

Descriptors: **Insect-pests. Plant-pests. Damage. Genotype-mixtures. Crop-yield. Pest-resistance. Insect-control. Root-vegetables. Potatoes. Resistance. Control. Cultural-control. Root-crops. Pest-control. Agricultural-entomology**

38. An experimental approach to simulate transgene pyramiding for the deployment of cry genes to control potato tuber moth (Phthorimaea operculella)

Source: Annals of Applied Biology. 2006. 148 (3). 231-238

Author(s): Meiyalaghan-S. Butler-R-C. Wratten-S-D. Conner-A-J

Abstract:

Alternating the daily feeding of potato tuber moth (Phthorimaea operculella) larvae (PTM) between isogenic pairs of potato plants provides an effective experimental approach to simulate transgene pyramiding in a clonal crop. This involves an experimental design with all six possible pairwise combinations of two transgenic lines expressing different cry genes and the non-transgenic control. In this manner, we have simulated the pyramiding of pairwise combinations of cry1Ac9, cry9Aa2 and cry1Ba1 genes in potato and evaluated how pairs of these three cry genes interact to influence the growth rate of PTM larvae. The results show that all combinations of the three cry genes were largely consistent with additive impacts on PTM larval growth, although results from the combination of the cry1Ac9 and cry9Aa2 genes were suggestive of slight synergistic effects. Pyramiding the cry1Ac9, cry9Aa2 and cry1Ba1 genes in potato could therefore

provide a more effective strategy to control PTM compared to single cry gene transgenic plants

Descriptors: **Crystal-proteins. Gene-expression. Genes. Genetic-engineering. Genetic-transformation. Genetically-engineered-organisms. Growth-rate. Insect-control. Insect-pests. Lines. Pest-control. Pest-resistance. Plant-pests. Potatoes. Transgenic-plants**

39. Mating frequency in dispersing potato tuber moth, Phthorimaea operculella, and its influence on the design of refugia to manage resistance in Bt transgenic crops

Source: Entomologia Experimentalis et Applicata. 2005. 115 (2). 323-332

Author(s): Cameron-P-J. Wallace-A-R. Madhusudhan-V-V. Wigley-P-J. Qureshi-M-S. Walker-G-P

Abstract:

Mating of potato tuber moth, Phthorimaea operculella (Zeller) (Lepidoptera: Gelechiidae), was investigated in relation to the dispersal of males in laboratory and field trials. The effect of stimulating the flight of males to light sources in a large cage on their mating ability was estimated for three age groups, and compared with similar estimates for confined moths. Although the mating of males declined with ages of up to 15 days, simulated dispersal had no effect on subsequent mating when the males were paired with virgin females. The dispersal of male moths was also categorised by the initial flight activity of untethered moths to a light source. Scores for poor, moderate, and good flight provided a repeatable measure of initial male flight activity, but the degree of activity was not related to their subsequent mating ability. In the field, virgin female potato tuber moths were tethered at various distances from the edge of isolated potato crops and then dissected to determine their mating status. Female mating frequency averaged 75% at the crop margin, remained above 50% up to 200 m, and then declined to 19% at 360 m from the margin. Derivation of the mating probability for an individual male potato tuber moth confirmed earlier work by other researchers that has indicated a tendency for dispersal prior to mating, and that males retain their ability to mate as they disperse from a crop. The influence of dispersal and mating on gene flow between crops, and its potential effects on refuge size required to minimise the development of resistance to Bt transgenic potato crops was examined

Descriptors: **Age. Bacterial-insecticides. Biological-control-agents. Dispersal. Flight. Gene-flow. Genetic-engineering. Genetic-transformation. Insect-pests. Light. Mating-ability. Mating-frequency. Natural-enemies. Pathogens. Plant-pests. Potatoes. Transgenic-plants. Virgin-females**

40. Molecular controls of tuberization

Source: American Journal of Potato Research. 2004. 81 (4). 263-274

Author(s): Hannapel-D-J. Chen-H. Rosin-F-M. Banerjee-A-K. Davies-P-J

Abstract:

Tuber formation in potatoes (Solanum tuberosum L.) is a complex developmental process involving a number of important biological systems. Under conditions of a short-day photoperiod and cool temperature, a transmissible signal is activated that initiates cell division and expansion and a change in the orientation of cell growth in the subapical region of the stolon tip. In this signal transduction pathway, perception of the appropriate environmental cues occurs in leaves and is mediated by phytochrome and gibberellins (GA). Phytohormones also play a prominent role in regulating the morphological events of tuberization activated in the stolon apex. GA, cytokinins, and jasmonate-like compounds have all been implicated in regulating tuber development. High levels of GA are correlated with the inhibition of tuberization, whereas low levels are associated with induction. Transcription factors are proteins that bind to DNA to regulate gene activity and, in some cases, to mediate hormone levels. Several of these DNA-binding proteins are involved in regulating plant growth and meristem development in potato, including tuber formation. One type, designated POTM1, regulates cytokinin levels in potato meristems and controls branching of axillary shoots. Two other types that physically interact, the BEL and KNOX proteins, mediate vegetative development. Transgenic plants that overexpressed BEL and KNOX proteins exhibited enhanced tuber formation even under long-day conditions. KNOX overexpressers exhibited abnormal leaf architecture and dwarfism. These transgenic lines exhibited a decrease in the levels of GA and an increase in cytokinin levels. In addition, the BEL transgenic lines grew more rapidly than wild-type plants. Our results indicate that DNA-binding proteins of potato mediate tuberization by enhancing or repressing the activity of specific target genes

Descriptors: Cell-growth. cytokinins. DNA. DNA-binding-proteins. endogenous-growth-regulators. gene-expression. genes. gibberellins. growth. jasmonic-acid. leaves. meristems. photoperiod. phytochrome. plant-development. plant-growth-regulators. potatoes. reviews. signal-transduction. stolons. temperature. transcription-factors. transgenic-plants. tubers

41. Overproduction of sweet potato peroxidases in transgenic tobacco plants

Source: Phytochemistry. 1998. 47 (5). 695-700

Author(s): Huh-GyungHye. Yun-ByungWook. Lee-HaengSoon. Jo-JinKi. Kwak-SangSoo

Abstract:

Two peroxidase (POD) cDNAs, anionic (swpa 1) and neutral (swpn 1) POD derived from suspension cultures of sweet potato (Ipomoea batatas), were used to express high levels in transgenic plants. Two sweet potato PODs were overproduced in two cultivars of transformed tobacco (Nicotiana tabacum) plants, Bel W3 and Samsun, by introducing a chimaeric gene composed of the cauliflower mosaic caulimovirus 35S promoter and POD cDNA. Young fully expanded leaves of transgenic plants of both cultivars showed higher POD activity than those of untransformed plants. Bel W3 transgenic plants carrying anionic POD had total POD activity approximately five times higher than control plants. However, no significant differences were observed in superoxide dismutase activity between transgenic and untransformed plants. Transgenic Bel W3 and Samsun tobacco plants with either anionic or neutral POD isoenzyme did not show distinctive phenotypes compared with untransformed plants

Descriptors:Transgenic-plants. Peroxidase. Superoxide-dismutase. Peroxidases. Tobacco. Sweet-potatoes. Genetic-transformation. Gene-expression. Cell-culture. Enzyme-activity. Genetic-engineering. Root-crops. Biotechnology. Stimulant-plants

42. The loss of expression of the H1 gene in Bt transgenic potatoes

Source: American Journal of Potato Research. 2003. 80 (2). 135-139

Author(s): Brodie-B-B

Abstract:

During evaluation of potato clones and cultivars from the Cornell seed production programme to confirm their resistance to golden nematode (Globodera rostochiensis) pathotype Ro1, several cysts developed on the transgenic cultivar Atlantic NewLeaf. This transformed cultivar resulted from the insertion of a Bt endotoxin gene into the golden-nematode-resistant cultivar Atlantic. In subsequent bioassay tests, golden nematode cysts developed freely on the transgenic cultivar that originated from Atlantic NewLeaf clone 6, but not on Atlantic NewLeaf clones 31 and 36. Clones 31 and 36 were from different Bt transformation events of the cultivar Atlantic that were never commercialized. RFLP analysis of Atlantic used in the transformations and the Atlantic NewLeaf clones 6, 31, and 36 showed that they possessed the marker for the H1 gene that confers resistance to golden nematode pathotype Ro1. These data indicate that the Bt transformation process adversely affected the expression of the H1 gene in the transgenic cultivar Atlantic NewLeaf. This finding highlights the importance of pre-release evaluation of transgenic plants for any previously known major traits such as pest and disease resistance before they are commercialized

Descriptors:Cysts-(developmental-stages). Gene-expression. Genes. Pest-resistance. Plant-parasitic-nematodes. Plant-pests. Potatoes. Transgenic-plants

43. Protection against potato virus Y (PVY) in the field in potatoes transformed with the PVY P1 gene

Source: American Journal of Potato Research. 2001. 78 (3). 209-214

Author(s): Maki-Valkama-T. Valkonen-J-P-T. Lehtinen-A. Pehu-E

Abstract:

Lines of potato cv. Pito transformed with the P1 gene of potato virus Y (PVYO) in sense or antisense orientation were evaluated for resistance to PVY in the field in 1997 and 1998. The transgenic resistance fully protected the crop from infection with PVYO transmitted by aphids in both years. These plants were not resistant to the field isolates of the PVYN strain group, which is in agreement with our greenhouse experiments. Consequently, several transgenic lines produced higher yields than the non-transgenic cv. Pito plants. These results showed that the P1 gene-mediated resistance provides significant benefits under conditions where the incidence of infections and damage by PVYO are considerable

Descriptors:Crop-yield. Disease-resistance. Genes. Plant-pathogens. Potatoes. Transgenic-plants

44. Current and potential role of transgenic crops in U.S. agriculture

Source: Journal of Crop Production. 2003. 9 (1-2). 501-530

Author(s): Silvers-C-S. Gianessi-L-P. Carpenter-J-E. Sankula-S

Abstract:

Transgenic crop cultivars with resistance to insects, pathogens, and herbicides offer growers powerful new pest management tools. We reviewed the observed and potential farm-level impacts of transgenic cultivars, including those with regulatory approval and commercial availability as well as those still being researched and developed. Direct grower benefits, such as yield and production increases and decreased management costs, have led to rapid and extensive adoption of Bt maize and cotton, herbicide-resistant cotton, soyabean, and rape, and virus-resistant papaya. Other transgenic crops, including Bt sweetcorn and potato, and herbicide-resistant sugarbeet and maize, have not been adopted despite strong agronomic and pest management performance, largely because growers fear there will be no market for their harvests. Despite inconsistent adoption of transgenic cultivars, demonstrated benefits of the technology encourage ongoing efforts to incorporate pest management traits into a wider variety of crops, including broccoli, tomato, lettuce, grape, citrus, pineapple, raspberry, groundnut, wheat, barley, and rice. Potential impacts of these upcoming transgenic cultivars range from a decrease in weed management costs for lettuce and tomato growers, to the defence of stone fruit, grape, and citrus against devastating new pests

Descriptors:Barley. Broccoli. Costs. Cotton. Crop-yield. Cultivars. Disease-resistance. Genetically-engineered-organisms. Grapes. Groundnuts. Herbicide-resistance. Insect-control. Insect-pests. Lettuces. Maize. Pawpaws. Pest-control. Pest-resistance. Pineapples. Plant-diseases. Plant-pathogens. Plant-pests. Plant-viruses. Potatoes. Rape. Raspberries. Reviews. Rice. Soyabeans. Stone-fruits. Sugarbeet. Swede-rape. Sweetcorn. Tomatoes. Transgenic-plants. Weed-control. Weeds. Wheat

45. Predation of Colorado potato beetle eggs by a polyphagous ladybeetle in the presence of alternate prey: potential impact on resistance evolution

Source: Entomologia Experimentalis et Applicata. 2005. 114 (1). 47-54

Author(s): Mallampalli-N. Gould-F. Barbosa-P

Abstract:

The influence of prey choice on the predation of a target prey item by a polyphagous insect predator was investigated in field plot studies. The target prey consisted of eggs of the Colorado potato beetle (CPB), Leptinotarsa decemlineata Say (Coleoptera: Chrysomelidae), and the predator was the 12-spotted ladybeetle, Coleomegilla maculata Lengi (Coleoptera: Coccinellidae). Eggs of the

European corn borer (ECB), Ostrinia nubilalis Hubner (Lepidoptera: Pyralidae), and nymphs and adults of the green peach aphid, Myzus persicae Sulzer (Homoptera: Aphididae), comprised the alternative prey choices. The objectives of these studies were to: (1) examine predation in a multiprey scenario likely to occur in an agroecosystem, and (2) use the data to simulate the impact of predator-induced mortality on the evolution of resistance to Bt-transgenic plants in the target herbivore. Simulations of the rate of resistance evolution were carried out using a deterministic genetic model. Experiments were performed using potato field plots planted in a manner reflecting a 25% or 50% non-transgenic refuge. CPB eggs were infested so as to mimic the densities of resistant and susceptible populations that might occur in commercial Bt-transgenic plantings. Densities of predators and alternate prey species were chosen to represent those that might typically occur in potato crops in the eastern USA. Simulation results indicated that when ECB eggs were present, predation on CPB eggs either became inversely spatially density-dependent, or increased significantly in a density-dependent manner. When aphids were present, predation became positively density-dependent. Model simulations predicted that ECB egg presence is beneficial, in that resistance was delayed by up to 40 pest generations (as compared to the scenario with CPB as the only prey), while aphid presence accelerated resistance evolution by 18 generations. Results suggest that resistance management strategies should take into account the composition of prey species available to generalist predators typically present, so as to best delay pest adaptation to Bt-toxins

Descriptors:Insect-pests. Insecticide-resistance. Plant-pests. Population-density. Potatoes. Predation. Predator-prey-relationships. Predators. Predatory-insects. Prey. Transgenic-plants

46. The influence of modified 14-3-3 protein synthesis in potato plants on the nutritional value of the tubers

Source: Food Chemistry. 2003. 82 (4). 611-617

Author(s): Prescha-A. Biernat-J. Weber-R. Zuk-M. Szopa-J

Abstract:

The recently created six transgenic potato genotypes with overexpressed or underexpressed P14-3-3a (29G) and P14-3-3c (20R) isoforms of 14-3-3 protein were field-trialled (1998-2001). The contents of protein, starch, reducing sugars, sucrose and lipids were determined in the transgenic and control tubers harvested from the field. The obtained results showed a significant increase in crude protein content in potatoes with repression of P14-3-3c isoform and in potatoes with blocked P14-3-3a synthesis in comparison to the control line. A stable increase in lipid content of potatoes with overexpression of 14-3-3 protein from Cucurbita pepo in the field trials was observed. The variability of the investigated genotypes, in respect to the nutritional components, was statistically analysed using discriminant function and cluster analyses. The dominant influence of the variability of the genotypes exerted significant differentiation of protein, lipid and starch contents. These components showed the greatest discriminant power in

the variability of genotypes. These results confirm the suggestion that 14-3-3 protein co-ordinates primary metabolite synthesis in plants

Descriptors: **Chemical-composition. Gene-expression. Genetic-transformation. Genetic-variation. Genotypes. Lipids. Marrows. Metabolites. Nutritive-value. Potatoes. Protein-content. Protein-synthesis. Reducing-sugars. Starch. Sucrose. Transgenic-plants. Tubers**

47. Induction of defence responses against Erwinia soft rot by an endogenous pectate lyase in potatoes

Source: Physiological and Molecular Plant Pathology. 2002. 60 (2). 91-100

Author(s): Wegener-C-B

Abstract:

Pectate lyase (PL) enzymes are major virulence factors of Erwinia carotovora (Ec) bacteria. They degrade plant cell wall pectin into unsaturated oligogalacturonates (OG) known to elicit plant defence responses. Therefore, a gene encoding the isoenzyme PL3 of Ec ssp. atroseptica was transformed by means of Agrobacterium into potatoes of cv. Desiree. Four PL-transgenic potato plant lines selected on the basis of greenhouse experiments were grown over a period of 4 years (1997-2000) in the field. It is shown that the heterologous PL enzyme mediated an enhanced resistance to Erwinia soft rot in field grown tubers. Thus compared to the non-transgenic counterpart extension of rotting was significantly reduced ($P<0.001$) on the wound surface of PL-expressing tubers. Moreover, the threshold density of Ec-bacteria causing a progressive soft rot was up to 19-fold higher on tuber tissue containing the PL enzyme. An induction of plant defence responses in PL-transgenic potatoes may be indicated by an enhanced resistance of tuber tissue cell walls to Erwinia-derived enzymes, an increased PPO- and PAL-activity in tuber tissue as well as by a strengthened formation of necrosis on the wound surface of tubers after infection with Ec-bacteria

Descriptors: **Catechol-oxidase. Defence. Disease-resistance. Enzyme-activity. Genes. Induced-resistance. Isoenzymes. Pectate-lyase. Phenylalanine-ammonia-lyase. Plant-diseases. Plant-pathogenic-bacteria. Plant-pathogens. Potatoes. Transgenic-plants**

48. Expression of the chicken lysozyme gene in potato enhances resistance to infection by Erwinia carotovora subsp. atroseptica

Source: American Journal of Potato Research. 2000. 77 (3). 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

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**

49. Erwinia soft rot resistance of potato cultivars transformed with a gene construct coding for antimicrobial peptide cecropin B is not altered

Source: American Potato Journal. 1995. 72 (8). 437-445
Author(s): Allefs-S-J-H-M. Florack-D-E-A. Hoogendoorn-C. Stiekema-W-J

Abstract:

Cecropin B is a peptide of approximately 4 kDA which shows antimicrobial activity in vitro against Gram positive and Gram negative bacteria. Potato cultivars Agria, Bintje, Karnico, Kondor and Producent were transformed using Agrobacterium tumefaciens with a gene construct encoding a cecropin B precursor polypeptide. In total, 49 independent transgenic potato clones were obtained. Northern blot analysis of these plants revealed that the introduced gene was transcribed to detectable levels in almost all plants, the highest transcription level being approximately 0.6% of total mRNA. No cecropin B peptide could be detected in transgenic plants, probably as a result of rapid proteolytic degradation of newly synthesized cecropin B by potato endogenous proteinases. Neither small tubers of a group of 11 clones with moderate to high transcription levels nor slices from field grown tubers of any of the transgenic clones obtained showed significantly less rot after inoculation with soft rot pathogens Erwinia carotovora subsp atroseptica or E. chrysanthemi than untransformed controls

Descriptors: **Potatoes. Transgenic-plants. Disease-resistance. Plant-pathogenic-bacteria. Transcription. Genetic-transformation. Plant-diseases. Plant-pathogens. Root-crops. Resistance. Biotechnology. Plant-pathology**

50. **Effects of Galanthus nivalis agglutinin (GNA) expressed in tomato leaves on larvae of the tomato moth Lacanobia oleracea (Lepidoptera: Noctuidae) and the effect of GNA on the development of the endoparasitoid Meteorus gyrator (Hymenoptera: Braconidae)**

Source: Bulletin of Entomological Research. 2006. 96 (1). 43-52

Author(s): Wakefield-M-E. Bell-H-A. Fitches-E-C. Edwards-J-P. Gatehouse-A-M-R

Abstract:

The effect of ingestion of transgenic tomato leaves expressing the plant lectin Galanthus nivalis agglutinin (GNA) on development of larvae of Lacanobia oleracea (Linnaeus) was studied under laboratory conditions. When L. oleracea larvae were fed on tomato line 14.1H, expressing approximately 2.0% GNA, significant increases in the mean larval weight and in the amount of food consumed were found. This resulted in an overall reduction in the mean development time to the pupal stage of approximately 7 days. A significant increase in the percentage survival to the adult moth was also recorded when newly hatched larvae were reared on transgenic tomato leaves (72%) compared to larvae reared on untransformed leaves (40%). The effects of ingestion of GNA by L. oleracea larvae, via artificial diet or the leaves of transgenic tomato or potato plants, on the subsequent development of its solitary endoparasitoid Meteorus gyrator (Thunberg) was also studied. No significant effects on the life cycle parameters of M. gyrator developing in L. oleracea fed on GNA-containing diets were observed. Experiments with transgenic potato plants indicated that the stadium of the host larvae at parasitism had a greater influence on M. gyrator development than the presence of GNA. Potential GNA-binding glycoproteins were detected in the gut and body tissues of larval M. gyrator. Despite detection in host tissues, GNA could not be detected in adult M. gyrator and therefore it is likely that at the time of pupation M. gyrator are able to void the GNA in the meconial pellet

Descriptors: **Agglutinins; biological development; genetic engineering; genetic transformation; insect pests; leaves; life cycle; parasitoids; plant pests; potatoes; survival; tomatoes; transgenic plants Galanthus; Amaryllidaceae; Liliales; monocotyledons; angiosperms; Spermatophyta; plants; Lacanobia; Noctuidae; Lepidoptera; insects; arthropods; invertebrates; animals; Lycopersicon; Solanaceae; Solanales; dicotyledons; Braconidae; Hymenoptera; natural enemies; Meteorus; Solanum**

51. **Potato proteins, and other plant proteins, as potential transgenic resistance factors to pollen beetles in oilseed rape**

Source: Annals of Applied Biology. 2003. 143 (2). 253-260

Author(s): Ahman-I. Melander-M

Abstract:

Proteinase inhibitors (PIs), lectin and patatin purified from potato tubers were tested in no-choice feeding assays with pollen beetle larvae (Meligethes spp.). The idea was to search for resistance factors possible to introduce into oilseed rape (Brassica napus) by genetic engineering. The larval diet was prepared by soaking oilseed rape anthers in protein solutions of known concentrations. Potato lectin was the most potent in that it was the only of these proteins that reduced both larval survival and growth rate, while cysteine, aspartic and metallo PIs and patatin only reduced larval growth rate. Serine PIs had no significant effect on larval performance. Subsequently, the effect of potato lectin was compared to that of lectins from other food or feed crops, resulting in the following mortalitybased ranking of activity: Con A from jackbean > wheat germ lectin > potato lectin > peanut lectin. In choice tests, larvae did not discriminate between Con A- and control-diets. These results suggest that the effect of Con A on larvae is toxic, not deterrent. Adult response was stronger to Con A than to potato lectin in no-choice tests, just as it was in larvae. However, adult survival rate and weight was not affected by Con A but the lectin significantly reduced adult feeding as well as oviposition rates. A resistance factor that suppresses adult feeding on flower buds is important for reduced impact of the pollen beetle on the Brassica oilseed crop

Descriptors:Adults. Anthers. Buds. Cysteine. Genetic-engineering. Groundnuts. Growth. Induced-resistance. Insect-pests. Insecticidal-properties. Larvae. Lectins. Mortality. Oviposition. Pest-resistance. Plant-pests. Plant-proteins. Potato-protein. Potatoes. Proteinase-inhibitors. Rape. Survival. Toxicity. Transgenic-plants. Tubers. Wheat

52. Induction of the maize GapC4 promoter in transgenic potato under anaerobiosis and in Erwinia carotovora-inoculated tuber tissue

Source: Molecular Plant Microbe Interactions. 1999. 12 (3). 182-188

Author(s): Bulow-L. Kohler-U. Cerff-R. Hehl-R. During-K

Abstract:

The induction pattern of the GapC4 promoter from maize in transgenic potato has been analysed by fusion to the beta -glucuronidase (gus) gene. Under anaerobic conditions this promoter confers high level expression not only in leaves, stems, and roots but also in tubers. After inoculation of potato tuber disks with E. carotovora subsp. atroseptica, beta -glucuronidase (GUS) activity could be detected in macerated tissue as well as in surrounding intact tissue. In mock controls no induction was detected, ruling out any induction due to an overall limitation in oxygen in the experimental system. In addition, it could be proven that no diffusion of GUS protein from macerated into intact tissue occurred. The promoter was shown to be aerobically induced even in the absence of live bacteria by incubation with purified Erwinia spp. pectolytic enzymes alone. Therefore, promoter induction seems to be mediated by a mobile factor instead of by limitation in oxygen. These results demonstrated that the maize GapC4 promoter is suitable for directing foreign genes encoding antibacterial proteins in transgenic potato

Descriptors:Anaerobiosis. Maize. Transgenics. Diffusion. Genes. Induction. Inoculation. Beta-glucuronidase. Plant-pathogenic-bacteria. Plant-pathogens. Disease-resistance. Root-crops. Cereals. Plant-pathology

53. **Pectate lyase in transgenic potatoes confers pre-activation of defence against Erwinia carotovora**

Source: Physiological and Molecular Plant Pathology. 1996. 49 (6). 359-376

Author(s): Wegener-C. Bartling-S. Olsen-O. Weber-J. Wettstein-D-von

Abstract:

The regeneration and resistance of transgenic potato plants transformed with chimeric genes encoding PL3 of E. carotovora subsp. atroseptica under control of the patatin B33 gene promoter and cauliflower mosaic caulimovirus (CaMV) 35S promoter were investigated. The DNA sequence encoding the mature enzyme was fused to the promoter of the potato patatin B33 gene and to the 35S promoter of CaMV. The expression cassettes were inserted into the binary vector pBin19. The plasmids pB33-PL3 and P35S-PL3 were used for Agrobacterium-mediated transformation of potato cv. Desiree. Enzyme production in plant lines transformed with plasmid pB33-PL3 was confined to tuber tissue, yielding a max. of 340 mU/ml extract. Plants harbouring the 35S-PL3 chimeric gene exhibited constitutive expression of PL in various tissues, with activities up to 280 mU/ml in leaf extracts and 50 mU/ml in tuber tissue. After wounding the tuber tissue, the liberated PL3 caused decrease in cell viability. Compared with non-transformed plants, the transgenic lines which synthesized PL3 were more resistant to tissue maceration by E. carotovora and its enzymes. Wounding produced the transcription of the plant defence related gene encoding phenylalanine ammonia-lyase to a high level in tubers of a PL3-expressing transgenic line. Possible implications of PLs and their enzymatic products for plant protection are discussed

Descriptors:Pectate-lyase. Plant-diseases. Plant-pathogens. Plant-pathogenic-bacteria. Disease-resistance. Potatoes. Genetic-transformation. Resistance. Enzymes. Molecular-genetics. Diseases. Root-crops. Plant-pathology

54. **Transgenic potato plants with enhanced resistance to the peach-potato aphid Myzus persicae**

Source: Entomologia Experimentalis et Applicata. 1996. 79 (3). 295-307

Author(s): Gatehouse-A-M-R. Down-R-E. Powell-K-S. Sauvion-N. Rahbe-Y. Newell-C-A. Merryweather-A. Hamilton-W-D-O. Gatehouse-J-A

Abstract:

Potato plants (Solanum tuberosum) cv. Desiree were transformed with the genes encoding the protein bean chitinase (BCH), snowdrop lectin (GNA) and wheat alpha -amylase inhibitor (WAI) under the control of the constitutive CaMV 35S promoter. Transgenic plants with detectable levels of foreign RNA were then selected for further characterization with respect to protein expression levels by immunodot blot analysis using polyclonal antibodies raised against the respective protein. With the exception of WAI, plants expressing high levels of RNA expressed correspondingly high levels of the foreign protein (1.5-2.0% of the total soluble protein). Although high levels of WAI mRNA were detected in some of the transformants, the protein could not be detected. On the bases of expression levels, 2 lines, designated PWG6#85 (transformed with the double construct WAI/GNA) and PBG6#47 (transformed with the double construct BCH/GNA), were selected for testing in aphid trials (using Myzus persicae) for enhanced levels of resistance. Both transgenic lines had a marked and significant effect on fecundity. The number of nymphs produced per female per day peaked at 4.1 and 4.2 for lines PBG6#47 and PWG6#85, resp., compared to a value of 5.4 on control plants. Total nymphal production was also significantly lower on either of the transgenic lines compared to control plants ($P < 0.001$) with the differences between the lines being only just significant ($P = 0.058$). On line PBG6#47 there was a delay in nymphal production of 1.6 days, representing a delay of 15%, and on line PWG6#85 this was 3.2 days, representing a delay of ca. 30%. The intrinsic rates of increase (rm) were also significantly lower on both of the transgenic lines in comparison to that on control plants ($P < 0.001$), but the differences between the lines were not significant. The potential of using such genes as part of an overall strategy for the control of aphid populations is discussed

Descriptors:Lectins. Pest-resistance. Insect-pests. Plant-pests. Genetic-engineering. Potatoes. Resistance. Transgenic-plants. Genetic-transformation. Root-crops. Techniques. Pest-control. Control. Agricultural-entomology

55. Salicylic acid is important for basal defense of Solanum tuberosum against Phytophthora infestans

Source: Molecular Plant Microbe Interactions. 2007. 20 (11). 1346-1352

Author(s): Halim-V-A. Eschen-Lippold-L. Altmann-S. Birschwilks-M. Scheel-D. Rosahl-S

Abstract:

The importance of the signaling compound salicylic acid for basal defense of potato (Solanum tuberosum L. cv. Desiree) against Phytophthora infestans, the causal agent of late blight disease, was assessed using transgenic NahG potato plants which are unable to accumulate salicylic acid. Although the size of lesions caused by P. infestans was not significantly different in wild-type and transgenic NahG plants, real-time polymerase chain reaction analyses revealed a drastic enhancement of pathogen growth in potato plants depleted of salicylic acid. Increased susceptibility of NahG plants correlated with compromised callose formation and reduced early defense gene expression. NahG plants pretreated with the salicylic acid analog 2,6-dichloro-isonicotinic acid allowed pathogen growth to a similar extent as did wild-type plants, indicating that salicylic acid is an important compound required for basal defense of potato against P. infestans

Descriptors:Defence-mechanisms. Induced-resistance. Plant-pathogenic-fungi. Plant-pathogens. Potatoes. Salicylic-acid. Signal-transduction. Transgenic-plants

56. Heterologous pectate lyase isoenzymes are not different in their effects on soft rot resistance in transgenic potatoes

Source: Physiological and Molecular Plant Pathology. 2004. 65 (2). 59-66

Author(s): Wegener-C-B. Olsen-O

Abstract:

Pectate lyase (PL) isoenzymes secreted by Erwinia carotovora (Ec) bacteria are of central interest to both basic and applied plant physiology because they depolymerise cell wall pectin into unsaturated oligogalacturonates that trigger various plant defence responses. Therefore, the effects of heterologously expressed PL1 and PL3 were examined with emphasis on plant resistance to soft rot disease caused by Ec bacteria. Agrobacterium-mediated, transformation resulted in transgenic potato lines of cv. Desiree, with activities of the recombinant PL1 ranging between 22 and 1402 mU ml-1. Compared with the non-transgenic plants, potato lines expressing PL1 provided enhanced resistance to soft rot-causing Erwinia bacteria. Thus, the degree of cell lysis caused by bacterial maceration as well as the extension of Ec-rotting was significantly diminished in PL-expressing tuber tissue. This was coincident with a strengthened formation of necrosis on the wound surface of tubers. Spreading of Ec bacteria appear to be prevented--most likely because of enhanced activities of polyphenol oxidase, phenylalanine ammonia-lyase and peroxidase in PL-transgenic tubers. However, key finding reveal that there are no significant differences in resistance to soft rot between potato lines expressing PL1 and PL3. Despite differences in their action patterns and reaction products, it is shown that both PL isoenzymes share similar molecular roles in the events leading to induction of plant defence responses

57. Modulation of the cellulose content of tuber cell walls by antisense expression of different potato (Solanum tuberosum L.) CesA clones

Source: Phytochemistry. 2004. 65 (5). 535-546

Author(s): Oomen-R-J-F-J. Tzitzikas-E-N. Bakx-E-J. Straatman-Engelen-I. Bush-M-S. McCann-M-C. Schols-H-A. Visser-R-G-F. Vincken-J-P

Abstract:

Four potato cellulose synthase (CesA) homologs (StCesA1, 2, 3 and 4) were isolated by screening a cDNA library made from developing tubers. Based on sequence comparisons and the fact that all four potato cDNAs were isolated from this single cDNA-library, all four StCesA clones are likely to play a role in primary cell wall biosynthesis. Several constructs were generated to modulate cellulose levels in potato plants in which the granule-bound starch synthase promoter was used to target the modification to the tubers. The StCesA3 was used for up- and down-regulation of the cellulose levels by sense (SE-StCesA3) and antisense (AS-StCesA3) expression of the complete cDNA. Additionally, the class-specific regions (CSR) of all four potato cellulose synthase genes were used for specific down-regulation (antisense) of the corresponding CesA genes (csr1, 2, 3 and 4). None of the transformants showed an overt developmental phenotype. Sections of tubers were screened for altered cell wall structure by Fourier Transform Infrared microspectroscopy (FTIR) and exploratory Principal Component Analysis (PCA), and those plants discriminating from WT plants were analysed for cellulose content and monosaccharide composition. Several transgenic lines were obtained with mainly decreased levels of cellulose. These results show that the cellulose content in potato tubers can be reduced down to 40% of the WT level without affecting normal plant development, and that constructs based on the CSR alone are specific and sufficient to down-regulate cellulose biosynthesis

Descriptors:Cell-wall-components. Cell-walls. Cellulose. Clones. Complementary-DNA. Enzyme-activity. Enzymes. Gene-expression. Genes. Plant-development. Potatoes. Tubers

58. **Accumulation of tyrosol glucoside in transgenic potato plants expressing a parsley tyrosine decarboxylase**

Source: Phytochemistry. 2002. 60 (7). 683-689

Author(s): Landtag-J. Baumert-A. Degenkolb-T. Schmidt-J. Wray-V. Scheel-D. Strack-D. Rosahl-S

Abstract:

As part of the response to pathogen infection, potato plants accumulate soluble and cell wall-bound phenolics such as hydroxycinnamic acid tyramine amides. Since incorporation of these compounds into the cell wall leads to a fortified barrier against pathogens, raising the amounts of hydroxycinnamic acid tyramine amides might positively affect the resistance response. To this end, we set out to increase the amount of tyramine, one of the substrates of the hydroxycinnamoyl-CoA:tyramine N-(hydroxycinnamoyl)-transferase reaction, by placing a cDNA encoding a pathogen-induced tyrosine decarboxylase from parsley under the control of the 35S promoter and introducing the construct into potato plants via Agrobacterium tumefaciens-mediated transformation. While no alterations were observed in the pattern and quantity of cell wall-bound phenolic compounds in transgenic plants, the soluble fraction contained several new compounds. The major one was isolated and identified as tyrosol glucoside by liquid chromatography-electrospray ionization-high resolution mass spectrometry and NMR analyses. Our results indicate that expression of a tyrosine decarboxylase in potato does not channel tyramine into the hydroxycinnamoyl-CoA:tyramine N-(hydroxycinnamoyl)-transferase reaction but rather unexpectedly, into a different pathway leading to the formation of a potential storage compound

Descriptors:cell-walls. Enzymes. Gene-expression. Genetic-transformation. Phenolic-compounds. Potatoes. Transgenic-plants. Tyramine

59. **Bromoxynil resistance in transgenic potato clones expressing the bxn gene**

Source: Weed Science. 1998. 46 (2). 150-157

Author(s): Eberlein-C-V. Guttieri-M-J. Steffen-Campbell-J

Abstract:

To broaden the spectrum of herbicides useful in potato production, the bxn gene for bromoxynil resistance, which encodes a nitrilase specific for bromoxynil, was introduced into cv. Lemhi Russet by Agrobacterium tumefaciens-mediated transformation. In GR50 studies, transformed potato clones were at least 70-fold more resistant to bromoxynil than untransformed controls. Resistance was due to rapid metabolism of bromoxynil to 3,5-dibromo-4-hydroxybenzoic acid, followed by conjugation to polar compounds. In field trials with cv. Lemhi Russet and Russet Burbank during 1993-94 in Idaho, USA, the best performing transgenic clones had total tuber yields equal to untreated, untransformed controls, but U.S. No. 1 tuber yields were 15 to 30% lower than untreated, untransformed controls. Tubers from 3 out of 4 transgenic clones had specific gravities, percentage solids and fry colour similar to or better than untreated, untransformed controls. Data suggest that lower U.S. No. 1 yields in transgenic clones were due to somaclonal variation and that expression of the bxn transgene had no consistent, detrimental effect on internal tuber quality

Descriptors:Genetic-engineering. Herbicide-resistance. Herbicides. Bromoxynil. Resistance. Clones. Transgenics. Potatoes. Somaclonal-variation. Transformation. Crop-yield. Tubers. Crop-quality. Genes. Genetic-transformation. Root-crops

60. Chimeric cDNA sequences from Citrus tristeza virus confer RNA silencing-mediated resistance in transgenic Nicotiana benthamiana plants

Source: Phytopathology. 2006. 96 (8). 819-827

Author(s): Roy-G. Sudarshana-M-R. Ullman-D-E. Ding-S-W. Dandekar-A-M. Falk-B-W

Abstract:

RNA silencing has been shown to be an important mechanism for conferring resistance in transgenic, virus-resistant plants. We used this approach to evaluate resistance in Nicotiana benthamiana plants transformed with chimeric coding and noncoding sequences from Citrus tristeza virus (CTV). Several independent transgenic plant lines were generated, using two constructs (pCTV1 and pCTV2) designed to produce self-complementary transcripts. The pCTV1 contained cDNA sequences from the CTV capsid protein (CP), p20, and 3' untranslated region (UTR); and pCTV2 contained CP, p23, and 3' UTR sequences. Heterologous recombinant Potato virus X (PVX) containing either homologous or heterologous CTV sequences was used to challenge plants and resistance was evaluated phenotypically and validated with reverse-transcriptase polymerase chain reaction and northern hybridization analysis. Transgenic plants (T1 generation) for each construct showed resistance to recombinant PVX constructs used for challenge experiments when PVX contained p20 or UTR (for CTV1 plants), or p23 or UTR (for CTV2 plants). However, no resistance was seen when plants were challenged with PVX containing the CTV CP. T2 generation plants also showed resistance even when challenged with PVX containing the cognate CTV sequences obtained from heterologous CTV isolates. The presence of transgene-specific small interfering RNAs in the resistant CTV1 and CTV2 plants indicated that resistance was mediated by post-transcriptional gene silencing

Descriptors:Complementary-DNA. Disease-resistance. Gene-silencing. Genetic-engineering. Genetic-transformation. Genetically-engineered-organisms. Messenger-RNA. Plant-diseases. Plant-pathogens. Plant-viruses. Transgenic-plants

61. The influence of Potato virus Y infection on the ultrastructure of Pssu-ipt transgenic tobacco

Source: International Journal of Plant Sciences. 2005. 166 (5). 713-721

Author(s): Schnablova-R. Synkova-H. Cerovska-N

Abstract:

We studied the effect of Potato virus YNTN (PVY) on the cell ultrastructure of control (rooted control plants [C] and control plants grafted onto control rootstock [C/C]) and transgenic Pssu-ipt plants overproducing cytokinins (CK; rooted [T] or grafted [T/C]). The PVY infection caused visible symptoms, i.e., reduction of leaf surface and plant growth, acceleration of leaf senescence, veinal necrosis, and leaf distortion in all infected C plants; in T and C/C plants, plant age affected whether symptoms of infection occurred. Even though DAS-ELISA proved the presence of virus coat protein in all studied plants, the symptoms of infection were never observed in T/C plants. Relative content of virus proteins in cells correlated with the stage of symptom development in infected plants. A massive accumulation of virus proteins was found in the cytoplasm of infected plants, and it was proved by immunocytochemical methods. The most prominent effect of viral infection was a decrease of volume density of starch, an increase of volume density of plastoglobuli in chloroplasts, and more abundant cores inside peroxisomes in C plants. Although virus particles were not found inside chloroplasts, they formed large aggregates adjacent to cell organelles - nuclei, chloroplasts, mitochondria, and peroxisomes. Both transgenic plants and C/C plants were less sensitive to viral infection. We concluded that not only CK overproduction but also the cultivation method of plants may influence the sensitivity of plants to biotic stress

Descriptors: Age. **Cell-ultrastructure. Coat-proteins. Leaves. Organelles. Peroxisomes. Plant-diseases. Plant-pathogens. Starch. Symptoms. Tobacco. Transgenic-plants. Viral-proteins**

62. Telling Transgenic Technology Tales: Lessons from the Agricultural Biotechnology Support Project (ABSP) Experience

Source: ISAAA Briefs. 2004. (31). 1-105

Author(s): Brenner-C

Abstract:

Booklet includes the following: 1) An overview of ABSP (Agricultural Biotechnology Support Project); 2) Country profiles of Egypt, Indonesia, and South Africa; 3) Two near-market biotechnologies developed under ABSP (transgenic potato resistant to potato tuber moth; transgenic and non-transgenic disease and virus-resistant cucurbits); 4) Key lessons from ABSP; 5) Narrowing the gap between biotechnology research and technology diffusion, including: the experience of other publicly-funded initiatives for transgenic crops; new approaches to narrowing the gap between research and technology diffusion (developing country policies and regulations, the changing roles and responsibilities of public research institutions in developing countries, changing role of the scientific community; the scope for public/private sector collaboration, project approach, design and management); and strategic options and issues for donors

63. **Characterization of susceptibility and resistance responses to potato cyst nematode (Globodera spp.) infection of tomato lines in the absence and presence of the broad-spectrum nematode resistance Hero gene**

Source: Molecular Plant Microbe Interactions. 2005. 18 (2). 158-168

Author(s): Sobczak-M. Avrova-A. Jupowicz-J. Phillips-M-S. Ernst-K. Amar-Kumar

Abstract:

The tomato Hero A gene is the only member of a multigene family that confers a high level (>80%) of resistance to all the economically important pathotypes of potato cyst nematode (PCN) species Globodera rostochiensis and G. pallida. Although the resistance levels of transgenic tomato lines were similar to those of the tomato line LA1792 containing the introgressed Hero multigene family, transgenic potato plants expressing the tomato Hero A gene are not resistant to PCNs. Comparative microscopy studies of in vitro infected roots of PCN-susceptible tomato cv. Money Maker, the resistant breeding line LA1792, and transgenic line L10 with Ro1 pathotype have revealed no statistically significant difference in the number of juveniles invading roots. However, syncytia (specialized feeding cells) induced in LA1792 and L10 roots mostly were found to have degenerated a few days after their induction, and a few surviving syncytia were able to support only the development of males rather than females. Thus, the ratio between males and females was biased towards males on LA1792 and L10 roots. A series of changes occur in resistant plants leading to formation of a layer of necrotic cells separating the syncytium from stellar conductive tissues and this is followed by degradation of the syncytium. Although the Hero A gene is expressed in all tissues, including roots, stems, leaves, and flower buds, its expression is upregulated in roots in response to PCN infection. Moreover, the expression profiles of the Hero A correlates with the timing of death of the syncytium

Descriptors: **Buds. gene-expression. genes. genetic-transformation. leaves. pest-resistance. plant-parasitic-nematodes. plant-pests. roots. sex-ratio. stems. syncytia. tomatoes. transgenic-plants**

64. **Homology-dependent virus resistance in transgenic plants with the coat protein gene of sweet potato feathery mottle potyvirus: target specificity and transgene methylation**

Source: Phytopathology. 1999. 89 (5). 385-391

Author(s): Sonoda-S. Mori-M. Nishiguchi-M

Abstract:

Nicotiana benthamiana plants were transformed with the coat protein (CP) coding sequence and the 3' nontranslated region (NTR) of the severe strain of sweet potato feathery mottle virus (SPFMV-S). Regenerated lines were screened for virus resistance using recombinant potato virus X (PVX) engineered to contain the sequence homologous to the transgene. Out of 19 transgenic lines, 7 showed virus resistance after inoculation by the recombinant PVX. In most of the resistant lines, relatively low steady-state accumulation of the CP gene mRNA and little or no protein products were observed, suggesting that the resistance was manifested by a post-transcriptional gene-silencing mechanism. The resistant lines could be divided into two groups according to the target specificity of the silencing mechanism; one group recognizing the 3' part of the transgene mRNA and the other not only the 3' part, but also the 5' and the central part of the transgene mRNA. Particular regions of the transgene corresponding to the RNA target in the resistant lines were differentially methylated compared with the transgene sequence in a susceptible line

Descriptors:Sweet-potatoes. Transgenic-plants. Messenger-RNA. Coat-proteins. Molecular-genetics. Disease-resistance. Plant-pathogens

65. Potato mop-top virus RNA can move long distance in the absence of coat protein: evidence from resistant, transgenic plants

Source: Molecular Plant Microbe Interactions. 2000. 13 (1). 125-128

Author(s): McGeachy-K-D. Barker-H

Abstract:

Transgenic expression of a translatable version of the potato mop-top virus (PMTV) coat protein (CP) gene (encoded by RNA 3) in Nicotiana benthamiana prevented production of symptoms and infective virus particles. RNAs 1 and 2 accumulated in inoculated and systemic leaves but, apart from small amounts of CP transgene RNA transcript, no genomic-length RNA 3 was found. Crude leaf extracts from inoculated plants were not infective. However, when RNA extracts from such transgenic plants were inoculated to nontransgenic N. benthamiana and N. clevelandii, RNA 1 and RNA 2 replicated in systemic leaves of both species in the absence of RNA 3 and virus particles, but symptoms did not develop. It is suggested that the triple-gene block proteins of PMTV (encoded by RNA 2) represent a class of long-distance RNA movement factors

Descriptors:Plant-diseases. Plant-pathogens. RNA. Transgenics. Transgenic-plants. Symptoms. Coat-proteins. Movement-proteins. Plant-pathology

66. Consequences of the expression of a bacterial glucokinase in potato tubers, both in combination with and independently of a yeast-derived invertase

Source: Australian Journal of Plant Physiology. 2000. 27 (8-9). 827-833

Author(s): Fernie-A-R. Riesmeier-J-W. Martiny-A. Ramalingam-S. Willmitzer-L. Trethewey-R-N

Abstract:

We previously found that glycolysis was induced (and starch accumulation reduced) in transgenic tubers in which a yeast invertase [beta-fructofuranosidase] and a glucokinase from the bacterium Zymomonas mobilis were expressed in the cytosol, whereas potato tuber size was increased when invertase expression was targeted to the apoplast. In this study, further characterization of potato (Solanum tuberosum cv. Desiree) tubers expressing a yeast invertase in the apoplast is described. The generation of 2 novel transgenic plants in which the Z. mobilis glucokinase gene is expressed tuber-specifically (either in the wild type or apoplastic invertase-expressing background) was reported. The effect of increasing the glucokinase activity, independent of invertase activity, on the shift in carbon partitioning was evaluated and the possibility of bringing hexoses produced by the apoplastic cleavage of sucrose into metabolism was assessed. Expression of glucokinase either in the wild type or in the apoplastic invertase-expressing background led to changes in the levels of glucose and glucose 6-phosphate. However, these changes had little effect on carbon partitioning or tuber size with respect to the parent line. It is concluded that neither the accumulation nor the phosphorylation of glucose plays a pivotal role in the regulation of metabolism or morphology in the potato tuber

Descriptors: beta-fructofuranosidase. Carbohydrate-metabolism. Cytosol. Enzymes. Gene-expression. Genetic-transformation. Glucokinase. Glucose. Glucose-6-phosphate. Potatoes. Transgenic-plants. Tubers. Carbohydrates

67. Resistance reactions of leaves and tubers of rolC transgenic tetraploid potato to bacterial and fungal pathogens. Correlation with sugar, starch and chlorophyll content

Source: Physiological and Molecular Plant Pathology. 1993. 42 (2). 123-132

Author(s): Fladung M. Gieffers W

Abstract:

Infection of plants with Agrobacterium rhizogenes results in hairy root disease. Four different loci (rolA, B, C, D) located on the TL-DNA of the Ri plasmid are involved in the establishment of this disease. When the rolC gene was expressed alone in tetraploid potato plants, the transgenic plants displayed severe phenotypic and physiological alterations compared with untransformed controls. The resistance reaction of these transgenic plants to pathogens was tested to determine differences caused by the introduction of this foreign gene. The level of infection was correlated to contents of some leaf and tuber metabolites. A new bioassay was used to measure the resistance of leaves and tubers. The pathogens used were Alternaria alternata, Botrytis cinerea and Erwinia carotovora subsp. atroseptica. On leaves, the mean level of infection with both fungi was between 10 and 20% in both controls, whereas in rolC transformed potato clones the infection increased significantly up to 95%. The correlation between level of infection of the 2 fungi was high and significant. The infection level was positively correlated with fructose and glucose content. However, in tuber discs of all rolC potato clones the mean level of infection was lower (between 15 and 55%) than in the controls (between 75 and 95%). Measurements of the tuber content of the metabolites studied in leaves revealed a positive correlation of the infection level with glucose, dry matter and starch content. Considering the results obtained from both leaves and tubers, only glucose content was positively correlated with infection rates

Descriptors:Potatoes. Genetic-transformation. Resistance. Diseases. Breeding. Disease-resistance. Biotechnology. Root-crops. Plant-pathogenic-bacteria. Plant-pathology

68. Field performance of transgenic Russet Burbank and Lemhi Russet potatoes

Source: American Potato Journal. 1994. 71 (5). 285-296

Author(s): Belknap W R. Corsini D. Pavek J J. Snyder G W. Rockhold D R. Vayda M E

Abstract:

Agrobacterium tumefaciens-mediated transformation was used to introduce three different transgene constructs (containing GUS; cDNA encoding a tyrosine rich arylphorin, a larval serum protein from Galleria mellonella, fused to the signal peptide from Phaseolus vulgaris phytohaemaglutinin; and sequences encoding a lytic peptide (cecropin B)) into Russet Burbank and Lemhi Russet clones. The transformants were evaluated for performance under field conditions in Idaho, USA during 1990-92. They were characterized over two growing seasons using plants grown from greenhouse produced minitubers (first year) and field grown seed (second year). Individual clones were evaluated for a variety of agronomic and quality properties. Many of the transformed clones showed reduced yield, and increases in percent malformed and undersized tubers. Characteristics such as specific gravity and chip colour showed less variability. The variation observed in non-transgenic clones regenerated from tissue culture was less than that of the transformed lines. Out of an original population of 57 transgenic lines in tissue culture, maintenance of key agronomic and quality properties of the parental material was observed in only four clones. The results suggested that experiments designed to generate transgenic lines should be initiated with a large number of transgenic clones

Descriptors: P**otatoes. Transgenic-plants. -beta--glucuronidase. Reporter-genes. Crop-yield. Tubers. Insertional-mutagenesis. Specific-gravity. Colour. Food-processing-quality. Chips-(french-fries). Genetic-transformation. Yield-components. Processing-quality. Cultivars. Root-crops. Biotechnology**

69. Microbial and nematode communities associated with potatoes genetically modified to express the antimicrobial peptide magainin and unmodified potato cultivars

Source: Soil Biology & Biochemistry. 2008. 40 (6). 1446-1459

Author(s): O'Callaghan-M. Gerard-E-M. Bell-N-L. Waipara-N-W. Aalders-L-T. Baird-D-B. Conner-A-J

Abstract:

The antimicrobial peptide magainin II has activity against a range of micro-organisms. Tubers harvested from potatoes genetically modified (GM) to express a synthetic magainin gene show improved resistance to the bacterial pathogen Erwinia carotovora. The microbial and nematode communities associated with three magainin-expressing potato lines, their near-isogenic, unmodified parental cultivar (Iwa) and an unrelated cultivar (Karaka) were investigated on field-grown plants. Heterotrophic plate counts were used to enumerate aerobic culturable bacterial and fungal populations, while cultivation-independent analysis of bacterial communities was based on denaturing gradient gel electrophoresis (DGGE) of 16S rRNA gene fragments amplified from community DNA from phyllosphere, rhizosphere and geocaulosphere (tuber surface) samples. Small but statistically significant differences in the population sizes of culturable bacteria, fungi and yeast were detected among some GM magainin-expressing lines and the unmodified control. However, these differences were typically smaller than the differences between the unmodified parental line control (Iwa) and the unrelated cultivar control (Karaka). Similarly, the difference in the proportion of the nematode population belonging to the fungal feeding trophic group between Iwa and Karaka was greater than that amongst Iwa and its near-isogenic GM lines, and was significantly so for the genus Aphelenchus. The nematode channel ratio (NCR) indicated a more fungal-dominated decomposition channel in soil beneath Karaka compared to Iwa at harvest. In general, eubacterial phylloplane communities were similar for all lines, while the rhizosphere communities associated with two of the three GM lines differed from communities associated with their unmodified parental line control. When roots were senescent, there was no significant difference among potato lines in rhizosphere eubacterial communities or individual trophic groups of the nematode community. Greater diversity was found in geocaulosphere; -proteobacteria and actinomycete communities of two of the three GM lines differed significantly from their unmodified parental line control and the unrelated cultivar control, while the communities associated with the third GM line were more similar to those of the two control lines. This highlights the importance of testing several GM lines when assessing non-target effects. Results suggest that there is little likelihood of any major sustained non-target effect of genetic modification using a magainin II transgene on plant-associated and soil microflora and function

Descriptors:Biological-indicators. Cultivars. Decomposition. DNA. Gene-expression. Genes. Indicator-species. Nucleotide-sequences. Peptides. Phyllosphere. Plant-pathogenic-bacteria. Plant-pathogens. Potatoes. Rhizosphere. Ribosomal-RNA. Soil-bacteria. Soil-fungi. Transgenic-plants

70. Potato glycosterol rhamnosyltransferase, the terminal step in triose side-chain biosynthesis

Source: Phytochemistry. 2007. 68 (3). 327-334

Author(s): McCue-K-F. Allen-P-V. Shepherd-L-V-T. Blake-A. Maccree-M-M. Rockhold-D-R. Novy-R-G. Stewart-D. Davies-H-V. Belknap-W-R

Abstract:

Steroidal glycoalkaloids (SGAs) are potentially harmful specialty metabolites found in Solanaceous plants. Two tri-glycosylated alkaloids, alpha -chaconine and alpha -solanine accumulate in potato tubers. Expressed sequence tags (ESTs) were identified in the available database by searching for protein homology to the Sgt1 (SOLtu:Sgt1) steriodalalkaloid galactosyltransferase. The EST sequence data was used to isolate Sgt3 cDNA sequences by polymerase chain reaction (PCR) from a wounded potato tuber cDNA library. The resulting 1515 bp open reading frame of Sgt3, encodes a predicted SGT3 amino acid sequence that is 18 residues longer than, 45% identical to, and 58% homologous to the SGT1 protein. The amino-terminal region of the Sgt3 cDNA was used to create an antisense

transgene under control of the granule bound starch synthase, GBSS6, promoter and the ubiquitin, Ubi3, polyadenylation signal. Analysis of SGA metabolites in selected transgenic tubers revealed a dramatic decrease in the accumulation of alpha -chaconine and alpha -solanine. This decrease was compensated by an increase in beta -solanine and beta -chaconine with minor accumulation of alpha -SGAs. These results allowed the identification of the function for SGT3 as the beta -solanine/ beta -chaconine rhamnosyl transferase, the terminal step in formation of the potato glycoalkaloid triose side chains

Descriptors:amino-acid-sequences. biosynthesis. complementary-DNA. enzymes. expressed-sequence-tags. genetic-engineering. genetic-transformation. nucleotide-sequences. phytosterols. polymerase-chain-reaction. potatoes. steroid-alkaloids. transferases. transgenic-plants. tubers

71. The primary in vivo steroidal alkaloid glucosyltransferase from potato

Source: Phytochemistry. 2006. 67 (15). 1590-1597

Author(s): McCue-K-F. Allen-P-V. Shepherd-L-V-T. Blake-A. Whitworth-J. Maccree-M-M. Rockhold-D-R. Stewart-D. Davies-H-V. Belknap-W-R

Abstract:

To provide tools for breeders to control the steroidal glycoalkaloid (SGA) pathway in potato, we have investigated the steroidal alkaloid glycosyltransferase (Sgt) gene family. The committed step in the SGA pathway is the glycosylation of solanidine by either UDP-glucose or UDP-galactose leading to alpha -chaconine or alpha -solanine, respectively. The Sgt2 gene was identified by deduced protein sequence homology to the previously identified Sgt1 gene. SGT1 has glucosyltransferase activity in vitro, but in vivo serves as the UDP-galactose:solanidine galactosyltransferase. Two alleles of the Sgt2 gene were isolated and its function was established with antisense transgenic lines and in vitro assays of recombinant protein. In tubers of transgenic potato (Solanum tuberosum) cvs. Lenape and Desiree expressing an antisense Sgt2 gene construct, accumulation of alpha -solanine was increased and alpha -chaconine was reduced. Studies with recombinant SGT2 protein purified from yeast show that SGT2 glycosylation activity is highly specific for UDP-glucose as a sugar donor. This data establishes the function of the gene product (SGT2), as the primary UDP-glucose:solanidine glucosyltransferase in vivo

Descriptors:Alleles. Amino-acid-sequences. Biochemical-pathways. Enzyme-activity. Enzymes. Genes. Genetic-engineering. Genetic-transformation. Genetically-engineered-organisms. Genomics. Lines. Potatoes. Recombinant-proteins. Solanine. Steroid-alkaloids. Sugar-phosphates. Transgenic-plants. Tubers

72. Expression of beta -1,3-glucanase in flax causes increased resistance to fungi

Source: Physiological and Molecular Plant Pathology. 2004. 65 (5). 245-256

Author(s): Wrobel-Kwiatkowska-M. Lorenc-Kukula-K. Starzycki-M. Oszmianski-J. Kepczynska-E. Szopa-J

Abstract:

Flax (Linum usitatissimum L.) is an annual plant cultivated in moderate climates. Although the genus Linum contains about 230 species, Linum usitatissimum is the only species which fulfills a commercial function, serving as a fiber donor for the textile industry and the production of linseed oil. The flax breeding is often limited due to the decrease in yield caused by fungi infection. The ectopic expression of a potato beta -1,3-glucanase cDNA in flax has improved the plant's defence against pathogen. The resistance of transgenic lines against Fusarium oxysporum and Fusarium culmorum was about threefold higher than for the non-transformed plants. In an in vitro experiment the transgenic plant extract inhibited fungi growth and the inhibition was abolished by extract heating and anti-beta -glucanase antibody treatment. By further investigation into the molecular basis of transgenic flax resistance, the metabolic profiling of the plant was performed. The significant decrease in the content of carbohydrate, fatty acids and organic acids and the increase in the level of selected amino acids, polyamines and antioxidant were revealed. What is interesting is that the transgenic plants showed a significant decrease in lignin content, which may lead to the improvement of flax fibre retting.

Descriptors:Amino-acids; antioxidants-; beta-glucanase-; carbohydrates-; disease-resistance; enzyme-activity; enzymes-; fatty-acids; flax-; fungal-diseases; genetic-control; genetic-resistance; genetic-transformation; lignin-; metabolism-; organic-acids; plant-diseases; plant-pathogenic-fungi; plant-pathogens; polyamines-; transgenic-plants Fusarium-; Deuteromycotina-; Eumycota-; fungi-; Linum-; Linaceae-; Linales-; dicotyledons-; angiosperms-; Spermatophyta-; plants- Field-Crops; Plant-Breeding-and-Genetics; Plant-Physiology-and-Biochemistry; Viral-Bacterial-and-Fungal-Diseases-of-Plants; Host-Resistance-and-Immunity; Other-Control-Measures; Genetic-Engineering-Gene-Transfer-and-Transgenics

73. Expression of beta -1,3-glucanase in flax causes increased resistance to fungi

Source: Physiological and Molecular Plant Pathology. 2004. 65 (5). 245-256

Author(s): Wrobel-Kwiatkowska-M. Lorenc-Kukula-K. Starzycki-M. Oszmianski-J. Kepczynska-E. Szopa-J

Abstract:

Flax (Linum usitatissimum L.) is an annual plant cultivated in moderate climates. Although the genus Linum contains about 230 species, Linum usitatissimum is the only species which fulfills a commercial function, serving as a fiber donor for the textile industry and the production of linseed oil. The flax breeding is often limited due to the decrease in yield caused by fungi infection. The ectopic expression of a potato beta -1,3-glucanase cDNA in flax has improved the plant's defence against pathogen. The resistance of transgenic lines against

Fusarium oxysporum and Fusarium culmorum was about threefold higher than for the non-transformed plants. In an in vitro experiment the transgenic plant extract inhibited fungi growth and the inhibition was abolished by extract heating and anti-beta -glucanase antibody treatment. By further investigation into the molecular basis of transgenic flax resistance, the metabolic profiling of the plant was performed. The significant decrease in the content of carbohydrate, fatty acids and organic acids and the increase in the level of selected amino acids, polyamines and antioxidant were revealed. What is interesting is that the transgenic plants showed a significant decrease in lignin content, which may lead to the improvement of flax fibre retting.

Descriptors:Amino-acids; antioxidants-; beta-glucanase-; carbohydrates-; disease-resistance; enzyme-activity; enzymes-; fatty-acids; flax-; fungal-diseases; genetic-control; genetic-resistance; genetic-transformation; lignin-; metabolism-; organic-acids; plant-diseases; plant-pathogenic-fungi; plant-pathogens; polyamines-; transgenic-plants Fusarium-; Deuteromycotina-; Eumycota-; fungi-; Linum-; Linaceae-; Linales-; dicotyledons-; angiosperms-; Spermatophyta-; plants- Field-Crops; Plant-Breeding-and-Genetics; Plant-Physiology-and-Biochemistry; Viral-Bacterial-and-Fungal-Diseases-of-Plants; Host-Resistance-and-Immunity; Other-Control-Measures; Genetic-Engineering-Gene-Transfer-and-Transgenics

74. Transgenic resistance to PVYO associated with post-transcriptional silencing of P1 transgene is overcome by PVYN strains that carry highly homologous P1 sequences and recover transgene expression at infection

Source: Molecular Plant Microbe Interactions. 2000. 13 (4). 366-373

Author(s): Maki-Valkama-T. Valkonen-J-P-T. Kreuze-J-F. Pehu-E

Abstract:

Resistance to potato virus Y (PVY) has been obtained in our previous studies through expression of the PVY P1 gene in sense or antisense orientation in potato cv. Pito. In the present study, the mechanism and strain specificity of the resistance were analysed. Several features including low steady-state P1 mRNA expression in the resistant P1 plants indicated that resistance was based on post-transcriptional gene silencing (PTGS). Resistance was specific to PVYO isolates, the PVY strain group from which the P1 transgene was derived. However, according to group analyses, there was no distinguishing characteristic between the PVYO and PVYN strains P1 gene sequences. Therefore, the ability of the PVYN strains to overcome resistance could not be explained solely based on their P1 gene sequences. Infection with PVYN of the PVYO-resistant transgenic lines led to a recovery of expression of the P1 transgene. These data suggested that factors other than sequence homology are required in determination of the resistance specificity

Descriptors:Plant-diseases. Plant-pathogens. Potatoes. Transgenic-plants. Molecular-genetics. Gene-expression. Disease-resistance.

Determination. Strains. Transgenics. Nucleotide-sequences. Genetic-transformation. Root-crops. Control. Plant-pathology

75. **Transformation of Nicotiana benthamiana with the potato mop-top virus coat protein gene produces a novel resistance phenotype mediated by the coat protein**

Source: Molecular Plant Microbe Interactions. 1998. 11 (7). 626-633

Author(s): Barker-H. Reavy-B. McGeachy-K-D. Dawson-S

Abstract:

Transformed lines of Nicotiana benthamiana expressing a translatable transgene (CPtrans) encoding the coat protein (CP) gene of potato mop-top furovirus (PMTV) differed considerably in steady-state levels of transgene RNA transcript and CP that were positively correlated. A mean of 88% of transgenic T1 plants from 7 transgenic lines were resistant to manual PMTV inoculation. Resistance was identified by failure to develop symptoms in plants and inability to recover infectious virus with a sensitive infectivity assay: many of the 12% of transgenic plants that gave a positive infectivity assay did not produce symptoms and virus was not detected in repeat assays on the same plants. Resistant plants did not express a "recovery" phenotype and resistance was not overcome by use of RNA inoculum. Strong resistance was expressed in all CPtrans lines irrespective of the amount of transcript RNA or CP detected, and there was no evidence that resistance was mediated by a "transgene silencing" mechanism. Lines transformed with PMTV CP gene sequence in a nontranslatable form (CPnontrans) also contained differing steady-state levels of RNA transcript, but were not resistant to PMTV, although in some lines symptoms were slightly milder and were slower to develop than those in nontransgenic control plants. It is suggested that CPtrans is unique because, although it depends on CP translation to be effective, it mediates very strong resistance in 10 independent transformed lines (tested here and in other work)

Descriptors:Plant-diseases. Plant-pathogens. Coat-proteins. RNA. Genetic-transformation. Transgenic-plants. Disease-resistance. Phenotypes. Gene-expression. Molecular-genetics. Stimulant-plants. Plant-pathology

76. **Effects of chloroplast targeted potato virus Y coat protein on transgenic plants**

Source: Physiological and Molecular Plant Pathology. 1997. 50 (2). 67-83

Author(s): Naderi-M. Berger-P-H

Abstract:

The effects of potato Y potyvirus (PVY) coat protein (CP) accumulation in the chloroplast stroma compartment of a transgenic tobacco line (cv. Xanthi) were investigated. Leaf discs were transformed with PVY coat protein with (TP-CP) or without (CP) the ribulose bisphosphate carboxylase small subunit (rbcs) transit peptide (TP). When only PVY-CP lacking the rbcs transit peptide was transformed into tobacco, nearly all transformants were phenotypically normal, whereas many

TP-CP+ transformants were chlorotic or pale green. Western blot analyses indicated that CP in TP-CP+ plants is processed and accumulated in chloroplasts of transgenic plants. Transgenic lines expressing high levels of TP-CP were adversely affected, and this effect appeared to be solely due to CP. Light and electron microscopy revealed that chloroplast targeted PVY-CP disrupted chloroplast development and structure in cells. Western analysis of fractioned chloroplast proteins from TP-CP plants indicated that chloroplastic CP was associated with the thylakoid membrane fraction. The study showed that the PVY-CP is toxic to chloroplasts and is possibly involved with the development of symptoms

Descriptors:Plant-diseases. plant-pathogens. coat-proteins. molecular-genetics. tobacco. interactions. genetic-transformation. transgenic-plants. stimulant-plants. plant-pathology

77. The Rx gene confers resistance to a range of Potexviruses in transgenic Nicotiana plants

Source: Molecular Plant Microbe Interactions. 2008. 21 (9). 1154-1164

Author(s): Baures-I. Candresse-T. Leveau-A. Bendahmane-A. Sturbois-B

Abstract:

Rx-mediated resistance was analyzed in Rx-expressing transgenic Nicotiana plants. The infection outcome of nine Potato virus X isolates mutated at amino acid positions 121 and 127 of the coat protein (CP) confirmed the key role of these amino acids but provided a more complex picture than previously reported. In particular, in Rx-expressing Nicotiana spp., eliciting activity modulated by amino acid 121 was conditioned by the nature of amino acid 127. These results suggest that the specificity of recognition might be modulated by host factors that are somehow subtly modified between Rx-expressing potato and Rx-expressing transgenic Nicotiana plants. Moreover, the CP of three Potexviruses, Narcissus mosaic virus (NMV), White clover mosaic virus (WClMV), and Cymbidium mosaic virus (CymMV), are all recognized by the Rx-based machinery and able to trigger an Rx-dependant hypersensitive response. A smaller elicitor of 90 amino acids was identified in the CP of NMV and WClMV, which contains the previously identified key positions 121 and 127. This elicitor is only weakly conserved (approximately 40% identity) among the CP of the various recognized viruses, suggesting that the Rx molecular machinery targets a conserved structural element of the Potexvirus CP rather than a conserved amino acid motif

Descriptors:Disease-resistance. Gene-expression. Genes. Plant-pathogens. Plant-viruses. Transgenic-plants

78. Characterization of the recombinant forms arising from a Potato virus X chimeric virus infection under RNA silencing pressure

Source: Molecular Plant Microbe Interactions. 2006. 19 (8). 904-913

Author(s): Barajas-D. Tenllado-F. Diaz-Ruiz-J-R

Abstract:

Recombination is a frequent phenomenon in RNA viruses whose net result is largely influenced by selective pressures. RNA silencing in plants acts as a defence mechanism against viruses and can be used to engineer virus resistance. Here, we have investigated the influence of RNA silencing as a selective pressure to favour recombinants of PVX-HCT, a chimeric Potato virus X (PVX) vector carrying the helper-component proteinase (HC-Pro) gene from Plum pox virus (PPV). All the plants from two lines expressing a silenced HC-Pro transgene were completely resistant to PPV. However a significant proportion became infected with PVX-HCT. Analysis of viral RNAs accumulating in silenced plants revealed that PVX-HCT escaped silencing-based resistance by removal of the HC-Pro sequences that represented preferential targets for transgene-promoted silencing. The virus vector also tended to lose the HC-Pro insert when infecting transgenic plants containing a nonsilenced HC-Pro transgene or wild-type (wt) Nicotiana benthamiana plants. Nevertheless, loss of HC-Pro sequences was faster in nonsilenced transgenic plants than in wt plants, suggesting the transgene plays a role in promoting a higher selective pressure in favour of recombinant virus versions. These results indicate that the outcome of recombination processes depends on the strength of selection pressures applied to the virus

Descriptors: **Characterization. Gene-expression. Gene-silencing. Genes. Genetic-engineering. Genetic-transformation. Genetically-engineered-organisms. Plant-diseases. Plant-pathogens. Plant-viruses. RNA. Transgenic-plants**

79. The utility and management of transgenic plants with Bacillus thuringiensis genes for protection from pests

Source: Journal of New Seeds. 2003. 5 (1). 53-76

Author(s): Sharma-C. Sharma-K-K. Nadoor-Seetharama. Crouch-J-H

Abstract:

Recombinant DNA technology offers opportunities for widening the available gene pool for crop improvement. Genetic engineering also allows the introduction of several desirable genes in a single event, and can reduce the time to introgress novel genes into elite backgrounds. Genes conferring resistance to insects have been inserted into crop plants such as cotton, maize, potato, tobacco, rice, broccoli, lettuce, walnut, apple, lucerne, and soyabean. Genetically transformed crops with B. thuringiensis (Bt) genes have been deployed for cultivation primarily in the USA, China, Argentina, Canada, Mexico, South Africa, and Australia. The potential of insect-resistant transgenic plants with Bt genes can be enhanced when deployed in combination with alternate protective genes such as protease inhibitors, enzymes, and plant lectins, or in combination with insect-resistant cultivars derived through conventional breeding. While several transgenic crops with insecticidal genes have been introduced in the temperate regions, very little has been done to use this technology for improving crop production in the harsh environments of the tropics, where the need for increasing food production is most urgent. This may be due to the lack of infrastructure, biosafety regulations, intellectual property rights, or market potential. There is an urgent need to develop a scientifically sound strategy to deploy exotic and plant derived genes through transgenic plants for minimizing the extent of losses caused by insect pests. Equally important is the need for observance of biosafety regulations, a responsible public debate, and a better presentation of the benefits to sustainable crop production of a rational deployment of genetically transformed plants

Descriptors:Biological-control. Biological-control-agents. Crop-production. Genes. Genetically-engineered-organisms. Insecticide-resistance. Pest-control. Resistance-management. Transgenic-plants

80. Inhibitor potential of protease and alpha -amylase inhibitors of sweet potato and taro on the digestive enzymes of root crop storage pests

Source: Journal of Stored Products Research. 2004. 40 (4). 461-470
Author(s): Rekha-M-R. Sasikiran-K. Padmaja-G
Abstract:

The inhibitory potential of purified protease and [alpha]-amylase isoinhibitors of sweet potato and taro (5 accessions each) on the digestive enzymes of four major root crop pests viz, Araecerus fasciculatus, Sitophilus oryzae, Cylas formicarius elegantulus and Tribolium castaneum was studied under in vitro conditions. Wide differences in inhibitory potential were noticed among the isoinhibitors of a single accession as well as among the same isoinhibitor of the different accessions. The isoinhibitor SPAI1 from Kanhangad was inhibitory to all the four insect [alpha]-amylases (25-58% inhibition), while only 0.8-15% inhibition was exerted by the isoinhibitor SPAI1 from S 1195. Very high inhibition of A. fasciculatus and C. formicarius elegantulus [alpha]-amylases (73-94%) was caused by isoinhibitors SPAI2 and SPAI4 from the sweet potato accession S 56-2. Cylas formicarius elegantulus [alpha]-amylases were inhibited to a greater extent by the taro [alpha]-amylase inhibitor. Among the four insect proteases, those from A. fasciculatus and T. castaneum were not appreciably inhibited by the protease isoinhibitors of sweet potato and taro. The S. oryzae protease was inhibited by 51% by isoinhibitor SPI2, while only 3% inhibition was caused by isoinhibitor SPI4. The selective inhibitory potential of the isoinhibitors of sweet potato and taro on the digestive enzymes of root crop pests could be exploited for making transgenic plants with improved resistance against major pests

81. Combining genetic engineering and traditional breeding to provide elevated resistance in potatoes to Colorado potato beetle

Source: Entomologia Experimentalis et Applicata. 2004. 112 (1). 37-46

Author(s): Cooper-S-G. Douches-D-S. Grafius-E-J

Abstract:

The sustainable deployment of resistant crop varieties is a critical issue for the implementation of biotechnology in crop pest management. Feeding, biomass accumulation, and mortality were evaluated for susceptible, insecticide-resistant, and Bacillus thuringiensis (Bt) Cry 3A-selected Colorado potato beetle (Leptinotarsa decemlineata Say) (Coleoptera, Chrysomelidae) larvae fed on: cultivated potato, a Solanum chacoense line expressing leptine glycoalkaloids, a transformed line expressing Bt toxin, or the leptine line transformed to express Bt toxin. Larvae selected for resistance to Bt-Cry3A performed better on Bt foliage, but not as well on the leptine foliage, compared to susceptible or insecticide-resistant larvae. Neither leptine nor Bt toxin completely inhibited the feeding and growth of 3rd and 4th instars of all three strains of Colorado potato beetle. However, for all three strains of Colorado potato beetle on leptine+Bt foliage, feeding was almost zero, growth was zero or negative, and mortality was near 100%

Descriptors:Bacterial-toxins. Developmental-stages. Foliage. Genetic-engineering. Genetic-transformation. Glycoalkaloids. Pest-resistance. Susceptibility. Transgenic-plants

82. **Elicitation of Rx-mediated resistance to PVX in potato does not require new RNA synthesis and may involve a latent hypersensitive response**

Source: Molecular Plant Microbe Interactions. 1998. 11 (8). 833-835

Author(s): Gilbert-J. Spillane-C. Kavanagh-T-A. Baulcombe-D-C

Abstract:

The Rx gene in potatoes confers extreme resistance against potato X potexvirus (PXV) that is elicited by the viral coat protein (CP). Using actinomycin D to inhibit transcription of nuclear genes, it was shown that Rx is expressed prior to virus inoculation, and that induction of the resistance mechanism does not require novel gene expression or continued transcription of previously expressed genes. It was also shown that transgenic plants carrying a CP transgene from an Rx-avirulent PXV in an Rx background could not be produced. It is suggested that Rx-mediated resistance involves a mechanism that suppresses viability of plant cells

Descriptors:Disease-resistance. Protoplasts. Potatoes. Plant-diseases. Plant-pathogens. Gene-expression. Genes. Coat-proteins. Hypersensitivity. Transgenic-plants. Genetic-transformation. RNA. Molecular-genetics. Root-crops. Plant-pathology

83. **Expression of an engineered cecropin gene cassette in transgenic tobacco plants confers disease resistance to Pseudomonas syringae pv. tabaci**

Source: Phytopathology. 1997. 87 (5). 494-499

Author(s): Huang-Y. Nordeen-R-O. Di-M. Owens-L-D. McBeath-J-H

Abstract:

A chimaeric gene fusion cassette, consisting of a secretory sequence from barley alpha -amylase joined to a modified cecropin (MB39) coding sequence, and placed under control of the promoter and terminator from the potato proteinase inhibitor II (PiII) gene, was introduced into tobacco by Agrobacterium-mediated transformation. Transgenic and control plants reacted differently when inoculated with P. s. pv. tabaci at various cell concn. With control plants (transformed with a PiII-GUS (beta -D-glucuronidase) gene fusion), necrosis was clearly visible in leaf tissue infiltrated with bacterial inoculum levels of 102, 103, 104, 105 and 106 c.f.u./ml. With MB39-transgenic plants, necrosis only occurred in the areas infiltrated with 105 or 106 c.f.u./ml. No necrosis occurred in areas infiltrated with bacterial concn of 104 c.f.u./ml or less. Bacterial multiplication in leaves of MB39-transgenic plants was suppressed >10-fold compared with control plants, and absence of disease symptom development was associated with this growth suppression. It is concluded that the pathogen-induced promoter and the secretory sequence were competent elements for transforming a cecropin gene into an effective disease-control gene for plants

Descriptors: **Molecular-genetics. Disease-resistance. Plant-diseases. Plant-pathogens. Plant-pathogenic-bacteria. Transgenic-plants. Tobacco. Genetic-engineering. Resistance. Genetic-transformation. Stimulant-plants. Biotechnology. Plant-pathology**

84. Growth and phenotype of potato plants expressing an antisense gene of P-protein of glycine decarboxylase under control of a promoter with preference for the mesophyll

Source: Annals of Applied Biology. 2001. 138 (1). 9-15
Author(s): Winzer-T. Heineke-D. Bauwe-H
Abstract:

A cDNA encoding P-protein of glycine decarboxylase was expressed in antisense orientation in leaves of potato (Solanum tuberosum cv. Solara) under control of the promoter of a P-protein gene of glycine decarboxylase from Flaveria pringlei. This promoter targets gene expression preferentially to the leaf mesophyll cells. In two of the transgenic lines, mitochondria oxidized glycine only with extremely low rates. Phenotypically, these transgenic lines were only marginally different from wild-type plants under ambient carbon dioxide concentrations and indistinguishable from wild-type plants when grown under 800 ppm carbon dioxide. When grown in ambient carbon dioxide, transgenic plants accumulated high amounts of glycine during the light period followed by nearly complete degradation in the following night

Descriptors:Carbon-dioxide. Complementary-DNA. Gene-expression. Genes. Glycine. Growth. Mesophyll. Phenotypes. Potatoes. Promoters

85. Resistance of tomato infected with cucumber mosaic virus satellite RNA to potato spindle tuber viroid

Source: Annals of Applied Biology. 1996. 129 (3). 543-551
Author(s): Yang-XiCai. Kang-LiangYi. Tien-Po
Abstract:

Tomato cultivars Rutgers and Lichun plants were firstly pre-inoculated either with a cucumber mosaic cucumovirus (CMV) isolate containing satellite RNA (CMV-S52) or with a CMV isolate without satellite RNA, and then challenged 14 d later with a severe strain of potato spindle tuber viroid (PSTVd). In addition, tomato plants transformed with CMV satellite cDNA and non-transgenic control plants were directly inoculated with PSTVd. Protection effects were assessed by observation of symptoms and by assay of PSTVd accumulation in tomato plants using return PAGE and silver staining. The results indicated that satellite-transgenic plants and plants pre-inoculated with CMV-S52 showed much milder symptoms of PSTVd infection than the respective control plants. Concn of PSTVd RNA in the satellite-transgenic plants and CMV-S52 pre-inoculated plants was reduced to c. 0.02-0.03 of the controls. PSTVd infection did not increase the amount of satellite dsRNA in plants. It is concluded that the plant resistance to PSTVd is induced by the presence of satellite RNA rather than the CMV infection. It is suggested that as there is considerable sequence similarity between satellite RNA and PSTVd, base pairings may be a cause of reduction of both symptoms and the accumulation of PSTVd

Descriptors:Plant-diseases. Plant-pathogens. Disease-resistance. Transgenic-plants. Rna. Tomatoes. Induced-resistance. Genetic-transformation. Vegetables. Plant-patho

86. Genetically engineered protection against viruses in transgenic plants

Source: Annual Review of Microbiology. 1993. 47 . 739-763

Author(s): Fitchen J H. Beachy R N

Abstract:

Transgenic plants carrying nucleotide sequences derived from plant viruses can exhibit increased resistance to viral disease. Many viral sequences confer some level of either resistance to infection or suppression of disease symptoms (tolerance). The transgene may act on initiation of infection, replication of virus, spread of the infection throughout the plant and symptom development. More than one of these processes can be impaired by a single transgene derived from a single viral gene. The level of protection ranges from very low to high, while the breadth of protection ranges from very narrow, where protection is only observed against closely related strains of the virus from which the transgene was derived, to moderately broad, extending to other viruses. Data are insufficient to establish a molecular mechanism of resistance for most of the described examples. In addition, although the use of a particular segment of the viral genome confers resistance in one virus-host system, analogous sequences from a different virus in another host may be ineffective. Information is reviewed under the following headings: protection conferred by sequences encoding viral coat proteins, including individual examples of resistance, mechanisms of resistance, and application to virology and agriculture; protection conferred by sequences encoding replicase-related proteins, including resistance to tobacco mosaic tobamovirus, pea early browning tobravirus, potato virus X [potato X potexvirus] and cucumber mosaic cucumovirus, and mechanisms of replicase-mediated resistance; protection conferred by the accumulation of RNA; and protection conferred by transgenic copies of mild strains, satellites and satellite RNAs, and defective interfering viruses

Descriptors: **Disease-resistance. RNA. Transgenic-plants. Genetic-engineering. Reviews. Coat-proteins. Plant-pathogens. Resistance. Plant-pathology**

87. **Modification at the N-terminus of the potato virus Y capsid protein CP does not interfere with Cp-mediated virus resistance in transgenic potato (Solanum tuberosum L.)**

Source: Journal of Genetics & Breeding. 1993. 47 (1). 89-93

Author(s): Wefels E. Salamini F. Rohde W

Abstract:

Two strategies for expression of the potato Y potyvirus capsid protein (CP) gene in transgenic potato lines are described. Utilization of the potyviral NIa protease activity or of in frame AUG translational start codons located upstream of the CP coding region regulate the synthesis of either wild-type or N-terminally modified capsid proteins. Both approaches result in virus resistance, and the N-terminal extension of PVY CP by up to 41 amino acid residues does not interfere with CP-mediated virus resistance

Descriptors: **Potatoes. Biotechnology. Genetic-transformation. Molecular-genetics. Gene-expression. Coat-proteins. Diseases. Resistance. Root-crops. Plant-pathology**

88. **Prospects for using transgenic resistance to insects in crop improvement**

Source: Electronic Journal of Biotechnology. 2000. 3 (2). 76-95

Author(s): Sharma-H-C. Sharma-K-K. Nadoor-Seetharama. Ortiz-R

Abstract:

Integrated pest management has historically placed great hopes on host plant resistance. However, conventional host-plant resistance to insects involves quantitative traits at several loci. As a result, the progress has been slow and difficult to achieve. With the advent of genetic transformation techniques, it has become possible to clone and insert genes into the crop plants to confer resistance to insect pests. Resistance to insects has been demonstrated in transgenic plants expressing genes for delta -endotoxins from Bacillus thuringiensis (Bt), protease inhibitors, enzymes and plant lectins. Most of the plant derived genes produce chronic rather than toxic effects and some insect pests are not sensitive to some of these factors. The potential of plant derived genes can be realized by deploying them in combination with host plant resistance and exotic genes. Genes conferring resistance to insects have been inserted into crop plants such as maize, cotton, potato, tobacco, potatoes, rice, broccoli, lettuce, walnuts, apples, alfalfa and soyabean. Genetically transformed crops with Bt genes have been deployed for cultivation in USA, China and Australia. However, very little has been done to use this technology for improving crop production in the harsh environments of the tropics, where the need for increasing food production is most urgent. International agricultural research centres, advanced research institutes and the seed sector should make an effort to use these new tools for increasing food production in poorer regions of the world. There is an urgent need to develop a scientifically sound strategy to deploy exotic and plant derived genes for minimizing the extent of losses caused by insect pests. Equally important is the need for following the biosafety regulations, more responsible public debate, social attitude and better presentation of the benefits for a rational deployment of the genetically transformed plants

Descriptors:Apples. Broccoli. Endotoxins. Gene-expression. Gene-transfer. Genes. Genetic-improvement. Genetic-transformation. Genetically-engineered-organisms. Induced-resistance. Insect-pests. Lettuces. Lucerne. Maize. Pest-resistance. Plant-pests. Potatoes. Reviews. Rice. Soyabeans. Tobacco. Transgenic-plants. Walnuts

89. Reduction of divinyl ether-containing polyunsaturated fatty acids in transgenic potato plants

Source: Phytochemistry. 2007. 68 (6). 797-801

Author(s): Eschen-Lippold-L. Rothe-G. Stumpe-M. Gobel-C. Feussner-I. Rosahl-S

Abstract:

Oxygenated polyunsaturated fatty acids synthesized via the lipoxygenase pathway play a role in plant responses to pathogen attack. In solanaceous plants, the preferential stimulation of the 9-lipoxygenase pathway in response to pathogen infection leads to the formation of the divinyl ether-containing polyunsaturated fatty acids colneleic and colnelenic acid, as well as hydroxy and trihydroxy polyunsaturated fatty acids. To functionally assess the role of divinyl ethers, transgenic potato plants were generated which express an RNA interference construct directed against the pathogen-inducible 9-divinyl ether synthase. Efficient reduction of 9-divinyl ether synthase transcript accumulation correlated with reduced levels of colneleic and colnelenic acid. However, in response to infection with virulent Phytophthora infestans, the causal agent of late blight disease, no significant differences in pathogen biomass could be detected suggesting that the levels of antimicrobial divinyl ethers are not critical for defence against Phytophthora infestans in a compatible interaction

Descriptors:biochemical-pathways. Disease-resistance. Fungal-diseases. Induced-resistance. Plant-diseases. Plant-pathogenic-fungi. Plant-pathogens. Polyenoic-fatty-acids. Potatoes. Transgenic-plants

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Descriptors: **Biochemical-pathways. Disease-resistance. Fungal-diseases. Induced-resistance. Plant-diseases. Plant-pathogenic-fungi. Plant-pathogens. Polyenoic-fatty-acids. Potatoes. Transgenic-plants**

91. Expression of the peroxidase gene promoter (Shpx6b) from Stylosanthes humilis in transgenic plants during insect attack

Source: Entomologia Experimentalis et Applicata. 2004. 111 (3). 165-171

Author(s): Perera-M-R. Jones-M-G-K

Abstract:

Inducible promoters are important in regulating the expression of resistance genes when plants are attacked by insects or pathogens. Evaluation of the Shpx6b peroxidase promoter from the tropical forage legume Stylosanthes humilis [Curtis MD, Rae AL, Rusu AG, Harrison SJ & Manners JM (1997) A peroxidase gene promoter induced by phytopathogens and methyl jasmonates in transgenic plants. Molecular Plant Microbial Interactions 10: 326-338] in transgenic tobacco plants Nicotiana tabacum L. (Solanaceae) demonstrated that this promoter could drive expression of both the beta -glucuronidase (GUS uidA gene of E. coli) and green fluorescent protein (GFP) reporter genes in leaf tissues during attack by chewing insects - larvae of potato tuber moth (PTM) Phthorimaea operculella Zeller (Lepidoptera: Gelechiidae) and sucking insects - green peach aphids Myzus persicae Sulzer (Homoptera: Aphididae). Strong GUS expression was present in tissues next to cells damaged by PTM larvae 24 h after infestation. With aphid infestation, GUS expression was limited to sites of feeding, and was observed 48 h after infestation. The expression of GFP mirrored that of GUS expression for both treatments, but was normally detected 48 h after infestation. Similarly, the exogenous application of methyl jasmonate (MeJa) induced GUS uniformly across leaf tissue, and mechanical wounding activated GUS expression at wound sites, similar to PTM larvae. GFP expression was observed 48 h after treatment, and for mechanical wounding GFP was localized in a manner similar to PTM damage. For MeJa treatment, GFP expression was more pronounced in cells around the midrib, and it was not uniformly induced across the leaf tissue. GUS reporter gene levels were also assayed to quantify expression, and the results were consistent with the observed histological patterns of expression. The results presented here show that the Shpx6b promoter switches on the expression of linked genes after damage by insect herbivores, and could be useful in regulating the expression of heterologous genes for insect and/or pathogen resistance in transgenic plants

Descriptors: **beta-glucuronidase. Enzymes. Gene-expression. Genes. Genetic-transformation. Insect-pests. Leaves. Methyl-jasmonate. Peroxidase. Plant-pests. Promoters. Reporter-genes. Tobacco. Transgenic-plants**

92. The effect of genetic transformations for pest resistance on foliar solanidine-based glycoalkaloids of potato (Solanum tuberosum)

Source: Annals of Applied Biology. 2002. 140 (2). 143-149

Author(s): Birch-A-N-E. Geoghegan-I-E. Griffiths-D-W. McNicol-J-W

Abstract:

Foliage of potato cv. Desiree was harvested from glasshouse-cultivated plants of five experimental transgenic lines expressing three different insecticidal proteins (snowdrop lectin, Galanthus nivalis agglutinin (GNA); jackbean lectin, Concanavalin A (Con A), cowpea trypsin inhibitor; (CpTi)), tissue-cultured control plants and standard control (non-tissue cultured) plants. The foliage was subdivided into stems, upper, middle and lower leaves and analysed separately by HPLC for the solanidine-based glycoalkaloids alpha -solanine and alpha -chaconine. The results demonstrate that one or more stages in the plant transformation process (i.e. insecticidal- and marker-gene insertions, gene expression and tissue culture) resulted in a lower level of leaf glycoalkaloids than that found in either the tissue-cultured controls or standard controls, based on the selected potato lines transformed for insecticidal protein expression. However, the distribution of glycoalkaloids throughout the plant foliage was unaffected by genetic transformation and tissue culture, with the highest glycoalkaloid levels being observed in the top third of the plant. The importance of investigating unexpected effects of genetic engineering on plant secondary metabolism is discussed from an ecological viewpoint

Descriptors:Agglutinins. Concanavalin-A. Foliage. Gene-expression. Genes. Genetic-engineering. Genetic-transformation. Glycoalkaloids. In-vitro-culture. In-vitro-regeneration. Insect-pests. Insecticidal-properties. Lectins. Lines. Marker-genes. Pest-resistance. Plant-pests. Potatoes. Secondary-metabolites. Tissue-culture. Transgenic-plants. Trypsin-inhibitors

93. Potential impact of Coleomegilla maculata predation on adaptation of Leptinotarsa decemlineata to Bt-transgenic potatoes

Source: Entomologia Experimentalis et Applicata. 1997. 82 (1). 91-100

Author(s): Arpaia-S. Gould-F. Kennedy-G

Abstract:

The relationship between Leptinotarsa decemlineata egg density and Coleomegilla maculata predatory behaviour was investigated at different spatial scales (plant-to-plant and plot-to-plot). Both adult C. maculata location and daily egg consumption rates were monitored over time in greenhouse and field tests in North Carolina. Despite aggregation in areas of highest prey density by C. maculata, egg consumption was inversely related to egg mass density at the smallest and the largest spatial scales tested. The experimental data on predation rates in high and low density field treatments were included in a mathematical model to simulate impact of natural enemies on the rate of L. decemlineata adaptation to Bt [Bacillus thuringiensis]-toxin-expressing transgenic potato plants when Bt-expressing plants are mixed at the plot-to-plot level with normal potato plants. Results showed that C. maculata predatory behaviour could decrease the rate at which L. decemlineata adapted to Bt-toxins if plot-to-plot mixed-plantings were used

Descriptors:Models. Predatory-arthropods. Transgenic-plants. Natural-enemies. Entomopathogenic-bacteria. Predators. Prey. Potatoes. Pest-resistance. Genetic-engineering. Fields. Behaviour. Insect-pests. Genetic-transformation. Root-crops. Biotechnology. Genetics. Biology. Agricultural-entomology

94. Pathogenesis-related protein 1a is induced in potato virus Y-infected plants as well as by coat protein targeted to chloroplasts

Source: Physiological and Molecular Plant Pathology. 1997. 51 (1). 41-44
Author(s): Naderi-M. Berger-P-H
Abstract:

Previously, the presence of potato Y potyvirus (PYV) coat protein (PYV-CP) was observed inside chloroplasts of infected tobacco plant cells. Induction of symptoms reminiscent of virus infection was observed only in transgenic plants accumulating CP in the chloroplasts but not in the cytoplasm. The results suggested that PYV-CP plays a role in symptom development. Plants with high levels of CP in their chloroplasts were more susceptible to PYV, suggesting that there was a host response to the presence of PYV-CP in the chloroplasts. To investigate whether PYV infection and/or chloroplast-targeted PV-CP resulted in a host stress response, levels of pathogenesis-related protein 1-a (PR-1a) were determined in these plants as an indicator of the host response. The results indicated that the expression of PR-1a was induced in chloroplast-targeted PYV-CP transgenic plants, but not in transgenic plants expressing PYV-CP cytosolically. The level of PR-1a in plants appeared to correspond with the severity of symptoms

Descriptors:Plant-diseases. Plant-pathogens. Chloroplasts. Coat-proteins. Molecular-genetics. Pathogenesis-related-proteins. Tobacco. Symptoms. Genetic-transformation. Disease-resistance. Plant-pathology

95. Genetic engineering and the improvement of rice and cotton

Source: Agriculture et Developpement. 1995. (6). 16-27
Author(s): Pannetier-C. Guiderdoni-E. Hau-B
Abstract:

The transfer of genes encoding entomopathogenic proteins makes it possible to create rice and cotton cultivars with resistance to insect pests. Pest resistant lines have been developed in cotton [Gossypium hirsutum], poplar

[Populus spp.], potato, rice and maize through the introduction of genes encoding the insecticidal proteins of the bacterium Bacillus thuringiensis (Bt). Cotton was first transformed in 1987 using Agrobacterium tumefaciens-mediated transformation and regeneration via somatic embryogenesis. Insecticidal properties of several lines were confirmed in the field after modification of the nucleotide sequence of the Bt gene used, since Bt genes are very weakly expressed in plants. CIRAD, in collaboration with INRA, is studying the transformation of cotton using A. tumefaciens for resistance to Heliothis armigera (Bt gene, cryIA(b)) and to Spodoptera littoralis (Bt gene, cryIC). However, the use of plants synthesizing a single Bt toxin may result in the development of resistance in the insects targeted. Different strategies can be used to prevent the occurrence of such resistance. That studied by the CIRAD/INRA team consists of combining two genes encoding entomopathogenic proteins with different modes of action: Bt toxins and protease [proteinase] inhibitors. Transgenic cotton plants incorporating a Bt gene or expressing a protease inhibitor gene have been obtained and have set seed. CIRAD is developing Mediterranean rice cultivars with resistance to borers (Chilo suppressalis, Maliarpha separatella and C. zacconius) by genetic transformation of protoplasts. Overall, the application of genetic engineering to cultivated plants has been slower than expected, but transgenic cultivars will soon be available on the market. Analysis of the impact for cropping techniques and the environment should precede the release of transgenic cultivars

Descriptors:Cotton. Rice. Plant-breeding. Genetic-engineering. Insect-pests. Pest-resistance. Potatoes. Maize. Somatic-embryogenesis. In-vitro-culture. Genes. Toxins. Proteinase-inhibitors. Protoplasts. Transgenic-plants. Genetic-transformation. Gene-expression. Breeding. Biosafety. Fibre-plants. Biotechnology. Cereals

96. Phenotypes and functional effects caused by various viral RNA silencing suppressors in transgenic Nicotiana benthamiana and N. tabacum

Source: Molecular Plant Microbe Interactions. 2008. 21 (2). 178-187

Author(s): Siddiqui-S-A. Sarmiento-C. Truve-E. Lehto-H. Lehto-K

Abstract:

RNA silencing suppressor genes derived from six virus genera were transformed into Nicotiana benthamiana and N. tabacum plants. These suppressors were P1 of Rice yellow mottle virus (RYMV), P1 of Cocksfoot mottle virus, P19 of Tomato bushy stunt virus, P25 of Potato virus X, HcPro of Potato virus Y (strain N), 2b of Cucumber mosaic virus (strain Kin), and AC2 of African cassava mosaic virus (ACMV). HcPro caused the most severe phenotypes in both Nicotiana spp. AC2 also produced severe effects in N. tabacum but a much milder phenotype in N. benthamiana, although both HcPro and AC2 affected the leaf tissues of the two Nicotiana spp. in similar ways, causing hyperplasia and hypoplasia, respectively. P1-RYMV caused high lethality in the N. benthamiana plants but only mild effects in the N. tabacum plants. Phenotypic alterations produced by the other transgenes were minor in both species. Interestingly, the suppressors had very different effects on crucifer-infecting Tobamovirus (crTMV) infections. AC2 enhanced both spread and brightness of the crTMV-green fluorescent protein (GFP) lesions, whereas 2b and both P1 suppressors enhanced spread but not brightness of these lesions. P19 promoted spread of the infection into new foci within the infiltrated leaf, whereas HcPro and P25 suppressed the spread of crTMV-GFP lesions

Descriptors: **Genetic-engineering. Genetic-transformation. Phenotypes. Phenotypic-variation. Plant-diseases. Plant-pathogens. Plant-viruses. RNA-interference. Tobacco. Transgenic-plants**

97. **Some physical and nutritional characteristics of genetically modified potatoes varying in amylose/amylopectin ratios**

Source: Food Chemistry. 2007. 100 (1). 136-146

Author(s): Karlsson-M-E. Leeman-A-M. Bjorck-I-M-E. Eliasson-A-C

Abstract:

Transgenically modified potatoes with a large spread in amylose/amylopectin ratios were analysed both as tubers and in the form of isolated starch. Different microscopic techniques were used to study starch granules and tuber tissue. Starch gelatinisation properties and recrystallisation of amylopectin and amylose were studied by differential scanning calorimetry. Starch bioavailability and resistant starch (RS) were evaluated using enzymatic in vitro procedures. Glyc'mic indices (GI) were predicted from low molecular weight carbohydrates (LMWC) contents and the in vitro hydrolysis rate of the starch moiety. For many of the examined parameters, differences of varying magnitude were found between the potato lines, especially for high amylose lines. High amylose starch granules had irregular shapes and showed only a limited swelling. Moreover, contents of RS and recrystallised amylose were elevated. GI's for the starch moiety were reduced, though elevated contents of LMWC caused a high over-all predicted GI

Descriptors: **Amylopectin. Amylose. Bioavailability. Carbohydrates. Genetic-engineering. Genetic-transformation. Genetically-engineered-organisms. Hydrolysis. Lines. Nutritive-value. Plant-tissues. Potato-starch. Potatoes. Recrystallization. Transgenic-plants. Tubers**

98. **Potato plants genetically modified to produce N-acylhomoserine lactones increase susceptibility to soft rot Erwiniae**

Source: Molecular Plant Microbe Interactions. 2004. 17 (8). 880-887

Author(s): Toth-I-K. Newton-J-A. Hyman-L-J. Lees-A-K. Daykin-M. Ortori-C. Williams-P. Fray-R-G

Abstract:

Many gram-negative bacteria employ N-acylhomoserine lactones (AHL), to regulate diverse physiological processes in concert with cell population density (quorum sensing (QS)). In the plant pathogen Erwinia carotovora, the AHL synthesized via the carI/expI genes are responsible for regulating the production of secreted plant cell wall-degrading exoenzymes and the antibiotic carbapen-3-em carboxylic acid. We have previously shown that targeting the product of an AHL synthase gene (yenI), from Yersinia enterocolitica to the chloroplasts of transgenic tobacco plants caused the synthesis in planta of the cognate AHL signalling molecules N-(3-oxohexanoyl)-L-homoserine lactone (3-oxo-C6-HSL), and N-hexanoylhomoserine lactone (C6-HSL), which in turn, were able to complement a carI- QS mutant. In the present study, we demonstrate that transgenic potato plants containing the yenI gene are also able to express AHL and that the presence and level of these AHL in the plant increases susceptibility to infection by E. carotovora. Susceptibility is further affected by both the bacterial level and the plant tissue under investigation

Descriptors:Gene-expression. Genes. Genetic-transformation. Lactones. Plant-pathogenic-bacteria. Plant-pathogens. Potatoes. Susceptibility. Transgenic-plants

99. The fungal gene Avr9 and the oomycete gene inf1 confer avirulence to potato virus X on tobacco

Source: Molecular Plant Microbe Interactions. 1999. 12 (5). 459-462

Author(s): Kamoun-S. Honee-G. Weide-R. Lauge-R. Kooman-Gersmann-M. Groot-K-de. Govers-F. Wit-P-J-G-M-de

Abstract:

The AVR9 peptide of Cladosporium fulvum [Fulvia fulva] and the INFI protein of Phytophthora infestans elicit the hypersensitive response (HR) on Cf9 tomato or Cf-9 transgenic tobacco and on all cultivars of tobacco, respectively. Expression of either the functional Avr9 or inf1 genes from engineered potato X potexvirus (PVX) genomes resulted in localized HR lesions on tobacco plants responsive to the elicitors and inhibited spread of the recombinant virus. In contrast, PVX derivatives producing mutant forms of AVR9 and INF1 with reduced elicitor activity caused systemic necrotic and/or mosaic symptoms, and were unable to inhibit PVX spread. These results demonstrated that HR is a highly versatile defense mechanism active against unrelated pathogens irrespective of the HR-inducing agent, and that resistance to recombinant PVX in tobacco is correlated with the strength of the transgene-encoded elicitor

Descriptors:Tomatoes. Transgenics. Tobacco. Gene-expression. Cultivars. Defence-mechanisms. Derivatives. Genes. Genomes. Mutants. Plant-pathogens. Responses. Symptoms. Plant-pathogenic-fungi. Disease-resistance. Transgenic-plants. Stimulant-plants. Plant-pathology

100. Comparison of the hypersensitive response induced by the tomato Cf-4 and Cf-9 genes in Nicotiana spp

Source: Molecular Plant Microbe Interactions. 2000. 13 (4). 465-469

Author(s): Thomas-C-M. Tang-SaiJun. Hammond-Kosack-K. Jones-J-D-G

Abstract:

We have previously shown that tomato Cf-9 induces an Avr9-dependent hypersensitive response (HR) in Nicotiana tabacum and potato. We show here that Cf-4 also induces an Avr4-dependent HR in two tobacco species (N. tabacum and N. benthamiana). The HR induced by Cf-4 and Cf-9 was compared in stable tobacco transgenics by a seedling lethal assay and resistance to recombinant potato virus X expressing Avr4 or Avr9. We also compared HR induction with Agrobacterium-mediated transient expression. The Cf-4/Avr4 combination induced a more rapid HR than Cf-9/Avr9. Sensitive assays for Cf-9 and Cf-4 function should prove useful for structure/function analyses of these resistance proteins in tobacco

Descriptors:Plant-diseases. Plant-pathogens. Tobacco. Disease-resistance. Transgenic-plants. Transgenics. Molecular-genetics. Gene-expression. Genes. Genetic-transformation. Stimulant-plants. Control. Plant-pathology. Tomatoes

101. Consumer acceptance of genetically modified potatoes

Source: American Journal of Potato Research. 2002. 79 (5). 309-316

Author(s): Guenthner-J-F

Abstract:

Slow consumer acceptance has inhibited the market for genetically modified (GM) potato products. Logistic growth functions were used to model market development patterns for three comparable products - diet sodas, frozen potatoes and microwave ovens.

Descriptors:Biotechnology. Consumer-attitudes. Models. Potatoes. Prediction. Transgenic-plants

102. Minor modifications to the cry1Ac9 nucleotide sequence are sufficient to generate transgenic plants resistant to Phthorimaea operculella

Source: Annals of Applied Biology. 2001. 138 (3). 281-292

Author(s): Beuning-L-L. Mitra-D-S. Markwick-N-P. Gleave-A-P

Abstract:

Minor modifications were made sequentially to the nucleotide sequence of truncated cry1Ac9 to produce cry1Ac9A (one nucleotide change) and then cry1Ac9B (seven nucleotide changes). The derivative genes under the control of the CaMV 35S promoter were transformed into Nicotiana tabacum (cv. Samsun) to determine whether these modified genes conferred resistance on the resulting transgenic tobacco plants to larvae of the potato tuber moth (PTM, P. operculella). Over two trials with PTM larvae on the transgenic plants expressing the cry1Ac9B gene, lower larval growth, development and survival was evident for most of the lines compared to the control plants. In the second trial, for four of these lines (7, 25, 26 and 28) larval growth rates were very low (0.28, 0.3, 0.42 and 0.28, respectively) compared to the control growth rate (4.18) and leaf damage was minimum. Northern and

Descriptors:Genes. Genetic-transformation. Growth. Insect-pests. Lines. Messenger-RNA. Nucleotide-sequences. Pest-resistance. Plant-pests. Promoters. Survival. Tobacco. Transgenic-plants

103. Longevity of phytophagous heteropteran predators feeding on transgenic Btt-potato plants

Source: Entomologia Experimentalis et Applicata. 2000. 95 (3). 329-333
Author(s): Armer-C-A. Berry-R-E. Kogan-M
Abstract:

The effect of direct feeding of plant-feeding predatory Heteroptera on transgenic Btt (Bacillus thuringiensis subsp. tenebrionis) potatoes was examined and the results are presented

Descriptors: **Feeding. Predators. Transgenics. Nontarget-effects. Transgenic-plants. Potatoes. Predatory-arthropods**

104. Herbicide metabolism and cross-tolerance in transgenic potato plants co-expressing human CYP1A1, CYP2B6, and CYP2C19

Source: Pesticide Biochemistry and Physiology. 2000. 66 (2). 116-129
Author(s): Inui-Hideyuki. Kodama-Takuya. Ohkawa-Yasunobu. Ohkawa-Hideo
Abstract:

The transgenic potato plants T1977, co-expressing human CYP1A1, CYP2B6, and CYP2C19; S1965, expressing human CYP1A1; S1972. expressing human CYP2B6; and S1974, expressing human CYP2C19 were selected by the combination of kanamycin-resistance, PCR, 7- ethoxycoumarin O-deethylase assay, and Western blot analysis. The 7- ethoxyresorufin O-deethylase activity of both T1977 and S1965 expressing CYP1A1 were 27 and 53 times higher, respectively, than that of the control. T1977 exhibited remarkable cross-tolerance toward the photosynthesis-inhibiting herbicides atrazine (AT), chlortoluron (CT), and methabenzthiazuron (MT), the lipid biosynthesis-inhibiting herbicides acetochlor (AC) and metolachlor (MC), and the carotenoid biosynthesis-inhibiting herbicide norflurazon (NR), although the control did not show tolerance toward these herbicides. In addition, T1977 showed high tolerance toward pyributicarb (PC), which inhibits root elongation, whereas S1974 expressing CYP2C19 showed a weak resistance to the herbicide, which was found to be metabolized by CYP2C19 in vitro. S1965, S1972, and S1974 showed cross-tolerance toward AT, CT, MT, and NR; AC and MC; and AT, AC, and MC; respectively. These results suggested that T1977 co-expressing CYP1A1, CYP2B6, and CYP2C19 was highly cross-tolerant toward all the herbicides tested, probably by cooperative herbicide metabolism of three P450 species, which were found to metabolize these herbicides in vitro. The transgenic plants expressing human P450 species metabolizing xenobiotics seem to be useful for breeding of herbicide-tolerant crops as well as for phytoremediation of environmental contaminants

Descriptors: **Cross-tolerance; environmental contamination: phytoremediation; herbicide metabolism; herbicide resistance. Molecular Genetics (Biochemistry and Molecular Biophysics); Pest Assessment Control and Management. Acetochlor: herbicide; atrazine: herbicide; chlortoluron: herbicide; methabenzthiazuron: herbicide; metolachlor: herbicide; norflurazon: herbicide, lipid biosynthesis inhibitor**

105. Transformation of potato with cucumber peroxidase: expression and disease response

Source: Physiological and Molecular Plant Pathology. 1998. 53 (2). 93-103

Author(s): Ray-H. Douches-D-S. Hammerschmidt-R

Abstract:

An anionic peroxidase gene from cucumber under the control of the cauliflower mosaic caulimovirus 35S promoter, was introduced into potato cultivars Snowden, Lemhi Russet, Superior and Desiree. Transgenic plants were raised and the tubers were tested for peroxidase activity and lignification. Resistance against the pathogen Fusarium sambucinum [Gibberella pulicaris] was tested in the tuber tissue, and leaf resistance to Phytophthora infestans and Erwinia carotovora was also tested. Tuber tissue showed high levels of expression of the transgene were observed in the tuber tissue in all of the potato cultivars. Increased peroxidase activity did not affect susceptibility to G.pulicaris, P. infestans and E. carotovora. The levels of soluble phenolics and polyphenol oxidase was unaffected in the tuber tissue and lignin levels were reduced

Descriptors: **Peroxidase. Transgenic-plants. Potatoes. Lignification. Plant-pathogens. Plant-pathogenic-fungi. Plant-diseases. Plant-pathogenic-bacteria. Gene-expression. Molecular-genetics. Disease-resistance. Varietal-reactions. Root-crops. Plant-pathology**

106. Suppression of PLRV titer in transgenic Russet Burbank and Ranger Russet

Source: American Potato Journal. 1995. 72 (10). 589-597

Author(s): Brown-C-R. Smith-O-P. Damsteegt-V-D. Yang-ChingPa. Fox-L.

Abstract:

Potato varieties Russet Burbank and Ranger Russet were transformed with a cDNA version of the 23 kDa coat protein cistron (CP) of the potato leaf roll luteovirus (PLRV) using the Agrobacterium tumefaciens-mediated procedure. Clones were assayed for presence of the nptII marker gene and CP genes using Southern analysis, for expression of CP mRNA using Northern analysis, and for the presence of PLRV coat protein in uninoculated and aphid-inoculated plants using ELISA and Western blot analysis in uninoculated plants. Two putative Russet Burbank transformants were escapes, lacking either nptII or CP, while one putative Ranger Russet transformant possessed the nptII gene but not the CP gene. In Russet Burbank and Ranger Russet, some transformants had statistically lower virus titre. The lowered titre was consistent in assays conducted at three stages during primary infection and once during secondary infection. The ranking of virus titre across all tests was statistically consistent. Russet Burbank and Ranger Russet transformants with the lowest secondary titres had virus contents 15 and 31% of the titres of untransformed controls, respectively. The virus titre of the two Russet Burbank escapes and the Ranger Russet with only the nptII gene did not differ significantly from their respective untransformed controls

Descriptors: **Transgenic-plants. Potatoes. Genetic-transformation. Southern-blotting. Northern-blotting. Elisa. Disease-resistance. Genetic-**

engineering. Coat-proteins. Plant-diseases. Plant-pathogens. Root-crops. Biotechnology. Plant-pathology

107. Evaluation of foliar fungal endophyte incidence in field-grown transgenic Bt white spruce trees

Source: Canadian Journal of Botany. 2006. 84 (10). 1573-1580

Author(s): Stefani-F-O-P. Berube-J-A

Abstract:

A total of 770 transgenic Bt white spruce needles were collected and plated on potato dextrose agar to determine their foliar endophyte diversity. The ribosomal internal transcribed spacer regions for 310 foliar endophytes were amplified by polymerase chain reaction (PCR) and digested using CfoI and MspI, which created 21 restriction groups. Isolates from each restriction group were sequenced and compared with reference sequences in GenBank. Eighteen sequence groups were obtained, of which five were identified at the species level. The most common endophytic fungi identified by PCR-RFLP was Lophodermium piceae (incidence of 74.5%). The second and third most common ones were Hypoxylon fragiforme (3.63%) and Lophodermium nitens (3.18%). A statistical analysis performed on the most common endophyte groups showed no statistical difference in endophyte frequency or distribution between the control white spruce needles (nontransgenic) and saplings with constructs containing the reporter gene GUS or the Bt Cry1A(b) gene and kanamycin.

Descriptors: **Endophytes-; genetic-transformation; intergenic-DNA; ribosomal-DNA; transgenic-plants Bacillus-; Bacillaceae-; Firmicutes-; bacteria-; prokaryotes-; Sphaeriales-; Ascomycotina-; Eumycota-; fungi-; eukaryotes-; Hypoxylon-; Rhytismatales-; Lophodermium-; Picea-; Pinaceae-; Pinopsida-; gymnosperms-; Spermatophyta-; plants- Plant-Breeding-and-Genetics; Forests-and-Forest-Trees-Biology-and-Ecology; Genetic-Engineering-Gene-Transfer-and-Transgenics**

108. Transgenic vegetable crops

Source: Journal of New Seeds. 2004. 6 (4). 411-431

Author(s): Ram-R-B. Dasgupta-S-K

Abstract:

Modern gene transfer based on recombinant DNA technology is a rapidly growing subject and offers vast opportunity for manifesting the utility of this technology in economic terms. Various areas where there is an enormous scope for this technology application in vegetables include improved yield, altered nutrition quality, improved resistance to diseases, pests and herbicides and in food stuffs having therapeutic value. Accordingly, the preferred target area of research in gene transfer, apart from the ones cited above, include tolerance to various abiotic stresses, plant productivity genes, genes affecting nitrogen fixation, usage of male sterility for production of hybrids, increased storage life, and various aesthetic aspects of the product. Keeping these advantages in view, there has been a drastic increase in the total cultivable area under transgenic crops globally. Among all vegetable crops, potato, tomato, aubergine, peppers, cucumber, cauliflower, cabbage and carrot, has received the maximum attention particularly in the areas relating to insect pests, disease and herbicide resistance and quality improvement. The paper discusses on the specific technology adopted in these areas. It also discusses the various issues relating to biosafety issues, current constraints in transformation

Descriptors: **Biosafety. Cabbages. Carrots. Cauliflowers. Crop-quality. Cucumbers. Isease-resistance. Gene-transfer. Genetic-engineering. Genetic-transformation. Genetically-engineered-organisms. Herbicide-resistance. Pest-resistance. Potatoes. Recombinant-DNA. Transgenic-plants. Vegetables**

109. A suite of novel promoters and terminators for plant biotechnology

Source: Functional Plant Biology. 2003. 30 (4). 443-452

Author(s): Schunmann-P-H-D. Llewellyn-D-J. Surin-B. Boevink-P. Feyter-R-C-de.

Abstract:

The gene regulation signals from subterranean clover stunt virus (SCSV) were investigated for their expression in dicot plants. The SCSV genome has at least eight circular DNA molecules. Each circular DNA component contains a promoter element, a single open reading frame and a terminator. The promoters from seven of the segments were examined for their strength and tissue specificity in transgenic tobacco (Nicotiana tabacum), potato (Solanum tuberosum) and cotton (Gossypium hirsutum) using a GUS reporter gene assay system. While the promoters of many of the segments were poorly expressed, promoters derived from segments 4 and 7 were shown to direct high levels of expression in various plant tissues and organs. The segment 1 promoter directs predominantly callus-specific expression and, when used to control a selectable marker gene, facilitated the transformation of all three species (tobacco, potato and cotton). From the results, a suite of plant expression vectors derived from the SCSV genome were constructed and used here to produce herbicide- and insect-resistant cotton, demonstrating their utility in the expression of foreign genes in dicot crop species and their potential for use in agricultural biotechnology

Descriptors: **Biotechnology. Callus. Cotton. DNA. Gene-expression. Genes. Genetic-regulation. Genetic-transformation. Genomes. Herbicide-resistance. Pest-resistance. Plant-diseases. Plant-organs. Plant-pathogens. Plant-tissues. Potatoes. Tobacco. Transgenic-plants**

110. A prospective evaluation of biotechnology in semi-subsistence agriculture

Source: Agricultural Economics. 2001. 25 (2-3). 165-175

Author(s): Qaim-M

Abstract:

This paper analyses ex ante the economic implications of transgenic virus- and weevil-resistant sweet potatoes in Kenya. These technologies are being developed within international projects, involving public and private organizations. It is expected that the resistant varieties will significantly reduce the crop losses in farmers' fields. Model calculations show that both innovations are likely to bring about substantial growth in economic surplus. The projected annual gross benefit is US$5.4 million for virus resistance and US$9.9 million for weevil resistance. Due to the semi-subsistence nature of sweet potato, the producing households will be the main beneficiaries. However, market consumers will also capture about one-fourth of the aggregate welfare gains. The high profitability of the projects is confirmed by significantly positive returns on research investments. The examples demonstrate the viability of successful research partnerships between the public and private sectors. As most of the basic biotechnology tools available to date are patented by private companies in the North, which often do not have sufficient market incentives to develop end-technologies for the South, more interactions of this kind are required from a development policy perspective. Working with typical semi-subsistence crops is particularly appealing because it immediately targets the poor and avoids conflicts with the private sector's commercial interests

Descriptors: agricultural-research. biotechnology. economic-evaluation. improved-varieties. returns. sweet-potatoes. transgenic-plants. varietal-resistance. welfare-economics

111. The NIa-proteinase of different plant potyviruses provides specific resistance to viral infection

Source: Crop Science. 1998. 38 (5). 1309-1319

Author(s): Fellers-J-P. Collins-G-B. Hunt-A-G

Abstract:

The genome-linked protein-proteinase (NIa) genes of three potyviruses (tobacco vein mottling potyvirus (TVMV), tobacco etch potyvirus (TEV) and potato Y potyvirus (PVY)) were introduced into tobacco (Nicotiana tabacum) cultivar Burley 21 and transgenic plant lines were evaluated for viral symptoms and virus accumulation. Plant lines that expressed the TVMV NIa gene were resistant to infection by TVMV; inoculated plants did not develop disease symptoms after inoculation, and virus did not accumulate. Most lines that carried the TEV NIa and PVY NIa genes did develop symptoms after inoculation with TEV and PVY, respectively, but these symptoms abated with time (a response termed as recovery). Three genes, each consisting of two NIa coding regions (TEV NIa-PVY NIa, TEV NIa-TVMV NIa, and TVMV NIa-PVY NIa) were also introduced into Burley 21. Transgenic lines that carried either TEV NIa-PVY NIa or TEV NIa-TVMV NIa constructs either did not develop disease symptoms or exhibited the process of recovery after inoculation with TEV. TEV NIa-TVMV NIa and TVMV NIa-PVY NIa lines recovered from an initial infection after inoculation with TVMV. Likewise, TEV NIa-PVY NIa and TVMV NIa-PVY NIa transformed lines recovered from initial infection after inoculation with PVY. These results demonstrate that different potyvirus NIa-proteinase genes can be used for protection against virus infection and that multiple NIa genes may be used to produce plants that are protected against more than one potyvirus

Descriptors: **Resistance. Infection. Proteinases. Genetic-transformation. Transgenic-plants. Disease-resistance. Stimulant-plants. Biotechnology. Plant-pathology. Tobacco**

112. Transgenic Populus: in vitro screening for resistance to cottonwood leaf beetle (Coleoptera: Chrysomelidae)

Source: Canadian Journal of Forest Research. 1997. 27 (6). 943-944

Author(s): Kang-HoDuck. Hall-R-B. Heuchelin-S-A. McNabb-H-S-Jr. Mize-C-W. Hart-E-R

Abstract:

Resistance of a nontransgenic Populus euramericana [P. canadensis] clone, 'Ogy', and three transgenic 'Ogy' lines (containing the pin2 proteinase inhibitor gene from potato) to the cottonwood leaf beetle, Chrysomela scripta, was evaluated by in vitro feeding on tissue-culture plantlets. Resistance of the transgenic lines was investigated in terms of effects on leaf area consumed and insect larval weight. Leaf area consumed and insect weight were both less with transformants than with control plantlets in the laboratory tests

Descriptors: **Gene-transfer. Genetic-transformation. Proteinase-inhibitors. Potatoes. Insect-pests. Plant-pests. Forest-pests. Pest-resistance. Broadleaves. Trees. Forest-trees. Pest-control. Control.**

113. The R3 resistance to Phytophthora infestans in potato is conferred by two closely linked R genes with distinct specificities

Source: Molecular Plant Microbe Interactions. 2004. 17 (4). 428-435

Author(s): Huang-SanWen. Vleeshouwers-V-G-A-A. Werij-J-S. Hutten-R-C-B. Eck-H-J-van. Visser-R-G-F. Jacobsen-E

Abstract:

The R3 locus of potato confers full resistance to avirulent isolates of Phytophthora infestans, the causal agent of late blight. R3 resides in the distal part of chromosome 11 and segregates in a potato mapping population, from which a well-saturated amplified fragment length polymorphism map is available. Using a population of 1748 plants, we constructed a high-resolution genetic map at the R3 locus. Using the combination of fine mapping and accurate disease testing with specific P. infestans isolates, we detected that the R3 locus is composed of 2 genes with distinct specificities. The genes R3a and R3b are 0.4 cM apart and have both been introgressed from Solanum demissum, the 'donor' species of most characterized race-specific R genes to P. infestans. A natural recombinant between R3a and R3b was discovered in one accession of S. demissum. The synteny between the R3 locus and the tomato I2 locus is discussed

Descriptors: **Chromosome-maps. Disease-resistance. Fungal-diseases. Gene-location. Genes. Genetic-mapping. Genetic-resistance. Linkage.**

Loci. Plant-diseases. Plant-pathogenic-fungi. Plant-pathogens. Potatoes. Transgenic-plants. Wild-relatives

114. Effect of diet and feeding history on flight of Colorado potato beetle, Leptinotarsa decemlineata

Source: Entomologia Experimentalis et Applicata. 2003. 107 (3). 207-213

Author(s): MacQuarrie-C-J-K. Boiteau-G

Abstract:

We evaluated the hypothesis that Colorado potato beetle (Leptinotarsa decemlineata Say) (CPB) flight frequency is related to diet, and that it changes with duration of food unavailability or exposure to poor quality food by exposing adult overwintered and summer CPB populations to an acceptable host plant (conventional foliage), a poor host (insect resistant transgenic foliage expressing Bacillus thuringiensis tenebrionis [Btt] Cry3a toxin) and no host. Exposure to poor host and no host treatments (with or without water) decreased mean daily flight frequencies and the overall number of overwintered CPB flying, but increased the mean daily flight frequency and number of summer population CPB that flew. Overwintered CPB did not react to an absence of plants at emergence whereas summer CPB increased mean daily flight frequencies when plants and water were not available. The flight response to insect resistant foliage was similar to that for starvation treatments in both populations indicating that flight may not be triggered by Btt toxins but by starvation brought on by feeding on poor quality food. Flight was observed in all treatments for the duration of the test with two exceptions; overwintered beetles fed insect resistant foliage ceased flying after day 17 and summer beetles starved without water ceased after day 8 of a 29-day study

Descriptors: Bacterial-toxins. Biological-control-agents. Eclosion. Evaluation. Flight. Insect-pests. Overwintering. Plant-pests

115. Patterns of phenylpropanoids in non-inoculated and potato virus Y-inoculated leaves of transgenic tobacco plants expressing yeast- derived invertase

Source: Phytochemistry. 2001. 56 (6). 535-541

Author(s): Baumert-Alfred. Mock-Hans-Peter. Schmidt-Juergen. Herbers-Karin.

Abstract:

The patterns of secondary metabolites in leaves of yeast invertase-transgenic tobacco plants (Nicotiana tabacum L. cv. Samsun NN) were analyzed. Plants expressing cytosolic yeast-derived invertase (cytInv) or apoplastic (cell wall associated) yeast invertase (cwInv) showed a characteristic phytochemical phenotype compared to untransformed controls (wild-type plants). The level of phenylpropanoids decreased in the cytInv plants but increased in the cwInv plants, which showed an induced de novo synthesis of a caffeic acid amide, i.e. N-caffeoylputrescine. In addition, the level of the coumarin glucoside scopolin was markedly enhanced. Increased accumulation of scopolin in the cwInv plants is possibly correlated with the induction of defense reactions and the appearance of necrotic lesions similar to the hypersensitive response caused by avirulent pathogens. This is consistent with results from potato virus Y-infected plants. Whereas there was no additional increase in the coumarins in leaves following infection in cwInv plants, wild-type plants showed a slight increase and cytInc a marked increase

Descriptors: Agronomy (Agriculture); Enzymology (Biochemistry and Molecular Biophysics); Infection. Caffeic acid conjugates; phenylpropanoids: patterns; scopolin; yeast-derived invertase: expression

116. Potato microtubers as research tools: a review

Source: American Journal of Potato Research. 2001. 78 (1). 47-55

Author(s): Coleman-W-K. Donnelly-D-J. Coleman-S-E

Abstract:

Although in vitro production of potato tubers or microtuberization was achieved more than 40 years ago, the application of microtubers in reliable model research systems has been slow to develop. Several factors such as the use of growth regulators in microtuber induction and growth media, the mixotropic nature of the in vitro system, and cultivar-specific responses have led to interpretive difficulties. A cautionary note is also necessary in view of apparent growth and development differences, metabolic alterations, and somaclonal variation encountered in microtubers that may not be found in field-grown tubers. Evidence for strong and consistent analogies between microtubers and field-grown tubers for their induction; growth and development; and metabolism often is lacking. However, several components such as the rapid and near-synchronous induction and growth, which can be modified by a range of exogenous compounds or conditions, make the microtuber a valuable model system. Complex problems such as dormancy also appear to be particularly amenable to examination by the microtuber system. In addition, the use of microtubers as experimental research tools has potential in the areas of plant metabolism, germplasm selection and evaluation, genetic transformation, somatic hybridization and molecular farming

Descriptors: Abscisic-acid. Carbohydrate-metabolism. Cytokinins. Dormancy. Dormancy-breaking. Ethylene. Genetic-transformation. Gibberellins. In-vitro. Potatoes. Reviews. Transgenic-plants. Tubers

117. Suppression of marker genes in sequentially transformed potato (Solanum tuberosum L.)

Source: American Potato Journal. 1995. 72 (10). 599-604

Author(s): Park-Y-D. Ronis-D-H. Lorenzen-J-H

Abstract:

Transgenic potato lines were developed from the advanced selection ND860-2 by sequential transformation using Agrobacterium tumefaciens and two different constructs: the binary vector pBI121, containing the GUS and NPTII reporter genes, and the binary vector pBV6, containing the hygR and OCS genes. Five doubly-transformed lines were utilized to study gene expression of the first construct. Three doubly-transformed lines had less NPTII antigen than the singly-transformed counterpart from which each was derived. GUS activity was reduced in all doubly-transformed lines compared to their singly-transformed original genotypes. Thus, NPTII and GUS genes in the first construct were suppressed to varying degrees by a second construct

Descriptors: marker-genes. Suppression. Potatoes. -beta--glucuronidase. Genetic-transformation. Gene-expression. Reporter-genes. Root-crops. Biotechnology

118. Expression of a pea disease resistance response gene in the potato cultivar Shepody

Source: American Potato Journal. 1993. 70 (9). 635-647

Author(s): Chang M M. Chiang C C. Martin M W. Hadwiger L A

Abstract:

The coding sequence from the pea disease resistance response gene 49 (DRR49) was transferred into cv. Shepody via Agrobacterium-mediated transformation. Leaf explants were co-cultivated with A. tumefaciens harbouring a binary vector containing the coding sequence from DRR49 under the control of the CaMV 35S promoter. Transformed plants were selected by their resistance to kanamycin. The insertion of foreign DNA was detected by polymerase chain reaction (PCR) and Southern blot analysis. Expression of the DRR49 coding sequence was confirmed by the detection of the corresponding mRNA in northern blots. Field pathogenicity tests indicated that transgenic plants expressing the pea DRR49 mRNA had higher tuber yields than the control plants when grown in potato early dying disease (Verticillium spp.) infested soil

Descriptors: Potatoes. Disease-resistance. Genes. Molecular-genetics. Genetic-transformation. Gene-expression. Peas. Genetic-engineering. Diseases. Resistance. Plant-diseases. Plant-pathogens. Plant-pathogenic-fungi. Root-crops. Biotechnology. Grain-legumes. Plant-pathology

119. Digestive alpha -amylases from Tecia solanivora larvae (Lepidoptera: Gelechiidae): response to pH, temperature and plant amylase inhibitors

Source: Bulletin of Entomological Research. 2008. 98 (6). 575-579

Author(s): Valencia-Jimenez-A. Arboleda-V-J-W. Lopez-Avila-A. Grossi-de-Sa-M-

Abstract:

The biochemical properties of the digestive alpha-amylase from Tecia solanivora larvae, an important and invasive insect pest of potato (Solanum tuberosum), were studied. This insect has three major digestive alpha -amylases with isoelectric points 5.30, 5.70 and 5.98, respectively, which were separated using native and isoelectric focusing gels. The alpha-amylase activity has an optimum pH between 7.0 and 10.0 with a peak at pH 9.0. The enzymes are stable when heated to 50 deg C and were inhibited by proteinaceous inhibitors from Phaseolus coccineus (70% inhibition) and P. vulgaris cv. Radical (87% inhibition) at pH 6.0. The inhibitors present in an amaranth hybrid inhibited 80% of the activity at pH 9.0. The results show that the alpha-amylase inhibitor from amaranth seeds may be a better candidate to make genetically-modified potatoes resistant to this insect than inhibitors from common bean seeds

Descriptors:Alpha-amylase. Amylases. Cultivars. Enzyme-inhibitors. Enzymes. Hybrids. Insect-pests. Larvae. Pest-resistance. Ph. Plant-pests. Potatoes. Seeds. Temperature. Transgenic-plants

120. Transgenic virus resistant potatoes in Mexico: potential socioeconomic implications of North-South biotechnology transfer

Source: ISAAA Briefs. 1998. (7). vi
Author(s): Qaim-M
Abstract:

Despite the rapid international development of biotechnology, we still lack knowledge and information about how low- and middle-income countries can best access this promising technology. Nor are the socio-economic repercussions of applying biotechnology in these countries' agricultural sectors well understood. This study seeks to fill in some of the gaps in our knowledge by analyzing a biotechnology transfer project that provided proprietary recombinant potato technology to Mexico

Descriptors:Agricultural-economics. Agribusiness. Biotechnology. Transgenics. Plant-viruses. Potatoes. Low-income-groups. Technology-transfer

121. Production of antimicrobial defensin in Nicotiana benthamiana with a potato virus X vector

Source: Molecular Plant Microbe Interactions. 2001. 14 (2). 111-115
Author(s): Saitoh-H. Kiba-A. Nishihara-M. Yamamura-S. Suzuki-K. Terauchi-R
Abstract:

A recombinant plasmid, pTXS.TH, was constructed to express the gene encoding wasabi (Wasabia japonica [Eutrema wasabi]) defensin with the potato virus X (PVX) vector. pTXS.TH allows the expression of defensin in the host Nicotiana benthamiana, and the defensin protein WT1 can be purified from virus-infected leaves by heat treatment and affinity chromatography. WT1 exhibits strong antifungal activity toward the phytopathogenic fungi Magnaporthe grisea (50% inhibitory concentration (IC50) = 5 micro g/ml) and Botrytis cinerea (IC50 = 20 micro g/ml) but is weakly active against the phytopathogenic bacterium Pseudomonas cichorii. This virus-mediated expression system is a rapid and efficient method to produce and characterize antimicrobial proteins in plants. It is particularly useful for the study of proteins that are difficult to produce with other expression systems

Descriptors:Genetic-engineering. Genetic-transformation. Gene-expression. Transgenic-plants. Disease-resistance. Antifungal-properties. Plant-pathogens. Plant-pathogenic-fungi. Fungal-diseases.

Plant-diseases. Plant-pathogenic-bacteria. Bacterial-diseases. Tobacco

122. Tombusvirus P19-mediated suppression of virus-induced gene silencing is controlled by genetic and dosage features that influence pathogenicity

Source: Molecular Plant Microbe Interactions. 2002. 15 (3). 269-280

Author(s): Qiu-W-P. Park-J-W. Scholthof-H-B

Abstract:

The p19 protein (P19) of Tomato bushy stunt virus (TBSV) is a pathogenicity determinant with host-dependent effects on virus spread and symptom induction. In addition, results in this study confirm that Potato virus X-mediated delivery of P19 suppresses posttranscriptional gene silencing (PTGS). To study the relevance of this activity for TBSV biology, we evaluated whether TBSV activates virus-induced gene silencing (VIGS) and if this process is suppressed by P19. TBSV vectors with the green fluorescent protein (GFP) gene, either active or inactive for P19 expression, were inoculated onto GFP-transgenic Nicotiana benthamiana plants. In the absence of P19 expression, VIGS was activated, as evidenced by the disappearance of GFP mRNA and green fluorescence. Coexpression of GFP and P19 from the TBSV vector suppressed VIGS, except in the newly emerging leaves. The suppressor activity required a central P19 region that is also known to be essential for host-dependent virus spread and symptom induction. Defective interfering RNAs (DIs) that contained the 3' end of the GFP gene induced silencing very effectively. The concomitant DI-instigated reduction in P19 accumulation failed to suppress this process, analogous to the known P19 dosage effects for other biological activities. In conclusion, (i) TBSV and its DIs are very effective inducers of VIGS, (ii) P19 is a strong suppressor of PTGS, (iii) P19 is a moderate suppressor of VIGS, and (iv) the suppressor activity is influenced by genetic and dosage features that are also important for P19-associated pathogenesis

Descriptors: **Gene-expression. Genes. Leaves. Messenger-RNA. Pathogenicity. Plant-pathogens. Transgenic-plants. Viral-proteins**

123. Effects of GNA and other mannose binding lectins on development and fecundity of the peach-potato aphid Myzus persicae

Source: Entomologia Experimentalis et Applicata. 1996. 79 (3). 285-293

Author(s): Sauvion-N. Rahbe-Y. Peumans-W-J. Damme-E-J-M-van. Gatehouse-J-A. Gatehouse-A-M-R

Abstract:

Three mannose-binding lectins were assayed in artificial diets for their toxic and growth-inhibitory effects on nymphal development of Myzus persicae. The snowdrop (Galanthus nivalis) lectin GNA was the most toxic, with an induced nymphal mortality of 42% at 1500 micro g/ml (30 micro M) and an IC50 (50% growth inhibition) of 630 micro g/ml (13 micro M). The daffodil (Narcissus pseudonarcissus) lectin NPA and a garlic (Allium sativum) lectin ASA induced no significant mortality in the range 10-1500 micro g/ml, but did result in growth inhibition of 59% (NPA) and 26% (ASA) at 1500 micro g/ml (40 micro M for NPA, 63 micro M for ASA). All 3 lectins were responsible for a slight but significant growth stimulation when ingested at 10 micro g/ml, reaching +26%, +18% and +11% over the control values for the garlic lectin, the daffodil lectin and the snowdrop lectin, resp. GNA, as well as the glucose/mannose binding lectin concanavalin A, were also provided at sublethal doses throughout the life cycle of the aphids, and effects on adult performance were monitored. Adult survival was not significantly altered, but both lectins adversely affected total fecundity and the dynamics of reproduction, resulting in significant reduction in calculated rm's (population intrinsic rate of natural increase) on lectin-containing diets. These effects are discussed in relation to the use of transgenic plants expressing these toxic lectins for potential control of aphid populations

Descriptors: Mannose. Lectins. Development. Fecundity. Plant-pests. Insect-pests. Survival. Reproduction. Garlic. Effects. Plant-extracts. Insecticidal-plants. Insecticidal-properties. Pesticides. Biology. Agricultural-entomology

GANDUM

1. **An Evergreen Revolution**
   Source: Crop Science. 2006. 46 (5). 2293-2303
   Author(s): Swaminathan-M-S
   Abstract:

   The Green Revolution was the product of alteration in plant architecture and physiological properties through breeding in wheat (Triticum aestivum L.), rice (Oryza sativa L.), corn (Zea mays L.), sorghum (Sorghum bicolor L.), and other crops. The semidwarf plant stature contributed to providing adequate nutrition to the plant for high productivity, without inducing lodging. It also increased the harvest index. Similarly, photoinsensitivity helped to match the crop cultivar to seasons with appropriate moisture availability. The Green Revolution led to increased production through higher productivity and, thereby, conserved arable land and forests. Green Revolution technology, however, was criticized by environmentalists, economists, and social scientists for its deficiencies. Economists stressed that, because market-purchased inputs are needed for output, only resource-rich farmers are able to take advantage of high-yielding cultivars. Environmentalists emphasized that the excessive use of fertilizers and pesticides, as well as the monoculture of a few crop cultivars, will create serious environmental problems, including the breakdown of resistance and the degradation of soil fertility. Social scientists stressed that often women were excluded from technology-based agriculture, leading to their marginalization. The Green Revolution, however, helped many developing countries, including India and China, to achieve a balance between population growth and food production. It contributed to an alignment of population growth to the human capacity to produce the needed food and other agricultural commodities

   Descriptors:Crop Production; Crop Yield; Harvest Index; High Yielding Varieties; Maize; Photosensitivity; Plant Nutrition; Rice; Wheat

Oryza; Poaceae; Cyperales; Monocotyledons; Angiosperms; Spermatophyta; Plants; Eukaryotes; Sorghum; Triticum; Zea

2. **Simulation-based analysis of effects of Vrn and Ppd loci on flowering in wheat**
   Source: Crop Science. 2008. 48 (2). 678-687
   Author(s): White-J-W. Herndl-M. Hunt-L-A. Payne-T-S. Hoogenboom-G
   Abstract:
   Cereal production is strongly influenced by flowering date. Wheat (Triticum aestivum L.) models simulate days to flower by assuming that development is modified by vernalization and photoperiodism. Cultivar differences are parameterized by vernalization requirement, photoperiod sensitivity, and earliness per se. The parameters are usually estimated by comparing simulations with field observations but appear estimable from genetic information. For wheat, the Vrn and Ppd loci, which affect vernalization and photoperiodism, were logical candidates for estimating parameters in the model CSM-Cropsim-CERES. Two parameters were estimated conventionally and then re-estimated with linear effects of Vrn and Ppd. Flowering data were obtained for 29 cultivars from international nurseries and divided into calibration (14 locations) and evaluation (34 locations) sets. Simulations with a generic cultivar explained 95% of variation in flowering for calibration data (10 d RMSE) and 89% for evaluation data (10 d RMSE), indicating the large effect of environment. Nonetheless, for the calibration data, the gene-based model explained 29% of remaining variation, and the conventional model, 54%. For the evaluation data, the gene-based model explained 17% of remaining variation, and the conventional model, 27%. Gene-based prediction of wheat phenology appears feasible, but more extensive genetic characterization of cultivars is needed
   Descriptors: flowering. genetic-effects. loci. simulation. wheat

3. **Modeling a wheat-maize double cropping system in China using two plant growth modules in RZWQM**
   Source: Agricultural Systems. 2006. 89 (2-3). 457-477
   Author(s): Yu-Q. Saseendran-S-A. Ma-L. Flerchinger-G-N. Green-T-R. Ahuja-L-
   Abstract:
   Agricultural system models are potential tools for evaluating soil-water-nutrient management in intensive cropping systems. In this study, we calibrated and validated the Root Zone Water Quality Model (RZWQM) with both a generic plant growth module (RZWQM-G) and the CERES plant growth module (RZWQM-C) for simulating winter wheat (Triticum aestivum L.) and maize (Zea mays L.) double cropping systems in the Northern China Plain (NCP), China. Data were obtained from an experiment conducted at Yucheng Integrated Agricultural Experimental Station (36 deg 57'N, 116 deg 36'E, 28 m asl) in the North China Plain (NCP) from 1997 to 2001 (eight crop seasons) with field measurements of evapotranspiration, soil water, soil temperature, leaf area index (LAI), biomass and grain yield. Using the same soil water and nutrient modules, both plant modules were calibrated using the data from one crop sequence

during 1998-1999 when detailed measurements of LAI and biomass growth were available. The calibrated models were then used to simulate maize and wheat production in other years. Overall simulation runs from 1997 to 2001 showed that the RZWQM-C model simulated grain yields with a RMSE of 0.94 Mg ha-1 in contrast to a RMSE of 1.23 Mg ha-1 with RZWQM-G. The RMSE for biomass simulation was 2.07 Mg ha-1 with RZWQM-G and 2.26 Mg ha-1 with RZWQM-C model. The RMSE values of simulated evapotranspiration, soil water, soil temperature and LAI were 1.4 mm, 0.046 m3 m-3, 1.75 deg C and 1.0 for RZWQM-G and 1.4 mm, 0.047 m3 m-3, 1.84 deg C and 1.1 for RZWQM-C, respectively. The study revealed that both plant models were able to simulate the intensive cropping systems once they were calibrated for the local weather and soil conditions. Sensitivity analysis also showed that a reduction of 25% of current water and N applications reduced N leaching by 24-77% with crop yield reduction of 1-9% only

Descriptors: biomass. crop-yield. cropping-systems. growth. leaching. leaf-area-index. maize. models. nitrogen-fertilizers. wheat. winter-wheat

4. **A wheat biorefining strategy based on solid-state fermentation for fermentative production of succinic acid**

Source: Bioresource Technology. 2008. 99 (17). 8310-8315

Author(s): Du-ChenYu. Lin-SzeKi. Koutinas-A. Wang-RuoHang. Dorado-P.

Abstract:

In this study, a novel generic feedstock production strategy based on solid-state fermentation (SSF) has been developed and applied to the fermentative production of succinic acid. Wheat was fractionated into bran, gluten and gluten-free flour by milling and gluten extraction processes. The bran, which would normally be a waste product of the wheat milling industry, was used to produce glucoamylase and protease enzymes via SSF using Aspergillus awamori and Aspergillus oryzae, respectively. The resulting solutions were separately utilised for the hydrolysis of gluten-free flour and gluten to generate a glucose-rich stream of over 140 g l-1 glucose and a nitrogen-rich stream of more than 3.5 g l-1 free amino nitrogen. A microbial feedstock consisting of these two streams contained all the essential nutrients required for succinic acid fermentations using Actinobacillus succinogenes. In a fermentation using only the combined hydrolysate streams, around 22 g l-1 succinic acid was produced. The addition of MgCO3 into the wheat-derived medium improved the succinic acid production further to more than 64 g l-1. These results demonstrate the SSF-based strategy is a successful approach for the production of a generic feedstock from wheat, and that this feedstock can be efficiently utilised for succinic acid production

Descriptors: feedstocks. fermentation. glucan-1,4-alpha-glucosidase. magnesium-carbonate. methodology. proteinases. succinic-acid. techniques. wheat. wheat-bran. wheat-flour. wheat-gluten

5. **Coexistence of related pathogen species on arable crops in space and time**
Source: Annual Review of Phytopathology. 2006. 44 . 163-182
Author(s): Fitt-B-D-L. Huang-YongJu. Bosch-F-van-den. West-J-S
Abstract:

This review considers factors affecting the coexistence of closely related pathogen species on arable crops, with particular reference to data available at Rothamsted for Septoria tritici/Stagonospora nodorum (Mycosphaerella graminicola/Phaeosphaeria nodorum) (septoria leaf blotch diseases on winter wheat), Oculimacula yallundae/O. acuformis (eyespot disease of winter cereals), and Leptosphaeria maculans/L. biglobosa (phoma stem canker on winter oilseed rape). Factors affecting the short-term, medium-term, and long-term coexistence of such related pathogen species are reviewed, and their evolution from common ancestors considered. Small niche differences between the related pathogen species enable them to coexist on the same host. The niche differences result from small differences in their biology/epidemiology, leading to separation in space, time, or resource use. Changes in both natural (e.g., fluctuating temperature) and man-made (e.g., agronomic practices, pollution) factors influence the coexistence. Such factors may result in coexistence between the related species in some parts of the world, whereas in other parts only one species occurs. These principles illustrated with pathogens of arable crops are generic to other host-pathogen systems

Descriptors: coevolution. epidemiology. evolution. plant-pathogenic-fungi. plant-pathogens. rape. reviews. swede-rape. wheat. winter-wheat

6. **Nonsystemic bunt fungi - Tilletia indica and T. horrida: a review of history, systematics, and biology**
Source: Annual Review of Phytopathology. 2006. 44 . 113-133
Author(s): Carris-L-M. Castlebury-L-A. Goates-B-J
Abstract:

The genus Tilletia is a group of smut fungi that infects grasses either systemically or locally. Basic differences exist between the systemically infecting species, such as the common and dwarf bunt fungi, and locally infecting species. Tilletia indica, which causes Karnal bunt of wheat, and Tilletia horrida, which causes rice kernel smut, are two examples of locally infecting species on economically important crops. However, even species on noncultivated hosts can become important when occurring as contaminants in export grain and seed shipments. In this review, we focus on T. indica and the morphologically similar but distantly related T. horrida, considering history, systematics, and biology. In addition, the controversial generic placement and evolutionary relationships of these two species are discussed in light of recent molecular studies

Descriptors: epidemiology. evolution. fungal-morphology. fungal-spores. history. plant-pathogenic-fungi. plant-pathogens. reviews. rice. sporulation. taxonomy. wheat

7. **InfoCrop: a dynamic simulation model for the assessment of crop yields, losses due to pests, and environmental impact of agro-ecosystems in tropical environments. II. Performance of the model**
   Source: Agricultural Systems. 2006. 89 (1). 47-67
   Author(s): Aggarwal-P-K. Banerjee-B. Daryaei-M-G. Bhatia-A. Bala-A. Rani-S. Chander-S. Pathak-H. Kalra-N
   Abstract:
   InfoCrop, a generic crop model, simulates the effects of weather, soils, agronomic management (planting, nitrogen, residues and irrigation) and major pests on crop growth, yield, soil carbon, nitrogen and water, and greenhouse gas emissions. This paper presents results of its evaluation in terms of its validation for rice and wheat crops in contrasting agro-environments of tropics, sensitivity to the key inputs, and also illustrates two typical applications of the model. Eleven diverse field experiments, having treatments of location, seasons, varieties, nitrogen management, organic matter, irrigation, and multiple pest incidences were used for validation. Grain yields in these experiments varied from 2.8 to 7.2 ton ha-1 in rice and from 3.6 to 5.5 ton ha-1 in wheat. The results indicated that the model was generally able to explain the differences in biomass, grain yield, emissions of carbon dioxide, methane and nitrous oxides, and long-term trends in soil organic carbon, in diverse agro-environments. The losses in dry matter and grain yield due to different pests and their populations were also explained satisfactorily. There were some discrepancies in the simulated emission of these gases during first few days after sowing/transplanting possibly because of the absence of tillage effects in the model. The sensitivity of the model to change in ambient temperature, crop duration and pest incidence was similar to the available field knowledge. The application of the model to quantify multiple pests damage through iso-loss curves is demonstrated. Another application illustrated is the use of InfoCrop for analyzing the trade-offs between increasing crop production, agronomic management strategies, and their global warming potential
   Descriptors: biomass-production. carbon-dioxide. climatic-change. crop-production. crop-yield. emission. environmental-impact. flooding. flowering. food-production. frost. global-warming. greenhouse-gases. growth. insect-pests. irrigation. leaf-area. leaf-area-index. methane. nitrogen. nitrogen-fertilizers. nitrous-oxide. nutrient-balance. organic-carbon. plant-diseases. plant-pests. rice. simulation-models. soil-fertility. soil-organic-matter. soil-water-balance. soil-water-content. water-use-efficiency. wheat. yield-losses

8. **Modeling the effect of Russian wheat aphid, Diuraphis noxia (Mordvilko) and weeds in winter wheat as guide to management**
   Source: Agricultural Systems. 2006. 88 (2-3). 494-513
   Author(s): Subhash-Chander. Ahuja-L-R. Peairs-F-B. Aggarwal-P-K. Naveen-

Abstract:

Infocrop, a generic crop growth model, was used to simulate the effect of Russian wheat aphid (Diuraphis noxia) damage on winter wheat at Fort Collins and Akron, Colorado state, USA. Observed and simulated yield reductions in four experiments over a period of two years were found to be closely related (R2=0.85). The aphid damage mechanisms coupled to the crop growth model could thus be validated through field experimental data. Economic injury levels for Russian wheat aphids determined with the validated model revealed that winter wheat was more prone to aphid attack during early growth stages than during late tillering and heading. Economic injury level changed among years and were directly related to cost of control but inversely related to market value of winter wheat. Infocrop and GPFARM were used to simulate effect of downy brome weed (Bromus tectorum) at Hays, Kansas state, USA and Cheyenne, Wyoming state, USA and jointed goat grass (Aegilops cylindrica) at Archer, Wyoming, USA on winter wheat. Both models simulated the effect of downy brome on winter wheat well. The average observed and simulated yield reductions with Infocrop over a period of three years were closely related (R2=0.941). The effect of jointed goat grass on winter wheat was simulated appropriately by GPFARM but not by Infocrop for want of required data on relative weed cover. Validated simulation models can be used for various applications such as for establishing economic thresholds and devising iso-loss curves for the pests. Simulation models have a great potential as guides for optimal pesticide use

Descriptors: crop-damage. crop-losses. crop-yield. farm-management. insect-pests. plant-pests. simulation-models. weeds. wheat. winter-wheat. yield-losses

9. **Nutrient content and in vitro dry matter digestibility of silages made from various grain sorghum and sweet sorghum cultivars**

Source: Journal of Sustainable Agriculture. 2000. 17 (1). 55-70

Author(s): Lema-M. Felix-A. Salako-S. Bishnoi-U

Abstract:

In the tropics, sorghum is an important grain and forage crop. However, information on silage made from various cultivars, including nutrient content and digestibility for livestock, is not available. Therefore, silages made from eleven grain sorghum (Sorghum bicolor) and ten sweet sorghum varieties were studied to determine the effect of sorghum variety and type on nutrient content and in vitro dry matter digestibility (IVDMD). Silage samples were analysed for Ca, P, Mg, K, Mg, crude protein (CP), ether extract (EE), gross energy (GE), neutral-detergent fibre (NDF), acid-detergent fibre (ADF), cellulose, acid-detergent lignin (ADL) and IVDMD. Results from silage analysis revealed significant ($P < 0.05$) varietal differences in CP, Ca, P, Mg, K, Na, GE, ash, NDF, ADL, cellulose, hemicellulose contents and IVDMD among grain sorghum varieties. However, the silage values for EE and NDF contents were not significantly different. Similarly, sweet sorghum varieties were significantly different ($P < 0.05$) in all of the above variables. Among sorghums, grain sorghum silage had higher (P

<0.05) CP, Ca, P, K, Na and IVDMD and lower ($P < 0.05$) NDF, ADF, cellulose and GE than sweet sorghum silage

Descriptors:Cellulose. Cultivars. Fibre-content. In-vitro-digestibility. Lignin. Nutrient-content. Nutritive-value. Protein-content. Silage. Sorghum-silage Zones on chemical components of stored sorghum grain in hararghe,

10. **Relative resistance of some sorghum varieties to the rice weevil, Sitophilus oryzae (Linnaeus) (Coleoptera: Curculionidae)**

Source: Journal of Sustainable Agriculture. 1998. 13 (2). 5-11

Author(s): Bamaiyi-L-J. Uvah-I-I. Dike-M-C. Onu-I

Abstract:

The relative resistances of 36 improved and local sorghum varieties to the storage pest S. oryzae were assessed at Samaru, Nigeria. For each variety, 200 g of sorghum were placed in a jar and infested with 10 pairs of adult S. oryzae. Adult S. oryzae were removed after 10 days. S. oryzae F1 progeny were counted at 35 days post-infestation. S. oryzae median developmental period, and percentage damage and weight loss of sorghum after 50 days were assessed. An index of susceptibility was calculated and used as the basis for determining the level of susceptibility. Varieties SINGE-2, SK5912, IC5V902NG, KSV8, 18495, ICSV210 and MORI (a local variety) were found to be highly susceptible, containing large numbers of S. oryzae progeny after 35 days. Varieties BES, ICSV111, ICSV247, ICSV1079BF and ICSH89009NG were highly resistant and contained low numbers of S. oryzae progeny. The index of susceptibility was positively correlated to F1 progeny emergence and negatively correlated to the median developmental period

Descriptors: Agricultural-entomology. Cereals. Control. Development. Insect-pests. Pest-control. Pest-resistance. Reproduction. Stored-products-pests. Susceptibility. Varietal-resistance. Varieties

11. **Sorghum and salinity: I. Response of growth, water relations, and ion accumulation to NaCl salinity**

Source: Crop Science. 2004. 44 (3). 797-805

Author(s): Netondo-G-W. Onyango-J-C. Beck-E

Abstract:

Crops grown in salt affected soils may suffer from drought stress, ion toxicity, and mineral deficiency leading to reduced growth and productivity. The present study was conducted to determine how salinity affects growth, water relations, and accumulation of cations of nutritional importance in various organs of grain sorghum [Sorghum bicolor (L.) Moench]. Two Kenyan sorghum varieties, Serena and Seredo, were grown in a greenhouse in quartz sand supplied with a complete nutrient solution to which 0 (control), 50, 100, 150, 200, and 250 mM NaCl was added. The 250 mM NaCl treatment significantly reduced the relative shoot growth rates, measured 25 d after the start of salt application, by 75 and 73%, respectively, for Serena and Seredo, and stem dry weight by 75 and 53%.

In a similar way, young leaves were affected, with leaf blades of both varieties being reduced by 67% while sheaths were reduced by 83 and 87% for Serena and Seredo, respectively. Leaf water potential, osmotic potential, leaf pressure potential, and relative water content significantly declined with increasing salt stress. Roots and stems accumulated substantial amounts of sodium, saturating at 150 mM external NaCl. Accumulation of K+ and Ca2+ in the roots, stems, and leaves was strongly inhibited by salinity. Magnesium concentration of the roots was minimally impaired but that of the stems and leaves was strongly affected. Leaves continuously accumulated sodium, which was preferentially deposited in the sheaths. Mature leaves contained more Ca2+ and Mg2+ than young ones. The two sorghum varieties appear to sequester Na+ predominantly in roots, stems, leaf sheaths, and older leaf blades sparing the growing tissues as a salt tolerance mechanism. Nevertheless, greatly reduced concentrations of Ca2+, K+, and Mg2+ in leaves under salinity could cause cation deficiency which reduces plant growth

Descriptors: Calcium-ions. Cations. Chemical-composition. Cultivars. Drought. Growth. Leaf-sheaths. Leaf-water-potential. Magnesium. Metabolism. Osmotic-pressure. Plant-composition. Plant-water-relations. Potassium. Productivity. Protected-cultivation. Salinity. Sodium-chloride. Stress. Water-content

12. **Effect of plant population density on the growth and yield of sorghum varieties grown on a Vertisol**

Source: African Crop Science Journal. 2002. 10 (1). 31-38

Author(s): Tabo-R. Olabanji-O-G. Ajayi-O. Flower-D-J

Abstract:

Sorghum (Sorghum bicolor (L.) Moench) is an important crop that is usually grown on the Vertisols of north eastern Nigeria during the dry season. The crop is grown on soils with residual moisture, and thus exposing it to terminal drought stress. Improvement of resource use efficiency and yields is probably possible through the use of appropriate plant densities. Field trials were therefore conducted to study the effects of four plant densities, varying from 2.0 to 12.5 plants m-2 on water and radiation use and performance of two Masakwa sorghum varieties grown on a Vertisol under residual soil moisture conditions. At higher plant densities the locally adapted Nigerian variety, Bulwalana produced higher grain yields than the selection from Cameroun, Bourgouri-28. It also had more efficient water use and better light interception. At low plant densities, Bourgouri-28 yielded higher than Bulwalana. Leaf area index and radiation interception increased with increasing plant density. Stem borer incidence decreased with increasing plant density. More stem borer holes and stem tunnelling were recorded in Bulwalana than in Bourgouri-28. Covered kernel smut [Sporisorium sorghi (Ehrenberg) Link] appeared to be a potentially serious disease of the crop. The study showed that the performance of the crop can be improved through manipulation of plant population and use of early maturing cultivars

Descriptors: sorghum bicolor; transplanted sorghum; water use efficiency; yield

13. **Fatty acid composition of seed oil of different Sorghum bicolor varieties**
Source: Food Chemistry. 2008. 109 (4). 855-859
Author(s): Mehmood-Saji. Orhan-Ka. Ahsan-Zahee. Aslan-Sine. Gulfraz-
Abstract:

In order to find out new sources of premium quality edible oil in the country, seeds of ten varieties of Sorghum bicolor were initially analyzed for their total oil contents. The seed oil was later fractionated into eight fatty acids including two new saturated fatty acids. The oil contents were determined by Soxhlet method and compared with the results obtained by NMR analysis. The total oil contents in the seeds of sorghum ranged from 5.0 to 8.2 % (w/w), indicating non significant difference obtained by two different techniques. The results revealed that oleic acid (31.12-48.99%), Palmitoleic acid (0.43-0.56%), linoleic acids (27.59-50.73%), linolenic acid (1.71-3.89%), stearic acid (1.09-2.59%) and palmitic acid (11.73-20.18%) was present in the seed oil of different sorghum varieties when analyzed by GC-MS. It was observed that in most of the varieties polyunsaturated fatty acids (PUFA) were higher than monounsaturated fatty acids (MUFA). The two atypical SFAs, octanedioic (C8:0) and azelaic acid (C9:0) were found in some varieties. These results suggest that these S. bicolor varieties could be additional sources of edible oil due to presence of clinically important saturated and high concentration of unsaturated fatty acids. A large scale production of the seed oil after refining process can contribute towards alleviation of edible oil shortage in the country with increased use of premium quality oil. (c) 2008 Elsevier Ltd. All rights reserved

Descriptors: Biochemistry and Molecular Biophysics; Foods edible oil (fats and oil)

14. **Genetic evaluation of seedling heat tolerance in sorghum**
Source: African Crop Science Journal. 2007. 15 (1). 33-42
Author(s): Setimela-P-S. Andrews-D-J. Eskridge-K-M. Partridge-J
Abstract:

This study was conducted to estimate sorghum seedling tolerance to heat, determine individual parental contribution and estimate additive, dominance and epistatic effects for seedling tolerance. In our experiments, seedling heat tolerance, termed heat tolerance index (HTI), was defined as a ratio of resumed coleoptile growth after a controlled heat shock, compared to normal growth. Genetic parameters of HTI were determined by crossing four lines with varying HTI, with three tester lines, and deriving F1, F2, F3, BC1 and BC11 families for generation means analysis. Line IS20969 from Egypt showed the highest HTI of 0.71, while 290R, an experimental line from the University of Nebraska was the lowest at 0.51. Additive and dominance effects contributed to coleoptile elongation under normal conditions, but only additive effects were significant in recovery growth. Epistatic effects were present in both conditions. General combining ability (GCA) effects for HTI were highly significant in both conditions, but specific combining ability effects were negligible. These results indicate that it is possible to improve seedling heat tolerance and, thus, improve sorghum variety and hybrid plant populations in tropical areas where hot soil temperatures occur

Descriptors:Epistasis. General-combining-ability. Genetic-effects. Heat-shock. Heat-stress. Heat-tolerance. Seedlings

15. **Improved cowpea-cereals-based cropping systems for household food security and poverty reduction in West Africa**

Source: Journal of Crop Improvement. 2007. 19 (1-2). 157-172

Author(s): Singh-B-B. Ajeigbe-H

Abstract:

Food production in West Africa has not been keeping pace with the population growth because the bulk of the agriculture in this region is still based on traditional inter-cropping systems with little or no application of fertilizers and chemicals. The average use of fertilizers in West Africa is less than 10 kg/ha/year. This leads to a negative balance of nutrients in the soil and continuous decline in crop yields, which perpetuates malnutrition, hunger and poverty through the vicious circle of 'low input-low production-low income' and food insecurity. How to reverse this trend is one of the major challenges of agricultural research in this region. The International Institute of Tropical Agriculture (IITA), in collaboration with relevant national, regional and international partners, has developed an appropriate model that seems to hold great promise for increasing food production in West Africa without affecting the environment and degrading the soils. This model involves a holistic combination of new, more productive dual purpose and resilient cultivars of cowpea [Vigna unguiculata (L.) Walp.], maize (Zea mays L.), sorghum [Sorghum bicolor (L.) Moench] and millet (Pennisetum glaucum and other species) in a strip-cropping pattern with a minimum and selective application of fertilizers and pesticides, feeding of crop residues to small ruminants in permanent enclosures on the home compound and returning of manure to the field. Based on this model, two 'best bet' options have become popular with farmers in northern Nigeria. These are: (1) an improved strip-cropping system involving two rows of a densely planted, improved sorghum variety: four rows of a densely planted, improved medium-maturity cowpea variety in the Sudan savanna where the rainfall is about 600 mm and (2) an improved strip-cropping system involving two rows of a densely planted, improved maize variety: four rows of densely planted double cropping of an improved 60-day cowpea in the northern Guinea savanna where the rainfall is about 1000 mm. The two-third cowpea and one-third cereal combination minimizes fertilizer use and maximizes profit because of the higher prices of cowpea grain and fodder and at the same time it leaves positive residual soil nitrogen balance and reduces Striga hermonthica seed bank, both of which benefit the cereal crops. This combination is also appropriate in view of the global surplus of cereals and global deficit of legumes. The on-station and on-farm evaluation of these systems covering several states and more than 2000 farmers in northern Nigeria, with the financial support from USAID, Gatsby

Foundation and DFID, has shown over 300% increase in productivity, enhanced income generation and improved livelihoods of the farm families

Descriptors: **Cereals. Cowpeas. Food-security. Intercropping. Poverty. Strip-cropping**

16. **Farm-level adoption of sorghum technologies in Tigray, Ethiopia**

Source: Agricultural Systems. 2006. 91 (1-2). 122-134

Author(s): Wubeneh-N-G. Sanders-J-H

Abstract:

Curtailing the effect of Striga weed, improving moisture availability and increasing soil fertility are essential strategies to increase the productivity of agriculture in the sorghum producing semi-arid areas of Ethiopia. The adoption of Striga resistant sorghum varieties and inorganic fertilizer on small subsistence farms in Tigray, Ethiopia was analysed to identify the factors determining farmers' adoption decisions. Separate Tobit regression models were estimated on survey data of a random sample of 90 farm households conducted in 2001. Results indicate that access to information, soil type, and farmers' perceptions of technology characteristics and rainfall risk were the factors associated with the adoption of the new sorghum cultivars. In contrast, availability of adult family labour, farm size, manure use, and soil type were the major determinants of the adoption of inorganic fertilizers. Farm size is negatively related to fertilizer adoption as small farms are more pressured to adopt inorganic fertilizer and intensive production techniques. Instead of the over emphasis of on short cycle varieties as a means of coping with drought and Striga, breeders need to generate intermediate and longer season Striga resistant cultivars to increase productivity during moderate and good rainfall years. Varieties combining the desirable characteristics of higher grain and biomass yields of the traditional cultivars with Striga resistance are expected to be more successfully adopted

Descriptors: **Crop-production. Fertilizers. Improved-varieties. Innovation-adoption. Pest-resistance. Small-farms. Subsistence-farming**

17. **Effects of irrigation and plant density on yield, composition and in vitro digestibility of a new forage sorghum variety, Tal, at two maturity stages**

Source: Animal Feed Science and Technology. 2006. 131 (1-2). 120-132

Author(s): Carmi-A. Aharoni-Y. Edelstein-M. Umiel-N. Hagiladi-A. Yosef-E. Nikbachat-M. Zenou-A. Miron-J

Abstract:

Most of the commercial varieties of forage sorghum belong to the tall types. Use of low types is limited, mainly due to their lower forage productivity. Recently a new low variety of forage sorghum, Tal, was developed in Israel. This study examined effects of irrigation level (IL) and plant density (PD) on Tal productivity and quality, as measured by field performance, chemical composition and in vitro digestibility. The optimal harvest stage for getting the best combination of yield amount and forage quality was explored. Irrigation included levels of 20, 100 and 180 mm, and PD consisted of 200,000, 260,000 and 330,000 plants/ha. Harvests were carried out at maturity stages of early heading

(EH) and soft dough (SD). Tal resistance to lodging was high. High irrigation increased plant height and dry matter (DM) yield in both harvests, and enhanced the content of neutral detergent fibre (NDF) and lignin, at EH. In most cases, additional irrigation decreased DM content, DM ratio of leaves/stems, and in vitro DM digestibility (IVDMD). Plant density did not affect significantly plant height or DM yield at either harvest, but did affect DM digestibility at EH. Maturation from EH to SD increased considerably DM content under all irrigation levels, and DM yield only under high irrigation. Maturation increased DM allocation to the panicles and enhanced their DM digestibility. Tal has the potential to become a successful forage crop, which under sufficient irrigation attains the best digestible DM and NDF yields at SD

Descriptors: Chemical-composition. crop-yield. cultivars. dry-matter. forage. in-vitro-digestibility. irrigation. lignin. maturity. new-cultivars. plant-composition. plant-density. plant-height

18. **Assessing production constraints, management and use of sorghum diversity in north-east Ghana: a diagnostic study**

Source: Netherlands Journal of Agricultural Science. 2004. 52 (3-4). 371-392

Author(s): Kudadjie-C-Y. Struik-P-C. Richards-P. Offei-S-K

Abstract:

This paper reports on the results of a diagnostic study conducted to assess the problems and needs of sorghum farmers in north-east Ghana with the aim of determining the type of research that would be useful for them in their own context. The importance of the crop and its position within the cropping system are identified. Sorghum is still an integral part of the livelihoods of farmers. The crop is very versatile and not only contributes to food security but also plays a part in the socio-cultural, socioeconomic, and religious aspects of the lives of farmers. Farmers have different uses for the varieties they grow, which depends on the morphological, agronomic and gastronomic traits of the crop. Sorghum varieties introduced from the research institutions have several problems including lodging, poor grain quality, bird damage and precocious germination. Farmers have developed management strategies for dealing with some of these problems. Nevertheless, further work is required by breeders to make the varieties more acceptable to users. Sorghum production constraints identified include poor soils, erratic rainfall and pest infestation of the grain during storage. The diagnostic study suggests that because farmers produce their own seed, enhancing their ability to improve the quality of their seed would be of benefit to them. The study further underscores the importance and value of diversity for farmers. It also highlights their understanding of diversity, and management and use of variation in their agronomic practices. Areas identified for further research together with farmers aim at enhancing farmers' knowledge towards strengthening their practices in diversity management and improving seed storage practices

Descriptors: F**armersÆ-knowledge; Sorghum-bicolor; maize; seed-management; biodiversity; variety**

19. Yield, composition and in vitro digestibility of new forage sorghum varieties and their ensilage characteristics

Source: Animal Feed Science and Technology. 2005. 120 (1-2). 17-32

Author(s): Miron-J. Zuckerman-E. Sadeh-D. Adin-G. Nikbachat-M. Yosef-E. Ben-Ghedalia-D. Carmi-A. Kipnis-T. Solomon-R

Abstract:

The objective of this study was to examine the effect of the ensilage process on yield, composition and in vitro digestibility of three new forage sorghum (Sorghum bicolor) varieties: Silobuster, Supersile 20, and the brown-midrib hybrid BMR-101. The commercial forage sorghum FS-5 was used as reference variety. Varieties were irrigated during summer with 242 mm water and harvested at their soft dough (SD) stage. All varieties were tall (>2.5 m), and their dry matter (DM) content at harvest was similar (270-280 g DM/kg green forage). FS-5 and BMR-101 contained higher proportion of heads on the account of lower proportion of leaves in FS-5, and stems in BMR-101. In all varieties the leaves tended to contain more neutral detergent fibre (aNDFom) and were characterized by lower DM digestibility as compared with the stems and heads organs. Silobuster and BMR-101 suffered from high lodging (43-65%), whereas FS-5 and Supersile 20 were characterized by moderated levels of lodging (27-30%) at harvest. Dry matter yield of the green forage was similar (15.3-16.5 t/ha) in all varieties. The ensilage of all varieties in glass silos resulted in moderated DM losses (<0.09 of yield) mostly as volatile gases, solubilization of 0.05-0.15 hemicellulose, and high conversion of water soluble carbohydrate (WSC) mostly into lactate, traces of ethanol and traces of volatile fatty acids (VFA). Consequently, similar pH (<4) was obtained in the silages of all varieties. In vitro DM digestibility of silage was similar in all varieties and ranged between 0.67 and 0.69. Silage aNDFom digestibility and yields per hectare of digestible silage DM and aNDFom were also similar. Ensilage resulted in 0.09-0.15 loss of digestible DM yield per hectare, and 0.04-0.14 loss of digestible aNDFom yield per hectare. Efficiency of water utilization for the production of digestible silage DM was high in all varieties. This study shows advantage of commercial FS-5 over the new varieties due to its better resistance to lodging and high quality silage

Descriptors: **Dry-matter. Ethanol. Fibre. Forage. Hemicelluloses. In-vitro-digestibility. Lactic-acid. Nutritive-value. Ph. Silage-making. Silage-quality. Volatile-fatty-acids**

20. Anthocyanins from black sorghum and their antioxidant properties

Source: Food Chemistry. 2005. 90 (1-2). 293-301

Author(s): Awika-J-M. Rooney-L-W. Waniska-R-D

Abstract:

A black, high anthocyanin sorghum variety (Tx430) grown in several environments was analyzed for anthocyanins by spectrophotometric and HPLC methods. The samples were also analyzed for antioxidant activity using the 2,2'-azinobis (3-ethyl-benzothiaziline-6-sulfonic acid) method. Two extracting solvents, 1% HCl in methanol and 70% aqueous acetone, were compared. Sorghum brans had three to four times higher anthocyanin contents than the whole grains. The brans were a good source of anthocyanin (4.0-9.8 mg luteolinidin equivalents/g) compared to pigmented fruits and vegetables (0.2-10 mg/g), fresh weight basis. Acidified methanol extracted the anthocyanins better than aqueous acetone. Luteolinidin and apigeninidin accounted for about 50% of the anthocyanins in the black sorghums. The sorghum grains and their brans had high antioxidant activity (52-400 micro mol TE/g) compared to other cereals (<0.1-34 mg TE/g). Black sorghum should be useful in food and other applications, because it is a valuable source of anthocyanins with good antioxidant activity

Descriptors: **Anthocyanins. bran**

21. **Changes in sorghum enzyme inhibitors, phytic acid, tannins and in vitro protein digestibility occurring during Khamir (local bread) fermentation**

    Source: Food Chemistry. 2004. 88 (1). 129-134

    Author(s): Osman-M-A

    Abstract:

    Effects of traditional fermentation on enzyme inhibitors, phytic acid, tannin content and in vitro digestibility of three local sorghum varieties were investigated. During a 24 h fermentation, enzyme inhibitory activities were significantly decreased. Trypsin inhibitory activity was reduced by 58%, 43% and 31% in Hamra, Shahla and Baidha, respectively, whereas amylase inhibitory activity was reduced by 74, 75 and in the three varieties after a 24 h fermentation. Phytic acid contents of the three varieties were markedly reduced as a result of fermentation. Tannin content of Hamra, Shahla and Baidha were significantly reduced by, respectively, 31%, 15% and 35% after fermentation. Fermentation significantly improved the in vitro digestibility of sorghum proteins

    Descriptors: Asmylases. Bread. Enzyme-inhibitors. Fermentation. In-vitro-digestibility. Phytic-acid. Protein-digestibility. Tannins. Trypsin

22. **Sorghum and salinity: II. Gas exchange and chlorophyll fluorescence of sorghum under salt stress**

    Source: Crop Science. 2004. 44 (3). 806-811

    Author(s): Netondo-G-W. Onyango-J-C. Beck-E

    Abstract:

    Photosynthetic activity decreases when plants are grown under saline conditions leading to reduced growth and productivity. Leaf growth, gas exchange, and chlorophyll fluorescence of two sorghum [Sorghum bicolor (L.) Moench] varieties, Serena and Seredo, were measured in response to increasing NaCl concentration. Sorghum plants were grown in sand culture under controlled greenhouse conditions. The NaCl concentrations in complete nutrient solution were 0 (control), 50, 100, 150, 200, and 250 mM. Salinity significantly (Pless than or equal to 0.01) reduced leaf area by about 86% for both varieties of sorghum. Chlorophyll a and b, net CO2 assimilation, stomatal conductance, and transpiration rate decreased significantly (Pless than or equal to 0.01) with the increase in salinity, and these decreases were similar for the two sorghum varieties. Salt induced decreases for these physiological traits ranged from 75 to

94%. Photochemical efficiency of PSII (Fv/Fm) and photochemical quenching coefficient (qP) decreased by about 9 and 10%, respectively, for both varieties, and electron transport rate (ETR) decreased by 20 and 25% for Serena and Seredo. In contrast, non-photochemical quenching (NPQ) significantly (Pless than or equal to 0.01) increased by 44 and 50% for Serena and Seredo. The results indicate that salinity affected photosynthesis per unit leaf area indirectly through stomatal closure, and to a smaller extent through direct interference with the photosynthetic apparatus. In addition, salinity decreases whole plant photosynthesis by restricting leaf area expansion. This effect starts from low levels of salinity, in contrast to that of net photosynthesis per unit leaf area, which occurs at higher levels of NaCl concentration

Descriptors:Chlorophyll. Cultivars. Electron-transfer. Growth. Leaf-area. Leaf-conductance. Photosynthesis. Plant-water-relations. Productivity. Protected-cultivation. Salinity. Stomata. Stress. Transpiration

23. **Effect of moisture stress on sorghum yield and its components**

Source: South African Journal of Plant and Soil. 1999. 16 (3). 153-157

Author(s): Wenzel-W-G

Abstract:

A sample of 48 sorghum varieties and inbred lines were planted in randomized block designs in two field trials, one of which was irrigated. The effect of moisture stress on grain yield, tillering, seeds per ear, ear mass, seeds per plot, 1000-seed weight, stover mass, biomass and harvest index was quantified for each genotype. Moisture stress resulted in increased tillering, while means of all other characteristics were reduced. Increased tillering caused an increase in grain yield under dryland conditions in those genotypes that indicated least reductions in seed number per ear and seed mass. The value of this screening method which includes both yield and drought resistance is discussed with respect to developing improved cultivars for the target environment

Descriptors: biomass. Drought-resistance. Harvest-index. Screening. Stover. Tillering. Inbred-lines. Water-stress. Yield-components. Cereals

24. **Physiology and histology of resistance to Striga hermonthica in Sorghum bicolor var. Framida**

Source: Australian Journal of Plant Physiology. 1999. 26 (1). 63-70

Author(s): Arnaud-M-C. Veronesi-C. Thalouarn-P

Abstract:

Germination, attachment to host root and growth of Striga hermonthica seeds and seedlings were studied in in vitro co-culture with Sorghum bicolor and in pot experiments. Two sorghum varieties were used, the resistant Framida and the susceptible CK-60B. Histological, morphological and physiological studies revealed the key stages of resistance mechanisms involved. Resistance of Framida to Striga does not occur at the germination or the attachment stages, since its roots do not support fewer Striga than roots of CK-60B. As Framida roots support the lowest number of young Striga stems with scale leaves, its resistance appears to occur during the establishment of a functional haustorium. Metabolite uptake by the haustorium and growth rate of the young parasite were lower on Framida roots than on CK-60B roots, even when similarly developed haustoria were compared. Furthermore, at a later stage of infestation, significant accumulation of a coloured material likely to be rich in phenolic compounds was observed in and around Framida conductive tissues, but not CK-60B tissues. These features indicate the involvement of at least three steps in the development of resistance in Framida roots: the first is linked to a partial inhibition of development of the young haustorium; the second could play a role in the physiological events that decrease nutrient translocation towards the haustoria; and the last seems to be associated with the accumulation of a coloured phenolic-like material

Descriptors: weeds. Seedlings. Seeds. Seed-germination. Weed-biology. Parasitic-plants. Parasitic-weeds. Resistance. Plant-development. Cereals

25. **Effects of steeping condition and germination time on the alpha-amylase activity, phenolics content and malting loss of Nigerian local red and hybrid short Kaura sorghum malts**

Source: Food Chemistry. 1997. 58 (4). 289-295

Author(s): Iwuoha-C-I. Aina-J-O

Abstract:

The effects of steeping condition (STC) and germination time (GMT) on the phenolics content (PC), alpha -amylase activity (DP) and malting loss (ML) of Nigerian local red (LRS) and hybrid (HSK) grain sorghum were investigated in 6-day micro-malting trials. Air-rested steeping (ARM) effected the highest increase in DP of both LRS (51.7%) and HSK (30.2%), which occurred on the fifth day of germination, while the lowest increase was from the low-temperature steeping treatment (LTM) in LRS (12.6%) and HSK (5.32%), based on the control (CSM). Reduction in PC was proportional to GMT. The greatest reduction, which occurred on the sixth day, in LRS (71.4%) was caused by formalin re-steeping of ARM germinates, while the least reduction was caused by ARM (28.3%) in HSK. Malting loss (ML) increased with GMT while ARM caused the greatest loss (46.2%) in the 6-day LRS malt. On average, ML of LTM was not significantly different from that of CSM in HSK, but it was in LRS. Results of second-order ANOVA showed that the main factors (STC (A), GMT (B) and sorghum variety (SGV; C)) significantly influenced DP and ML, while SGV did not influence PC. The interaction A x B affected DP and ML; A x C exerted no statistically significant effects on any of the three quality attributes, while B x C influenced only DP

Descriptors: seed-germination. alpha-amylase. enzyme-activity. malting. phenolic-compounds. quality. malting-quality. cereals

26. **Release of three grain sorghum pure line varieties in Botswana**
Source: South African Journal of Plant and Soil. 1997. 14 (3). 137-138
Author(s): Setimela-P. Manthe-C-S. Mazhani-L. Obilana-A-B
Abstract:

Sorghum varieties Macia, SDS 2583 and Bot 79 were cooperatively developed by the Botswana National Agricultural Research System (NARS) and the Southern African Development Community/International Crops Research Institute for the Semi-Arid Tropics (SADC/ICRISAT). They were jointly tested over 4 years followed by on-farm verification. Milling and grain quality traits were also evaluated. All 3 varieties are more resistant to drought and aphids and more adaptable to arid production systems than control variety Segaolane. They were released by Botswana's Department of Agricultural Research on 19 July 1994 as Phofu (Macia), Mahube (SDS 2583) and Mmabaitse (Bot 79)

Descriptors: cultivars. characteristics. drought-resistance. cereals

27. **Studies on genetic variations in a sorghum variety irradiated with cobalt 60 (Co60)**
Source: African Crop Science Journal. 2001. 9 (2). 377-384
Author(s): Aba-D-A. Nwasike-C-C. Yeye-M. Zaria-A-A
Abstract:

Genetic variability was created in a common sorghum (Sorghum bicolor) cultivar SK5912 (SAM-SORG 17) using gamma-ray irradiation from Cobolt 60 (Co60) source. The M0 seeds were grown in the off-season of 1985/86. This was bulk harvested and planted as M1 bulk in 1986. In 1986, ninety (90) M2 single seed selections were made as single plants selected based on height, yield and disease resistance. These were advanced to M3 in 1987, out of which 34 M4 family selections were harvested, threshed and evaluated for 3 years (1989-1991). The seeds from each family were divided into three equal portions for three years evaluation (1989, 1990 and 1991) in a ramdomized complete block design (RCBD) at the Institute for Agricultural Research, northern Nigeria. Data were collected on 22 characters ((i) eight panicle, (ii) eight leaf, and (iii) six stem (culm) characters). Coefficients of variability were higher for panicle characters than for leaf and stem characters. They ranged from 1.65% for days to 50% flowering to 4.15% for grain weight per spikelet. Broadsense heritability estimates were high for most panicle characters (45%), while they were moderate for both the leaf and stem characters (40%). The mean squares for all characters, except for grain weight per spikelet, were highly significant in a combined analysis. There were high and significant correlations (r=>0.5) between the lengths of first and second leaf sheaths (r=0.689) and also the lengths of internodes (r=0.652, 0.628 and 0.634). Highly significant but negative correlation was found between length of first leaf sheath and width of spikelet (r=0.840) in 1991. Variance components from the combining ability analysis showed that genotypic variance was high for all characters except for protein percentage and weight of spikelet. All other characters had lower genotypic variances than their respective phenotypic and error variances. Principal components extracted from the combining ability correlation matrix showed high variability in leaf and stem characters than in the panicle characters. Internode length and leaf sheaths length load significantly (SEL=0.417, i.e., standard error of significant loading) on the first factor in the individual years as well as in the combined. Plotting of the first two factors of all the years (F1 and F2) in a common scale showed that internode length and leaf sheath length were clustered together in one quadrant; grain weight per panicle, grain weight per spikelet, days to 50% flowering and width of spikelet were also clustered together, indicating a close relationship between these characters and that these characters could be selected together in order to improve sorghum yield

Descriptors: cobalt. Gamma-radiation. Genetic-variation. Heritability. Irradiation. Phenotypic-variation. Seeds. Selection. Yield-components

28. **Growth, carcass and sensory characteristics of m. longissimus lumborum from wethers fed silage diets made from maize or various sorghum varieties**

Source: South African Journal of Animal Science. 2000. 30 (1). 36-42

Author(s): Bosman-M-J-C. Webb-E-C. Cilliers-H-J. Steyn-H-S

Abstract:

Growth, carcass characteristics and eating quality of meat from South African Mutton Merino wethers fed maize or different sorghum silage diets were studied. Forty newly weaned wethers (20 kg) were randomly allocated to 10 dietary treatments: non-bird-resistant grain sorghum silage (NGS), maize silage (MS), bird-resistant grain sorghum silage (BGS), forage sorghum silage (FSS) and a standard non-silage control diet consisting of equal proportions of maize meal and milled lucerne hay (C). Silage was included at 50 or 70% of the total diet on a dry matter basis. Average daily gains of wethers were recorded from weaning to slaughter at 45 kg live mass. Carcass mass, dressing percentage, subcutaneous fat thickness and carcass length were recorded. Samples from the left m. longissimus lumborum were minced and stewed to determine foreign odours and flavours, while samples from the right m. longissimus lumborum were oven-roasted for subsequent sensory evaluation by an analytical sensory panel. Growth responses did not differ between wethers fed MS, NGS or BGS at inclusion levels of 50% or 70%. FSS at the 70% inclusion level resulted in poorer growth rates ($p<0.05$) and longer feeding periods ($p<0.05$) compared with the other silage diets. The best feed conversion efficiencies and shortest finishing periods were recorded by feeding MS at either the 50% or the 70% inclusion level, NGS at the 50% inclusion level, or BGS at the 50% inclusion level. Dressing percentages and subcutaneous fat thicknesses of wethers fed BGS and FSS at a 70% inclusion level were lower ($p<0.05$) compared to those fed the other silage diets. No significant differences in sensory characteristics or cooking losses and no sensory defects were observed among wethers fed different silage diets

Descriptors: growth. Performance. Sheep-feeding. Liveweight-gain. Carcass-weight. Carcass-yield. Backfat. Body-measurements.

Muscles. Meat-quality. Sheepmeat. Organoleptic-traits. Maize-silage. Sorghum-silage

SAPI

1. **Lipoxygenase product formation and cell adhesion during neutrophil-glomerular endothelial cell interaction**
Source: American Journal of Physiology. 1995. 268 (1_Pt_2). F1-12
Author(s): Brady H R. Lamas S. Papayianni A. Takata S. Matsubara M.
Abstract:

Leukotriene (LT) and lipoxin (LX) levels were monitored in ionophore-stimulated coincubations of polymorphonuclear neutrophils (PMN) and microvascular kidney glomerular endothelial cells (GEN) to determine the profile of lipoxygenase (LO) products generated during cell-cell interactions and the relative contributions of transcellular pathways to LO product biosynthesis in this setting. LTB4 and LTC4 were the major products formed, as determined by reverse-phase high-performance liquid chromatography and radioimmunoassay. LTB4 and LTC4 levels were increased by 23 and 185%, respectively, in coincubations of PMN and GEN, compared with incubations of PMN alone. In contrast, LXA4 and LXB4 levels were not changed in the presence of GEN. These data suggested that GEN utilize PMN-derived LTA4 to generate LT. In keeping with this hypothesis, LT biosynthesis was enhanced if PMN were primed with human granulocyte-macrophage colony-stimulating factor (GM-CSF), a cytokine that augments LTA4 biosynthesis by activated PMN. The influence of LT on PMN adhesion to GEN was also assessed, since adhesion appears to be a pivotal event in recruitment of PMN in acute glomerulonephritis. Under basal conditions, LTB4 provoked low levels of adhesion via a PMN-directed CD11/CD18-dependent mechanism. The level of adhesion was markedly enhanced by prior priming of PMN with GM-CSF or activation of GEN with tumor necrosis factor-alpha (TNF). LTB4 was as potent in this regard as the complement component C5a, platelet-activating factor (PAF), and interleukin-8 (IL-8), other mediators that contribute to the entrapment of PMN in inflamed glomeruli. LTC4 also provoked PMN-GEN adhesion via a CD11/CD18-dependent mechanism, but, in contrast to LTB4, via actions with GEN. This action of LTC4 appeared to be mediated, at least in part, by induction of PAF synthesis by GEN. Interestingly, LT-induced PMN-GEN adhesion was markedly attenuated following remodeling of PMN phospholipids with 15(S)-hydroxyeicosatetraenoic acid, a product of 15-LO, which has been implicated as an anti-inflammatory eicosanoid in some experimental and human inflammatory diseases. Taken together, these results provide further evidence that 1) transcellular biosynthetic pathways may amplify the profiles of inflammatory mediators and thereby contribute to leukocyte recruitment in acute glomerulonephritis and 2) that products of the 5-LO and 15-LO pathways may exert opposing actions on PMN trafficking during glomerular inflammation in vivo

Descriptors: Amino Acid Sequence. Base Sequence. Cattle. Cell Adhesion. Cells, Cultured. Chemotaxis, Leukocyte. Cloning, Molecular. DNA, Complementary. Eicosanoids. Endothelium, Vascular. Gene Expression. Intercellular Adhesion Molecule-1. Kidney Glomerulus. Leukotriene B4. Leukotriene C4. Lipoxygenase. Molecular Sequence Data. Neutrophils. Renal Circulation. Tumor Necrosis Factor

2. **Breeding value estimation for fat percentage using dense markers on Bos taurus autosome 14**

Source: Journal of Dairy Science. 2007. 90 (10). 4821-4829

Author(s): Roos-A-P-W-de. Schrooten-C. Mullaart-E. Calus-M-P-L. Veerkamp-

Abstract:

Prediction of breeding values using whole-genome dense marker maps for genomic selection has become feasible with the advances in DNA chip technology and the discovery of thousands of single nucleotide polymorphisms in genome-sequencing projects. The objective of this study was to compare the accuracy of predicted breeding values from genomic selection (GS), selection without genetic marker information (BLUP), and gene-assisted selection (GEN) on real dairy cattle data for 1 chromosome. Estimated breeding values of 1,300 bulls for fat percentage, based on daughter performance records, were obtained from the national genetic evaluation and used as phenotypic data. All bulls were genotyped for 32 genetic markers on chromosome 14, of which 1 marker was the causative mutation in a gene with a large effect on fat percentage. In GS, the data were analyzed with a multiple quantitative trait loci (QTL) model with haplotype effects for each marker bracket and a polygenic effect. Identical-by-descent probabilities based on linkage and linkage disequilibrium information were used to model the covariances between haplotypes. A Bayesian method using Gibbs sampling was used to predict the presence of a putative QTL and the effects of the haplotypes in each marker bracket. In BLUP, the haplotype effects were removed from the model, whereas in GEN, the haplotype effects were replaced by the effect of the genotype at the known causative mutation. The breeding values from the national genetic evaluation were treated as true breeding values because of their high accuracy and were used to compute the accuracy of prediction for GS, BLUP, and GEN. The allele substitution effect for the causative mutation, obtained from GEN, was 0.35% fat. The accuracy of the predicted breeding values for GS (0.75) was as high as for GEN (0.75) and higher than for BLUP (0.51). When some markers close to the QTL were omitted from the model, the accuracy of prediction was only slightly lower, around 0.72. The removal of all markers within 8 cM from the QTL reduced the accuracy to 0.64, which was still much higher than BLUP. It is concluded that, when applied to 1 chromosome and if genetic markers close to the QTL are available, the presented model for GS is as accurate as GEN

Descriptors: Alleles. Autosomes. Breeding-value. Bulls. Chromosomes. Dairy-bulls. Dairy-cattle. Genetic-markers. Haplotypes.

Linkage-disequilibrium. Mathematical-models. milk. milk-composition. milk-fat-percentage.

3. **Glomerular endothelial cells in culture express and secrete vascular endothelial growth factor**
Source: American Journal of Physiology. 1994. 266 (1_Pt_2). F81-F88
Author(s): Uchida K. Uchida S. Nitta K. Yumura W. Marumo F. Nihei H
Abstract:
Vascular endothelial growth factor (VEGF) is a specific growth factor for endothelial cells, and its abundant expression has been reported in kidney glomeruli. In this study, we focused on glomerular endothelial cells (GEN) as a possible source of VEGF secretion and sought to uncover a potential autocrine role of VEGF for GEN. Ribonuclease protection assay demonstrated VEGF mRNA expression in cultured GEN, and 46-kDa VEGF protein was detected in the conditioned medium by immunoblot analysis using polyclonal antibody raised against the NH2-terminal portion of VEGF. Removal of fetal bovine serum (FBS) from the culture medium for 2 h decreased VEGF mRNA abundance, which was restored by the readdition of FBS (10%) within 2 h. The effect of FBS was completely abolished by protein kinase inhibitor H-7 (10 microM), suggesting that FBS- stimulated VEGF mRNA induction involves activation of protein kinases. The treatment of GEN with 10(-7) M 12-O- tetradecanoylphorbol-13-acetate (TPA) increased the VEGF mRNA abundance fivefold, supporting the idea that VEGF expression is regulated by protein kinase C. [3H]thymidine incorporation into GEN treated with TPA (10(-7) M) was inhibited by neutralizing antibody for VEGF. Thus VEGF was identified as an autocrine growth factor for GEN in vitro. Its physiological role might be the regulation of GEN proliferation, and the induction of VEGF expression by FBS and TPA suggests its involvement in the response of glomerular capillary endothelial cells to injury in certain pathophysiological states
Descriptors: Capillaries. Cattle. Cells, Cultured. Culture Media. Endothelial Growth Factors. Endothelium, Vascular. Kidney Glomerulus. Lymphokines. RNA, Messenger

4. **Identification of Brucella abortus S19 vaccinal strain in cow milk samples**
Source: Veterinaria Mexico. 2006. 37 (4). 479-486
Author(s): Martinez-Chavarria-L-C. Verdugo-Rodriguez-A. Hernandez-Castro-R
Abstract:
Brucellosis is an infectious disease caused by Brucella sp. which affects several domestic and wild animals, as well as humans. Until the past decade, strain 19 (S19) of B. abortus was used as the vaccine strain for brucellosis in cattle in Mexico. Brucella abortus S19 carries a deletion in two genes of the operon ery, responsible for the erythritol catabolic pathway. Since 1997, B. abortus strain RB51 was officially approved in Mexico for its use as a vaccine for cattle. This strain has an insertion sequence (IS) named IS711, which interrupts the wboA gen. Based on this knowledge, two PCR assays were standardized to allow the identification of strains S19 and RB51, and distinguish them from other

Brucella species and biotypes. These assays were used for characterization of 11 field strains of B. abortus isolated from milk of cattle. A 456-bp DNA fragment was amplified from all strains when PCR, that identifies RB51, was used, discarding the presence of vaccine strain RB51 among the field strains. In contrast, when the assay to identify strain S19 was performed, a 1063-bp DNA fragment was amplified from nine strains, while the other two were identified as vaccine strain S19 by amplification of a 361-bp DNA fragment. The finding of vaccine strains among this isolates is important to both epidemiological and government level, due to their direct and indirect implications on the National Campaign for Control and Eradication of Bovine Brucellosis

Descriptors:Biotypes. brucellosis. identification. loci. milk. operons. reviews. strain-differences. vaccine-development. vaccines

5. **Cloning and prokaryotic expression of the mature fragment of the Chinese yellow bovine myostatin gene**

Source: Asian-Australasian Journal of Animal Sciences. 2007. 20 (6). 827-831

Author(s): Lu-WenFa. Zhao-Jing. Wei-GuoJian. Shan-XueSong

Abstract:

Myostatin is a member of the transforming growth factor- beta (TGF- beta) super-family. It acts as a negative regulator for skeletal muscle growth. Myostatin mutations are characterized by a visible, generalized increase in muscle mass in double muscled cattle breeds. To understand the biochemistry and physiology of the Chinese Yellow bovine myostatin gene, we report here for the first time expression of the gene in Escherichia coli (E. coli). Primers of the myostatin gene of Chinese Yellow Cattle were designed on the basis of the reported bovine myostatin mRNA sequence (Gen-Bank Accession No. NM005259) and optimized for E. coli codon usage. XhoI and EcoRI restriction enzyme sites were incorporated in the primers, and then cloning vector and expression vector were constructed in a different host bacterium. The expressed protein had a molecule mass of about 16 kDa as determined by SDS-PAGE under reducing conditions. The expressed protein reacted specifically with myostatin monoclonal antibody on immunoblots. Our studies should lead to the investigation of the differences in myostatin genes of various cattle and could benefit human health and food animal agriculture

Descriptors:Codons. DNA-cloning. Gene-expression. Genes. Genetic-vectors. Messenger-RNA. Monoclonal-antibodies. Nucleotide-sequences. Transforming-growth-factor

6. **SAGE-based comparison between glomerular and aortic endothelial cells**

Source: American Journal of Physiology. 2005. 288 (6 Part 2). F1290-F1300

Author(s): Sengoelge-G. Luo-W. Fine-D. Perschl-AM. Fierlbeck-W. Haririan-A. Sorensson-J. Rehman-TU. Hauser-P. Trevick-JS. Kulak-SC. Wegner-B. Ballermann-BJ

Abstract:

Endothelial cells have many characteristics in common, but significant morphological and functional differences exist between endothelial cells from different anatomic sites. The specific glomerular endothelial (GEn) cell transcript repertoire is unknown. We sought to determine whether endothelial cells derived from bovine glomeruli display a distinct transcriptional profile compared with bovine aortic endothelium (BAE) under identical conditions. Serial analysis of gene expression (SAGE), which includes known and unknown transcripts, was used to make the comparison. The GEn and BAE SAGE libraries contain 36,844 and 26,452 total tag sequences, respectively. Among 6,524 unique tag sequences represented at least 2 times in the 2 libraries, 2,094 (32%) were matched to well-characterized bovine cDNA sequences (358 tags) or expressed sequence tags (EST). Identification of the human homolog was achieved for 1,035 of these tags. Forty-two tags were differentially expressed in GEn. For 25 of these, the bovine cDNA or EST, and for 17 the human homolog was identified. Among all transcripts with a known bovine and human tag, seven were expressed at levels more than 10-fold higher in cultured GEn cells compared with all other SAGE libraries. The transcript "DKFZp564B076" was localized by in situ hybridization to glomerular endothelium in vivo and was shown by real-time RT-PCR to be highly abundant in glomeruli compared with aortic intima. This work supports the concept that differences in the transcriptional profile of endothelial cells from distinct origins are observed under otherwise equivalent conditions. Furthermore, we have identified the first known transcript predominant in glomerular endothelium in vivo

Descriptors: Animals. Aorta. Cattle. Cells, Cultured. Comparative Study. Databases, Genetic. Endothelium, Vascular. Gene Expression Profiling. Gene Library. Kidney Glomerulus. RNA, Messenger. Research Support

7. **Cyllamyces aberensis gen.nov. sp.nov., a new anaerobic gut fungus with branched sporangiophores isolated from cattle**

Source: Canadian Journal of Botany. 2001. 79 (6). 666-673

Author(s): Ozkose-Emin. Thomas-Barry-J. Davies-David-R. Griffith-Gareth-W. Theodorou-Michael-K

Abstract:

A new genus of the anaerobic gut fungi (Neocallimastigales), Cyllamyces aberensis gen.nov. sp.nov., with bulbous holdfast, branched sporangiophores and limited polycentric thallus development is described. The fungus was isolated from fresh cattle faeces. Free-swimming zoospores were spherical, uninucleate, and uniflagellate. After encystment, zoospores germinated and gave rise to a single, bulbous holdfast. One or several branched sporangiophores were produced from different locations on the holdfast, each bearing several spherical sporangia. DAPI staining of thalli indicated that nuclei were present in the holdfast, sporangiophores, and sporangia. As many as 12 sporangia were observed per thallus on up to 5 sporangiophores, with zoosporogenesis beginning 16-18 h after encystment. Zoospore ultrastructure was examined by transmission electron microscopy and found to be similar to that reported for other anaerobic chytrid fungi. Organelles were evenly distributed throughout the cell, except for the posteriorly attached flagellum and associated attachment apparatus, the hydrogenosomes, which were mainly situated in the posterior parts of the cell and a posteriorly directed, beak-shaped nucleus. Limited polycentric thallus development (including branched sporangiophores), the possession of a single bulbous holdfast and the absence of rhizoids were stable features of this fungus that distinguished it from the other five genera of gut fungi. Therefore, we have used these characteristics to assign the fungus to a new genus, Cyllamyces, with the specific name C. aberensis

Descriptors: Systematics and Taxonomy

8. **Inter-animal variation in the biological characteristics of muscle tissue in male limousin cattle**

   Source: Meat Science. 1995. 39 (3). 415-425

   Author(s): Jurie-C. Robelin-J. Picard-B. Renand-G. Geay-Y

   Abstract:

   The biochemical, metabolic and contractile characteristics of semitendinosus (ST) and longissimus thoracicus (LT) muscles were studied in 147 male Limousin cattle. The animals, which were slaughtered at 16 months, were the offspring of 15 different sires. Weight gain and carcass tissue composition (proportion of muscle and adipose tissue) were also measured. The biochemical characteristics of the two muscles studied had coefficients of variation between 13 and 30%, markedly higher than for proximate characteristics of the carcass, in which coefficients were all lower than 18%. There were significant differences between the two muscles: ST had a higher protein/DNA ratio and greater lactate dehydrogenase (LDH) activity than LT, also a lower isocitrate dehydrogenase (ICDH) activity and lower slow myosin heavy chain (MHCI) content. The percentage of MHC I was positively correlated with ICDH activity and negatively with LDH activity and protein/DNA ratio. These muscle characteristics were also correlated with weight gain: animals with greater weight gain had a higher protein/DNA ratio and lower oxidative activity, with differences in the level of significance of the correlations according to muscles. Selection of animals on the basis of muscle growth may therefore be a means of improving the quality of meat

   Descriptors: Enzymes-Physiological Studies. Food Technology-Meats and Meat By-Products. Food Technology-Evaluations of Physical and Chemical Properties (1970-). Muscle-Physiology and Biochemistry. Animal Production-Breeds and Breeding

9. **cDNA cloning of p42, a shared subunit of two proteasome regulatory proteins, reveals a novel member of the AAA protein family**

   Source: FEBS Letters. 1996. 387 (2-3). 184-188

   Author(s): Fujiwara-T. Watanabe-T-K. Tanaka-K. Slaughter-C-A. DeMartino-G-

   Abstract:

   We have employed cDNA cloning to deduce the complete primary structure of p42, a protein previously identified as a common subunit of two proteasome regulatory proteins: PA700, a 700000-Da multisubunit complex that binds to the proteasome and promotes the ATP-dependent degradation of ubiquitinated proteins, and modulator, a 250000-Da PA700-dependent proteasome activator. Computer analysis reveals that p42 is a novel member of a large protein family characterized by a conserved 200 amino acid domain which contains a consensus sequence for ATP binding. Five other members of this family, termed AAA proteins (ATPases associated with a variety of cellular activities) are also subunits of PA700. Gel filtration chromatography was employed to determine the qualitative and quantitative distribution of p42 in crude soluble lysates of bovine red blood cells. These studies demonstrated that p42 was found in two multi-protein complexes: the 26S proteasome (formed from the 20S proteasome and PA700) and the modulator. These results establish the identity of a new protein involved in the regulation of proteasome function and indicate that this protein is found in at least two different protein complexes

Descriptors: Adenosinetriphosphatase. Amino Acid Sequence. Base Sequence. Cattle. Cell Extracts. Cloning, Molecular. DNA, Complementary. Erythrocytes. Molecular Sequence Data. Peptide Hydrolases. Proteins. Sequence Homology, Amino Acid

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11. Identification of Brucella abortus S19 vaccinal strain in cow milk samples

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