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 No.    Records    Request
   1       7462    RICE
   2       4374    ORYZA
   3       7668    SATIVA
   4        432    PADDY
   5       7933    RICE or ORYZA SATIVA OR PADDY
   6      16957    PY=2004
*  7        434    #5 and (PY=2004)

Record 1 of 434 - AGRICOLA 1998-2004/09
AU:   Gitsopoulos,-T.K.; Froud-Williams,-R.J.
TI:   Effects of oxadiargyl on direct-seeded rice and Echinochloa
      crus-galli under aerobic and anaerobic conditions.
SO:   Weed research. 2004 Aug., v. 44, no. 4 p. 329-334.
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Record 2 of 434 - AGRICOLA 1998-2004/09
AU:   Shiu,-S.H.; Karlowski,-W.M.; Pan,-R.; Tzeng,-Y.H.; Mayer,-K.F.X.;
      Li,-W.H.
TI:   Comparative analysis of the receptor-like kinase family in
      Arabidopsis and rice.
SO:   Plant cell. 2004 May,  v. 16, no. 5 p. 1220-1234.
AB:   Receptor-like kinases (RLKs) belong to the large RLK/Pelle gene
      family, and it is known that the Arabidopsis thaliana genome
      contains >600 such members, which play important roles in plant
      growth, development, and defense responses. Surprisingly, we
      found that rice (Oryza sativa) has nearly twice as many RLK/Pelle
      members as Arabidopsis does, and it is not simply a consequence
      of a larger predicted gene number in rice. From the inferred
      phylogeny of all Arabidopsis and rice RLK/Pelle members, we
      estimated that the common ancestor of Arabidopsis and rice had >
      440 RLK/Pelles and that large-scale expansions of certain RLK/
      Pelle members and fusions of novel domains have occurred in both
      the Arabidopsis and rice lineages since their divergence. In
      addition, the extracellular domains have higher nonsynonymous
      substitution rates than the intracellular domains, consistent
      with the role of extracellular domains in sensing diverse
      signals. The lineage-specific expansions in Arabidopsis can be
      attributed to both tandem and large-scale duplications, whereas
      tandem duplication seems to be the major mechanism for recent
      expansions in rice. Interestingly, although the RLKs that are
      involved in development seem to have rarely been duplicated after
      the ArabidopsisÆrice split, those that are involved in defense/
      disease resistance apparently have undergone many duplication
      events. These findings led us to hypothesize that most of the
      recent expansions of the RLK/Pelle family have involved defense/
      resistance-related genes.
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Record 3 of 434 - AGRICOLA 1998-2004/09
AU:   Kristensen,-B.K.; Askerlund,-P.; Bykova,-N.V.; Egsgaard,-H.;
      Moller,-I.M.
TI:   Identification of oxidised proteins in the matrix of rice leaf
      mitochondria by immunoprecipitation and two-dimensional liquid
      chromatography-tandem mass spectrometry.
SO:   Phytochemistry. 2004 June, v. 65, no. 12 p. 1839-1851.
AB:   Highly purified mitochondria were isolated from green 7-day-old
      rice leaves. The mitochondria were sonicated and the matrix
      fraction isolated as the 100,000g supernatant. Part of the matrix
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fraction was left untreated while the other part was subjected to a mild oxidative treatment (0.5 mM H_2O_2 + 0.2 mM $CuSO_4$ for 10 min at room temperature). The oxidised proteins in both samples were tagged with dinitrophenylhydrazine (DNP), which forms a covalent bond with carbonyl groups. The DNP-tagged proteins were immunoprecipitated using anti-DNP antibodies and digested with trypsin. The mixture of peptides was analysed by nano-HPLC coupled online to an ESI-Quad-TOF mass spectrometer. The peptides were separated by stepwise ion exchange chromatography followed by reverse phase chromatography (2D-LC), and analysed by MS/MS. Proteins were identified by un-interpreted fragment ion database searches. Using this approach we identified 20 oxidised proteins in the control sample and a further 32 in the oxidised sample. Western blots of 2D-gels of the same samples prior to immunoprecipitation verified that the oxidation treatment increases protein oxidation also for specific proteins. Likewise Western blots showed that neither the isolation of mitochondria nor their subfractionation introduced carbonyl groups. We therefore conclude that a number of proteins are oxidised in the matrix of rice leaf mitochondria in vivo and further identify a group of proteins that are particularly susceptible to mild oxidation in vitro.

Record 4 of 434 - AGRICOLA 1998-2004/09

AU: Panahi,-M.; Alli,-Z.; Cheng,-X.; Belbaraka,-L.; Belgoudi,-J.; Sardana,-R.; Phipps,-J.; Altosaar,-I.

TI: Recombinant protein expression plasmids optimized for industrial E. coli fermentation and plant systems produce biologically active human insulin-like growth factor-1 in transgenic rice and tobacco plants.

SO: Transgenic research. 2004 June, v. 13, no. 3 p. 245-259.

Record 5 of 434 - AGRICOLA 1998-2004/09

AU: Brugiere,-S.; Kowalski,-S.; Ferro,-M.; Seigneurin-Berny,-D.; Miras,-S.; Salvi,-D.; Ravanel,-S.; d'Herin,-P.; Garin,-J.; Bourguignon,-J.

TI: The hydrophobic proteome of mitochondrial membranes from Arabidopsis cell suspensions.

SO: Phytochemistry. 2004 June, v. 65, no. 12 p. 1693-1707.

AB: The development of mitochondria and the integration of their function within a plant cell rely on the presence of a complex biochemical machinery located within their limiting membranes. The aim of the present work was: (1) to enhance our understanding of the biochemical machinery of mitochondrial membranes and (2) to test the versatility of the procedure developed for the identification of the hydrophobic proteome of the chloroplast envelope [Molecular and Cellular Proteomics 2 (2003) 325-345]. A proteomic analysis was performed, to provide the most exhaustive view of the protein repertoire of these membranes. For this purpose, highly purified mitochondria were prepared from Arabidopsis cultured cells and membrane proteins were extracted. To get a more exhaustive array of membrane proteins from Arabidopsis mitochondria, from the most to the less hydrophobic ones, various extraction procedures (chloroform/methanol extraction, alkaline or saline treatments) were applied. LC-MS/MS analyses were then performed on each membrane subfraction, leading to the identification of more than 110 proteins. The identification of these proteins is discussed with respect to their mitochondrial localization, their physicochemical properties and their implications in the metabolism of mitochondria. In order to provide a new overview of the biochemical machinery of the plant mitochondria, proteins identified during this work were compared to the lists of proteins identified during previous proteomic analyses performed on plant and algae mitochondria (Arabidopsis, pea, Chlamydomonas, rice, etc.). A total of 502 proteins are listed. About 40% of the 114 proteins identified during this work were not identified during previous proteomic studies performed on mitochondria.

Record 6 of 434 - AGRICOLA 1998-2004/09
AU: Khan,-M.M.K.; Komatsu,-S.
TI: Rice proteomics: recent developments and analysis of nuclear proteins.
SO: Phytochemistry. 2004 June, v. 65, no. 12 p. 1671-1681.
AB: Rice is the most important cereal crop in Asia, and is considered as a model cereal plant for genetic and molecular studies. An immense progress has been made in rice genome sequence analysis during the last decade. This prompted the researcher to identify the functions, modifications, and regulations of every encoded protein. Proteome analysis provides information to predict the translation and relative concentration of gene products, including the extent of modification, none of which can be accurately predicted from the nucleic acid sequence alone. During the last couple of years, considerable researches were conducted to analyze rice proteome, and only recently a remarkable progress has been made to systematically analyze and characterize the functional role of various tissues and organelles in rice. In this review, the rice proteomic research has been compiled and also presented a comprehensive analysis of rice nuclear proteins. In rice nucleus, 549 proteins were resolved using 2D-PAGE. Among them, 257 proteins were systematically analyzed by Edman sequencing and mass spectrometry and identified 190 proteins following database searching (http://gene64.dna.affrc.go.jp/RPD/main.html). The identified proteins were sorted into different functional categories. In these data, the proteins involved in signaling and gene regulations dominated others, reflecting the role of nucleus in gene expression and regulation.

Record 7 of 434 - AGRICOLA 1998-2004/09
AU: Bao,-J.; Corke,-H.; Sun,-M.
TI: Genetic diversity in the physicochemical properties of waxy rice (Oryza sativa L) starch.
SO: Journal of the science of food and agriculture. 2004 Aug. 30, v. 84, issue 11 p. 1299-1306.
AB: The genetic diversity in the physicochemical properties of starches from 56 waxy rice (Oryza sativa L) genotypes (34 of indica and 22 of japonica) was studied. The parameters included thermal and retrogradation properties tested by differential scanning calorimetry (DSC), pasting viscosity tested by rapid viscoanalyser (RVA), and flour swelling volume (FSV). Wide diversity was found in all the parameters. According to their gelatinisation temperature (GT), the waxy rice genotypes could be divided into two groups, a high-GT group and a low-GT group. A total of 15 genotypes were identified as high-GT, all belonging

to the indica subspecies. There was about a 5 ÀC difference within each group and a 10 ÀC difference between groups. Many parameters were correlated with each other in all 56 waxy rices, but some correlations were also consistent and significant when comparing the high-GT group and the low-GT group separately. For example, hot paste viscosity (HPV) was positively correlated with onset temperature (To) and enthalpy of gelatinisation (deltaHg). The results suggested that initial screening in waxy rice breeding programmes for varieties with desirable starch properties for specific food uses could be efficiently accomplished using pasting profiles from the RVA.

Record 8 of 434 - AGRICOLA 1998-2004/09

AU: Takle,-E.S.; Massman,-W.J.; Brandle,-J.R.; Schmidt,-R.A.; Xinhua,-Z.; Litvina,-I.V.; Garcia,-R.; Doyle,-G.; Rice,-C.W.

TI: Influence of high-frequency ambient pressure pumping on carbon dioxide efflux from soil.

SO: Agricultural and forest meteorology. 2004 Aug. 20, v. 124, issue 3-4 p. 193-206.

Record 9 of 434 - AGRICOLA 1998-2004/09

AU: Lissowska,-J.; Gail,-M.H.; Pee,-D.; Groves,-F.D.; Sobin,-L.H.; Nasierowska-Guttmejer,-A.; Sygnowska,-E.; Zatonski,-W.; Blot,-W.J.; Chow,-W.H.

TI: Diet and stomach cancer risk in Warsaw, Poland.

SO: Nutrition and cancer. 2004, v. 48, no. 2 p. 149-159.

AB: Some of the world's highest rates of stomach cancer are found in Poland. Reasons for the increased incidence are not known, but high intake of sausages and other preserved foods and low intake of fresh fruits and vegetables may be involved. A case-control study comprising residents newly diagnosed with stomach cancer during 1994-96 and controls randomly selected from the general population was conducted in Warsaw, Poland. Standardized interviews were conducted to ascertain usual consumption of 118 common foods and beverages and other exposures. Using data from direct interviews with 274 cases and 463 controls, odds ratios of stomach cancer were calculated as estimates of risks associated with dietary factors, adjusting for age, sex, education, smoking, and caloric intake. Risk of stomach cancer was inversely related to intake of total fruits and dark green-yellow vegetables and to indices of vitamins C and E and alpha- and beta-carotenes. However, risk was not significantly increased among those with high intake of pickled/salted vegetables and sausages. Risks were positively associated with increased intake of breads/cereals/rice/pasta and other refined grains, as well as a high carbohydrate index. Our findings add to the evidence of a protective effect of fruits and certain vegetables on stomach cancer risk, but do not indicate that high intake of sausage and other preserved foods typical in the Polish diet has contributed to the country's elevated stomach cancer incidence. Our data also suggest that high carbohydrate consumption may influence risk, but further confirmation is needed.

Record 10 of 434 - AGRICOLA 1998-2004/09

AU: Xuan,-T.D.; Shinkichi,-T.; Hong,-N.H.; Khanh,-T.D.; Min,-C.I.

TI: Assessment of phytotoxic action of Ageratum conyzoides L. (billy goat weed) on weeds.

SO: Crop protection. 2004 Oct., v. 23, issue 10 p. 915-922.

AB: Ageratum conyzoides L. (billy goat weed), showed strong inhibition on Raphanus sativus L. (radish) germination and growth in a bioassay. The leaves exhibited a greater suppression than the stem and root. The leaves of A. conyzoides applied at 2 t ha-1 reduced about 70% of the growth of Echinochloa crus-galli var. formosensis Ohwi. and completely inhibited emergence of Monochoria vaginalis (Burm.f. Persil var. plantaginea Solms.) and Aeschynomene indica L. in calcareous soil condition. Application of A. conyzoides leaves at 2 t ha-1 in a paddy field 2 d after transplanting caused about 75% paddy weed reduction and increased yield by 14% compared with a herbicide treatment. Three phenolic compounds were identified in the leaves, stem and root including gallic acid, coumalic acid, and protocatechuic acid, and catechin was found only in the stem. p-hydroxybenzoic acid was detected in both A. conyzoides leaves and stem. Three additional putative allelochemicals were found in the leaves consisting of p-coumaric acid, sinapic acid, and benzoic acid. The greater number of growth inhibitors found in the leaves might result in the stronger inhibitory activity than the stem and root. A. conyzoides might be a natural herbicide for weed control in paddy fields to reduce the dependence on synthetic herbicides.

Record 11 of 434 - AGRICOLA 1998-2004/09

AU: Ross,-E.J.H.; Stone,-J.M.; Elowsky,-C.G.; Arredondo-Peter,-R.; Klucas,-R.V.; Sarath,-G.

TI: Activation of the Oryza sativa non-symbiotic haemoglobin-2 promoter by the cytokinin-regulated transcription factor, ARR1.

SO: Journal of experimental botany. 2004 Aug., v. 55, no. 403 p. 1721-1731.

Record 12 of 434 - AGRICOLA 1998-2004/09

AU: Liu,-W.J.; Zhu,-Y.G.; Smith,-F.A.; Smith,-S.E.

TI: Do iron plaque and genotypes affect arsenate uptake and translocation by rice seedlings (Oryza sativa L.) grown in solution culture.

SO: Journal of experimental botany. 2004 Aug., v. 55, no. 403 p. 1707-1713.

Record 13 of 434 - AGRICOLA 1998-2004/09

AU: Sajidan,-A.; Farouk,-A.; Greiner,-R.; Jungblut,-P.; Muller,-E.C.; Borriss,-R.

TI: Molecular and physiological characterisation of a 3-phytase from soil bacterium Klebsiella sp. ASR1.

SO: Applied microbiology and biotechnology. 2004 July, v. 65, no. 1 p. 110-118.

AB: Klebsiella sp. strain ASR1 isolated from an Indonesian rice field is able to hydrolyse myo-inositol hexakis phosphate (phytate). The phytase protein was purified and characterised as a 42 kDa protein accepting phytate, NADP and sugar phosphates as substrates. The corresponding gene (phyK) was cloned from chromosomal DNA using a combined approach of protein and genome analysis, and expressed in Escherichia coli. The recombinant enzyme was identified as a 3-phytase yielding myo-inositol monophosphate, Ins(2)P, as the final product of enzymatic phytate hydrolysis. Based on its amino acid sequence, PhyK appears to be a member of a hitherto unknown subfamily of histidine acid phytate-degrading enzymes with the active site RHGXRXP and HD sequence motifs, and is different from other general phosphatases and phytases. Due to its ability to degrade sodium phytate to the mono phosphate ester, the phyK gene product is an interesting candidate for industrial and agricultural applications to make phytate phosphorous available for plant and animal nutrition.

Record 14 of 434 - AGRICOLA 1998-2004/09

AU: Malone,-R.W.; Weatherington-Rice,-J.; Shipitalo,-M.J.; Fausey,-N.; Ma,-L.; Ahuja,-L.R.; Wauchope,-R.D.; Ma,-Q.

TI: Herbicide leaching as affected by macropore flow and within-storm rainfall intensity variation: a RZWQM simulation.

SO: Pest management science. 2004 Mar., v. 60, issue 3 p. 277-285.

AB: Within-event variability in rainfall intensity may affect pesticide leaching rates in soil, but most laboratory studies of pesticide leaching use a rainfall simulator operating at constant rainfall intensity, or cover the soil with ponded water. This is especially true in experiments where macropores are present - macroporous soils present experimental complexities enough without the added complexity of variable rainfall intensity. One way to get around this difficulty is to use a suitable pesticide transport model, calibrate it to describe accurately a fixed-intensity experiment, and then explore the affects of within-event rainfall intensity variation on pesticide leaching through macropores. We used the Root Zone Water Quality Model (RZWQM) to investigate the effect of variable rainfall intensity on alachlor and atrazine transport through macropores. Data were used from an experiment in which atrazine and alachlor were surface-applied to 30 x 30 x 30 cm undisturbed blocks of two macroporous silt loam soils from glacial till regions. One hour later the blocks were subjected to 30-mm simulated rain with constant intensity for 0.5 h. Percolate was collected and analyzed from 64 square cells at the base of the blocks. RZWQM was calibrated to describe accurately the atrazine and alachlor leaching data, and then a median Mid-west variable-intensity storm, in which the initial intensity was high, was simulated. The variable-intensity storm more than quadrupled alachlor losses and almost doubled atrazine losses in one soil over the constant-intensity storm of the same total depth. Also rainfall intensity may affect percolate-producing macroporosity and consequently pesticide transport through macropores. For example, under variable rainfall intensity RZWQM predicted the alachlor concentration to be 2.7 microgram ml-1 with an effective macroporosity of 2.2 E-4 cm3 cm-3 and 1.4 microgram ml-1 with an effective macroporosity of 4.6 E-4 cm3 cm-3. Percolate-producing macroporosity and herbicide leaching under different rainfall intensity patterns, however, are not well understood. Clearly, further investigation of rainfall intensity variation on pesticide leaching through macropores is needed.

Record 15 of 434 - AGRICOLA 1998-2004/09

AU: Huang,-F.; Subramanyam,-B.

TI: Responses of Corcyra cephalonica (Stainton) to pirimiphos-methyl, spinosad, and combinations of pirimiphos-methyl and synergized pyrethrins.

SO: Pest management science. 2004 Feb., v. 60, issue 2 p. 191-198.

AB: Field control failures with pirimiphos-methyl against the rice moth, Corcyra cephalonica (Stainton), in Weslaco, Texas, USA, led us to investigate the susceptibility of this particular strain to pirimiphos-methyl, spinosad, pyrethrins synergized with piperonyl butoxide, and pirimiphos-methyl combined with synergized pyrethrins. In laboratory bioassays, 50 eggs of C cephalonica were exposed to untreated and insecticide-treated corn and sunflower seeds to determine larval survival after 21 days, egg-to-adult emergence after 49 days, and larval damage to seeds at both exposure periods. Pirimiphos-methyl at both 4 and 8 mg kg-1 did not prevent larval survival or egg-to-adult emergence of C cephalonica on either corn or sunflower seeds, and seed damage was evident at both rates. The C cephalonica strain was highly susceptible to spinosad at 0.5 and 1 mg kg-1. At both spinosad rates, reduction in larval survival, egg-to-adult emergence, and seed damage relative to the control treatment was > = 93% on both corn and sunflower seeds. Pirimiphos-methyl and spinosad were generally more effective against C cephalonica on corn than sunflower seeds. The C cephalonica strain was completely controlled on corn treated with 1.5 mg kg-1 of pyrethrins synergized with 15 mg kg-1 of piperonyl butoxide. Many larvae survived and became adults on corn treated with synergized pyrethrins at < = 0.75 mg kg-1. Corn treated with pirimiphos-methyl at 4, 6 or 8 mg kg-1 in combination with 0.38 to 1.5 mg kg-1 of synergized pyrethrins reduced larval survival by > = 95%, egg-to-adult emergence by > = 97%, and seed damage by > = 94%. Our results suggest that the C cephalonica strain can be controlled on corn by combining pirimiphos-methyl with synergized pyrethrins or with synergized pyrethrins at the labeled rate. Although spinosad is not currently labeled for use on stored corn and sunflower seeds, it appears to be effective against C cephalonica on both commodities at very low rates.

Record 16 of 434 - AGRICOLA 1998-2004/09

AU: Goyal,-S.K.; Berg,-E.

TI: An analysis of marketed surplus response of cereals in Haryana State of India.

SO: Agribusiness an international journal. 2004 Summer, v. 20, no. 3 p. 253-268.

AB: This report uses a model that considers the effect of both factor and output prices on marketed surplus. To derive input demand and output supply elasticities, the normalized quadratic profit function and demand equations were estimated jointly with the seemingly unrelated regressions (SUR) estimation technique using farm level panel data. The data confirm the theoretical framework. The derived price elasticities of input demand, output supply, and marketed surplus have been simulated to examine alternative price policies for securing different levels of marketed surplus. At the observed price structure, the marketed surplus of wheat will increase almost equal to population growth, but in case of paddy it will grow at a very low rate. The study further reveals that besides price adjustment, technological improvement and non-price factors are also of critical importance for increasing output supply and, hence, marketed surplus.

Record 17 of 434 - AGRICOLA 1998-2004/09

AU: Omokawa,-H.; Murata,-H.; Kobayashi,-S.

TI: Chiral response of Oryzeae and Paniceae plants in alpha-methylbenzyl-3-p-tolyl urea agar medium.

SO: Pest management science. 2004 Jan., v. 60, issue 1 p. 59-64.

AB: The results presented here support the hypothesis that plants of the tribe Oryzeae respond enantioselectively and homogeneously to optically active 1-alpha-methylbenzyl-3-p-tolylurea (MBTU) in root growth inhibition, in contrast to Echinochloa species. The Oryzeae plants tested in this study belong to different genera (Oryza, Leersia, Chikusichloa and Zizania), to different species (O sativa, O glaberrima, O alta, O coarctata, O latifolia, O minuta, O rufipogon), to various ecospecies of Oryza (japonica, indica, japonica x indica, javanica) and to different levels of evolution [cultivated rice (O sativa and O glaberrima) and ancestral wild rice species]. In spite of their different phylogenic status and diverse sensitivity, the root growth of all members of the genus Oryza was inhibited more by R-MBTU than by S-MBTU. Zizania palustris, Z latifolia, Leersia oryzoides and Chikusichloa aquatica belonging to the tribe Oryzeae exhibited similar chiral recognition to the Oryza plants, suggesting that Oryzeae have a common chiral recognition mechanism in their response to optically active MBTUs. In contrast, Echinochloa plants (E crus-galli (L) Beauv var crus-galli and E colonum (L) Link), belonging into subfamily Panicoideae tribe Paniceae, responded in a different way, where their root growth was more sensitive to S-MBTU than to the antipodal R-MBTU. A reverse chiral response between the tribe Oryzeae and the genus Echinochloa was clearly indicated in this study. This diverse response may be relevant to Gramineae classification.

Record 18 of 434 - AGRICOLA 1998-2004/09

AU: Mahmoud,-C.; Shively,-G.

TI: Agricultural diversification and integrated pest management in Bangladesh.

SO: Agricultural economics the journal of the International Association of Agricultural Economists. 2004 May, v. 30, no. 3 p. 187-194.

AB: We study factors associated with a shift toward diversified, high-valued vegetable crops and the incentives associated with the use of IPM methods for vegetable producers in Bangladesh. The primary objective is to measure how IPM technologies affect the crop and technology choices of low-income rice farmers. A three-season household optimisation model is used to study crop and technology choice under price and yield uncertainty. The model is parameterised using data from vegetable farms and experimental IPM trials conducted in Bangladesh. Simulation results show that access to IPM technology and IPM availability combined with access to credit increase household welfare and lead to higher rates of vegetable adoption. Off-farm employment opportunities work against vegetable cultivation and IPM use by risk-averse farmers. Implications for policy and extension efforts are highlighted.

Record 19 of 434 - AGRICOLA 1998-2004/09

AU: Yano,-S.; Arata,-K.; Suzuki,-S.; Yamazaki,-K.; Suzuki,-N.; Kanzaki,-Y.

TI: Pulse NMR study of refrigerated cooked rice and comparison with physicochemical properties.

SO: Food science and technology research. 2004 May, v. 10, no. 2 p.

218-223.

Record 20 of 434 - AGRICOLA 1998-2004/09

AU: Reddy,-B.S.; Chakraverty,-A.

TI: Physical properties of raw and parboiled paddy.

SO: Biosystems engineering. 2004 Aug., v. 88, issue 4 p. 461-466.

AB: The physical properties namely, size and shape, bulk density, true density, and angle of repose at moisture contents ranging from 7.19 to 28.28% d.b. for raw paddy (IR-36) and from 12.24 to 43.53% d.b. for parboiled paddy were determined using standard techniques. In the case of raw paddy, the thousand grain weight increased from 23.04 to 27.16 g with an increase in moisture content from 10.45 to 32.13% d.b. Bulk density and angle of repose increased from 522 to 566 kg/m3 and 42.35 to 49.30À, respectively, with an increase in moisture content from 7.19 to 27.86% d.b. True density and porosity decreased from 1405 to 1348 kg/m3 and from 62.84 to 58.01% respectively, with an increase in moisture content from 7.19 to 27.86% (d.b.). In the case of parboiled paddy, bulk density and angle of repose increased from 507 to 564.8 kg/m3 and 39.90 to 43.89À, respectively, with an increase in moisture content from 12.24 to 43.53% d.b. True density and porosity decreased from 1411 to 1342 kg/m3 and from 64.08 to 57.91% respectively, with an increase in moisture content from 12.24 to 43.53%. The physical properties were linearly dependent upon moisture content.

Record 21 of 434 - AGRICOLA 1998-2004/09

AU: Rohrer,-C.A.; Siebenmorgen,-T.J.

TI: Nutraceutical concentrations within the bran of various rice kernel thickness fractions.

SO: Biosystems engineering. 2004 Aug., v. 88, issue 4 p. 453-460.

AB: Several important nutraceutical compounds, such as tocotrienols, tocopherols, and oryzanols, can be extracted from rice bran, a by-product of milling. This study was conducted to not only provide information regarding nutraceutical concentrations within the rice kernel based on bran collected from successive milling, but also to determine levels of nutraceutical concentrations across several different thickness fractions. Nutraceutical compounds were measured in the bran from two long-grain rice varieties, Cypress and Drew. Rough rice was separated into three thickness fractions (<1.84, 1.84-1.98, and >1.98 mm) and each fraction milled for three successive 10 s milling durations. Bran was collected from each milling duration of each thickness fraction to allow quantification of the nutraceutical content. Results showed that bran collected from rice milled for longer durations (30 s) had lower levels of tocotrienols and tocopherols compared to bran from shorter milling durations (10 s). The highest concentration of oryzanols was in the rice bran from the first 10 s milling duration. Overall, compared to bran from thinner kernels (<1.84 mm), the bran from thicker kernel fractions contained a higher content of nutraceuticals.

Record 22 of 434 - AGRICOLA 1998-2004/09

AU: Iguaz,-A.; Arroqui,-C.; Esnoz,-A.; Virseda,-P.

TI: Modelling and validation of heat transfer in stored rough rice without aeration.

SO: Biosystems engineering. 2004 Aug., v. 88, issue 4 p. 429-439.

AB: Temperature and moisture content are the two main factors that affect grain storage without aeration. A two-dimensional, finite difference model was developed to predict temperature and moisture content of rough rice stored in a cylindrical bin subjected to variations in ambient air temperature variation. Mass transfer is considered to affect heat transfer model and also mass and heat transfer are linked by the moisture content dependent thermo-physical properties of rough rice. Model validation was made by comparing predicted with experimental measured temperature data at different points of a pilot silo. The proposed model can be used to optimise the design and operation of rough rice storage systems.

Record 23 of 434 - AGRICOLA 1998-2004/09

AU: Joseph,-M.; Gopalakrishnan,-S.; Sharma,-R.K.; Singh,-V.P.; Singh,-A.K.; Singh,-N.K.; Mohapatra,-T.

TI: Combining bacterial blight resistance and Basmati quality characteristics by phenotypic and molecular marker-assisted selection in rice.

SO: Molecular breeding new strategies in plant improvement. 2004 May, v. 13, no. 4 p. 377-387.

AB: Bacterial Blight (BB) caused by Xanthomonas oryzae pv. oryzae is a major disease of rice in tropical Asia. Since all the Basmati varieties are highly susceptible and the disease is prevalent in the entire Basmati growing region of India, BB is a severe constraint in Basmati rice production. The present study was undertaken with the objective of combining the important Basmati quality traits with resistance to BB by a combination of phenotypic and molecular marker-assisted selection (MAS). Screening of 13 near-isogenic lines of rice against four isolates of the pathogen from Basmati growing regions identified the Xa4, xa8, xa13 and Xa21 effective against all the isolates tested. Two or more of these genes in combination imparted enhanced resistance as expressed by reduced average lesion length in comparison to individual genes. The two-gene pyramid line IRBB55 carrying xa13 and Xa21 was found equally effective as three/four gene pyramid lines. The two BB resistance genes present in IRBB55 were combined with the Basmati quality traits of Pusa Basmati-1 (PB-1), the most popular high yielding Basmati rice variety used as recurrent parent. Phenotypic selection for disease resistance, agronomic and Basmati quality characteristics and marker-assisted selection for the two resistance genes were carried out in BC1F1, BC1F2 and BC1F3 generations. Background analysis using 252 polymorphic amplified fragment length polymorphism (AFLP) markers detected 80.4 to 86.7% recurrent parent alleles in BC1F3 selections. Recombinants having enhanced resistance to BB, Basmati quality and desirable agronomic traits were identified, which can either be directly developed into commercial varieties or used as immediate donors of BB resistance in Basmati breeding programs.

Record 24 of 434 - AGRICOLA 1998-2004/09

AU: Azanza,-M.P.V.; Centeno,-E.D.F.

TI: Inactivation of Bacillus cereus spores during rice cooking.

SO: Food science and technology research. 2004 May, v. 10, no. 2 p. 161-163.

Record 25 of 434 - AGRICOLA 1998-2004/09
AU: Bashir,-K.; Husnain,-T.; Fatima,-T.; Latif,-Z.; Mehdi,-S.A.; Riazuddin,-S.
TI: Field evaluation and risk assessment of transgenic indica basmati rice.
SO: Molecular breeding new strategies in plant improvement. 2004 May, v. 13, no. 4 p. 301-312.
AB: We report the first field trial of different transgenic lines of Indica Basmati rice (B-370) expressing cry1Ac and cry2A genes. Different transgenic lines were grown under field conditions for two consecutive years, according to RCBD and Split Plot Design respectively. All the biosafety measures were taken into consideration. Sixty neonate larvae of yellow stem borer were artificially infested into each plant in three installments. Data was recorded in terms of dead hearts and white heads at vegetative and flowering stage respectively. Transgenic lines exhibited inherent ability to protect rice plants from target insects ($p<0.01$). Natural infestations of rice skipper and rice leaf folder were also observed and transgenic plants were statistically superior to their untransformed counterparts. Green house whole plant bioassays were done by infesting two 2nd instar larvae of rice leaf folder per tiller. Transgenics were 96% more resistant than untransformed control plants. The presence of cry genes was observed with Dot blot, PCR and Southern blot analysis, while ELISA and Western blot analysis confirmed the expression of Cry proteins. All lines expressed higher level of Cry proteins when compared with commercially released cultivars of Bt cotton, maize and potato. It was also observed that although toxin titer substantially decreased with increasing age of the plants, it remained well within the limits to kill the target insects. Morphological studies showed significant variation for days to maturity, plant height and panicle length. Cooking qualities of seeds harvested from these lines were compared with the untransformed control. The transgenic lines had no effect on non-target insects (insects belonging to orders other than diptera and lepidoptera) and germination of three local varieties of wheat. Chances of gene spread were calculated at a level of 0.18% cross pollination in experimental lines.

Record 26 of 434 - AGRICOLA 1998-2004/09
AU: Roy,-P.; Shimizu,-N.; Kimura,-T.
TI: Energy conservation in cooking of milled raw and parboiled rice.
SO: Food science and technology research. 2004 May, v. 10, no. 2 p. 121-126.

Record 27 of 434 - AGRICOLA 1998-2004/09
AU: Yamamoto,-H.; Matsunaga,-R.
TI: Group discriminant method of rice cultivar and producing district based on parameters representing the contour of rice grain.
SO: Food science and technology research. 2004 May, v. 10, no. 2 p. 114-120.

Record 28 of 434 - AGRICOLA 1998-2004/09
AU: Pirmoradian,-N.; Sepaskhah,-A.R.; Maftoun,-M.
TI: Deficit irrigation and nitrogen effects on nitrogen-use efficiency and grain protein of rice.
SO: Agronomie. 2004 Apr., v. 24, no. 3 p. 143-153.

Record 29 of 434 - AGRICOLA 1998-2004/09

AU: Kakimoto,-T.; Koizumi,-F.; Hirase,-K.; Banba,-S.; Tanaka,-E.; Arai,-K.

TI: Novel 3,3a,5,9b-tetrahydro-2H-furo[3,2-c][2] benzopyran derivatives: synthesis of chiral glycol benzyl ether herbicides.

SO: Pest management science. 2004 May, v. 60, issue 5 p. 493-500.

AB: Novel tricyclic 3,3a,5,9b-tetrahydro-2H-furo[3,2-c][2]benzopyran (TFB) derivatives were synthesized, and their herbicidal activities were elucidated. They were synthesized from D-glucose as a natural chiral source. The formation of the TFB skeleton was achieved by a Friedel-Crafts type intramolecular cyclization of methyl 5-deoxy-2,3-O-dibenzyl-5-C-methyl-D-xylofranosides. The intramolecular cyclization was dependent upon the electronic effects of the substituents at the C-2 benzyloxy group of methyl xylofranosides. Some TFBs exhibited a remarkable herbicidal activity to annual paddy weeds, such as Echinochloa sp, without injury to the rice.

Record 30 of 434 - AGRICOLA 1998-2004/09

AU: Cruz,-V.C.; Pezzato,-A.C.; Ducatti,-C.; Pinheiro,-D.F.; Sartori,-J.R.; Goncalves,-J.C.

TI: Tracing metabolic routes of feed ingredients in tissues of broiler chickens using stable isotopes.

SO: Poultry science. 2004 Aug., v. 83, no. 8 p. 1376-1381.

AB: The present study aimed to quantify the proportion of 13C from energy and protein feed ingredients that follow the metabolic routing of the liver and muscle in broiler chickens. A stable isotope of carbon technique was used that is based on the isotopic discrimination that occurs in the plants during the photosynthesis process. One-day-old male chicks were subjected to treatments based on free choice of energy and protein sources. Rice bran (R) and soybean meal (S), C3 plants, have higher isotopic ratios than corn (C), a C4 plant, and corn gluten meal (G). Choices were R+S, C+G, R+G, C+S, or R+C+G+S. A complete feed (CF) was a sixth treatment. Feed intake and BW were measured at 30 d of age, when liver and breast muscle were collected for isotopic analysis. Treatments affected the amount of feed intake and the choices of energy or protein sources. Complete feed had the largest intake, differing from the other treatments that had free-choice feeding. Final BW was a direct reflection of consumption by these birds in all treatments. The isotopic results indicated that the 13C/12C ratio was generally higher in breast muscle than in liver, probably because of higher protein content. Moreover, in the liver, the proportion of 13C retained from the energy ingredient was greater than the proportion from the protein ingredient. That is in contrast to muscle, where the proportion of 13C retained from the protein ingredient was greater than from the energy ingredient that was self-selected.

Record 31 of 434 - AGRICOLA 1998-2004/09

AU: Takehisa,-H.; Shimodate,-T.; Fukuta,-Y.; Ueda,-T.; Yano,-M.; Yamaya,-T.; Kameya,-T.; Sato,-T.

TI: Identification of quantitative trait loci for plant growth of rice in paddy field flooded with salt water.

SO: Field crops research. 2004 Sept. 10, v. 89, issue 1 p. 85-95.

Record 32 of 434 - AGRICOLA 1998-2004/09
AU: Shimono,-H.; Hasegawa,-T.; Fujimura,-S.; Iwama,-K.
TI: Responses of leaf photosynthesis and plant water status in rice to low water temperature at different growth stages.
SO: Field crops research. 2004 Sept. 10, v. 89, issue 1 p. 71-83.

Record 33 of 434 - AGRICOLA 1998-2004/09
AU: Bijay-Singh; Yadvinder-Singh; Imas,-P.; Xie,-J.C.
TI: Potassium nutrition of the rice-wheat cropping system.
SO: Advances in agronomy. 2004, v. 81 p. 201-259.

Record 34 of 434 - AGRICOLA 1998-2004/09
AU: Choi,-D.; Kim,-J.H.; Kende,-H.
TI: Whole genome analysis of the OsGRF gene family encoding plant-specific putative transcription activators in rice (Oryza sativa L.).
SO: Plant and cell physiology. 2004 July, v. 45, no. 7 p. 897-904.
AB: OsGRF1 (Oryza sativa GROWTH-REGULATING FACTOR1) is a rice gene encoding a putative novel transcriptional regulator. We identified and characterized eleven homologs of OsGRF1 in the rice genome. All twelve OsGRF proteins have two highly conserved regions, the QLQ (Gln, Leu, Gln) and WRC (Trp, Arg, Cys) domains, and sequences reminiscent of transcription factors. OsGRF genes were preferentially expressed in young and growing tissues, and applied gibberellic acid (GA3) enhanced the expression of seven OsGRF genes. In situ hybridization showed high levels of OsGRF1 transcripts in the shoot apical meristem and in cells surrounding the vasculature of the intercalary meristem. In a GAL4-based yeast assay, the C-terminal region of OsGRF1 was found to have transactivation activity. These results indicate that OsGRF1 acts as a transcriptional activator. Based on the in situ expression pattern of OsGRF1, we postulate that it may be involved in regulating vegetative growth in rice.

Record 35 of 434 - AGRICOLA 1998-2004/09
AU: Holweg,-C.; Susslin,-C.; Nick,-P.
TI: Capturing in vivo dynamics of the actin cytoskeleton stimulated by auxin or light.
SO: Plant and cell physiology. 2004 July, v. 45, no. 7 p. 855-863.
AB: We present here a transient expression system that allows the response of actin microfilaments to physiological stimuli (changes in auxin content, light) to be observed in single cells in vivo. Etiolated, intact rice seedlings are attached to glass slides, transfected biolistically with talin fused to yellow-fluorescent protein to visualize actin microfilaments, and either treated with auxin or irradiated. The talin marker labels distinct populations of actin that are differentially expressed depending on the physiological state of the coleoptile (active elongation versus ceased elongation). Whereas longitudinal transvacuolar bundles prevail in cells that have ceased to elongate, fine cortical strands are characteristic for elongating cells. The visualized actin structures remain dynamic and responsive to signals. Exogenous auxin triggers a loosening of the bundles and an extension of the cortical strands, whereas irradiation reorientates cortical strands into longitudinal arrays. These responses correspond in quality and timing to the signal responses inferred previously from fixed specimens and

biochemical studies. In big advantage over those methods it is now possible to observe them directly at the single cell level. Thus, the rice coleoptile system can be used as a convenient model to study actin dynamics in vivo, in response to physiologically relevant stimuli.

Record 36 of 434 - AGRICOLA 1998-2004/09

AU: Andrews,-M.; Lea,-P.J.; Raven,-J.A.; Lindsey,-K.

TI: Can genetic manipulation of plant nitrogen assimilation enzymes result in increased crop yield and greater N-use efficiency? An assessment.

SO: Annals of applied biology. 2004, v. 145, no. 1 p. 25-40.

Record 37 of 434 - AGRICOLA 1998-2004/09

AU: Gallagher,-C.E.; Matthews,-P.D.; Li,-F.; Wurtzel,-E.T.

TI: Gene duplication in the carotenoid biosynthetic pathway preceded evolution of the grasses.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1776-1783.

AB: Despite ongoing research on carotenoid biosynthesis in model organisms, there is a paucity of information on pathway regulation operating in the grasses (Poaceae), which include plants of world-wide agronomic importance. As a result, efforts to either breed for or metabolically engineer improvements in carotenoid content or composition in cereal crops have led to unexpected results. In comparison to maize (Zea mays), rice (Oryza sativa) accumulates no endosperm carotenoids, despite having a functional pathway in chloroplasts. To better understand why these two related grasses differ in endosperm carotenoid content, we began to characterize genes encoding phytoene synthase (PSY), since this nuclear-encoded enzyme appeared to catalyze a rate-controlling step in the plastid-localized biosynthetic pathway. The enzyme had been previously associated with the maize Y1 locus thought to be the only functional gene controlling PSY accumulation, though function of the Y1 gene product had never been demonstrated. We show that both maize and rice possess and express products from duplicate PSY genes, PSY1 (Y1) and PSY2; PSY1 transcript accumulation correlates with carotenoid-containing endosperm. Using a heterologous bacterial system, we demonstrate enzyme function of PSY1 and PSY2 that are largely conserved in sequence except for N- and C-terminal domains. By database mining and use of ortholog-specific universal PCR primers, we found that the PSY duplication is prevalent in at least eight subfamilies of the Poaceae, suggesting that this duplication event preceded evolution of the Poaceae. These findings will impact study of grass phylogeny and breeding of enhanced carotenoid content in an entire taxonomic group of plant crops critical for global food security.

Record 38 of 434 - AGRICOLA 1998-2004/09

AU: Castleden,-C.K.; Aoki,-N.; Gillespie,-V.J.; MacRae,-E.A.; Quick,-W.P.; Buchner,-P.; Foyer,-C.H.; Furbank,-R.T.; Lunn,-J.E.

TI: Evolution and function of the sucrose-phosphate synthase gene families in wheat and other grasses.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1753-1764.

AB: Suc-phosphate synthase (SPS) is a key regulatory enzyme in the pathway of Suc biosynthesis and has been linked to quantitative trait loci controlling plant growth and yield. In dicotyledonous plants there are three SPS gene families: A, B, and C. Here we report the finding of five families of SPS genes in wheat (Triticum aestivum) and other monocotyledonous plants from the family Poaceae (grasses). Three of these form separate subfamilies within the previously described A, B, and C gene families, but the other two form a novel and distinctive D family, which on present evidence is only found in the Poaceae. The D-type SPS proteins lack the phosphorylation sites associated with 14-3-3 protein binding and osmotic stress activation, and the linker region between the N-terminal catalytic glucosyltransferase domain and the C-terminal Suc-phosphatase-like domain is 80 to 90 amino acid residues shorter than in the A, B, or C types. The D family appears to have arisen after the divergence of mono- and dicotyledonous plants, with a later duplication event resulting in the two D-type subfamilies. Each of the SPS gene families in wheat showed different, but overlapping, spatial and temporal expression patterns, and in most organs at least two different SPS genes are expressed. Analysis of expressed sequence tags indicated similar expression patterns to wheat for each SPS gene family in barley (Hordeum vulgare) but not in more distantly related grasses. We identified an expressed sequence tag from rice (Oryza sativa) that appears to be derived from an endogenous antisense SPS gene, and this might account for the apparently low level of expression of the related OsSPS11 sense gene, adding to the already extensive list of mechanisms for regulating the activity of SPS in plants.

Record 39 of 434 - AGRICOLA 1998-2004/09

AU: Zhu,-Q.H.; Ramm,-K.; Shivakkumar,-R.; Dennis,-E.S.; Upadhyaya,-N.M.

TI: The ANTHER INDEHISCENCE1 gene encoding a single MYB domain protein is involved in anther development in rice.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1514-1525.

AB: Using a two-element iAc/Ds transposon-tagging system, we identified a rice (Oryza sativa L. cv Nipponbare) recessive mutant, anther indehiscence1 (aid1), showing partial to complete spikelet sterility. Spikelets of the aid1 mutant could be classified into three types based on the viability of pollen grains and the extent of anther dehiscence. Type 1 spikelets (approximately 25%) were sterile due to a failure in accumulation of starch in pollen grains. Type 2 spikelets (approximately 55%) had viable pollen grains, but anthers failed to dehisce and/or synchronize with anthesis due to failure in septum degradation and stomium breakage, resulting in sterility. Type 3 spikelets (approximately 20%) had normal fertility. In addition, aid1 mutant plants had fewer tillers and flowered 10 to 15 d later than the wild type. The Ds insertion responsible for the aid1 mutation was mapped within the coding region of the AID1 gene on chromosome 6, which is predicted to encode a novel protein of 426 amino acids with a single MYB domain. The MYB domain of AID1 is closely related to that of the telomere-binding proteins of human, mouse, and Arabidopsis, and of single MYB domain transcriptional regulators in plants such as PcMYB1 and ZmIBP1. AID1 was expressed in both the leaves and panicles of wild-type plants, but not in mutant plants.

Record 40 of 434 - AGRICOLA 1998-2004/09

AU: Ge,-L.; Chen,-H.; Jiang,-J.F.; Zhao,-Y.; Xu,-M.L.; Xu,-Y.Y.; Tan,-K.H.; Xu,-Z.H.; Chong,-K.

TI: Overexpression of OsRAA1 causes pleiotropic phenotypes in transgenic rice plants, including altered leaf, flower, and root development and root response to gravity.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1502-1513.

AB: There are very few root genes that have been described in rice as a monocotyledonous model plant so far. Here, the OsRAA1 (Oryza sativa Root Architecture Associated 1) gene has been characterized molecularly. OsRAA1 encodes a 12.0-kD protein that has 58% homology to the AtFPF1 (Flowering Promoting Factor 1) in Arabidopsis, which has not been reported as modulating root development yet. Data of in situ hybridization and OsRAA1::GUS transgenic plant showed that OsRAA1 expressed specifically in the apical meristem, the elongation zone of root tip, steles of the branch zone, and the young lateral root. Constitutive expression of OsRAA1 under the control of maize (Zea mays) ubiquitin promoter resulted in phenotypes of reduced growth of primary root, increased number of adventitious roots and helix primary root, and delayed gravitropic response of roots in seedlings of rice (Oryza sativa), which are similar to the phenotypes of the wild-type plant treated with auxin. With overexpression of OsRAA1, initiation and growth of adventitious root were more sensitive to treatment of auxin than those of the control plants, while their responses to 9-hydroxyfluorene-9-carboxylic acid in both transgenic line and wild type showed similar results. OsRAA1 constitutive expression also caused longer leaves and sterile florets at the last stage of plant development. Analysis of northern blot and GUS activity staining of OsRAA1::GUS transgenic plants demonstrated that the OsRAA1 expression was induced by auxin. At the same time, overexpression of OsRAA1 also caused endogenous indole-3-acetic acid to increase. These data suggested that OsRAA1 as a new gene functions in the development of rice root systems, which are mediated by auxin. A positive feedback regulation mechanism of OsRAA1 to indole-3-acetic acid metabolism may be involved in rice root development in nature.

Record 41 of 434 - AGRICOLA 1998-2004/09

AU: Wong,-H.L.; Sakamoto,-T.; Kawasaki,-T.; Umemura,-K.; Shimamoto,-K.

TI: Down-regulation of metallothionein, a reactive oxygen scavenger, by the small GTPase OsRac1 in rice.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1447-1456.

AB: Metallothioneins are small, ubiquitous Cys-rich proteins known to be involved in reactive oxygen species (ROS) scavenging and metal homeostasis. We found that the expression of a metallothionein gene (OsMT2b) was synergically down-regulated by OsRac1 and rice (Oryza sativa) blast-derived elicitors. Transgenic plants overexpressing OsMT2b showed increased susceptibility to bacterial blight and blast fungus. OsMT2b-overexpressing cells showed reduced elicitor-induced hydrogen peroxide production. In contrast, homozygous OsMT2b::Tos17-inserted mutant and OsMT2b-RNAi-silenced transgenic cells showed significantly higher elicitor-induced hydrogen peroxide production than the wild-type cells. In vitro assay showed that recombinant OsMT2b protein possessed superoxide- and hydroxyl radical-scavenging activities. Taken together, these results showed that OsMT2b is an ROS scavenger and its expression is down-regulated by OsRac1, thus potentiating ROS, which function as signals in resistance response. The results suggest that OsRac1 plays a dual role as an inducer of ROS production and a suppressor of ROS scavenging.

Record 42 of 434 - AGRICOLA 1998-2004/09
AU: Cagnac,-O.; Bourbouloux,-A.; Chakrabarty,-D.; Zhang,-M.Y.; Delrot,-S.
TI: AtOPT6 transports glutathione derivatives and is induced by primisulfuron.
SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1378-1387.
AB: The oligopeptide transporter (OPT) family contains nine members in Arabidopsis. While there is some evidence that AtOPTs mediate the uptake of tetra- and pentapeptides, OPT homologs in rice (Oryza sativa; OsGT1) and Indian mustard (Brassica juncea; BjGT1) have been described as transporters of glutathione derivatives. This study investigates the possibility that two members of the AtOPT family, AtOPT6 and AtOPT7, may also transport glutathione and its conjugates. Complementation of the hgt1met1 yeast double mutant by plant homologs of the yeast glutathione transporter HGT1 (AtOPT6, AtOPT7, OsGT1, BjGT1) did not restore the growth phenotype, unlike complementation by HGT1. By contrast, complementation by AtOPT6 restored growth of the hgt1 yeast mutant on a medium containing reduced (GSH) or oxidized glutathione as the sole sulfur source and induced uptake of [3H] GSH, whereas complementation by AtOPT7 did not. In these conditions, AtOPT6-dependent GSH uptake in yeast was mediated by a high affinity (K(m) = 400 micromolar) and a low affinity (K(m) = 5 mM) phase. It was strongly competed for by an excess oxidized glutathione and glutathione-N-ethylmaleimide conjugate. Growth assays of yeasts in the presence of cadmium (Cd) suggested that AtOPT6 may transport Cd and Cd/GSH conjugate. Reporter gene experiments showed that AtOPT6 is mainly expressed in dividing areas of the plant (cambium, areas of lateral root initiation). RNA blots on cell suspensions and real-time reverse transcription-PCR on Arabidopsis plants indicated that AtOPT6 expression is strongly induced by primisulfuron and, to a lesser extent, by abscisic acid but not by Cd. Altogether, the data show that the substrate specificity and the physiological functions of AtOPT members may be diverse. In addition to peptide transport, AtOPT6 is able to transport glutathione derivatives and metal complexes, and may be involved in stress resistance.

Record 43 of 434 - AGRICOLA 1998-2004/09
AU: Chen,-M.H.; Huang,-L.F.; Li,-H.M.; Chen,-Y.R.; Yu,-S.M.
TI: Signal peptide-dependent targeting of a rice alpha-amylase and cargo proteins to plastids and extracellular compartments of plant cells.
SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1367-1377.
AB: alpha-Amylases are important enzymes for starch degradation in plants. However, it has been a long-running debate as to whether alpha-amylases are localized in plastids where starch is stored. To study the subcellular localization of alpha-amylases in plant cells, a rice (Oryza sativa) alpha-amylase, alpha Amy3, with or without its own signal peptide (SP) was expressed in transgenic tobacco (Nicotiana tabacum) and analyzed. Loss-of-function analyses revealed that SP was required for targeting of alpha

Amy3 to chloroplasts and/or amyloplasts and cell walls and/or extracellular compartments of leaves and suspension cells. SP was also required for in vitro transcribed and/or translated alpha Amy3 to be cotranslationally imported and processed in canine microsomes. alpha Amy3, present in chloroplasts of transgenic tobacco leaves, was processed to a product with M(r) similar to alpha Amy3 minus its SP. Amino acid sequence analysis revealed that the SP of chloroplast localized alpha Amy3 was cleaved at a site only one amino acid preceding the predicted cleavage site. Function of the alpha Amy3 SP was further studied by gain-of-function analyses. beta-Glucuronidase (GUS) and green fluorescence protein fused with or without the alpha Amy3 SP was expressed in transgenic tobacco or rice. The alpha Amy3 SP directed translocation of GUS and green fluorescence protein to chloroplasts and/or amyloplasts and cell walls in tobacco leaves and rice suspension cells. The SP of another rice alpha-amylase, alpha Amy8, similarly directed the dual localizations of GUS in transgenic tobacco leaves. This study is the first evidence of SP-dependent dual translocations of proteins to plastids and extracellular compartments, which provides new insights into the role of SP in protein targeting and the pathways of SP-dependent protein translocation in plants.

Record 44 of 434 - AGRICOLA 1998-2004/09

AU: Shen,-Y.J.; Jiang,-H.; Jin,-J.P.; Zhang,-Z.B.; Xi,-B.; He,-Y.Y.; Wang,-G.; Wang,-C.; Qian,-L.; Li,-X.

TI: Development of genome-wide DNA polymorphism database for map-based cloning of rice genes.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1198-1205.

AB: DNA polymorphism is the basis to develop molecular markers that are widely used in genetic mapping today. A genome-wide rice (Oryza sativa) DNA polymorphism database has been constructed in this work using the genomes of Nipponbare, a cultivar of japonica, and 93-11, a cultivar of indica. This database contains 1,703,176 single nucleotide polymorphisms (SNPs) and 479,406 Insertion/Deletions (InDels), approximately one SNP every 268 bp and one InDel every 953 bp in rice genome. Both SNPs and InDels in the database were experimentally validated. Of 109 randomly selected SNPs, 107 SNPs (98.2%) are accurate. PCR analysis indicated that 90% (97 of 108) of InDels in the database could be used as molecular markers, and 68% to 89% of the 97 InDel markers have polymorphisms between other indica cultivars (Guang-lu-ai 4 and Long-te-pu B) and japonica cultivars (Zhong-hua 11 and 9522). This suggests that this database can be used not only for Nipponbare and 93-11, but also for other japonica and indica cultivars. While validating InDel polymorphisms in the database, a set of InDel markers with each chromosome 3 to 5 marker was developed. These markers are inexpensive and easy to use, and can be used for any combination of japonica and indica cultivars used in this work. This rice DNA polymorphism database will be a valuable resource and important tool for map-based cloning of rice gene, as well as in other various research on rice (http://shenghuan.shnu.edu.cn/ricemarker).

Record 45 of 434 - AGRICOLA 1998-2004/09

AU: Routledge,-A.P.M.; Shelley,-G.; Smith,-J.V.; Talbot,-N.J.; Draper,-J.; Mur,-L.A.J.

TI: Magnaporthe grisea interactions with the model grass Brachypodium distachyon closely resemble those with rice (Oryza sativa).

SO: Molecular plant pathology. 2004 July, v. 5, issue 4 p. 253-265.

Record 46 of 434 - AGRICOLA 1998-2004/09

AU: Graham,-M.A.; Silverstein,-K.A.T.; Cannon,-S.B.; VandenBosch,-K.A.

TI: Computational identification and characterization of novel genes from legumes.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1179-1197.

AB: The Fabaceae, the third largest family of plants and the source of many crops, has been the target of many genomic studies. Currently, only the grasses surpass the legumes for the number of publicly available expressed sequence tags (ESTs). The quantity of sequences from diverse plants enables the use of computational approaches to identify novel genes in specific taxa. We used BLAST algorithms to compare unigene sets from Medicago truncatula, Lotus japonicus, and soybean (Glycine max and Glycine soja) to nonlegume unigene sets, to GenBank's nonredundant and EST databases, and to the genomic sequences of rice (Oryza sativa) and Arabidopsis. As a working definition, putatively legume-specific genes had no sequence homology, below a specified threshold, to publicly available sequences of nonlegumes. Using this approach, 2,525 legume-specific EST contigs were identified, of which less than three percent had clear homology to previously characterized legume genes. As a first step toward predicting function, related sequences were clustered to build motifs that could be searched against protein databases. Three families of interest were more deeply characterized: F-box related proteins, Pro-rich proteins, and Cys cluster proteins (CCPs). Of particular interest were the >300 CCPs, primarily from nodules or seeds, with predicted similarity to defensins. Motif searching also identified several previously unknown CCP-like open reading frames in Arabidopsis. Evolutionary analyses of the genomic sequences of several CCPs in M. truncatula suggest that this family has evolved by local duplications and divergent selection.

Record 47 of 434 - AGRICOLA 1998-2004/09

AU: Krysan,-P.

TI: Ice-cap. A high-throughput method for capturing plant tissue samples for genotype analysis.

SO: Plant physiology. 2004 July, v. 135, no. 3 p. 1162-1169.

AB: High-throughput genotype screening is rapidly becoming a standard research tool in the post-genomic era. A major bottleneck currently exists, however, that limits the utility of this approach in the plant sciences. The rate-limiting step in current high-throughput pipelines is that tissue samples from living plants must be collected manually, one plant at a time. In this article I describe a novel method for harvesting tissue samples from living seedlings that eliminates this bottleneck. The method has been named Ice-Cap to reflect the fact that ice is used to capture the tissue samples. The planting of seeds, growth of seedlings, and harvesting of tissue are all performed in a 96-well format. I demonstrate the utility of this system by using tissue harvested by Ice-Cap to genotype a population of Arabidopsis seedlings that is segregating a previously characterized mutation. Because the harvesting of tissue is performed in a nondestructive manner, plants with the desired genotype can be transferred to soil and grown to maturity. I also show that Ice-Cap can be used to analyze genomic DNA from rice (Oryza sativa) seedlings. It is expected that this method will be applicable to high-throughput screening with many different plant species, making it a useful technology for performing marker assisted selection.

Record 48 of 434 - AGRICOLA 1998-2004/09
AU: Gutterson,-N.; Reuber,-T.L.
TI: Regulation of disease resistance pathways by AP2/ERF transcription factors.
SO: Current opinion in plant biology. 2004 Aug., v. 7, no. 4 p. 465-471.

Record 49 of 434 - AGRICOLA 1998-2004/09
AU: Sharma,-P.; Dubey,-R.S.
TI: Ascorbate peroxidase from rice seedlings: properties of enzyme isoforms, effects of stresses and protective roles of osmolytes.
SO: Plant science. 2004 Sept., v. 167, issue 3 p. 541-550.

Record 50 of 434 - AGRICOLA 1998-2004/09
AU: Tian,-S.; Nakamura,-K.; Kayahara,-H.
TI: Analysis of phenolic compounds in white rice, brown rice, and germinated brown rice.
SO: Journal of agricultural and food chemistry. 2004 July 28, v. 52, no. 15 p. 4808-4813.
AB: Two hydroxycinnamate sucrose esters, 6'-O-(E)-feruloylsucrose and 6'-O-(E)-sinapoylsucrose, were isolated from methanol extracts of rice bran. Soluble and insoluble phenolic compounds as well as 6'-O-(E)-feruloylsucrose and 6'-O-(E)-sinapoylsucrose from white rice, brown rice, and germinated brown rice were analyzed using HPLC. The results demonstrated that the content of insoluble phenolic compounds was significantly higher than that of soluble phenolics in rice, whereas almost all compounds identified in germinated brown rice and brown rice were more abundant than those in white rice. 6'-O-(E)-Feruloylsucrose (1.09 mg/100 g of flour) and 6'-O-(E)-sinapoylsucrose (0.41 mg/100 g of flour) were found to be the major soluble phenolic compounds in brown rice. During germination, an ~70% decrease was observed in the content of the two hydroxycinnamate sucrose esters, whereas free phenolic acid content increased significantly; the ferulic acid content of brown rice (0.32 mg/100 g of flour) increased to 0.48 mg/100 g of flour and became the most abundant phenolic compound in germinated brown rice. The content of sinapinic acid increased to 0.21 mg/100 g of flour, which is nearly 10 times as much as that in brown rice (0.02 mg/100 g of flour). In addition, the total content of insoluble phenolic compounds increased from 18.47 mg/ 100 g of flour in brown rice to 24.78 mg/100 g of flour in germinated brown rice. These data suggest that appropriate germination of brown rice may be a method to improve health-related benefits.

Record 51 of 434 - AGRICOLA 1998-2004/09
AU: Hur,-J.; Jung,-K.H.; Lee,-C.H.; An,-G.
TI: Stress-inducible OsP5CS2 gene is essential for salt and cold tolerance in rice.
SO: Plant science. 2004 Sept., v. 167, issue 3 p. 417-426.

Record 52 of 434 - AGRICOLA 1998-2004/09

AU: Bawadi,-H.A.; Antunes,-T.M.; Shih,-F.; Losso,-J.N.

TI: In vitro inhibition of the activation of pro-matrix metalloproteinase 1 (Pro-MMP-1) and pro-matrix metalloproteinase 9 (pro-MMP-9) by rice and soybean Bowman-Birk inhibitors.

SO: Journal of agricultural and food chemistry. 2004 July 28, v. 52, no. 15 p. 4730-4736.

AB: The in vitro inhibitory activity of the rice Bowman-Birk inhibitor (rBBI) or soybean Bowman-Birk inhibitor (sBBI) against trypsin-catalyzed activation of pro-matrix metalloproteinase 1 or 9 (pro-MMP-1 or pro-MMP-9), respectively, was investigated using electrophoresis with silver staining, heparin-enhanced zymography, biotinylated gelatin, Biotrak assay, and fluorescence quenched substrate hydrolysis. rBBI at concentrations of 0.08-0.352 mg/mL dose-dependently inhibited the in vitro activation of 45 microgram/mL pro-MMP-1 by trypsin. Heparin-enhanced zymography analysis of pro-MMP-1, trypsin-activated MMP-1, and a mixture of pro-MMP-1-trypsin-rBBI showed clear zones associated with trypsin-activated MMP-1 and the absence of clear zones in lanes containing pro-MMP-1 or a mixture of pro-MMP-1, trypsin, and rBBI. The results of the Biotrak assay also indicated that rBBI dose-dependently suppressed the activation of pro-MMP-1 by trypsin. sBBI dose-dependently inhibited the activation of 100 microgram/mL of pro-MMP-9 by trypsin. Biotinylated gelatin assays demonstrated that pro-MMP-9 or pro-MMP-9 in the presence of trypsin and BBI did not hydrolyze gelatin, whereas p-aminophenylmercury acetate (APMA)-activated MMP-9 and trypsin-activated MMP-9 caused significant hydrolysis of gelatin. Quenched fluorescence substrate hydrolysis for total MMP activity showed that pro-MMP-1 or pro-MMP-9 did not hydrolyze the substrate Mca-Pro-Leu-Gly-Leu-Dpa-Ala-Arg-NH2; active MMP-1 or MMP-9 hydrolyzed the substrate, but lower substrate hydrolysis was obtained when pro-MMP-1 or pro-MMP-9 was incubated with trypsin in the presence of increasing concentrations of rBBI. The results are discussed in light of the role of MMP-1 and MMP-9 in the process of angiogenesis and the potential of rBBI or sBBI as a functional food ingredient.

Record 53 of 434 - AGRICOLA 1998-2004/09

AU: Singh,-M.P.; Lee,-F.N.; Counce,-P.A.; Gibbons,-J.H.

TI: Mediation of partial resistance to rice blast through anaerobic induction of ethylene.

SO: Phytopathology. 2004 Aug., v. 94, no. 8 p. 819-825.

AB: The correlation between anaerobic soil conditions and increased resistance to rice blast disease has long been observed without benefit of an adequate explanation. We researched flood depth, dissolved oxygen (DO), and ethylene relative to expression of partial blast resistance in cvs. M-201, Newbonnet, LaGrue, Mars, and Cypress. Cultivar blast index (BI) and flood DO decreased with increasing flood depth. BIs were positively correlated with DO. Total leaf blast lesions were 3.4 and 3.2 times greater in cvs. M-201 and LaGrue growing in a 5.0-microliter liter-1 DO nutrient solution than when growing in a 0.1-microliter liter-1 DO solution. Treatment with 0.25 mM ethephon, which releases ethylene, lowered BIs of Newbonnet, LaGrue, and Cypress growing upland when applied drench, foliar, or foliar-drench. If flooded, BIs of ethephon-treated cultivars were decreased by drench and foliar-drench applications only. BIs of upland plants were unchanged, whereas BIs of analogous flooded plants increased following treatment with 0.31 mM aminoethoxyvinylglycine (AVG), an ethylene biosynthesis inhibitor. We hypothesize that varying anaerobic conditions mediate production of phytohormones, particularly ethylene, which modify expression of inherent partial blast resistance in these rice cultivars.

Record 54 of 434 - AGRICOLA 1998-2004/09

AU: Umemura,-K.; Tanino,-S.; Nagatsuka,-T.; Koga,-J.; Iwata,-M.; Nagashima,-K.; Amemiya,-Y.

TI: Cerebroside elicitor confers resistance to Fusarium disease in various plant species.

SO: Phytopathology. 2004 Aug., v. 94, no. 8 p. 813-818.

AB: In the rice blast fungus pathosystem, cerebroside, a compound categorized as a sphingolipid, was found in our previous study to be a non-race-specific elicitor, which elicits defense responses in rice. Here we describe that cerebroside C is produced in diverse strains of Fusarium oxysporum, a common soilborne agent of wilt disease affecting a wide range of plant species. In addition, some type of cerebroside elicitor involving cerebroside A, B, or C was detected in other soilborne phytopathogens, such as Pythium and Botrytis. Treatment of lettuce (Lactuca sativa), tomato (Lycopersicon esculentum), melon (Cucumis melo), and sweet potato (Ipomoea batatas) with cerebroside B resulted in resistance to infection by each pathogenic strain of F. oxysporum. Induction of pathogenesis-related genes and H(2)O(2) production by treatment with cerebroside B were observed in tomato root tissues. The cerebroside elicitor showed no antifungal activity against F. oxysporum in vitro, indicating that the cerebroside elicitor activates defense mechanisms to confer resistance to Fusarium disease. These results suggest that cerebroside functions as a non-race-specific elicitor in a wide range of plantÆphytopathogenic fungus interactions. Additionally, cerebroside elicitor serves as a potential biologically derived control agent.

Record 55 of 434 - AGRICOLA 1998-2004/09

AU: Qi,-Y.; Yamauchi,-Y.; Ling,-J.; Kawano,-N.; Li,-D.; Tanaka,-K.

TI: Cloning of a putative monogalactosyldiacylglycerol synthase gene from rice (Oryza sativa L.) plants and its expression in response to submergence and other stresses.

SO: Planta. 2004 July, v. 219, no. 3 p. 450-458.

AB: Suppression subtractive hybridization was used to construct a subtractive cDNA library from plants of non-submerged and 7-day-submerged rice (Oryza sativa L., FR13A, a submergence-tolerant cultivar). One clone of the subtractive cDNA library, S23, was expressed abundantly during submergence. The full length of S23 was amplified using 5'- and 3'-rapid amplification of cDNA ends, and found to consist of 1,671 bp with an open reading frame of 1,077 bp (181-1257) encoding 358 amino acids. Its deduced amino acid sequence showed a high homology with monogalactosyldiacylglycerol synthase (UDPgalactose: 1,2-diacylglycerol 3-beta-D-galactosyl transferase; EC 2.4.1.46, MGDG synthase) from Arabidopsis thaliana; therefore, we named the gene OsMGD. Time-course studies showed that the expression of

OsMGD in the rice cultivars FR13A and IR42 (submergence-susceptive cultivar) during submergence was gradually increased and that expression in FR13A was higher than in IR42. The expression of OsMGD in FR13A was influenced by benzyladenine and illumination. The accumulation of OsMGD mRNA in both FR13A and IR42 was also increased by ethephon, gibberellin, drought and salt treatment, but cold stress had no effect on the expression of the gene. These results suggest that the expression of OsMGD mRNA requires benzyladenine or illumination, and that the process is also mediated by ethephon and gibberellin. Salt and drought stress have an effect similar to that of submergence. Furthermore, the enhanced expression of OsMGD may relate to photosynthesis, and play an important role during submergence.

Record 56 of 434 - AGRICOLA 1998-2004/09
AU: Peabody,-E.
TI: Bolstering rice against blast.
SO: Agricultural research. 2004 Aug., v. 52, no. 8 p. 18-19.

Record 57 of 434 - AGRICOLA 1998-2004/09
AU: Sallaud,-C.; Gay,-C.; Larmande,-P.; Bes,-M.; Piffanelli,-P.; Piegu,-B.; Droc,-G.; Regad,-F.; Bourgeois,-E.; Meynard,-D.
TI: High throughput T-DNA insertion mutagenesis in rice: a first step toward in silico reverse genetics.
SO: Plant journal. 2004 Aug., v. 39, no. 3 p. 450-464.
AB: A library of 29 482 T-DNA enhancer trap lines has been generated in rice cv. Nipponbare. The regions flanking the T-DNA left border from the first 12 707 primary transformants were systematically isolated by adapter anchor PCR and sequenced. A survey of the 7480 genomic sequences larger than 30 bp (average length 250 bp), representing 56.4% of the total readable sequences and matching the rice bacterial artificial chromosome/ phage artificial chromosome (BAC/PAC) sequences assembled in pseudomolecules allowed the assigning of 6645 (88.8%) T-DNA insertion sites to at least one position in the rice genome of cv. Nipponbare. T-DNA insertions appear to be rather randomly distributed over the 12 rice chromosomes, with a slightly higher insertion frequency in chromosomes 1, 2, 3 and 6. The distribution of 723 independent T-DNA insertions along the chromosome 1 pseudomolecule did not differ significantly from that of the predicted coding sequences in exhibiting a lower insertion density around the centromere region and a higher density in the subtelomeric regions where the gene density is higher. Further establishment of density graphs of T-DNA inserts along the recently released 12 rice pseudomolecules confirmed this non-uniform chromosome distribution. T-DNA appeared less prone to hot spots and cold spots of integration when compared with those revealed by a concurrent assignment of the Tos17 retrotransposon flanking sequences deposited in the National Center for Biotechnology Information (NCBI). T-DNA inserts rarely integrated into repetitive sequences. Based on the predicted gene annotation of chromosome 1, preferential insertion within the first 250 bp from the putative ATG start codon has been observed. Using 4 kb of sequences surrounding the insertion points, 62% of the sequences showed significant similarity to gene encoding known proteins (E-value <1.00 e-05). To illustrate the in silico reverse genetic approach, identification of 83 T-DNA insertions

within genes coding for transcription factors (TF) is presented. Based both on the estimated number of members of several large TF gene families (e.g. Myb, WRKY, HD-ZIP, Zinc-finger) and on the frequency of insertions in chromosome 1 predicted genes, we could extrapolate that 7-10% of the rice gene complement is already tagged by T-DNA insertion in the 6116 independent transformant population. This large resource is of high significance while assisting studies unravelling gene function in rice and cereals, notably through in silico reverse genetics.

Record 58 of 434 - AGRICOLA 1998-2004/09

AU: Koike,-S.; Inoue,-H.; Mizuno,-D.; Takahashi,-M.; Nakanishi,-H.; Mori,-S.; Nishizawa,-N.K.

TI: OsYSL2 is a rice metal-nicotianamine transporter that is regulated by iron and expressed in the phloem.

SO: Plant journal. 2004 Aug., v. 39, no. 3 p. 415-424.

AB: We identified 18 putative yellow stripe 1 (YS1)-like genes (OsYSLs) in the rice genome that exhibited 36-76% sequence similarity to maize iron(III)-phytosiderophore transporter YS1. Of particular interest was OsYSL2, the transcripts of which were not detected in the roots of either iron-sufficient or iron-deficient plants, but dramatic expression was induced in the leaves by iron deficiency. Based on the nucleotide sequence, OsYSL2 was predicted to encode a polypeptide of 674 amino acids containing 14 putative transmembrane domains. OsYSL2:green fluorescent protein (GFP) was localized in the plasma membrane of onion epidermal cells. Promoter:beta-glucuronidase (GUS) analysis revealed that OsYSL2 was expressed in companion cells in iron-sufficient roots. GUS activity was increased in companion cells, but no GUS staining was observed in epidermal or cortex cells, even in iron-deficient roots. In the leaves and leaf sheaths of iron-sufficient rice, GUS staining was observed in phloem cells of the vascular bundles. In iron-deficient leaves, the OsYSL2 promoter was active in all tissues with particularly strong GUS activity evident in companion cells. The phloem-specific expression of the OsYSL2 promoter suggests that OsYSL2 is involved in the phloem transport of iron. Strong OsYSL2 promoter activity was also detected in developing seeds. Electrophysiological measurements using Xenopus laevis oocytes showed that OsYSL2 transported iron(II)-nicotianamine (NA) and manganese(II)-NA, but did not transport iron(III)-phyosiderophore. These results suggest that OsYSL2 is a rice metal-NA transporter that is responsible for the phloem transport of iron and manganese, including the translocation of iron and manganese into the grain.

Record 59 of 434 - AGRICOLA 1998-2004/09

AU: Xu,-M.; Hillwig,-M.L.; Prisic,-S.; Coates,-R.M.; Peters,-R.J.

TI: Functional identification of rice syn-copalyl diphosphate synthase and its role in initiating biosynthesis of diterpenoid phytoalexin/allelopathic natural products.

SO: Plant journal. 2004 Aug., v. 39, no. 3 p. 309-318.

AB: Rice produces a number of phytoalexins, and at least one allelopathic agent, from syn-copalyl diphosphate (CPP), representing the only known metabolic fate for this compound. Thus, the class II terpene synthase that converts the universal diterpenoid precursor geranylgeranyl diphosphate to syn-CPP catalyzes the committed step in biosynthesis of these natural products. Here the extensive sequence information available for rice was coupled to recombinant expression and functional analysis to identify syn-copalyl diphosphate synthase (OsCPSsyn). In addition, OsCPSsyn mRNA was found to be specifically induced in leaves by conditions that stimulate phytoalexin biosynthesis. Therefore, transcription of OsCPSsyn seems to be an important regulatory point for controlling the production of these defensive compounds. Finally, alignments carried out with OsCPSsyn revealed that class II terpene synthases exhibit a sequence conservation pattern substantially different from that of the prototypical class I enzymes. One particularly notable feature is the specific conservation of the functionally cryptic 'insertional' sequence element in class II terpene synthases, indicating that this region is important for the corresponding cyclization reaction.

Record 60 of 434 - AGRICOLA 1998-2004/09

AU: LeJeune,-J.T.; Besser,-T.E.; Rice,-D.H.; Berg,-J.L.; Stilborn,-R. P.; Hancock,-D.D.

TI: Longitudinal study of fecal shedding of Escherichia coli O157:H7 in feedlot cattle: predominance and persistence of specific clonal types despite massive cattle population turnover.

SO: Applied and environmental microbiology. 2004 Jan., v. 70, no. 1 p. 377-384.

AB: Identification of the sources and methods of transmission of Escherichia coli O157:H7 in feedlot cattle may facilitate the development of on-farm control measures for this important food-borne pathogen. The prevalence of E. coli O157:H7 in fecal samples of commercial feedlot cattle in 20 feedlot pens between April and September 2000 was determined throughout the finishing feeding period prior to slaughter. Using immunomagnetic separation, E. coli O157:H7 was isolated from 636 of 4,790 (13%) fecal samples in this study, with highest prevalence earliest in the feeding period. No differences were observed in the fecal or water trough sediment prevalence values of E. coli O157:H7 in 10 pens supplied with chlorinated drinking water supplies compared with nonchlorinated water pens. Pulsed-field gel electrophoresis of XbaI-digested bacterial DNA of the 230 isolates obtained from eight of the pens revealed 56 unique restriction endonuclease digestion patterns (REDPs), although nearly 60% of the isolates belonged to a group of four closely related genetic subtypes that were present in each of the pens and throughout the sampling period. The other REDPs were typically transiently detected, often in single pens and on single sample dates, and in many cases were also closely related to the four predominant REDPs. The persistence and predominance of a few REDPs observed over the entire feeding period on this livestock operation highlight the importance of the farm environment, and not necessarily the incoming cattle, as a potential source or reservoir of E. coli O157:H7 on farms.

Record 61 of 434 - AGRICOLA 1998-2004/09

AU: Frantz,-J.M.; Pinnock,-D.; Klassen,-S.; Bugbee,-B.

TI: Characterizing the environmental response of a gibberellic acid-deficient rice for use as a model crop.

SO: Agronomy journal. 2004 July-Aug, v. 96, no. 4 p. 1172-1181.

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Record 62 of 434 - AGRICOLA 1998-2004/09
AU:   Appleton,-D.J.; Rand,-J.S.; Priest,-J.; Sunvold,-G.D.; Vickers,-J.
      R.
TI:   Dietary carbohydrate source affects glucose concentrations,
      insulin secretion, and food intake in overweight cats.
SO:   Nutrition research. 2004 June, v. 24, no. 6 p. 447-467.
AB:   This study was undertaken to assess the impact of dietary
      carbohydrate source on food intake, body composition, glucose
      tolerance, insulin sensitivity, and glucose and insulin
      concentrations in overweight and obese cats with reduced insulin
      sensitivity. Sixteen overweight and obese cats were divided into
      two groups and randomly allocated one of two extruded diets
      formulated to contain similar starch content (33%) from different
      cereal sources (sorghum and corn versus rice). Meal response,
      glucose tolerance and insulin sensitivity tests were performed
      before and after a 6-week weight-maintenance phase and after an
      additional 8-week free-access feeding phase. Dual energy x-ray
      absorptiometry (DEXA)Æderived body composition was determined in
      each cat before the study and after each test phase. Food intake
      was measured daily and body weight measured twice weekly for the
      duration of the study. When compared with the sorghum/corn-based
      diet, cats fed the rice-based diet consumed more energy and
      gained more weight in response to free-access feeding. Cats fed
      the rice-based diet also tended to have higher glucose
      concentrations and insulin secretion in response to a glucose
      load or a test meal. We conclude that a sorghum and corn blend is
      a superior carbohydrate source than rice for overweight cats with
      glucose intolerance and reduced insulin sensitivity. Such a diet
      may help to minimize overeating and additional weight gain, and
      may also reduce the risk of developing type 2 diabetes mellitus.
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Record 63 of 434 - AGRICOLA 1998-2004/09
AU:   Coyne,-D.L.; Sahrawat,-K.L.; Plowright,-R.A.
TI:   The influence of mineral fertilizer application and plant
      nutrition on plant-parasitic nematodes in upland and lowland rice
      in Cote d'Ivoire and its implications in long term agricultural
      research trials.
SO:   Experimental agriculture. 2004 Apr., v. 40, no. 2 p. 245-256.
AB:   Mineral fertilizer application and consequent plant nutrition has
      long been observed to influence associated plant-parasitic
      nematode population densities, offering the potential as a
      nematode management option. Observations were made on the
      influence of mineral fertilizer application on nematode
      populations on three separate long-term rice experiments, (
      differential mineral application on upland and on lowland rice,
      and P application on upland rice) undertaken between 1994 and
      1997 in Cote d'Ivoire. In 1995, on upland rice, treatments with K
      or N withheld from the comprehensive mineral application
      treatment (range of elements including N, P, K, Ca, Mg and Zn)
      led to lower densities of Pratylenchus zeae at harvest than the
      comprehensive mineral application. By withholding K or Mg,
      Helicotylenchus pseudorobustus densities were greater than with
      either the control (no mineral application) or comprehensive
      mineral application in the same year. No differences were
      observed between treatments in 1994, or between treatments for
      densities of other nematode species present (Meloidogyne
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incognita, Criconemella tescorum) or for total nematode density. In the lowland rice trial, no treatment effects on nematode species (Hirschmanniella oryzae and Uliginotylenchus palustris) were observed. In the P application trial on a P-deficient Ultisol, Heterodera sacchari densities were lower in treatments receiving 180 kg P ha-1, than untreated in 1995; in 1996 no differences were observed between untreated and 135 kg P ha-1, while in 1997 higher densities of H. sacchari were present in 135 kg P ha-1 than untreated. Regression analysis of nematode densities against the mineral straw content in the P application trial revealed a negative correlation between M. incognita and Mn and Ca, and between P. zeae and Zn or Fe. A positive correlation was observed between Helicotylenchus spp. and Mg. This study provides strong arguments for taking plant parasitic nematodes into account when planning and executing long-term research trials.

Record 64 of 434 - AGRICOLA 1998-2004/09

AU: Rong,-J.; Xia,-H.; Zhu,-Y.; Wang,-Y.; Lu,-B.R.

TI: Asymmetric gene flow between traditional and hybrid rice varieties (Oryza sativa) indicated by nuclear simple sequence repeats and implications for germplasm conservation.

SO: New phytologist. 2004 Aug., v. 163, no. 2 p. 439-445.

Record 65 of 434 - AGRICOLA 1998-2004/09

AU: Kimura,-M.; Murase,-J.; Lu,-Y.

TI: Carbon cycling in rice field ecosystems in the context of input, decomposition and translocation of organic materials and the fates of their end products (CO_2 and CH_4).

SO: Soil biology and biochemistry. 2004 Sept., v. 36, no. 9 p. 1399-1416.

AB: Rice fields are intensively managed, unique agroecosystems, where soil flooding is general performance for rice cultivation. Flooding the field results in reductive soil conditions, under which decomposition of organic materials proceeds during the period of rice cultivation. A large variety of organic materials are incorporated into rice soils according to field management. In this review, the kind and abundance of organic materials entering carbon cycling in the rice field ecosystem are evaluated first. Then, decomposition of plant residues and soil organic matter in rice fields is reviewed quantitatively. Decomposition of plant residues is shown to be the active process in carbon cycling in rice fields. Rice releases photosynthates into the rhizosphere (rhizodeposition), and they follow a different avenue of decomposition in soil from that of plant residues. Incorporation of rhizodeposition into microbial biomass and soil organic matter during the period of rice cultivation, and their fates after harvesting are evaluated quantitatively from 13C pulse labeled experiments. Percolating water transports inorganic and organic carbon from the plow layer to the subsoil layer. The amounts of their transport and accumulation in the subsoil layer are evaluated in relation to the amounts of soil organic C in the plow layer. Not only CO_2 but also CH_4 are produced in the decomposition process of organic materials in flooded rice fields. CH_4 evolution from rice fields is of global concern from the viewpoint of global warming. Origins of CH_4 evolved from rice fields are estimated first, followed by the fates of CH_4 in rice field ecosystems. Rhizodeposition is shown to be the main origin of CH4 evolved from rice fields. Evolution to the atmosphere is not the sole pathway of CH4 produced in rice fields. The amounts of CH4 retained in soil, percolated to the subsoil layer and decomposed in soil are evaluated in the context of the amounts of CH4 efflux. Thus, this review focuses on carbon cycling in the rice field ecosystem from the viewpoints of input, decomposition, and translocation of organic materials and the fates of their end products (CO2 and CH4).

Record 66 of 434 - AGRICOLA 1998-2004/09

AU: Kennedy,-I.R.; Choudhury,--A.T.M.A.; Kecskes,-M.L.

TI: Non-symbiotic bacterial diazotrophs in crop-farming systems: can their potential for plant growth promotion be better exploited.

SO: Soil biology and biochemistry. 2004 Aug., v. 36, no. 8 p. 1229-1244.

AB: Biological N2 fixation (BNF) by associative diazotrophic bacteria is a spontaneous process where soil N is limited and adequate C sources are available. Yet the ability of these bacteria to contribute to yields in crops is only partly a result of BNF. A range of diazotrophic plant growth-promoting rhizobacteria participate in interactions with C3 and C4 crop plants (e.g. rice , wheat, maize, sugarcane and cotton), significantly increasing their vegetative growth and grain yield. We review the potential of these bacteria to contribute to yield increases in a range of field crops and outline possible strategies to obtain such yield increases more reliably. The mechanisms involved have a significant plant growth-promoting potential, retaining more soil organic-N and other nutrients in the plant-soil system, thus reducing the need for fertiliser N and P. Economic and environmental benefits can include increased income from high yields, reduced fertiliser costs and reduced emission of the greenhouse gas, N2O (with more than 300 times the global warming effect of CO2), as well as reduced leaching of NO3--N to ground water. Obtaining maximum benefits on farms from diazotrophic, plant growth promoting biofertilisers will require a systematic strategy designed to fully utilise all these beneficial factors, allowing crop yields to be maintained or even increased while fertiliser applications are reduced.

Record 67 of 434 - AGRICOLA 1998-2004/09

AU: Burt,-S.

TI: Essential oils: their antibacterial properties and potential applications in foods--a review.

SO: International journal of food microbiology. 2004 Aug. 1, v. 94, no. 3 p. 223-253.

AB: In vitro studies have demonstrated antibacterial activity of essential oils (EOs) against Listeria monocytogenes, Salmonella typhimurium, Escherichia coli O157:H7, Shigella dysenteria, Bacillus cereus and Staphylococcus aureus at levels between 0.2 and 10 microliter ml-1. Gram-negative organisms are slightly less susceptible than gram-positive bacteria. A number of EO components has been identified as effective antibacterials, e.g. carvacrol, thymol, eugenol, perillaldehyde, cinnamaldehyde and cinnamic acid, having minimum inhibitory concentrations (MICs) of 0.05-5 microliter ml-1 in vitro. A higher concentration is needed to achieve the same effect in foods. Studies with fresh meat,

meat products, fish, milk, dairy products, vegetables, fruit and cooked rice have shown that the concentration needed to achieve a significant antibacterial effect is around 0.5-20 microliter g-1 in foods and about 0.1-10 microliter ml-1 in solutions for washing fruit and vegetables. EOs comprise a large number of components and it is likely that their mode of action involves several targets in the bacterial cell. The hydrophobicity of EOs enables them to partition in the lipids of the cell membrane and mitochondria, rendering them permeable and leading to leakage of cell contents. Physical conditions that improve the action of EOs are low pH, low temperature and low oxygen levels. Synergism has been observed between carvacrol and its precursor p-cymene and between cinnamaldehyde and eugenol. Synergy between EO components and mild preservation methods has also been observed. Some EO components are legally registered flavourings in the EU and the USA. Undesirable organoleptic effects can be limited by careful selection of EOs according to the type of food.

Record 68 of 434 - AGRICOLA 1998-2004/09
AU: Rakwal,-R.; Yang,-G.; Komatsu,-S.
TI: Chitinase induced by jasmonic acid, methyl jasmonate, ethylene and protein phosphatase inhibitors in rice.
SO: Molecular biology reports. 2004 June, v. 31, no. 2 p. 113-119.

Record 69 of 434 - AGRICOLA 1998-2004/09
AU: Zhang,-Z.; Zhu,-Y.M.; Guo,-P.Y.; Liu,-G.S.
TI: Potential loss of phosphorus from a rice field in Taihu Lake basin.
SO: Journal of environmental quality. 2004 July-Aug, v. 33, no. 4 p. 1403-1412.
AB: Nonpoint-source pollution by phosphorus (P) poses a threat to waters in the Taihu Lake basin in China. The potential transfer of P in rice (Oryza sativa L.) fields through surface drainage and subsurface flow was investigated under simulated conventional irrigationÆdrainage management. Surface drainage events were conducted to avoid overflow across the plots after heavy rainfall and for rice harvest, at which time P losses were also investigated. This study was conducted in 2001 in a long-term rice field experiment. The experimental plots were treated with 0, 26, or 52 kg P ha-1 as superphosphate or 26 kg P ha-1 with equal parts of P supplied as superphosphate and pig manure. Phosphorus concentrations and loads in field floodwater on plots receiving P rapidly declined in a nonlinear manner before the first drainage, three weeks after fertilizer application. The combined application of fertilizer and manure P resulted in higher P transfer potential in field floodwater than with fertilizer P alone one week after P application. Phosphorus concentrations in interflow water sampled by Teflon suction cups inserted at a depth of 150 to 200 mm gradually increased within two weeks after P application, then declined. The concentration of P in interflow water was related to soil P buildup from long-term P application, as well as recently applied P. The 26 kg P ha-1 treatment (the conventional P rate in this region) resulted in a loss of 0.74 kg total phosphorus (TP) ha-1 and a drainage-weighted average concentration of 0.25 mg TP L-1 from the three surface drainage events. Results indicate that avoiding overflow drainage after P input and extending the time between P application and drainage

may reduce P losses from rice paddies.

Record 70 of 434 - AGRICOLA 1998-2004/09

AU: Sawada,-H.; Sugihara,-M.; Takagaki,-M.; Nagayama,-K.

TI: Monitoring and characterization of Magnaporthe grisea isolates with decreased sensitivity to scytalone dehydratase inhibitors.

SO: Pest management science. 2004 Aug., v. 60, issue 8 p. 777-785.

AB: Rice blast fungus isolates were collected in Kyushu to investigate resistance to scytalone dehydratase inhibitors of melanin biosynthesis (MBI-D). In 2001, failure of control of rice blast was reported in the Saga prefecture, where MBI-Ds have been used since 1998. At that time, the distribution of resistant isolates was mainly limited to that area. However, in 2002, resistant isolates were detected in all prefectures of Kyushu. DNA fingerprinting analysis showed that the mutation causing resistance to MBI-Ds had arisen independently in each area. These data suggest that resistant isolates may occur in any area and become dominant under continuous selection pressure for MBI-Ds. Nevertheless, resistant strains can be controlled by reductase inhibitors of melanin biosynthesis (MBI-R) or commercial rice seed disinfectants.

Record 71 of 434 - AGRICOLA 1998-2004/09

AU: Mohapatra,-D.; Bal,-S.

TI: Wear of rice in an abrasive milling operation. 1. Prediction of degree of milling.

SO: Biosystems engineering. 2004 July, v. 88, issue 3 p. 337-342.

AB: The abrasion coefficient of rice was determined at different degrees of milling levels, for three varieties of rice differing in slenderness ratio. The abrasion coefficient was found to decrease with the degree of milling, indicating the removal of asperities and progressive hardness of the core of the rice. The slenderness ratio was found to be negatively related with the value of the abrasion coefficient. The average values of the abrasion coefficient of rice on abrasive element (synthetic emery) varied between 0.03 and 0.05 for three varieties of rice differing in hardness and slenderness values. The average value of abrasion coefficient was used to predict the degree of milling using the principles of adhesive wear. The predicted values of the degree of milling fitted the experimental values adequately, with relative deviation modulus varying between 14 and 23% and good values for the coefficient of determination (R2>0.90).

Record 72 of 434 - AGRICOLA 1998-2004/09

AU: Mols,-J.; Peeters-Joris,-C.; Agathos,-S.N.; Schneider,-Y.J.

TI: Origin of rice protein hydrolysates added to protein-free media alters secretion and extracellular proteolysis of recombinant interferon-gamma as well as CHO-320 cell growth.

SO: Biotechnology letters. 2004 July, v. 26, no. 13 p. 1043-1046.

AB: CHO-320 cells, cultivated in suspension in a protein-free medium supplemented with rice protein hydrolysates (peptones), secrete recombinant interferon-gamma (IFN-gamma) that undergo will or will not proteolysis, depending on the origin of the peptones. This proteolytic event, as well as the appearance of an unidentified 70 kDa gelatinase-like protease, are attributed to a cysteine protease. Casein zymographies revealed that one rice protein hydrolysate, but not another, contains a papain-like cysteine protease whose activity is undetectable in solution. This work underlines the significance of the origin of peptones when considered as supplements in serum- and protein-free media for overproduction of recombinant proteins.

Record 73 of 434 - AGRICOLA 1998-2004/09

AU: Hirai,-Y.; Inoue,-E.; Mori,-K.

TI: Application of a quasi-static stalk bending analysis to the dynamic response of rice and wheat stalks gathered by a combine harvester reel.

SO: Biosystems engineering. 2004 July, v. 88, issue 3 p. 281-294.

AB: Horizontal and vertical reaction forces of rice and wheat stalks gathered by a combine harvester reel were measured by the experiment system, newly developed in order to clarify dynamic response of the crop stalks related to the gathering performance and to discuss the application of a quasi-static stalk bending analysis to the determination of the reaction force of crop stalks under dynamic loading conditions. The experiment was conducted under five different loading speeds, and the effect of the loading speed on the reaction force was investigated. As the loading speed increased, the horizontal force had a large positive peak value, while the vertical force involved the change in the force direction and had a negative peak value, depending on the initial deflection shape of crop stalks. Thus, the results simulated by the stalk bending analysis involved a large amount of error, and limitations of the analytical method were identified. The experimental results were examined in terms of acceleration at the loading point during the gathering operation. The location of a positive peak in the horizontal reaction force and a negative peak in the vertical one coincided with that of the negative peak in the horizontal acceleration and the positive peak in the vertical one, respectively. These results indicated that the peak values under high loading speeds were due to the effect of the inertial force of the crop stalks. Further, the error in the simulated results under high loading speeds was investigated in terms of the direction of the acceleration force determined by the difference between the simulated and measured values. The direction of the acceleration force coincided with the loading direction during the gathering operation, and the error was shown to be the force required for the accelerated motion.

Record 74 of 434 - AGRICOLA 1998-2004/09

AU: Siebenmorgen,-T.J.; Yang,-W.; Sun,-Z.

TI: Glass transition temperature of rice kernels determined by dynamic mechanical thermal analysis.

SO: Transactions of the ASAE. 2004 May-June, v. 47, no. 3 p. 835-839.

AB: A protocol was developed to measure the glass transition temperature (Tg) of brown rice kernels using dynamic mechanical thermal analysis (DMTA). In order to accommodate the sample requirements of the dynamic mechanical thermal analyzer and prevent moisture loss during experiments, kernels were first wrapped with a thin layer of parafilm and then a thin layer of aluminum foil. The wrapped kernels were then filed at both ends with fine sandpaper to produce 3 mm long rice cylinders with parallel ends. The dynamic mechanical properties of brown rice kernels were determined over a temperature range of -40ÀC to

120ÀC. During each DMTA test, the onset temperature of glass transition was measured as the Tg of a brown rice kernel, since moisture diffusion and other physical properties begin to change drastically above the onset temperature. No dramatic changes in both the storage modulus (E') and the loss modulus (E") of brown rice kernels were found around Tg, indicating that relaxation of the amorphous phase of the rice kernel was quite limited. However, E"/ E' (tandelta) showed a much better transition for brown rice kernels, and thus the E"/ E' vs. temperature curves were used to determine Tg values of rice kernels. It was found that the Tg values of rice kernels decreased linearly with increases in moisture content (MC) within the tested range. The Tg of rice kernels was not affected by variety.

Record 75 of 434 - AGRICOLA 1998-2004/09

AU: Sharda,-V.N.; Dhyani,-B.L.

TI: Economic analysis of conventional and conservation bench terrace systems in a sub-humid climate.

SO: Transactions of the ASAE. 2004 May-June, v. 47, no. 3 p. 711-720.

AB: Water scarcity, accelerated soil erosion, and food security are the basic concerns in rain-dependent agricultural systems. The conservation bench terrace (CBT) system, in conjunction with water harvesting and recycling techniques, is an efficient conservation measure for in situ rain water harvesting, minimizing soil erosion, and sustaining productivity in arid, semi-arid, and sub-humid climates. Economic analysis has revealed that the CBT system exhibited 71.7% and 58.5% higher net present value (NPV), respectively, when compared to a rainfed maize-wheat system and a conventional system of sloping borders (i.e., making plots on slopes at 2% to 4%) with supplemental irrigation from harvested runoff. Various combinations of conventional and CBT systems were analyzed for economic efficiency, nutrient loss, and food security under different probabilities of runoff-producing rainfall by extrapolating the experimental data. The pure CBT system was found to be inadequate to generate sufficient runoff to provide even one pre-sowing irrigation of 5 cm depth to winter wheat crop. In contrast, pure conventional and a combination of conventional and CBT systems in the ratios of 50:50 and 75:25 had the potential to yield runoff more than sufficient to provide two supplemental irrigations to wheat crop at all probability levels. However, these systems result in higher soil and nutrient losses. The conventional and CBT systems in the ratio of 25:75 produced sufficient runoff to provide two irrigations with negligible overflow. Benefit cost ratio (BCR), payback period (PBP), and internal rate of return (IRR) criteria favor the pure CBT system owing to its low initial investment on pond construction for less runoff storage. However, NPV was always superior for combinations of conventional and CBT systems in the ratios of 25:75 or 50:50 over other combinations. Total maize-equivalent and energy production criteria also confirm that these two combinations perform better than the others. It is thus concluded that conventional and CBT systems in the ratios of 50:50 or 25:75 are the best choices to maximize economic returns, ensure food security, minimize soil and nutrient losses, and produce sufficient runoff for harvesting and recycling under rainfed cropping systems in sub-humid climates.

Record 76 of 434 - AGRICOLA 1998-2004/09

AU: Goffman,-F.D.; Bergman,-C.J.

TI: Rice kernel phenolic content and its relationship with antiradical efficiency.

SO: Journal of the science of food and agriculture. 2004 Aug. 15, v. 84, issue 10 p. 1235-1240.

AB: Plant phenolics exert beneficial effects on human health and may also prevent oxidative deterioration of food. Two field experiments were carried out for characterising phenolics in rice . The first assay was conducted in 1999 and 2000 in Beaumont, TX and included five light-brown, two purple and 10 red pericarp coloured cultivars. 'Bran colour' was highly statistically significant for both bran phenolic concentration and antiradical efficiency ($p < 0.001$). 'Year' and its interaction with bran colour were not significant for the analysed traits, suggesting that seasonal differences and their interactions may not affect phenolic content or antiradical efficiency. The accessions ranged from 3.1 to 45.4 mg gallic acid equivalents (GAE) g-1 bran and from 10.0 to 345.3 micromolar trolox equivalents (TE) g-1 bran for total phenolic content and antiradical efficiency respectively. The light-brown bran genotypes exhibited the lowest values for phenolic content and antiradical efficiency, whereas red bran ones displayed ca 10 times higher total phenolic content and more than 50 times higher tannin content than light-brown ones. The two purple lines showed either low or high values for the studied traits. Antiradical efficiency of rice bran extracts was highly positively correlated with total phenolic content (r = 0.99***), suggesting that phenolics are the main compounds responsible for the free radical-scavenging activity in rice bran extracts. In the second field experiment (Stuttgart, AR, 2001 and Beaumont, TX, 2000), 133 coloured rice cultivars were analysed for total phenolic content in whole grain. The accessions showed a large variation for total phenolics, ranging from 0.69 to 2.74 mg GAE g-1 grain. The data confirmed previous results suggesting bran colour as the main factor affecting phenolic concentration in rice kernel and seasonal effects and their interactions as not significant. The results also confirm that within red and purple bran groups can be found the highest phenolic concentrations in rice kernel.

Record 77 of 434 - AGRICOLA 1998-2004/09

AU: Mosha,-T.C.E.; Bennink,-M.R.

TI: Protein quality of drum-processed cereal-bean-sardine composite supplementary foods for preschool-age children.

SO: Journal of the science of food and agriculture. 2004 Aug. 15, v. 84, issue 10 p. 1111-1118.

AB: Acute, severe undernutrition during childhood remains a common health problem in many parts of the world and makes a significant contribution to childhood mortality. This study was conducted to evaluate the protein quality and growth/rehabilitation potential of supplementary foods developed from locally produced materials in Tanzania. Six diets, namely rice meal (RM), bean meal (BM), rice-bean meal (RBM), rice-bean-sardines meal (RBSM), corn-bean-sardines meal (CBSM) and corn-bean meal (CBM), were formulated to maximise the amino acid score as recommended by FAO/WHO/UNU for preschool children. Biological qualities of the diets, including apparent and true protein digestibility, net protein retention ratio, food efficiency ratio, protein digestibility-corrected amino acid score and rehabilitation potential, were evaluated using Sprague Dawley weanling rats. Net protein retention ratio varied significantly ($p < 0.05$) among control diet (0.93), RBSM (0.92), CBSM (0.86), RM (0.66), RBM (0.44), CBM (0.28), BM (0.12) and corn meal (CM) diet (-0.40). True protein digestibility ranged between 82 and 99%, with BM showing the lowest digestibility. The protein digestibility-corrected amino acid scores were 100% (control diet), 77% (CBSM), 89% (RBSM), 58% (RM), 90% (RBM), 47% (CBM), 85% (BM) and 48% (CM). Two test diets, CBSM and RBSM, showed the greatest potential to support growth and rehabilitation of undernourished rats, while CBM, RBM, BM and CM did not display acceptable growth. These results suggest that cereal-bean-sardine composites are of high quality and have potential for use as supplementary/rehabilitation foods for preschool- and school-age children as well as adults.

Record 78 of 434 - AGRICOLA 1998-2004/09

AU: Zhang,-J.; Wang,-L.; Yang,-Z.

TI: Emission of biogenic sulfur gases from the microbial decomposition of cystine in Chinese rice paddy soils.

SO: Bulletin of environmental contamination and toxicology. 2004 Apr., v. 72, no. 4 p. 850-857.

Record 79 of 434 - AGRICOLA 1998-2004/09

AU: Nandakumar,-N.; Singh,-A.K.; Sharma,-R.K.; Mohapatra,-T.; Prabhu,-K.V.; Zaman,-F.U.

TI: Molecular fingerprinting of hybrids and assessment of genetic purity of hybrid seeds in rice using microsatellite markers.

SO: Euphytica international journal of plant breeding. 2004, v. 136, no. 3 p. 257-264.

Record 80 of 434 - AGRICOLA 1998-2004/09

AU: Jung,-S.; Chung,-J.S.; Chon,-S.U.; Kuk,-Y.I.; Lee,-H.J.; Guh,-J.O.; Back,-K.

TI: Expression of recombinant protoporphyrinogen oxidase influences growth and morphological characteristics in transgenic rice.

SO: Plant growth regulation. 2004 Mar., v. 42, no. 3 p. 283-288.

AB: Transgenic rice plants expressing a Bacillus subtilis protoporphyrinogen oxidase (Protox), the last shared enzyme of the porphyrin pathway, in the cytoplasm (C89) or the plastids (P72) were compared with wild-type rice plants in their growth characteristics. Production of tiller buds 18 d after seeding was more profuse in transgenic plants than in wild-type plants, especially in plastid-targeted plants. Transgenic plants had 12-27% increase in tiller number and 17-33% increase in above-ground biomass compared with wild-type plants 4 and 8 weeks after transplanting of 2-week-old rice seedlings, demonstrating that tiller production and above-ground biomass correlate with each other. Cytoplasm-expressed and plastid-targeted transgenic plants also had a distinct phenotypic characteristic of narrower and more horizontal leaves than wild-type plants. Phenotypic and anatomical characteristics of the transgenic plants were clearly different from wild-type plants, indicating that regulation of porphyrin biosynthesis by expression of B. subtilis Protox in rice influences morphological characteristics of plant growth as well as biomass.

Record 81 of 434 - AGRICOLA 1998-2004/09

AU: Shih,-Y.W.; Chou,-W.C.; Lin,-Y.M.; Huang,-D.D.; Liu,-Z.H.; Huang,-H.J.

TI: Changes in protein tyrosine phosphorylation during mannose and senescence induced cell death in rice.

SO: Plant growth regulation. 2004 Mar., v. 42, no. 3 p. 271-282.

AB: In mammals protein tyrosine phosphorylation plays an important role in the activation of apoptosis. However, tyrosine phosphorylation associated with cell death has not been examined in plants. We monitored changes in tyrosine phosphorylation during cell death in rice (Oryza sativa L.) suspension cultures. Cell death was induced in the cell cultures by mannose treatment or by allowing the cultures to senescence. We have demonstrated that both mannose and senescence induced DNA fragmentation in rice suspension cells. In the presence of mannose, the tyrosine phosphorylation patterns of mannose treated and non-treated cell proteins are basically the same, except the tyrosine phosphorylation intensity is considerably different. In aged suspension-cultured cells, the occurrence of DNA fragmentation was detected. In addition, the tyrosine phosphorylation pattern was changed. These results suggest that protein tyrosine phosphorylation may have a role in distinct signal transduction pathways responding to mannose and senescence. The expression of a gene that encodes mitogen-activated protein kinase (MAPK), OsMAPK2, is up-regulated during mannose treatment, suggesting the possible involvement of rice MAPK in pathways associated with rice cell death induced by D-mannose.

Record 82 of 434 - AGRICOLA 1998-2004/09

AU: Hsu,-Y.T.; Kao,-C.H.

TI: Cadmium toxicity is reduced by nitric oxide in rice leaves.

SO: Plant growth regulation. 2004 Mar., v. 42, no. 3 p. 227-238.

AB: We evaluate the protective effect of nitric oxide (NO) against Cadmium (Cd) toxicity in rice leaves. Cd toxicity of rice leaves was determined by the decrease of chlorophyll and protein contents. CdCl2 treatment resulted in (1) increase in Cd content, (2) induction of Cd toxicity, (3) increase in H2O2 and malondialdehyde (MDA) contents, (4) decrease in reduced form glutathione (GSH) and ascorbic acid (ASC) contents, and (5) increase in the specific activities of antioxidant enzymes (superoxide dismutase, glutathione reductase, ascorbate peroxidase, catalase, and peroxidase). NO donors [N-tert-butyl-alpha-phenylnitrone, 3-morpholinosydonimine, sodium nitroprusside (SNP), and ASC + NaNO2] were effective in reducing CdCl2-induced toxicity and CdCl2-increased MDA content. SNP prevented CdCl2-induced increase in the contents of H2O2 and MDA, decrease in the contents of GSH and ASC, and increase in the specific activities of antioxidant enzymes. SNP also prevented CdCl2-induced accumulation of NH4+, decrease in the activity of glutamine synthetase (GS), and increase in the specific activity of phenylalanine ammonia-lyase (PAL). The protective effect of SNP on CdCl2-induced toxicity, CdCl2-increased H2O2, NH4+, and MDA contents, CdCl2-decreased GSH and ASC, CdCl2-increased specific activities of antioxidant enzymes and PAL, and CdCl2-decreased activity of GS were reversed by 2-(4-carboxy-2-phenyl)-4,4,5,5-tetramethyl-imidazoline-1-oxyl-3-oxide, a NO scavenger, suggesting that protective effect by SNP is attributable to NO released. Reduction of CdCl2-induced toxicity by NO in rice leaves is most likely mediated through its ability to scavenge active oxygen species including H2O2.

Record 83 of 434 - AGRICOLA 1998-2004/09
AU: Ozdemir,-F.; Bor,-M.; Demiral,-T.; Turkan,-I.
TI: Effects of 24-epibrassinolide on seed germination, seedling growth, liquid peroxidation, proline content and antioxidative system of rice (Oryza sativa L.) under salinity stress.
SO: Plant growth regulation. 2004 Mar., v. 42, no. 3 p. 203-211.
AB: The effects of 24-epibrassinolide (24-epiBL) on seedling growth, antioxidative system, lipid peroxidation, proline and soluble protein content were investigated in seedlings of the salt-sensitive rice cultivar IR-28. Seedling growth of rice plants was improved by 24-epiBL treatment under salt stress conditions. When seedlings treated with 24-epiBL were subjected to 120 mM NaCl stress, the activities of superoxide dismutase (EC 1.15.1.1), catalase (EC 1.11.1.6) and glutathione reductase (EC 1.6.4.2) did not show significant difference, whereas the activity of ascorbate peroxidase (EC 1.11.1.11) significantly increased. Increased activity of peroxidase (EC 1.11.1.7) under NaCl stress showed remarkable decrease in the 24-epiBL+NaCl-applied group. Lipid peroxidation level significantly increased under salt stress but decreased with 24-epiBL application revealing that less oxidative damage occurred in this group (24-epiBL+NaCl). In addition, increased proline content in the NaCl-applied group was decreased by 24-epiBL application in the 24-epiBL+NaCl-applied group. Soluble protein content was increased by 24-epiBL application even under NaCl stress, being also higher than control conditions (no 24-epiBL or NaCl treatment). 24-epiBL treatment considerably alleviated oxidative damage that occurred under NaCl-stressed conditions and improved seedling growth in part under salt stress in sensitive IR-28 seedlings.

Record 84 of 434 - AGRICOLA 1998-2004/09
AU: Batal,-A.B.; Parsons,-C.M.
TI: Utilization of various carbohydrate sources as affected by age in the chick.
SO: Poultry science. 2004 July, v. 83, no. 7 p. 1140-1147.
AB: In 3 experiments, New Hampshire x Columbian male chicks were fed carbohydrate-soybean meal (SBM) or casein diets from 0 to 21 d of age, and MEn was determined at 0 to 2, 3 to 4, 7, 14, and 21 d of age. Carbohydrate sources evaluated in experiment 1 were dextrose (D-glucose), conventional cornstarch, dextrinized cornstarch, corn-syrup solids, pregelatinized unmodified cornstarch, pregelatinized tapioca starch, tapioca dextrin, high-amylose starch, and polycose (mixed glucose polymers). Carbohydrate sources evaluated in experiments 2 and 3 were conventional corn, waxy corn, high-oil corn, corn flour, rice flour, dextrose, and sucrose. In experiment 1, chicks fed the dextrose diet had the highest weight gains, and the chicks fed high-amylose starch and pregelatinized unmodified cornstarch diets had the lowest weight gains. The MEn values varied among carbohydrate sources with MEn being highest for the dextrose diet and lowest for the high amylose starch diet. In experiment 2, chicks fed waxy corn,

high-oil corn, or dextrose-SBM diets had ($P < 0.05$) higher growth rates than chicks fed conventional corn, corn flour, or rice flour. The MEn values increased with age for all diets except the dextrose-SBM, which was consistently high at all ages. In experiment 3, the dextrose diets (SBM or casein) yielded higher growth performance and MEn values than the sucrose-diets, and the differences were greater at younger ages. The MEn values were also much higher for the casein than the SBM diets, and MEn of the SBM diets increased with increasing age. The results of this study indicate that MEn varies among carbohydrate sources and increases with age for most carbohydrate-SBM diets.

Record 85 of 434 - AGRICOLA 1998-2004/09

AU: Tindall,-K.V.; Stout,-M.J.; Williams,-B.J.

TI: Effect of the presence of barnyardgrass on rice water weevil (Coleoptera: Curculionidae) and rice stink bug (Hemiptera: Pentatomidae) populations on rice.

SO: Environmental entomology. 2004 June, v. 33, no. 3 p. 720-726.

AB: Both the rice water weevil, Lissorhoptrus oryzophilus Kuschel, and rice stink bug, Oebalus pugnax (F.), are important pests of rice, Oryza sativa L., in the United States. The host ranges of both insects primarily consist of monocotyledonous plants. Previous research has shown that the rice water weevil prefers barnyardgrass, Echinochloa crus-galli Beauv., over rice for feeding and oviposition. Barnyardgrass is also a preferred host for rice stink bug. Thus, presence of barnyardgrass in rice fields may alter populations of one or both insects. Field experiments were conducted to determine how the presence of a preferred host influences rice water weevil and rice stink bug populations on rice. Mixed plots of barnyardgrass and rice were cultivated such that either rice was surrounded by barnyardgrass or barnyardgrass was surrounded by rice. Insects were collected from rice portions of mixed plots and compared with numbers collected from whole plots of rice in the same location. Presence of barnyardgrass had little impact on rice water weevil densities on rice. In contrast, presence of barnyardgrass influenced rice stink bug populations on rice. Rice stink bugs were found on barnyardgrass in mixed plots before panicle emergence of rice. After panicle emergence of rice, results varied from 2001 and 2002. In 2001 and 2003, rice stink bugs were up to 9 times more abundant on rice in mixed plots of barnyardgrass and rice compared with whole plots of rice. Rice stink bugs were up to 4 times greater on rice in whole plots of rice than in mixed plots in 2002. Differences are likely a result of the developmental stage of barnyardgrass relative to rice. Data suggest the presence and developmental stage of barnyardgrass can influence the severity and timing of rice stink bug infestations.

Record 86 of 434 - AGRICOLA 1998-2004/09

AU: Hou,-X.; Fields,-P.; Flinn,-P.; Perez-Mendoza,-J.; Baker,-J.

TI: Control of stored-product beetles with combinations of protein-rich pea flour and parasitoids.

SO: Environmental entomology. 2004 June, v. 33, no. 3 p. 671-680.

AB: Protein-rich pea flour is toxic and repellent to three major stored-grain pests: the rice weevil, Sitophilus oryzae L.; the red flour beetle, Tribolium castaneum (Herbst); and the rusty grain beetle, Cryptolestes ferrugineus (Stephens). This study found that protein-rich pea flour was not toxic to, and did not reduce the offspring of, Anisopteromalus calandrae (Howard), a parasitoid of S. oryzae, nor did it reduce offspring of Cephalonomia waterstoni (Gahan), a parasitoid of C. ferrugineus. Protein-rich pea flour was also not repellent to A. calandrae. Small-scale and large-scale tests of a combination of protein-rich pea flour and parasitoids were conducted in 2-liter jars and in barrels containing 330 kg wheat. A larger population of A. calandrae was found at a high host infestation rate (24 adults/kg for 25 d), but the parasitoid did not become established at middle and low host infestation rates (2.4; 0.24 adults/kg for 25 d). The combinations of protein-rich pea flour and parasitoids reduced populations of S. oryzae in both tests. Additional effects of protein-rich pea flour and parasitoids were found in the large-scale test. Releasing parasitoids alone reduced the populations of S. oryzae by 46% and C. ferrugineus by 49%. Treating wheat with 0.04 or 0.1% protein-rich pea flour reduced the population of S. oryzae by 26 and 79% and C. ferrugineus by 27 and 43%, respectively. Combining parasitoids with 0.04 or 0.1% protein-rich pea flour reduced S. oryzae populations by 76 and 98% and C. ferrugineus populations by 42 and 75%, respectively. At the end of the large-scale experiment, grain treated with protein-rich pea flour alone or in combination with parasitoids had better grain quality than the untreated controls.

Record 87 of 434 - AGRICOLA 1998-2004/09

AU: Malcomber,-S.T.; Kellogg,-E.A.

TI: Heterogeneous expression patterns and separate roles of the SEPALLATA gene LEAFY HULL STERILE1 in grasses.

SO: Plant cell. 2004 July, v. 16, no. 7 p. 1692-1706.

AB: SEPALLATA (SEP) genes exhibit distinct patterns of expression and function in the grass species rice (Oryza sativa) and maize (Zea mays), suggesting that the role of the genes has changed during the evolution of the family. Here, we examine expression of the SEP-like gene LEAFY HULL STERILE1 (LHS1) in phylogenetically disparate grasses, reconstruct the pattern of gene expression evolution within the family, and then use the expression patterns to test hypotheses of gene function. Our data support a general role for LHS1 in specifying determinacy of the spikelet meristem and also in determining the identity of lemmas and paleas; these two functions are separable, as is the role of the gene in specifying floret meristems. We find no evidence that LHS1 determines flower number; it is strongly expressed in all spikelet meristems even as they are producing flowers, and expression is not correlated with eventual flower number. LHS1 expression in only the upper flowers of the spikelet appears to be the ancestral state; expression in all flowers is derived in subfamily Pooideae. LHS1 expression in pistils, stamens, and lodicules varies among the cereals. We hypothesize that LHS1 may have affected morphological diversification of grass inflorescences by mediating the expression of different floral identity genes in different regions of the floret and spikelet.

Record 88 of 434 - AGRICOLA 1998-2004/09

AU: Kong,-C.; Liang,-W.; Xu,-X.; Hu,-F.; Wang,-P.; Jiang,-Y.

TI: Release and activity of allelochemicals from allelopathic rice seedlings.

SO: Journal of agricultural and food chemistry. 2004 May 19, v. 52, no. 10 p. 2861-2865.

AB: 3-Isopropyl-5-acetoxycyclohexene-2-one-1 (1), momilactone B (2), and 5,7,4'-trihydroxy-3',5'-dimethoxyflavone (3) were isolated and identified from an allelopathic rice accession PI312777. These three compounds at low concentrations could inhibit the growth of weeds Echinochloa crusgalli and Cyperus difformis associated with rice, especially mixtures of the compounds had stronger inhibitory activity than did individual compounds. Studies with hydroponic culture, continuous root exudates trapping system (CRETS), and direct resin adsorption methods showed that a total of 7.6 n moles 1, 2, and 3 were exuded from living roots of each seedling into the environment at 10 days after seedlings were transplanted. Furthermore, 1, 2, and 3 were found in the soil growing PI312777 seedlings at day 15 after seedlings emergence and reached a total of 39.5 g/g soil at day 30. The results indicated that PI 312777 seedlings could release sufficient quantities of 1, 2, and 3 into the environment to act as allelochemicals inhibiting the growth of associated weeds. Investigations on the distribution of 1, 2, and 3 in PI 312777 plant, and its root exudates showed that the levels of 1, 2, and 3 were significantly higher in the shoots and root exudates than in the roots, and only trace 1 was observed in the roots. The results suggest that the roots of rice seedlings are not major site of synthesis or accumulation 1, 2, and 3, but a pathway for their release into the environment. The levels of 1, 2, and 3 in the root exudates were over 2-folds higher under direct resin adsorption than under hydroponic culture and CRETS, and hence, it is the preferred method to collect and identify active allelochemicals in rice exudates in future studies on rice allelopathy.

Record 89 of 434 - AGRICOLA 1998-2004/09

AU: Cockell,-K.A.; Bonacci,-G.; Belonje,-B.

TI: Manganese content of soy or rice beverages is high in comparison to infant formulas.

SO: Journal of the American College of Nutrition. 2004 Apr., v. 23, no. 2 p. 124-130.

AB: Objective: Well-meaning but inadequately informed parents may perceive plant-based beverages such as soy beverages (SB) or rice beverages (RB) as an alternative to infant formula. Manganese (Mn) is an essential mineral nutrient found at high levels in plants such as soy and rice. Excessive Mn exposure increases the risk of adverse neurological effects. Methods: We analysed, by atomic absorption spectrometry, the Mn content of 36 SB, 5 RB, 6 evaporated milks (EM), 14 soy-based infant formulas (SF) and 16 milk-based infant formulas (MF), obtained from commercial outlets in Ottawa, Canada. Results: SB had the highest levels of Mn (16.5 « 8.6 micrograms/g dry wt, mean « s.d.), followed by RB (9.9 « 1.7 micrograms/g dry wt). Mn levels of individual SB/RB ranged from 2 to 17 times the mean Mn content of SF (2.4« 0.7 micrograms/g dry wt) and 7 to 56 times that of MF (0.70 « 0.35 micrograms/g dry wt). EM contained very little Mn (0.02 « 0.03 micrograms/g dry wt). Calculated mean Mn intakes from SB/RB by infants up to 6 months of age, assuming complete substitution of these products (0.78 L/day), approached the Tolerable Upper Intake Level (UL) for

1-3 year olds (no UL for Mn is available for infants under 1 year of age). Expressed as g Mn/100 kcal, SB/RB exceeded the range derived from ULs and typical energy intakes of 1-3 year olds. Conclusions: SB/RB should not be fed to infants because they are nutritionally inadequate and contain Mn at levels which may present an increased risk of adverse neurological effects if used as a sole source of nutrition.

Record 90 of 434 - AGRICOLA 1998-2004/09

AU: Wang,-X.; Ren,-X.; Zhu,-L.; He,-G.

TI: OsBi1, a rice gene, encodes a novel protein with a CBS-like domain and its expression is induced in responses to herbivore feeding.

SO: Plant science. 2004 June, v. 166, issue 6 p. 1581-1588.

Record 91 of 434 - AGRICOLA 1998-2004/09

AU: Ithal,-N.; Reddy,-A.R.

TI: Rice flavonoid pathway genes, OsDf and OsAns, are induced by dehydration, high salt and ABA, and contain stress responsive promoter elements that interact with the transcription activator, OsC1-MYB.

SO: Plant science. 2004 June, v. 166, issue 6 p. 1505-1513.

Record 92 of 434 - AGRICOLA 1998-2004/09

AU: De-Faveri,-D.; Torre,-P.; Perego,-P.; Converti,-A.

TI: Statistical investigation on the effects of starting xylose concentraiton and oxygen mass flowrate on xylitol production from rice straw hydrolyzate by response surface methodology.

SO: Journal of food engineering. 2004 Dec., v. 65, issue 3 p. 383-389.

AB: A 32 full-factorial design combined with response surface methodology was used to investigate the simultaneous effects of starting xylose concentration (S0) and oxygen mass flowrate (qO2) on xylitol production from rice straw hydrolyzate. Fermentations were performed at 30ÀC, using Debaryomyces hansenii NRRL Y-7426 as xylitol producer and varying S0 between 50 and 150 g/l and qO2 between 2.5 and 5.9 mgO2/s. At the lowest starting xylose concentration and an oxygen mass flowrate of 4.2 mgO2/s, volumetric productivity and xylitol yield reached maximum values (Qp=0.70 gP/l h and YP/S=0.73 gP/gS, respectively), but xylitol concentration was quite low (35.9 gP/l). The results were in close agreement with the model prediction. The statistical model also allowed identifying the optimum operating conditions (S0=71 g/l and qO2=4.1 mgO2/s) able to simultaneously maximize volumetric productivity (0.53 gP/l h), xylitol yield (0.71 gP/gS) and final xylitol concentration (42.2 gP/l).

Record 93 of 434 - AGRICOLA 1998-2004/09

AU: Chun,-S.Y.; Yoo,-B.

TI: Rheological behavior of cooked rice flour dispersions in steady and dynamic shear.

SO: Journal of food engineering. 2004 Dec., v. 65, issue 3 p. 363-370.

AB: The steady and dynamic rheological properties of Korean rice flour dispersions were evaluated at different concentrations (4%, 5%, 6%, 7%, and 8%). Rice flour dispersions at 25ÀC showed a high shear-thinning behavior (n=0.23-0.28) with low magnitudes of

Casson yield stresses (sigmaoc=4.1-20.1 Pa). The magnitudes of sigmaoc, consistency index (K) and apparent viscosity (etaa,100) increased with increase in concentration. The apparent viscosity over the temperature range of 25-70ÀC obeyed the Arrhenius temperature relationship, indicating that the magnitudes of activation energies (Ea) were in the range of 0.21-0.27 KJ/mol. The power law model was found to be more suitable than the exponential model in expressing the relationship between concentration and apparent viscosity (etaa). Storage (G') and loss (G") moduli increased with increase in frequency (omega) while complex viscosity (eta*) decreased. Magnitudes of G' and G" moduli increased with increase in concentration. Cox-Merz rule was not applicable to rice flour dispersions.

Record 94 of 434 - AGRICOLA 1998-2004/09

AU: Kim,-C.M.; Piao,-H.L.; Park,-S.J.; Chon,-N.S.; Je,-B.I.; Sun,-B.; Park,-S.H.; Park,-J.Y.; Lee,-E.J.; Kim,-M.J.

TI: Rapid, large-scale generation of Ds transposant lines and analysis of the Ds insertion sites in rice.

SO: Plant journal. 2004 July, v. 39, no. 2 p. 252-263.

AB: Rapid, large-scale generation of a Ds transposant population was achieved using a regeneration procedure involving tissue culture of seed-derived calli carrying Ac and inactive Ds elements. In the F2 progeny from genetic crosses between the same Ds and Ac starter lines, most of the crosses produced an independent germinal transposition frequency of 10-20%. Also, many Ds elements underwent immobilization even though Ac was expressed. By comparison, in a callus-derived regenerated population, over 70% of plants carried independent Ds insertions, indicating transposition early in callus formation. In the remaining population, the majority of plants carried only Ac. Most of the new Ds insertions were stably transmitted to a subsequent generation. An exceptionally high proportion of independent transposants in the regenerated population means that selection markers for transposed Ds and continual monitoring of Ac/Ds activities may not necessarily be required. By analyzing 1297 Ds-flanking DNA sequences, a genetic map of 1072 Ds insertion sites was developed. The map showed that Ds elements were transposed onto all of the rice chromosomes, with preference not only near donor sites (36%) but also on certain physically unlinked arms. Populations from both genetic crossing and tissue culture showed the same distribution patterns of Ds insertion sites. The information of these mapped Ds insertion sites was deposited in GenBank. Among them, 55% of Ds elements were on predicted open-reading frame (ORF) regions. Thus, we propose an optimal strategy for the rapid generation of a large population of Ds transposants in rice.

Record 95 of 434 - AGRICOLA 1998-2004/09

AU: Ma,-H.; Xu,-S.P.; Luo,-D.; Xu,-Z.H.; Xue,-H.W.

TI: OsPIPK1, a rice phosphatidylinositol monophosphate kinase, regulates rice heading by modifying the expression of floral induction genes.

SO: Plant molecular biology. 2004 Jan., v. 54, no. 2 p. 295-310.

AB: A rice gene, OsPIPK1, encoding a 792-aa putative phosphatidylinositol 4-phosphate 5-kinase (PIPK), was identified and characterized. Comparison between the cDNA and genomic sequences revealed the presence of 10 exons (39-1050 bp) and 9 introns (88-745 bp) in OsPIPK1 gene. The deduced amino acid sequence of OsPIPK1 contains a lipid kinase domain that is highly homologous to those of previously isolated PIPKs, and structural analysis revealed the intriguing presence of multiple MORN motifs at the N-terminus. The MORN motifs have also been detected in PIPKs from Arabidopsis thaliana and Oryza sativa, but not in the well-characterized PIPKs from animal and yeast cells. RT-PCR analysis indicated that OsPIPK1 was expressed almost constitutively in roots, shoots, stems, leaves and flowers, and up-regulated following treatment with plant hormones or application of various stresses. An antisense transgenic strategy was used to suppress the expression of OsPIPK1, and homozygous transgenic plants showed earlier heading (7-14 days earlier) than control plants, suggesting that OsPIPK1 negatively regulates floral initiation. This was further confirmed by morphologic observation showing earlier floral development in antisense plants, as well as leaf emergence measurement indicating delayed leaf development under OsPIPK1 deficiency, a common phenotype observed with earlier flowering. RT-PCR analysis and cDNA chip technology were used to examine transcripts of various genes in the transgenic plants and the results showed altered transcriptions of several flowering-time or -identity related genes, suggesting that OsPIPK1 is involved in rice heading through regulation of floral induction genes, signaling and metabolic pathways.

Record 96 of 434 - AGRICOLA 1998-2004/09

AU: Day,-R.B.; Tanabe,-S.; Koshioka,-M.; Mitsui,-T.; Itoh,-H.; Ueguchi-Tanaka,-M.; Matsuoka,-M.; Kaku,-H.; Shibuya,-N.; Minami,-E.

TI: Two rice GRAS family genes responsive to N-acetylchitooligosaccharide elicitor are induced by phytoactive gibberellins: evidence for cross-talk between elicitor and gibberellin signaling in rice cells.

SO: Plant molecular biology. 2004 Jan., v. 54, no. 2 p. 261-272.

AB: In this study, we present data showing that two members of the GRAS family of genes from rice, CIGR1 and CIGR2 (chitin-inducible gibberellin-responsive), inducible by the potent elicitor N-acetylchitooligosaccharide (GN), are rapidly induced by exogenous gibberellins. The pattern of mRNA accumulation was dependent on the dose and biological activity of the gibberellins, suggesting that the induction of the genes by gibberellin is mediated by a biological receptor capable of specific recognition and signal transduction upon perception of the phytoactive compounds. Further pharmacological analysis revealed that the CIGR1 and CIGR2 mRNA accumulation by treatment with gibberellin is dependent upon protein phosphorylation/dephosphorylation events. In rice calli derived from slender rice 1, a constitutive gibberellin-responsive mutant, or d1, a mutant deficient in the alpha-subunit of the heterotrimeric G-protein, CIGR1 and CIGR2 were induced by a GN elicitor, yet not by gibberellin. Neither gibberellin nor GN showed related activities in defense or development, respectively. These results strongly suggested that the signal transduction cascade from gibberellin is independent of that from GN, and further implied that CIGR1 and CIGR2 have dual, distinct roles in defense and development.

Record 97 of 434 - AGRICOLA 1998-2004/09

AU: Coca,-M.; Bortolotti,-C.; Rufat,-M.; Penas,-G.; Eritja,-R.; Tharreau,-D.; Martinez-del-Pozo,-A.; Messeguer,-J.; San-Segundo,-B.

TI: Transgenic rice plants expressing the antifungal AFP protein from Aspergillus giganteus show enhanced resistance to the rice blast fungus Magnaporthe grisea.

SO: Plant molecular biology. 2004 Jan., v. 54, no. 2 p. 245-259.

AB: The Aspergillus giganteus antifungal protein (AFP), encoded by the afp gene, has been reported to possess in vitro antifungal activity against various economically important fungal pathogens, including the rice blast fungus Magnaporthe grisea. In this study, transgenic rice (Oryza sativa) constitutively expressing the afp gene was generated by Agrobacterium-mediated transformation. Two different DNA constructs containing either the afp cDNA sequence from Aspergillus or a chemically synthesized codon-optimized afp gene were introduced into rice plants. In both cases, the DNA region encoding the signal sequence from the tobacco AP24 gene was N-terminally fused to the coding sequence of the mature AFP protein. Transgenic rice plants showed stable integration and inheritance of the transgene. No effect on plant morphology was observed in the afp-expressing rice lines. The inhibitory activity of protein extracts prepared from leaves of afp plants on the in vitro growth of M. grisea indicated that the AFP protein produced by the trangenic rice plants was biologically active. Several of the T2 homozygous afp lines were challenged with M. grisea in a detached leaf infection assay. Transformants exhibited resistance to rice blast at various levels. Altogether, the results presented here indicate that AFP can be functionally expressed in rice plants for protection against the rice blast fungus M. grisea.

Record 98 of 434 - AGRICOLA 1998-2004/09

AU: Zou,-L.; Stout,-M.J.; Ring,-D.R.

TI: Density-yield relationships for rice water weevil on rice for different varieties and under different water management regimes.

SO: Crop protection. 2004 June, v. 23, no. 6 p. 543-550.

AB: The rice water weevil, Lissorhoptrus oryzophilus Kuschel, is the most destructive insect pest of rice in the United States. Two years of field experiments were conducted to quantify relationships between densities of immature rice water weevils and yields for two rice varieties under early and delayed flooding regimes. Larval densities during earlier stages of rice growth were more strongly correlated with yield losses than were larval densities later in the growing season. Slopes of regression models were more negative for early-flood than for delayed-flood plots, and more negative for 'Bengal' than for ' Cocodrie'. The results of these experiments confirm that short delays in flooding reduce yield losses from the rice water weevil and that 'Bengal' is less tolerant of weevil feeding than ' Cocodrie'. Estimates of yield loss caused by each weevil provide a key parameter for the calculation of economic injury levels under different management regimes. Data from this study suggest that it is possible to integrate the use of insecticides, cultural practices and host plant resistance in a management system for the rice water weevil.

Record 99 of 434 - AGRICOLA 1998-2004/09

AU: Kawazu,-K.; Kamimuro,-T.; Kamiwada,-H.; Nagata,-K.; Matsunaga,-T.; Sugie,-H.; Fukumoto,-T.; Adati,-T.T.; Tatsuki,-S.

TI: Effective pheromone lures for monitoring the rice leaffolder moth, Cnaphalocrocis medinalis (Lepidoptera: Crambidae).

SO: Crop protection. 2004 July, v. 23, no. 7 p. 589-593.

AB: Several factors affecting the attractiveness of traps baited with synthetic sex pheromone components of Cnaphalocrocis medinalis were examined in the laboratory and field. In the laboratory, among the four pheromone components Z11-18:Ald, Z13-18:Ald, Z11-18:OH and Z13-18:OH, the major component, Z13-18:Ald, was shown to be essential for attraction and Z11-18:Ald was a potent synergist for the major component. The alcohols also showed an apparent synergistic effect in the laboratory bioassay when their mixture was combined with an aldehyde mixture. The addition of the geometric isomers of the four components at levels greater than 5% of the purified 4-component blend showed significant inhibitory effects on the pheromonal activity in the laboratory. In contrast, no synergistic effect of the alcohols on the aldehydes was shown in the field. A range of loadings of the pheromone rubber septa (0.01-3.42 mg) was tested and all remained attractive for at least 1 month with optimum attractiveness of 0.86 mg/septum. No significant effects were obtained when the ratio of Z11-18:Ald to Z13-18:Ald was changed. Rubber septa containing 0.86 mg of the four components (E-isomers <5%) at the natural ratio are being effectively used for monitoring C. medinalis.

Record 100 of 434 - AGRICOLA 1998-2004/09

AU: Nico,-A.I.; Jimenez-Diaz,-R.M.; Castillo,-P.

TI: Control of root-knot nematodes by composted agro-industrial wastes in potting mixtures.

SO: Crop protection. 2004 July, v. 23, no. 7 p. 581-587.

AB: The use of composted dry cork, dry-grape marc (fruit residue after pressing) and a 1:1 mixture of dry-olive marc+dry-rice husk as an amendment to potting mixtures was assessed for the management of Meloidogyne species. Amending the potting mixture with composted dry cork at rates of 0%, 25%, 50%, 75% and 100% v/v, reduced the root galling and final populations of Meloidogyne incognita race 1 and M. javanica in tomato, and final nematode population in olive plants, compared with the control. In tomato, increasing the rate of that amendment exponentially reduced the root galling caused by Meloidogyne incognita race 1 (40.8%) and the final nematode population (81.9%). Similarly, increasing rates of the amendment exponentially reduced the root galling of tomato caused by M. javanica (51.3%) and the final population (82.6%). Infection of olive roots by M. incognita race 1 did not cause visible galling; however, amendment with dry cork reduced the final nematode population by 87.9%. Amending the potting mixture with dry-grape marc also reduced the root galling and final populations of M. incognita race 1 and M. javanica in tomato, though the reductions in root galling (24.4% and 25.6%, respectively) and final nematode populations (34.2% and 34.7%, respectively) were not enough for effective nematode management. Root galling and final nematode population were not reduced in potting mixture amended with the 1:1 mixture of composted dry-olive marc and dry-rice husk.

Record 101 of 434 - AGRICOLA 1998-2004/09

AU: Liu,-Z.L.; Han,-F.P.; Tan,-M.; Shan,-X.H.; Dong,-Y.Z.; Wang,-X.Z.; Fedak,-G.; Hao,-S.; Liu,-B.

TI: Activation of a rice endogenous retrotransposon Tos17 in tissue culture is accompanied by cytosine demethylation and causes heritable alteration in methylation pattern of flanking genomic regions.

SO: Theoretical and applied genetics. 2004 June, v. 109, no. 1 p. 200-209.

AB: Tos17 is a copia-like, cryptic retrotransposon of rice, but can be activated by tissue culture. To study possible epigenetic mechanism controlling activity of Tos17, we subjected three rice lines (the parental line cv. Matsumae and two introgression lines, RZ2 and RZ35) that harbor different copies of the element to tissue culture. For each line, we investigated transcription and transposition of Tos17 in seed plants, calli and regenerated plants, cytosine-methylation status at CG and CNG positions within Tos17, effect of 5-azacytidine on methylation status and activity of Tos17, and cytosine-methylation states in genomic regions flanking original and some newly transposed copies of Tos17 in calli and regenerated plants. We found that only in introgression line RZ35 wasTos17 transcriptionally activated and temporarily mobilized by tissue culture, which was followed by repression before or upon plant regeneration. The activity and inactivity of Tos17 in calli and regenerated plants of RZ35 are accompanied by hypo- and hyper-CG methylation and hemi- and full CNG methylation, respectively, within the element, whereas immobilization of the element in the other two lines is concomitant with near-constant, full hypermethylation. Treatment with 5-azacytidine induced both CG and CNG partial hypomethylation of Tos17 in two lines (Matsumae and RZ35), which, however, was not accompanied by activation of Tos17 in any line. Heritable alteration in cytosine-methylation patterns occurred in three of seven genomic regions flanking Tos17 in calli and regenerated plants of RZ35, but in none of the five regions flanking dormant Tos17 in the other two lines.

Record 102 of 434 - AGRICOLA 1998-2004/09

AU: Aert,-R.; Sagi,-L.; Volckaert,-G.

TI: Gene content and density in banana (Musa acuminata) as revealed by genomic sequencing of BAC clones.

SO: Theoretical and applied genetics. 2004 June, v. 109, no. 1 p. 129-139.

AB: The complete sequence of Musa acuminata bacterial artificial chromosome (BAC) clones is presented and, consequently, the first analysis of the banana genome organization. One clone (MuH9) is 82,723 bp long with an overall G+C content of 38.2%. Twelve putative protein-coding sequences were identified, representing a gene density of one per 6.9 kb, which is slightly less than that previously reported for Arabidopsis but similar to rice. One coding sequence was identified as a partial M. acuminata malate synthase, while the remaining sequences showed a similarity to predicted or hypothetical proteins identified in genome sequence data. A second BAC clone (MuG9) is 73,268 bp long with an overall G+C content of 38.5%. Only seven putative coding regions were discovered, representing a gene density of only one gene per 10.5 kb, which is strikingly lower than that of the first BAC. One coding sequence showed significant homology to the soybean ribonucleotide reductase (large subunit). A transition point between coding regions and repeated sequences was found at approximately 45 kb, separating the coding upstream BAC end from its downstream end that mainly contained transposon-like sequences and regions similar to known repetitive sequences of M. acuminata. This gene organization resembles Gramineae genome sequences, where genes are clustered in gene-rich regions separated by gene-poor DNA containing abundant transposons.

Record 103 of 434 - AGRICOLA 1998-2004/09

AU: Raedschelders,-G.; Debefve,-C.; Goesaert,-H.; Delcour,-J.A.; Volckaert,-G.; Campenhout,-S.-van

TI: Molecular identification and chromosomal localization of genes encoding Triticum aestivum xylanase inhibitor I-like proteins in cereals.

SO: Theoretical and applied genetics. 2004 June, v. 109, no. 1 p. 112-121.

AB: TAXI (Triticum aestivum xylanase inhibitor) proteins are present in wheat flour and are known to inhibit glycosyl hydrolase family 11 endoxylanases, enzymes which are commonly applied in grain processing. Here, we describe the PCR-based molecular identification of genes encoding endoxylanase inhibitors HVXI and SCXI, the TAXI-like proteins from barley (Hordeum vulgare) and rye (Secale cereale) respectively. The HVXI coding sequence encodes a mature protein of 384 amino acids preceded by a 19 amino acid long signal sequence. SCXI-II/III has an open reading frame encoding a signal peptide of 21 amino acids and a mature protein of 375 amino acids. As for TAXI-I, no introns were detected in the untranslated regions and coding sequences identified. These newly identified sequences allowed us to perform a multiple sequence alignment with TAXI-I and similar proteins. Rice TAXI-type proteins clustered together with the cereal endoxylanase inhibitors. Dicotyledonous proteins with sequence similarity to TAXI-I, including the tomato xyloglucan-specific endoglucanase inhibiting protein, formed a different clade. The TAXI-type proteins may hence be part of a superfamily of proteins all involved in plant responses to biotic or abiotic stress and for which a function as glycosyl hydrolase inhibitors can be suggested. The chromosomal localization of the TAXI-I gene identified on wheat chromosome 3B, of the SCXI-II/III gene identified on rye chromosome 6R, and the presence of a cluster of TAXI-like genes on rice chromosome 1, allowed us to assign the location of TAXI-like genes to the wheat-rye translocation area 3BL/6RL characterized by RFLP markers XGlb33 and Xpsr454 and isozyme Est-5. In rice, RFLP marker C1310S corresponds to a TAXI-like protein encoding sequence.

Record 104 of 434 - AGRICOLA 1998-2004/09

AU: Zhao,-B.Y.; Ardales,-E.; Brasset,-E.; Claflin,-L.E.; Leach,-J.E.; Hulbert,-S.H.

TI: The Rxo1/Rba1 locus of maize controls resistance reactions to pathogenic and non-host bacteria.

SO: Theoretical and applied genetics. 2004 June, v. 109, no. 1 p. 71-79.

AB: Infiltration of different maize lines with a variety of bacterial pathogens of maize, rice and sorghum identified qualitative differences in resistant reactions. Isolates from two bacterial species induced rapid hypersensitive reactions (HR) in some maize lines, but not others. All isolates of the non-host pathogen Xanthomonas oryzae pv. oryzicola (bacterial leaf streak disease of rice) and some isolates of the pathogenic bacterium Burkholderia andropogonis induced HR when infiltrated into maize line B73, but not Mo17. Genetic control of the HR to both bacteria segregated as a single dominant gene. Surprisingly, both phenotypes mapped to the same locus, indicating they are either tightly linked or controlled by the same gene. The locus maps on the short arm of maize chromosome six near several other disease-resistance genes. Results indicate the same type of genes may contribute to both non-host resistance and resistance to pathogens.

Record 105 of 434 - AGRICOLA 1998-2004/09

AU: Nemoto,-K.; Ukai,-Y.; Tang,-D.Q.; Kasai,-Y.; Morita,-M.

TI: Inheritance of early elongation ability in floating rice revealed by diallel and QTL analyses.

SO: Theoretical and applied genetics. 2004 June, v. 109, no. 1 p. 42-47.

AB: In floating rice, stem elongation begins much earlier than in non-floating rice, which is the major survival mechanism for flooding. Inheritance of this early elongation ability was studied using diallel and quantitative trait locus (QTL) analyses. The diallel analysis was undertaken using a set of 6x6 half-diallel crosses involving four floating ('Goai', 'Habiganj Aman VIII', 'Badal 106', and Oryza rufipogon strain W120) and two non-floating ('Latisail' and 'Patnai 23') parents. The additive gene effects were higher than the dominant effects. The dominant alleles were concentrated in the cultivated floating parents (' Goai', 'Habiganj Aman VIII', and 'Badal 106'), whereas the recessive alleles were in the wild floating parent (W120). A QTL analysis using a 'Patnai 23' x 'Goai' F2 population detected two putative QTLs. Of these QTLs, the one on chromosome 12 behaved as a partially dominant major gene that explained more than half of the total genetic variation.

Record 106 of 434 - AGRICOLA 1998-2004/09

AU: Kim,-D.S.; Lee,-I.S.; Jang,-C.S.; Lee,-S.J.; Song,-H.S.; Lee,-Y.I. ; Seo,-Y.W.

TI: AEC resistant rice mutants induced by gamma-ray irradiation may include both elevated lysine production and increased activity of stress related enzymes.

SO: Plant science. 2004 Aug., v. 167, issue 2 p. 305-316.

Record 107 of 434 - AGRICOLA 1998-2004/09

AU: Yang,-Y.; Peng,-H.; Huang,-H.; Wu,-J.; Jia,-S.; Huang,-D.; Lu,-T.

TI: Large-scale production of enhancer trapping lines for rice functional genomics.

SO: Plant science. 2004 Aug., v. 167, issue 2 p. 281-288.

Record 108 of 434 - AGRICOLA 1998-2004/09

AU: Solfrizzo,-M.; Vitti,-C.; De-Girolamo,-A.; Visconti,-A.; Logrieco,-A.; Fanizzi,-F.P.

TI: Radicinols and radicinin phytotoxins produced by Alternaria radicina on carrots.
SO: Journal of agricultural and food chemistry. 2004 June 2, v. 52, no. 11 p. 3655-3660.
AB: The phytotoxin epi-radicinol, a diastereomer of radicinol, was isolated from large cultures of Alternaria radicina grown on carrot slices and identified by GC-MS, LC-MS, 1H NMR, and 13C NMR. Four strains of A. radicina isolated from rotted carrot produced epi-radicinol as the major metabolite (up to 39414 g/g) together with radicinol (up to 2423 microgram/g), and, to a lesser extent, radicinin when cultured on carrot slices, whereas on rice they mainly produced radicinin (2486-53800 microgram/g). Radicinin and epi-radicinol reduced root elongation of germinating carrot seeds at concentrations of 10-20 microgram/mL. Carrot samples naturally infected by A. radicina contained detectable quantities of epi-radicinol also in combination with lower levels of radicinin or radicinol. Accumulation of radicinols and radicinin in stored carrots, either naturally contaminated or artificially inoculated with A. radicina, was stimulated by successive temperature rises from 1 to 10 ÀC and from 10 to 20 ÀC, reaching maximum levels of 60 microgram/g epi-radicinol and 26 microgram/g radicinin. This is the first report on the production of radicinols by A. radicina and its natural occurrence in carrots in association with radicinin.

Record 109 of 434 - AGRICOLA 1998-2004/09
AU: Cho,-S.B.; Chang,-H.J.; Kim,-H.Y.L.; Kim,-W.J.; Chun,-H.S.
TI: Steeping-induced physicochemical changes of milled waxy rice and their relation to the quality of yukwa (an oil-puffed waxy rice snack).
SO: Journal of the science of food and agriculture. 2004 Apr. 15, v. 84, issue 5 p. 465-473.
AB: The influence of water-steeping periods (0 to 15 days, 25ÀC) on the physicochemical properties of raw waxy rice in relation to the yukwa quality was investigated. The moisture contents in waxy rice and reducing sugar in its steeping medium were increased, while contents of protein and minerals of raw waxy rice were decreased in proportion to the water-steeping duration. With longer steeping periods, swelling power, solubility and peak viscosity were increased, while grain hardness was decreased with apparent kernel structural change. Depending on the water-steeping duration of raw waxy rice, the hardness decreased from 26.0 to 1.8 g, and the expansion ratio of yukwa increased from 762 to 1539%. Correlations between the physicochemical properties and yukwa quality indicated that variables having the most positive influential on expansion ratio were reducing sugar (Wgc = 0.961, P < 0.01) and peak viscosity (Wgc = 0.897, P < 0.01), and those for hardness of yukwa were crude protein (Wgc = 0.875, P < 0.01) and hardness (Wgc = 0.887, P < 0.01) of the steeped waxy rice. It is suggested that steeping-induced physicochemical changes of raw waxy rice had a significant influence on the final quality of yukwa in terms of hardness and expansion ratio.

Record 110 of 434 - AGRICOLA 1998-2004/09
AU: Ding,-J.; Jia,-J.; Yang,-L.; Wen,-H.; Zhang,-C.; Liu,-W.; Zhang,-D.

TI: Validation of a rice specific gene, sucrose phosphate synthase, used as the endogenous reference gene for qualitative and real-time quantitative PCR detection of transgenes.
SO: Journal of agricultural and food chemistry. 2004 June 2, v. 52, no. 11 p. 3372-3377.
AB: With the development of transgenic crops, many countries have issued regulations to label the genetically modified organisms (GMOs) and their derived products. Polymerase Chain Reaction (PCR) methods are thought to be reliable and useful techniques for qualitative and quantitative detection of GMOs. These methods generally need to amplify the transgene and compare the amplified result with that of the corresponding reference gene to obtain reliable results. In this article, we reported the development of specific primers and probe for the rice (Oryza sativa) sucrose phosphate synthase (SPS) gene and PCR cycling conditions suitable for the use of this sequence as an endogenous reference gene in both qualitative and quantitative PCR assays. Both methods were assayed with 13 different rice varieties, and identical amplification products were obtained with all of them. No amplification products were observed when DNA samples from other species, such as wheat, maize, barley, tobacco, soybean, rapeseed, tomato, sunflower, carrot, pepper, eggplant, lupine, mung bean, plum, and Arabidopsis thaliana, were used as templates, which demonstrated that this system was specific for rice. In addition, the results of the Southern blot analysis confirmed that the SPS gene was a single copy in the tested rice varieties. In qualitative and quantitative PCR analyses, the detection sensitivities were 0.05 and 0.005 ng of rice genomic DNA, respectively. To test the practical use of this SPS gene as an endogenous reference gene, we have also quantified the beta-glucuronidase (GUS) gene in transgenic rice using this reference gene. These results indicated that the SPS gene was species specific, had one copy number, and had a low heterogeneity among the tested cultivars. Therefore, this gene could be used as an endogenous reference gene of rice and the optimized PCR systems could be used for practical qualitative and quantitative detection of transgenic rice.

Record 111 of 434 - AGRICOLA 1998-2004/09
AU: Obojska,-A.; Berlicki,-L.; Kafarski,-P.; Lejczak,-B.; Chicca,-M.; Forlani,-G.
TI: Herbicidal pyridyl derivatives of aminomethylene-bisphosphonic acid inhibit plant glutamine synthetase.
SO: Journal of agricultural and food chemistry. 2004 June 2, v. 52, no. 11 p. 3337-3344.
AB: A series of aminomethylene-bisphosphonic acid derivatives, previously synthesized and shown to be endowed with herbicidal properties, were evaluated as potential inhibitors of plant glutamine synthetase. The cytosolic form of the enzyme was partially purified from rice cultured cells and assayed in the presence of millimolar concentrations of the compounds by means of three different assay methods, respectively measuring the hemibiosynthetic, the transferase, and the full biosynthetic reactions. Several compounds were found to exert a remarkable inhibition, with I50 values similar to those obtained under the same conditions with a well-established inhibitor of glutamine synthetase, the herbicide phosphinothricin. Contrary to the

reference compound, enzyme kinetics accounted for a reversible inhibition mechanism. The biological activity of the most active derivatives was further characterized by measuring free glutamine levels in cell suspension rice cultures following treatment with the inhibitors. Results confirmed their ability to interfere in vivo with nitrogen metabolism. A preliminary analysis of structure-activity relationship allowed it to be hypothesized that steric rather than electronic factors are responsible for the inhibitory potential of these compounds.

Record 112 of 434 - AGRICOLA 1998-2004/09

AU: Latha,-R.; Rao,-C.S.; Subramaniam,-H.M.S.; Eganathan,-P.; Swaminathan,-M.S.

TI: Approaches to breeding for salinity tolerance--a case study on Porteresia coarctata.

SO: Annals of applied biology. 2004, v. 144, no. 2 p. 177-184.

Record 113 of 434 - AGRICOLA 1998-2004/09

AU: Kim,-B.R.; Nam,-H.Y.; Kim,-S.U.; Pai,-T.; Chang,-Y.J.

TI: Reverse transcription quantitative-PCR of three genes with high homology encoding 3-hydroxy-methylglutaryl-CoA reductase in rice.

SO: Biotechnology letters. 2004 June, v. 26, no. 12 p. 985-988.

AB: Reverse transcription followed by RT Q-PCR is useful for the systematic measurement of changes in gene expression. RT Q-PCR with two pairs of primers for each gene was used for relative expression of three genes with high homology encoding 3-hydroxy-methylglutaryl-CoA reductase (HMGR) in rice. At various growth stages of etiolated seedling and various times after UV-irradiation treatment, RT Q-PCR of each HMGR gene showed a consistent pattern of relative expression with the RT Q-PCR data, using two pairs of primers, giving a high degree of accuracy. Furthermore, the different expression levels of three HMGR genes in a sample were determined by diluting the cDNA concentration. These results indicate that RT Q-PCR with only one pair of primers for a gene can quantify the relative expression and that the high expression level of HMGR2 could be quantified in comparison to the low level of HMGR1 expression.

Record 114 of 434 - AGRICOLA 1998-2004/09

AU: Kim,-K.S.; Kang,-H.J.; Hwang,-I.K.; Hwang,-H.G.; Kim,-T.Y.; Choi,-H.C.

TI: Comparative ultrastructure of Ilpumbyeo, a high-quality Japonica rice, and its mutant, Suweon 464: scanning and transmission electron microscopy studies.

SO: Journal of agricultural and food chemistry. 2004 June 16, v. 52, no. 12 p. 3876-3883.

AB: A new rice mutant Suweon 464 (S-464), which has extreme contrast in cooking quality and physicochemical properties from those of its mother variety Ilpumbyeo (IP), revealed striking differences in ultrastructure in in situ, fractured whole grain, and isolated starch preparation. In scanning electron microscopy (SEM), compound starch granules (CSG) in whole grains of IP were readily split during fracturing, whereas those in S-464 were structurally intact and were enclosed within a sac-like structure tolerant of fracturing. In isolated preparation, IP starch consisted entirely of individual starch granules, whereas S-464 starch consisted of mostly large CSG enclosed within the sac, preventing the release of the individuals. In transmission electron microscopy (TEM), S-464 starch granules were smaller, solidly "condensed", and highly contrasted, whereas those of IP were larger, loosely " diffused", and less contrasted. The boundaries of amyloplasts and starch granules in S-464 were coated with a thin proteinaceous layer, presumed to be the counterpart of the sac that enclosed the CSG observed in SEM.

Record 115 of 434 - AGRICOLA 1998-2004/09
AU: Dang,-J.M.C.; Copeland,-L.
TI: Studies of the fracture surface of rice grains using environmental scanning electron microscopy.
SO: Journal of the science of food and agriculture. 2004 May, v. 84, issue 7 p. 707-713.
AB: Raw and processed grains of rice (Oryza sativa) were examined using the environmental scanning electron microscope (ESEM), which allows specimens to be imaged at high resolution with minimal preparation. Images were obtained for milled rice grains that were fractured along natural transverse fracture planes. The images showed two distinct features: a smooth surface, where the fracture plane is suggested to be between endosperm cells, and a rough, more disorganised surface, which is likely to correspond to the fracture plane passing through an endosperm cell. Individual starch granules exposed in the fractured surface ranged from 3 to 11 micrometer in diameter. The ESEM revealed morphological differences between grains of different varieties. Parboiled rice showed a glassy fracture surface in which features of endosperm cells and starch granules were clearly recognisable but smaller than those of uncooked rice grains. Rice grains that had been heated and puffed showed a complete loss of organisational structure. The ESEM was able to capture the effect of processing treatments on the organisational structure of the grains.

Record 116 of 434 - AGRICOLA 1998-2004/09
AU: Gujral,-H.S.; Rosell,-C.M.
TI: Improvement of the breadmaking quality of rice flour by glucose oxidase.
SO: Food research international. 2004, v. 37, no. 1 p. 75-81.

Record 117 of 434 - AGRICOLA 1998-2004/09
AU: Sangnark,-A.; Noomhorm,-A.
TI: Chemical, physical and baking properties of dietary fiber prepared from rice straw.
SO: Food research international. 2004, v. 37, no. 1 p. 66-74.

Record 118 of 434 - AGRICOLA 1998-2004/09
AU: Dalen,-G.-van.
TI: Determination of the size distribution and percentage of broken kernels of rice using flatbed scanning and image analysis.
SO: Food research international. 2004, v. 37, no. 1 p. 51-58.

Record 119 of 434 - AGRICOLA 1998-2004/09
AU: Tseng,-S.H.; Lo,-Y.W.; Chang,-P.C.; Chou,-S.S.; Chang,-H.M.
TI: Simultaneous quantification of glyphosate, glufosinate, and their major metabolites in rice and soybean sprouts by gas chromatography with pulsed flame photometric detector.

SO: Journal of agricultural and food chemistry. 2004 June 30, v. 52, no. 13 p. 4057-4063.

AB: Procedures were developed for the simultaneous determination of glyphosate [N-(phosphonomethyl)glycine] and glufosinate [DL-homoalanin-4-yl-(methyl)phosphinic acid] and their major metabolites, aminomethylphosphonic acid (AMPA) and 3-(methylphosphinico)propionic acid (3-MPPA), in rice and soybean sprouts by gas chromatography (GC) equipped with a pulsed flame photometric detector (PFPD). Herbicides and their major metabolites were previously derivatized with TMOA (trimethyl orthoacetate (TMOA) in the presence of acetic acid, and their GC responses versus heating temperature (70-90 ÀC) and heating time (30-120 min) were optimized. It was found that increases in heating temperature and heating time were unfavorable for the derivatization of glyphosate or glufosinate, whereas high temperature and extended reaction time remarkably facilitated that of AMPA and 3-MPPA except at 90 ÀC for an extended reaction time (120 min). Combination of AG1-X8 anion-exchange chromatography with a Florisil cartridge cleanup process was favorable for the GC-PFPD analysis. Four types of derivatives spiked in rice and soybean sprout matrices were eluted, reaching a baseline separation, in a sequence of 3-MPPA, AMPA, glyphosate, and glufosinate within 14 min using a DB-608 capillary column. Recoveries of glyphosate, AMPA, glufosinate, and 3-MPPA (0.5 ppm) spiked in both sample matrices were determined to be 72-81, 71-86, 101-119, and 83-90%, respectively, whereas the coefficient of variation was determined to be <10% in three repeated determinations. The instrumental limits of detection for glyphosate, AMPA, glufosinate, and 3-MPPA in sample matrices were 0.02, 0.03, 0.02, and 0.01 ppm, respectively. The limits of quantification for glyphosate, AMPA, glufosinate, and 3-MPPA in sample matrices were 0.06, 0.10, 0.06, and 0.04 ppm, respectively.

Record 120 of 434 - AGRICOLA 1998-2004/09

AU: Reversat,-G.; Fernandez,-L.

TI: Effect of inoculations with single and multiple juveniles on release of progeny of Meloidogyne graminicola from susceptible rice.

SO: Nematology international journal of fundamental and applied nematological research. 2004, v. 6, pt. 1 p. 1-6.

Record 121 of 434 - AGRICOLA 1998-2004/09

AU: Ramesh,-S.; Nagadhara,-D.; Pasalu,-I.C.; Kumari,-A.P.; Sarma,-N.P.; Reddy,-V.D.; Rao,-K.V.

TI: Development of stem borer resistant transgenic parental lines involved in the production of hybrid rice.

SO: Journal of biotechnology. 2004 July 15, v. 111, no. 2 p. 131-141.

Record 122 of 434 - AGRICOLA 1998-2004/09

AU: Perez-Mendoza,-J.; Throne,-J.E.; Dowell,-F.E.; Baker,-J.E.

TI: Chronological age-grading of three species of stored-product beetles by using near-infrared spectroscopy.

SO: Journal of economic entomology. 2004 June, v. 97, no. 3 p. 1159-1167.

AB: The accuracy of near-infrared spectroscopy (NIRS) for predicting the chronological age of adults of the rice weevil, Sitophilus

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      oryzae (L.); the lesser grain borer, Rhyzopertha dominica (F.);
      and the red flour beetle, Tribolium castaneum (Herbst), three
      pests of stored grain, was examined. NIRS-predicted age
      correlated well with actual age of these three species. Age
      predictions in S. oryzae by using the NIRS method are not
      dependent upon adult sex or temperatures to which adult weevils
      are exposed. Results indicated that water content decreased with
      increasing age in rice weevil adults, and excluding wavelengths
      at which water absorbs NIR radiation reduced the accuracy of
      correct classification. Additionally, removing cuticular lipids
      from insects resulted in a significant decrease in classification
      accuracy of weevils, indicating that these compounds may be
      partly responsible for the ability of NIRS to differentiate young
      from old beetles. NIRS is a nondestructive technique that can be
      used to age-grade large numbers of adult stored-product beetles,
      information that could help to increase the accuracy of
      population models for these pest species.
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Record 123 of 434 - AGRICOLA 1998-2004/09
AU:   High,-S.M.; Cohen,-M.B.; Shu,-Q.Y.; Altosaar,-I.
TI:   Achieving successful deployment of Bt rice.
SO:   Trends in plant science. 2004 June, v. 9, no. 6 p. 286-292.
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Record 124 of 434 - AGRICOLA 1998-2004/09
AU:   Jabbari,-K.; Cruveiller,-S.; Clay,-O.; Le-Saux,-J.; Bernardi,-G.
TI:   The new genes of rice: a closer look.
SO:   Trends in plant science. 2004 June, v. 9, no. 6 p. 281-285.
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Record 125 of 434 - AGRICOLA 1998-2004/09
AU:   Meeso,-N.; Nathakaranakule,-A.; Madhiyanon,-T.; Soponronnarit,-S.
TI:   Influence of FIR irradiation on paddy moisture reduction and
      milling quality after fluidized bed drying.
SO:   Journal of food engineering. 2004 Nov., v. 65, issue 2 p.
      293-301.
AB:   The influence of far-infrared (FIR) irradiation in multi-stage
      paddy drying process on moisture reduction and milling quality
      has been experimentally studied. The process, running in series,
      comprised fluidized bed drying, FIR irradiation, tempering and
      ambient air ventilation. The experimental results showed that the
      critical moisture content after the fluidized bed drying was
      around 23% d.b. whereas incorporating with the FIR irradiation
      could continuously reduced the moisture content to 21% d.b.
      without affecting paddy head rice yield and whiteness. Under the
      intensity of FIR irradiation, wet paddy was more sensitive than
      dry paddy. However, to maintain head rice yield, moisture
      equalization by a subsequent tempering stage was still required.
      Studying the microstructure of rice kernels and the pasting
      behavior of rice flours showed the presence of partial
      gelatinization resulted in the improvement of head rice yield.
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Record 126 of 434 - AGRICOLA 1998-2004/09
AU:   Bauer,-P.; Lubkowitz,-M.; Tyers,-R.; Nemoto,-K.; Meeley,-R.B.;
      Goff,-S.A.; Freeling,-M.
TI:   Regulation and a conserved intron sequence of liguleless3/4 knox
      class-I homeobox genes in grasses.
SO:   Planta. 2004 June, v. 219, no. 2 p. 359-368.
AB:   The nine class-I maize (Zea mays L.) knox genes are putative
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transcription factors normally expressed in shoot apices, but not in leaves. knotted1 (kn1) seems to function in shoot apical meristem maintenance, and rough sheath1 (rs1)-like genes may act in internode elongation. The function of liguleless3 (lg3)-type genes is still unknown. Here, we characterized lg3 as well as the two most closely related genes liguleless4a (lg4a, formerly knox11) and liguleless4b (lg4b, formerly knox5). We termed this subclass of knox genes lg3/4 genes. We studied the expression patterns of lg3/4 genes and compared their sequences. We obtained knockout mutants of lg3 by finding Mu transposon insertions into exons. Our results show that lg3 was not essential for plant development, and that lg4a and lg4b were likely to encode the redundant function. In addition, lg4a but not lg4b was ectopically expressed in the Lg4-O mutant, suggesting that this mutant was affected at the lg4a locus. We found that the lg3 gene was unique among knox genes as it was co-induced in the leaves of leaf mutants that ectopically expressed knox genes in the leaves. The leaf phenotype expressed in the dominant Rs1-O mutant was not altered when lg3 function was removed using the knockout. Genomic sequence comparisons of lg3, lg4a and lg4b from maize and the two homologous genes, osh6 and osh71, from rice revealed a 14-bp phylogenetic footprint in intron II. This sequence was conserved in nucleotide composition, position and polarity in the lg3/4 genes of divergent grasses representing six Gramineae subfamilies. In an independent experiment, this same conserved sequence was found in a yeast reverse one-hybrid screen for putative binding sites of the LG3 homeodomain protein. Distribution of this 14-bp sequence was examined within the public rice database. The possible function of this sequence in regulation of lg3/4 genes is discussed.

Record 127 of 434 - AGRICOLA 1998-2004/09

AU: Tyagi,-N.K.; Agrawal,-A.; Sakthivadivel,-R.; Ambast,-S.K.; Sharma,-D.K.

TI: Productivity of rice-wheat cropping system in a part of Indo-Gengetic plain: a spatial analysis.

SO: Irrigation and drainage systems. 2004 Feb., v. 18, no. 1 p. 73-88.

AB: Investigations were made to study the effect of unequal distribution of canal water in land and water productivity of the riceÆwheat cropping system in terms of headÆtail relationship in Bhakra Canal command, Haryana. Information on water supply, agronomic practices, crop yield, etc., were collected from 216 farmers comprising 36 farmers each from the head, middle, and tail watercourses of two minors during year 2000-01. The unequal supply of canal water and presence of marginal quality groundwater creates large variations in the cropping pattern, irrigation application, and land and water productivity of the irrigation system. The groundwater of tail reaches, being saline in nature, was about 25% less productive as compared to head reaches. The unavailability of canal water in the tail reaches creates more dependency on groundwater. Due to its poor quality the crop production in the tail reaches was less by 10 to 20% in case of wheat, and 20 to 40% in case of rice, as compared to head reaches. Groundwater transfer from head to tail reaches and cultivation of low water requiring salt tolerant crops/varieties would be helpful in reducing the productivity gap and increasing the profitability of the farms in the region.

Record 128 of 434 - AGRICOLA 1998-2004/09

AU: Bambaradeniya,-C.N.B.; Edirisinghe,-J.P.; Silva,-D.N.-de; Gunatilleke,-C.V.S.; Ranawana,-K.B.; Wijekoon,-S.

TI: Biodiversity associated with an irrigated rice agro-ecosystem in Sri Lanka.

SO: Biodiversity and conservation. 2004 Aug., v. 13, no. 9 p. 1715-1753.

Record 129 of 434 - AGRICOLA 1998-2004/09

AU: Datta,-K.K.; Tewari,-L.; Joshi,-P.K.

TI: Impact of subsurface drainage on improvement of crop production and farm income in north-west India.

SO: Irrigation and drainage systems. 2004 Feb., v. 18, no. 1 p. 43-55.

AB: The Indian Council of Agricultural research has given priority to control and manage salinity problems that have developed in north-west India. Multi-disciplinary taskforces have recommended installation of subsurface drainage for salinity control, based on design and management techniques developed by the Central Soil Salinity Research Institute (CSSRI), to rehabilitate lands with excess soil salinity. After small-scale studies, large-scale pilot projects were launched to install subsurface drainage in problem areas. One such attempt in was initiated in the north-west region of India where a large-scale drainage project was carried out with Dutch collaboration. We assessed the impact of investments in subsurface drainage in order to validate past funding on research of drainage in India. The important methods used for assessing the efficiency benefits of drainage investment were: to determine the impact of sub surface drainage in terms of net present value, internal rate of returns, consumers' surplus and producers' surplus; to assess the social welfare in terms of social equality and sustainability of the drainage system; and to examine the factors affecting the sustainability of the technology. The internal rate of return was computed to assess the efficiency parameter of subsurface drainage for salinity management. In order to measure the changes in inequality distribution of income, Gini concentration ratios were computed with and without installing sub surface drainage. The Radar Approach, a method based on a graphical display of differences between actual ideal performance, was used to quantify drainage sustainability in terms of optimizing gains and conserving, or improving the quality of soil and water resources. There were several farm-level benefits as a result of installing subsurface drainage: these included: (i) a substantial increase in farm income; (ii) cropping intensification and diversification toward high value crops; and (iii) generation employment. A high internal rate of return justified investment in subsurface drainage. Income inequalities across farms were reduced. The radar approach showed improvement in sustainability in terms of economic gains and resource conservation. Despite of these economic, social, and environmental benefits, the sustainability of subsurface drainage technology is questionable. The specific reasons include: (i) the nature of the technology; (ii) lukewarm collective action by the beneficiaries; (iii) conflicting objectives among beneficiaries; and (iv) growing numbers of free riders. To a large extent these were addressed in the study area by forming village committees. Without appropriate institutional arrangements, subsurface drainage may not yield the desired results, and in the long run may result in neglect of operation and maintenance needs and ultimately the abandonment of the technology.

Record 130 of 434 - AGRICOLA 1998-2004/09

AU: Srinivasulu,-A.; Sujani-Rao,-C.; Lakshmi,-G.V.; Satyanarayana,-T.V.; Boonstra,-J.

TI: Model studies on salt and water balances at Konanki pilot area, Andhra Pradesh, India.

SO: Irrigation and drainage systems. 2004 Feb., v. 18, no. 1 p. 1-17.

AB: The salt and water balances at Konanki pilot area in Nagarjunasagar project right canal command in Andhra Pradesh State of India were analysed using SALTMOD. The model was calibrated by using two-year data collected in the pilot area. From the calibration, the leaching efficiencies of the root and transition zone were estimated as 65% and the out going natural sub-surface drainage was determined as 50 mm per year. The model predicts that the root zone soil water salinity will be reduced to 4, 3 and 2.5 dS/m (from an initial value of 11.5 dS/m) during the first, second and third seasons within six years after installation of the drainage system. Next, the situation prior to the installation of the drainage system was reconstructed using the model. Finally, sensitivity analyses were made to study the effects of varying drain depth, spacing and amount of irrigation water applied on root zone salinity and depth to water table. Here, the model predicted that closer than the present spacing or further deepening of the drains from the present depth of 1 m to 1.4 m will not have any better influence on the reduction of the root zone salinity than in the present situation. These simulations also suggested that by applying 80% of the present amount of irrigation water, the root zone salinity can be brought down to 5 and 4 dS/m by second and fourth years, respectively and this will in turn reduce the problem of water logging and salinity to some extent.

Record 131 of 434 - AGRICOLA 1998-2004/09

AU: Biffi,-R.; Munari,-M.; Dioguardi,-L.; Ballabio,-C.; Cattaneo,-A.; Galli,-C.L.; Restani,-P.

TI: Ochratoxin A in conventional and organic cereal derivatives: a survey of the Italian market, 2001-02.

SO: Food additives and contaminants. 2004 June, v. 21, no. 6 p. 586-591.

AB: Ochratoxin A is a mycotoxin produced mainly by Penicillium verrucosum and Aspergillus ochraceus. Although typically considered a cereal contaminant, it has also been detected in dried fruit, nuts, meat and derivatives. To estimate the quantity of ochratoxin A that might be ingested by Italian consumers from these foods, 211 cereal derivatives (flours and bakery products) were analysed by high-performance liquid chromatography. Products were from conventional and organic agriculture and from integrated pest management agriculture. All commercial flours and derivatives examined contained ochratoxin A at concentrations very much below the legal limit (3 microgram kg-1): the highest value, 0.816 microgram kg-1, was detected in a sample of spelt whole flour from organic agriculture. In many samples, the ochratoxin content was below the limit of detection; only rarely did values exceed 0.5 microgram kg-1. In baby foods, four samples were above the particularly restrictive Italian legal limit of 0.5 microgram kg-1. Although some significant differences were found between samples from conventional and organic agriculture when some product categories were examined (namely, baby foods as semolina and rice creams), no important difference was found between the two types of agricultural practice when all types of cereal derivatives were considered together.

Record 132 of 434 - AGRICOLA 1998-2004/09

AU: Zheng,-X.; Chen,-X.; Zhang,-X.; Lin,-Z.; Shang,-J.; Xu,-J.; Zhai,-W.; Zhu,-L.

TI: Isolation and identification of a gene in response to rice blast disease in rice.

SO: Plant molecular biology. 2004 Jan., v. 54, no. 1 p. 99-109.

AB: We combined cDNA amplified fragment length polymorphism (cDNA-AFLP) with bulked segregant analysis (BSA) to detect genes that control rice blast (Magnaporthe grisea) resistance in a double-haploid (DH) population derived from a cross between a blast-resistant variety, Zhai Ye Qing8 (ZYQ8), and a blast-susceptible variety, Jin Xi17 (JX17). In cDNA-AFLP analysis between a blast resistance (R) pool and a blast susceptibility (S) pool from the DH population, 12 transcript-derived fragments (TDFs) that were present in only one of the two pools were detected, 8 of which were from the R pool and 4 from the S pool. Mapping analysis of these TDFs by using the DH mapping population showed that five of them, R1, R8, S9, S16 and S17, were located on chromosome 1. Sequence comparison and allelic analysis showed thatR1/S16 and R8/S9 were two pairs of allelic genes. The full-length cDNA sequences of R1/S16, S17 and R8/S were obtained through cDNA library screening, in which only the expression level of R8 cDNA was up-regulated by inoculation with the blast isolate zh10814 and not affected by mock treatment, suggesting that R8 was implicated in the signaling pathways of the rice blast resistance reaction. Protein function prediction showed that R8 cDNA encodes a protein with high identity to a putative calmodulin-binding protein in Arabidopsis thaliana which belongs to the P-loop-containing nucleotide triphosphate hydrolases superfamily that contains a number of various kinases.

Record 133 of 434 - AGRICOLA 1998-2004/09

AU: Kanno,-T.; Kasai,-K.; Ikejiri-Kanno,-Y.; Wakasa,-K.; Tozawa,-Y.

TI: In vitro reconstitution of rice anthranilate synthase: distinct functional properties of the alpha subunits OASA1 and OASA2.

SO: Plant molecular biology. 2004 Jan., v. 54, no. 1 p. 11-23.

AB: Anthranilate synthase (AS) is a key enzyme in the biosynthesis of various indole compounds including tryptophan. AS consists of two subunits, alpha and beta, and converts chorismate to anthranilate. Two or more AS alpha-subunit genes have been identified and characterized in several land plants. Although alpha subunits of AS induced by elicitation have been suggested to play significant roles in secondary metabolism, the biochemical and precise functional properties of individual AS isozymes have remained unclear. We have previously identified and characterized two AS alpha-subunit genes (OASA1 and OASA2) in rice

(Oryza sativa). To provide further insight into the enzymatic functions of AS isozymes in rice, we have now isolated rice cDNAs encoding the AS beta subunits OASB1 and OASB2 and reconstituted AS isozymes in vitro with the wheat germ cell-free system for protein expression. Both OASB subunits conferred glutamine-dependent AS activity on either OASA1 or OASA2, indicating the absence of a marked functional difference between the two beta subunits in terms of amidotransferase activity. Furthermore, both OASA subunits required assembly with a subunit to achieve maximal enzymatic activity even with NH4+ as the amino donor. The V(max) and K(i) for tryptophan of the OASA1-OASB1 isozyme with glutamine as the amino donor, however, were 2.4 and 7.5 times, respectively, those of OASA2-OASB1, suggesting that AS isozymes containing OASA1 possess a higher activity and are less sensitive to feedback inhibition than those containing OASA2. Our biochemical characterization of reconstituted AS isozymes has thus revealed distinct functional properties of these isozymes in rice.

Record 134 of 434 - AGRICOLA 1998-2004/09

AU: Alcantara,-E.P.; Aguda,-R.M.; Curtiss,-A.; Dean,-D.H.; Cohen,-M.B.

TI: Bacillus thuringiensis delta-endotoxin binding to brush border membrane vesicles of rice stem borers.

SO: Archives of insect biochemistry and physiology. 2004 Apr., v. 55, no. 4 p. 169-177.

AB: The receptor binding step in the molecular mode of action of five delta-endotoxins (Cry1Ab, Cry1Ac, Cry1C, Cry2A, and Cry9C) from Bacillus thuringiensis was examined to find toxins with different receptor sites in the midgut of the striped stem borer (SSB) Chilo suppressalis (Walker) and yellow stem borer (YSB) Scirpophaga incertulas (Walker) (Lepidoptera: Pyralidae). Homologous competition assays were used to estimate binding affinities (Kcom) of 125I-labelled toxins to brush border membrane vesicles (BBMV). The SSB BBMV affinities in decreasing order was: Cry1Ab = Cry1Ac > Cry9C > Cry2A > Cry1C. In YSB, the order of decreasing affinities was: Cry1Ac > Cry1Ab > Cry9C = Cry2A > Cry1C. The number of binding sites (Bmax) estimated by homologous competition binding among the Cry toxins did not affect toxin binding affinity (Kcom) to both insect midgut BBMVs. Results of the heterologous competition binding assays suggest that Cry1Ab and Cry1Ac compete for the same binding sites in SSB and YSB. Other toxins bind with weak (Cry1C, Cry2A) or no affinity (Cry9C) to Cry1Ab and Cry1Ac binding sites in both species. Cry2A had the lowest toxicity to 10-day-old SSB and Cry1Ab and Cry1Ac were the most toxic. Taken together, the results of this study show that Cry1Ab or Cry1Ac could be combined with either Cry1C, Cry2A, or Cry9C for more durable resistance in transgenic rice. Cry1Ab should not be used together with Cry1Ac because a mutation in one receptor site could diminish binding of both toxins.

Record 135 of 434 - AGRICOLA 1998-2004/09

AU: Rychlik,-M.

TI: Revised folate content of foods determined by stable isotope dilution assays.

SO: Journal of food composition and analysis an official publication of the United Nations University, International Network of Food

Data Systems. 2004 June-Aug, v. 17, no. 3-4 p. 475-483.

AB: Stable isotope dilution assays were applied to quantify folates in several vegetables, orange juice, meat, liver, bread, and rice . The results were compared to data in the literature and in food data bases revealing significantly lower folate contents in broccoli and bread. Applying the new folate values to the Bavarian Food Intake Survey of 1995 resulted in a reduced daily intake of about 10 microgram, which was caused primarily by the lower folate content in bread. However, the majority of foods contributing to folate intake still needs to be quantified by the new method to obtain accurate data on the estimated dietary intake to compare with the recommended daily intake.

Record 136 of 434 - AGRICOLA 1998-2004/09

AU: Barikmo,-I.; Ouattara,-F.; Oshaug,-A.

TI: Protein, carbohydrate and fibre in cereals from Mali--how to fit the results in a food composition table and database.

SO: Journal of food composition and analysis an official publication of the United Nations University, International Network of Food Data Systems. 2004 June-Aug, v. 17, no. 3-4 p. 291-300.

AB: During the past 5 years, the main staple foods (cereals) used in Mali have been collected to develop a food composition table and database. We present recent results of protein, carbohydrate and fibre content for some cereals. Samples were collected from five different regions. To reduce laboratory costs, composite samples (cs) were made. The cereals analysed were sorghum (Sorghum bicolor) (cs=142), millet (Pennisetum glaucum) (cs=163), maize (Zea mays) (cs=107), wheat (Triticum aestivum) (cs=123), rice (Oryza sativa) (cs=151) and fonio (Digitaria exilis) (cs=104). Fonio is an old cereal cultivated across the dry savannahs in West Africa, and is very popular in Mali. All samples were cleaned and processed (ready to cook) before analysis. Detailed sampling plans were used. For total nitrogen, Kjeldahl and Dumas combustion methods were used. Methods used for carbohydrate (sugar and starch) were polarimetric, spectrophotometric and HPLC, and a gravimetric method was used for fibre. The mean«S.D. content of protein for 100 g cereal was: in millet 7.9«1.4 g, sorghum 10.3«0.7 g, maize 7.6«1.1 g, rice 6.3«0.3 g, wheat 10.6«1.1 g and fonio 7.2«0.4 g. The mean«S.D. content of carbohydrate and fibre per 100 g cereal was: in millet 65.8«10.1 and 6.2«2.3 g, sorghum 73.5«4.3 and 4.7«0.1 g, maize 73.0«10.2 and 4.6«1.3 g, rice 83.7«7.8 and 1.1«0.0 g, wheat 75.1«1.8 and 3.0«0.0 g and fonio 74.3«0.1 and 2.2«0.3 g, respectively. As indicated by the standard deviations there were considerable geographical differences in nutrient content for the same cereal. There is no apparent explanation for these differences. Until this is explored further, it is necessary to develop separate tables for different regions.

Record 137 of 434 - AGRICOLA 1998-2004/09

AU: Miyazaki,-S.; Rice,-M.; Quigley,-F.; Bohnert,-H.J.

TI: Expression of plant inositol transporters in yeast.

SO: Plant science. 2004 Jan., v. 166, issue 1 p. 245-252.

Record 138 of 434 - AGRICOLA 1998-2004/09

AU: Dhingra,-A.; Khurana,-J.P.; Tyagi,-A.K.

TI: Involvement of G-proteins, calmodulin and tagetitoxin-sensitive

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      RNA polymerase in light-regulated expression of plastid genes (
      psbA, psaA and rbcL) in rice (Oryza sativa L.).
SO:   Plant science. 2004 Jan., v. 166, issue 1 p. 163-168.
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Record 139 of 434 - AGRICOLA 1998-2004/09
AU:   Martinez-Trujillo,-M.; Chavez-Barcenas,-T.; Limones-Briones,-V.;
      Simpson,-J.; Herrera-Estrella,-L.
TI:   Functional analysis of the promoter of the rice sucrose phosphate
      synthase gene (sps1).
SO:   Plant science. 2004 Jan., v. 166, issue 1 p. 131-140.
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Record 140 of 434 - AGRICOLA 1998-2004/09
AU:   Lee,-J.R.; Lee,-K.O.; Park,-J.H.; Yoo,-J.Y.; Kang,-J.S.; Jeon,-H.
      S.; Kim,-S.Y.; Lee,-Y.M.; Kim,-S.T.; Lim,-C.O.
TI:   Molecular and functional characterization of a PEX14 cDNA from
      rice.
SO:   Plant science. 2004 Jan., v. 166, issue 1 p. 123-130.
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Record 141 of 434 - AGRICOLA 1998-2004/09
AU:   Chen,-C.T.; Chen,-T.H.; Lo,-K.F.; Chiu,-C.Y.
TI:   Effects of proline on copper transport in rice seedlings under
      excess copper stress.
SO:   Plant science. 2004 Jan., v. 166, issue 1 p. 103-111.
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Record 142 of 434 - AGRICOLA 1998-2004/09
AU:   Wilkinson,-H.C.; Champagne,-E.T.
TI:   Value--added rice products in today's market.
SO:   Cereal foods world. 2004 May-June, v. 49, no. 3 p. 134-138.
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Record 143 of 434 - AGRICOLA 1998-2004/09
AU:   Zeng,-L.; Kwon,-T.R.; Liu,-X.; Wilson,-C.; Grieve,-C.M.; Gregorio,
      -G.B.
TI:   Genetic diversity analyzed by microsatellite markers among rice (
      Oryza sativa L.) genotypes with different adaptations to saline
      soils.
SO:   Plant science. 2004 May, v. 166, issue 5 p. 1275-1285.
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Record 144 of 434 - AGRICOLA 1998-2004/09
AU:   Lee,-S.C.; Kim,-J.Y.; Kim,-S.H.; Kim,-S.J.; Lee,-K.; Han,-S.K.;
      Choi,-H.S.; Jeong,-D.H.; An,-G.; Kim,-S.R.
TI:   Trapping and characterization of cold-responsive genes from T-DNA
      tagging lines in rice.
SO:   Plant science. 2004 Jan., v. 166, issue 1 p. 69-79.
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Record 145 of 434 - AGRICOLA 1998-2004/09
AU:   He,-Z.; Fu,-Y.; Si,-H.; Hu,-G.; Zhang,-S.; Yu,-Y.; Sun,-Z.
TI:   Phosphomannose-isomerase (pmi) gene as a selectable marker for
      rice transformation via Agrobacterium.
SO:   Plant science. 2004 Jan., v. 166, issue 1 p. 17-22.
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Record 146 of 434 - AGRICOLA 1998-2004/09
AU:   Ramesh,-S.; Nagadhara,-D.; Reddy,-V.D.; Rao,-K.V.
TI:   Production of transgenic indica rice resistant to yellow stem
      borer and sap-sucking insects, using super-binary vectors of
      Agrobacterium tumefaciens.
SO:   Plant science. 2004 Apr., v. 166, issue 4 p. 1077-1085.
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Record 147 of 434 - AGRICOLA 1998-2004/09
AU: Borges,-R.; Miguel,-E.C.; Dias,-J.M.R.; Cunha,-M.-da; Bressan-Smith,-R.E.; Oliveira,-J.G.-de; Souza-Filho,-G.A.-de
TI: Ultrastructural, physiological and biochemical analyses of chlorate toxicity on rice seedlings.
SO: Plant science. 2004 Apr., v. 166, issue 4 p. 1057-1062.

Record 148 of 434 - AGRICOLA 1998-2004/09
AU: Rakwal,-R.; Agrawal,-G.K.; Tamogami,-S.; Iwahashi,-H.
TI: Transcriptional profiling of OsHin1 in rice plants: a potential role in defense/stress and development.
SO: Plant science. 2004 Apr., v. 166, issue 4 p. 997-1005.

Record 149 of 434 - AGRICOLA 1998-2004/09
AU: Su,-J.; Wu,-R.
TI: Stress-inducible synthesis of proline in transgenic rice confers faster growth under stress conditions than that with constitutive synthesis.
SO: Plant science. 2004 Apr., v. 166, issue 4 p. 941-948.

Record 150 of 434 - AGRICOLA 1998-2004/09
AU: Lee,-H.J.; Lee,-D.E.; Ha,-S.B.; Jang,-S.W.; Lee,-I.J.; Ryu,-S.B.; Back,-K.
TI: The characterization of transgenic rice plants expressing a pepper 5-epi aristolochene synthase, the first committed step enzyme for capsidiol synthesis in isoprenoid pathway.
SO: Plant science. 2004 Apr., v. 166, issue 4 p. 881-887.

Record 151 of 434 - AGRICOLA 1998-2004/09
AU: Babu,-R.C.; Zhang,-J.; Blum,-A.; Ho,-T.H.D.; Wu,-R.; Nguyen,-H.T.
TI: HVA1, a LEA gene from barley confers dehydration tolerance in transgenic rice (Oryza sativa L.) via cell membrane protection.
SO: Plant science. 2004 Apr., v. 166, issue 4 p. 855-862.

Record 152 of 434 - AGRICOLA 1998-2004/09
AU: Yuan,-H.; Chen,-X.; Zhu,-L.; He,-G.
TI: Isolation and characterization of a novel rice gene encoding a putative insect-inducible protein homologous to wheat Wir1.
SO: Journal of plant physiology. 2004 Jan., v. 161, no. 1 p. 79-85.
AB: A full-length cDNA, designated BpHi008A, was cloned representing a rice (Oryza sativa) mRNA that accumulates after brown planthopper (BPH) Nilapar vata lugens Stål feeding. The cDNA encodes a putative 82 amino acid protein (BpHi008A) exhibiting about 37 % amino acid sequence identity to Wir1 family of proteins that are encoded by pathogen-induced transcripts in wheat. Like Wir1 proteins, it consists of a hydrophobic N-terminal half and a hydrophilic C-terminal half relatively rich in glycine and proline. These proteins are predicted to be integrated into the membrane, with the C-terminus being extracytoplastic. Genomic Southern analysis indicated that the BpHi008A gene was present as a single-copy sequence in the rice genome. Temporal and spatial studies showed that BpHi008A were systemically induced in rice when 2nd and 3rd-instars were feeding. The BpHi008A transcripts level was also increased in seedlings damaged by mechanical wounding. These data indicated that BphHi008A was implicated in the response of rice plants to BPH feeding and wounding.

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Record 153 of 434 - AGRICOLA 1998-2004/09
AU:   Meriga,-B.; Reedy,-B.K.; Rao,-K.R.; Reedy,-L.A.; Kishor,-P.B.K.
TI:   Aluminium-induced production of oxygen radicals, lipid
      peroxidation and DNA damage in seedlings of rice (Oryza sativa).
SO:   Journal of plant physiology. 2004 Jan., v. 161, no. 1 p. 63-68.
AB:   The effect of aluminium (Al) on seedlings of two rice cultivars,
      Pusa Basmati and Vikas was investigated after different hours of
      exposure to 80 micromol/L of external Al supply. With increasing
      time of exposure, the growing seedlings readily absorbed Al and
      its localization was greater in roots than shoots. Prolonged
      exposure to Al intensified lipid peroxidation, changed the
      activities of SOD and peroxidase and caused DNA damage. However,
      differential responses were observed between the seedlings of two
      rice cultivars under Al stress. A close inverse relationship
      existed between decreased root growth and increased Al
      accumulation, lipid peroxidation, SOD, peroxidase activities and
      DNA damage. The results demonstrate that roots are the major
      sites of Al localization and accumulation of Al promoted oxygen
      free radicals mediated peroxidation of membranes as evidenced by
      increased MDA levels and the activities of SOD and peroxidase.
      Our results for the first time showed that Al can cause DNA
      damage in rice.
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Record 154 of 434 - AGRICOLA 1998-2004/09
AU:   Zhang,-F.; Zhu,-L.; He,-G.
TI:   Differential gene expression in response to brown planthopper
      feeding in rice.
SO:   Journal of plant physiology. 2004 Jan., v. 161, no. 1 p. 53-62.
AB:   Plant responses to herbivores are complex. 108 cDNA clones
      representing genes relating to plant responses to chewing
      insect-feeding, pathogen infection, wounding and other stresses
      were collected. Northern blot and cDNA array analysis were
      employed to investigate gene expression regulated by
      piercing-sucking insect, brown planthopper (BPH), Nilaparvata
      lugens (Homoptera: Dephacidae) on both the resistant and
      susceptible rice genotypes. After BPH feeding in rice for 72 h,
      the expression of most tested genes was affected. 14 genes in
      resistant rice variety B5 and 44 genes in susceptible MH63 were
      significantly up- or down-regulated. Most of the well-regulated
      genes were grouped in the categories of signaling pathways,
      oxidative stress/apoptosis, wound-response, drought-inducible and
      pathogen-related proteins. Those related to the flavonoid
      pathway, aromatic metabolidsm and the octadecanoid pathway were
      mostly kept unchanged or down-regulated. Our results indicate
      that BPH feeding induces plant responses which would take part in
      a jasmonic acid-independent pathway and crosstalk with those
      related to abiotic stress, pathogen invasion and phytohormone
      signaling pathways.
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Record 155 of 434 - AGRICOLA 1998-2004/09
AU:   Hung,-K.T.; Kao,-C.H.
TI:   Nitric oxide acts as an antioxidant and delays methyl
      jasmonate-induced senescence of rice leaves.
SO:   Journal of plant physiology. 2004 Jan., v. 161, no. 1 p. 43-52.
AB:   In the present study, we evaluate the protective effect of nitric
      oxide (NO) against senescence of rice leaves promoted by methyl
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jasmonate (MJ). Senescence of rice leaves was determined by the decrease of protein content. MJ treatment resulted in (1) induction of leaf senescence, (2) increase in H2O2 and malondialdehyde (MDA) contents, (3) decrease in reduced form glutathione (GSH) and ascorbic acid (AsA) contents, and (4) increase in antioxidative enzyme activities (ascorbate peroxidase, glutathione reductase, peroxidase and catalase). All these MJ effects were reduced by free radical scavengers such as sodium benzoate and GSH. NO donors [N-tert-butyl-alpha-phenylnitrone (PBN), sodium nitroprusside, 3-morpholinosydonimine, and AsA+NaNO2] were effective in reducing MJ-induced leaf senescence. PBN prevented MJ-induced increase in the contents of H2O2 and MDA, decrease in the contents of GSH and AsA, and increase in the activities of antioxidative enzymes. The protective effect of PBN on MJ-promoted senescence, MJ-increased H2O2 content and lipid peroxidation, MJ-decreased GSH and AsA, and MJ-increased antioxidative enzyme activities was reversed by 2-(4-carboxy-2-phenyl)-4,4,5,5-tetramethyl-imidazoline-1-oxyl-3-oxide, a NO-specific scavenger, suggesting that the protective effect of PBN is attributable to NO released. Reduction of MJ-induced senescence by NO in rice leaves is most likely mediated through its ability to scavenge active oxygen species including H2O2.

Record 156 of 434 - AGRICOLA 1998-2004/09

AU: Maiale,-S.; Sanchez,-D.H.; Guirado,-A.; Vidal,-A.; Ruiz,-O.A.

TI: Spermine accumulation under salt stress.

SO: Journal of plant physiology. 2004 Jan., v. 161, no. 1 p. 35-42.

AB: Polyamines have long been recognized to be linked to stress situations, and it is generally accepted that they have protective characteristics. However, little is known about their physiological relevance in plants subjected to long-term salt stress. In order to precise their importance, two rice (Oryza sativa) cultivars differing in their salt tolerance were salinized for 7, 14 and 21 days. The activities of some of the enzymes involved in polyamine metabolism, free polyamines and proline contents were evaluated. Arginine decarboxylase and S-adenosyl-L-methionine decarboxylase activities were reduced in both cultivars as a consequence of salt treatment. However, spermidine synthase activity was reduced in the salt tolerant cultivar (var Giza) but not in the salt sensitive (var El Paso), while no polyamine oxidase activity was detected. During the salinization period, putrescine and spermidine levels decreased in both cultivars, although less dramatically in Giza. Simultaneously, spermine accumulations occur in both varieties, while proline accumulation was major in the sensitive one. However, spermine accumulation induced by treatment with spermidine synthase inhibitor cyclohexylamine, determined no reduction in leaf injury associated with salt stress in both cultivars. The data presented suggest that spermine accumulation is not a salt tolerance trait.

Record 157 of 434 - AGRICOLA 1998-2004/09

AU: Kato-Noguchi,-H.

TI: Allelopathic substance in rice root exudates: rediscovery of momilactone B as an allelochemical.

SO: Journal of plant physiology. 2004 Mar., v. 161, no. 3 p. 271-276.

AB: Much research on rice allelopathy has been directed toward the selection of allelopathic rice strains and the identification of allelochemicals in rice. This paper briefly summarizes recent progress in the rice allelopathy and focuses on rediscovery of momilactone B as an allelochemical. A large number of rice varieties were found to inhibit the growth of several plant species when grown together under field and/or laboratory conditions. These findings suggest that rice probably produces and releases allelochemical(s) into the environment. The putative compound causing the inhibitory effect of rice was recently isolated from rice root exudates, and the chemical structure of the inhibitor was determined by spectral data as momilactone B. In addition, it has been found that momilactone B is released from rice roots into the neighboring environment, and the release level of momilactone B from rice may be sufficient to cause growth inhibition of neighboring plants. These findings suggest that momilactone B may play an important role in rice allelopathy.

Record 158 of 434 - AGRICOLA 1998-2004/09

AU: Kurusu,-T.; Sakurai,-Y.; Miyao,-A.; Hirochika,-H.; Kuchitsu,-K.

TI: Identification of a putative voltage-gated Ca2+- permeable channel (OsTPC1) involved in Ca2+ influx and regulation of growth and development in rice.

SO: Plant and cell physiology. 2004 June, v. 45, no. 6 p. 693-702.

AB: Cytosolic free Ca2+ serves as an important second messenger participating in signal transduction of various environmental stresses. However, molecular bases for the plasma membrane Ca2+ influx and its regulation remain largely unknown. We here identified a gene (OsTPC1) encoding a putative voltage-gated Ca2+ channel from rice, ubiquitously expressed in mature leaves, shoots and roots as well as in cultured cells. OsTPC1 rescued the Ca2+ uptake activity and growth rate of a yeast mutant cch1. To elucidate its physiological roles, we generated transgenic rice plants and cultured cells overexpressing OsTPC1 mRNA. Furthermore, a retrotransposon (Tos17) insertional knockout mutant of OsTPC1 was isolated. OsTPC1-overexpressing cells showed hypersensitivity to excess Ca2+ but higher growth rate under Ca2+ limitation, while growth of the OsTPC1-knockout cultured cells was less sensitive to extracellular free Ca2+ concentration, suggesting that OsTPC1 has Ca2+ transport activity across the plasma membrane. OsTPC1-overexpressing plants showed reduced growth and abnormal greening of roots. Growth of Ostpc1 seedlings was comparable to the control on agar plates, while significantly reduced in adult plants. These results suggest that OsTPC1 functions as a Ca2+-permeable channel involved in the regulation of growth and development.

Record 159 of 434 - AGRICOLA 1998-2004/09

AU: Sharma,-A.; Isogai,-M.; Yamamoto,-T.; Sakaguchi,-K.; Hashimoto,-J.; Komatsu,-S.

TI: A novel interaction between calreticulin and ubiquitin-like nuclear protein in rice.

SO: Plant and cell physiology. 2004 June, v. 45, no. 6 p. 684-692.

AB: Calreticulin (CRT), a major Ca2+-sequestering protein, has been implicated in a variety of cellular functions such as Ca2+ storage, signaling and chaperone activity within the cytoplasm and endoplasmic reticulum. To investigate the biological role of

CRT in rice, 21 partial cDNAs, encoding proteins that interacted with rice CRT in a yeast two-hybrid interaction-cloning system, were characterized and the nucleotide sequences were found to be identical to each other. A full-length cDNA of 3.5 kb, obtained from rice genomic sequence data and 5' RACE, codes for a novel protein of 966 amino acid residues and was designated as CRTintP (CRT interacting protein). Primary sequence analysis of CRTintP showed no sequence homology with the known functional proteins; however, a potential ubiquitin-like domain at the N-terminal together with a putative leucine zipper, a nuclear localization signal and several sites for serine/threonine kinases were evident. Cellular localization of CRTintP demonstrated its role in directing green fluorescent protein to the nucleus in onion epidermal cells. Northern and immunoblot analysis showed increased expression of CRT and CRTintP in response to cold stress. Co-immunoprecipitation using anti-CRT antibodies confirmed the existence of the CRT-CRTintP complex in vivo in the stressed leaf tissue, suggesting their potential role in regulating stress response.

Record 160 of 434 - AGRICOLA 1998-2004/09
AU: Dasgupta,-T.; Hossain,-S.A.; Meharg,-A.A.; Price,-A.H.
TI: An arsenate tolerance gene on chromosome 6 of rice.
SO: New phytologist. 2004 July, v. 163, no. 1 p. 45-49.

Record 161 of 434 - AGRICOLA 1998-2004/09
AU: Nelson,-D.R.; Schuler,-M.A.; Paquette,-S.M.; Werck-Reichhart,-D.; Bak,-S.
TI: Comparative genomics of rice and Arabidopsis. Analysis of 727 cytochrome P450 genes and pseudogenes from a monocot and a dicot.
SO: Plant physiology. 2004 June, v. 135, no. 2 p. 756-772.
AB: Data mining methods have been used to identify 356 Cyt P450 genes and 99 related pseudogenes in the rice (Oryza sativa) genome using sequence information available from both the indica and japonica strains. Because neither of these genomes is completely available, some genes have been identified in only one strain, and 28 genes remain incomplete. Comparison of these rice genes with the 246 P450 genes and 26 pseudogenes in the Arabidopsis genome has indicated that most of the known plant P450 families existed before the monocot-dicot divergence that occurred approximately 200 million years ago. Comparative analysis of P450s in the Pinus expressed sequence tag collections has identified P450 families that predated the separation of gymnosperms and flowering plants. Complete mapping of all available plant P450s onto the Deep Green consensus plant phylogeny highlights certain lineage-specific families maintained (CYP80 in Ranunculales) and lineage-specific families lost (CYP92 in Arabidopsis) in the course of evolution.

Record 162 of 434 - AGRICOLA 1998-2004/09
AU: Hayama,-R.; Coupland,-G.
TI: The molecular basis of diversity in the photoperiodic flowering responses of Arabidopsis and rice.
SO: Plant physiology. 2004 June, v. 135, no. 2 p. 677-684.

Record 163 of 434 - AGRICOLA 1998-2004/09
AU: Rensink,-W.A.; Buell,-C.R.

TI: Arabidopsis to rice. Applying knowledge from a weed to enhance our understanding of a crop species.
SO: Plant physiology. 2004 June, v. 135, no. 2 p. 622-629.
AB: Although Arabidopsis is well established as the premiere model species in plant biology, rice (Oryza sativa) is moving up fast as the second-best model organism. In addition to the availability of large sets of genetic, molecular, and genomic resources, two features make rice attractive as a model species: it represents the taxonomically distinct monocots and is a crop species. Plant structural genomics was pioneered on a genome-scale in Arabidopsis and the lessons learned from these efforts were not lost on rice. Indeed, the sequence and annotation of the rice genome has been greatly accelerated by method improvements made in Arabidopsis. For example, the value of full-length cDNA clones and deep expressed sequence tag resources, obtained in Arabidopsis primarily after release of the complete genome, has been recognized by the rice genomics community. For rice >250,000 expressed sequence tags and 28,000 full-length cDNA sequences are available prior to the completion of the genome sequence. With respect to tools for Arabidopsis functional genomics, deep sequence-tagged lines, inexpensive spotted oligonucleotide arrays, and a near-complete whole genome Affymetrix array are publicly available. The development of similar functional genomics resources for rice is in progress that for the most part has been more streamlined based on lessons learned from Arabidopsis. Genomic resource development has been essential to set the stage for hypothesis-driven research, and Arabidopsis continues to provide paradigms for testing in rice to assess function across taxonomic divisions and in a crop species.

Record 164 of 434 - AGRICOLA 1998-2004/09
AU: Shibata,-M.; Mikota,-T.; Yoshimura,-A.; Iwata,-N.; Tsuyama,-M.; Kobayashi,-Y.
TI: Chlorophyll formation and photosynthetic activity in rice mutants with alterations in hydrogenation of the chlorophyll alcohol side chain.
SO: Plant science. 2004 Mar., v. 166, issue 3 p. 593-600.

Record 165 of 434 - AGRICOLA 1998-2004/09
AU: Sacchetti,-G.; Pinnavaia,-G.G.; Guidolin,-E.; Dalla-Rosa,-M.
TI: Effects of extrusion temperature and feed composition on the functional, physical and sensory properties of chestnut and rice flour-based snack-like products.
SO: Food research international. 2004, v. 37, no. 5 p. 527-534.
AB: Snack-like products were obtained by extrusion-cooking of chestnut-rice flour blend-based doughs, by forming the extruded dough in pellets and then baking them in a toaster, in order to obtain adequate puffing. The effects of chestnut flour content and of extrusion temperature on functional (water adsorption index, water-holding capacity and water solubility index) and physical (density, moisture content and color) properties of the extrudates were investigated. Since chestnuts are particularly rich in sugars, the flour content limited the gelatinization and the expansion of the product, moreover the combined effect of flour content and temperature enhanced the browning reactions. Chestnut flour was found to be suitable for the extrusion-cooking process adopted if properly mixed with rice flour, with 30%

chestnut flour percentage processed at 120 ÀC producing a snack-like product with limited density and browning that was judged good by a sensory panel.

Record 166 of 434 - AGRICOLA 1998-2004/09

AU: Iturriaga,-L.; Lopez,-B.; Anon,-M.

TI: Thermal and physicochemical characterization of seven argentine rice flours and starches.

SO: Food research international. 2004, v. 37, no. 5 p. 439-447.

AB: Differential scanning calorimetry (DSC) was used to evaluate phase transitions of rice flours and starches from seven new argentine genotypes in systems with different water content. Flours of high, medium and low TG (gelatinization temperature) were detected; deltaHG (total gelatinization enthalpy) showed two homogenous groups (8.1-9.2 and 10.1-10.4 mJ/mg). Amylose-lipid complex melting endotherm in waxy rice flours was observed despite the low amylose content. It is suggested that this complex could be originated in the longest amylopectin branches and extra granular complexing lipids. Differential behaviour in waxy genotypes was found with decrease of water content, probably due to the highest water absorption capacity of the AP (amylopectin). Genotypes with high (26.8-28.6 g/100 starch), medium (19.6-20.7 g/100 g starch) and low total amylose (TAM) content was found (1.3-2.1g/100 g starch). In using X-ray diffraction, the relative crystallinity in waxy genotypes was found to be higher (48%) than that corresponding to the non-waxy ones (37-40%). A linear correlation between gelatinization process cooperativity and TAM was found to exist but no between deltaHG and TG with crystallinity and TAM. Glass transitions (Tg) of gelatinized starch-water systems were also determined by DSC. Results indicated higher values (-5.0 to 6.3 ÀC) for flours than for starches (-10 ÀC).

Record 167 of 434 - AGRICOLA 1998-2004/09

AU: Barman,-S.R.; Gowda,-M.; Venu,-R.C.; Chattoo,-B.B.

TI: Identification of a major blast resistance gene in the rice cultivar 'Tetup'.

SO: Plant breeding = Zeitschrift fèur Pflanzenzuchtung. 2004 June, v. 123, no. 3 p. 300-302.

AB: Analysis of near-isogenic lines (NILs) indicated the presence of a novel resistance gene in the indica rice cultivar 'Tetep' which was highly resistant to the rice blast fungus Magnaporthe grisea. 'Tetep' was crossed to the widely used susceptible cultivar 'CO39' to generate the mapping population. A Mendelian segregation ratio of 3 : 1 for resistant to susceptible F2 plants further confirmed the presence of a major dominant locus, in 'Tetep', conferring resistance to the blast fungal isolate B157, corresponding to the international race IC9. Simple sequence length polymorphism (SSLP) was used for molecular genetic analysis. The analysis revealed that the SSLP marker RM 246 was linked to a novel blast resistance gene designated Pi-tp(t) in 'Tetep'.

Record 168 of 434 - AGRICOLA 1998-2004/09

AU: Latha,-R.; Thiyagarajan,-K.; Senthilvel,-S.

TI: Genetics, fertility behaviour and molecular marker analysis of a new TGMS line, TS6, in rice.

SO: Plant breeding = Zeitschrift fèur Pflanzenzuchtung. 2004 June, v.

123, no. 3 p. 235-240.

AB: The thermosensitive genic male sterility (TGMS) system has great potential for revolutionizing hybrid rice production through simple, less expensive and more efficient seed production technology. For the successful utilization of this novel male sterility system, knowledge of the breeding and fertility behaviour of a TGMS line is essential. In this study, the fertility transformation behaviour, the critical fertility and sterility temperatures and the mode of inheritance of male sterility were studied for a new TGMS line, TS6, identified at Tamil Nadu Agricultural University, Coimbatore, India. The pollen and spikelet fertilities recorded on plants raised at fortnightly intervals revealed that this line was completely sterile for 78 consecutive days (35/22 to 32/23ÀC, maximum/minimum temperatures) and reverted to fertile when the temperature was 30/18ÀC. It remained fertile continuously for 69 days and the maximum pollen and spikelet fertilities recorded were 75 and 70%, respectively. The fertility was highly influenced by daily maximum temperature followed by average and minimum temperatures. It was not influenced by relative humidity, sunshine hours or photoperiod. The critical temperature inducing sterility and fertility was 26.7 and 25.5ÀC, respectively. The male sterility in TS6 was inherited as a monogenic recessive in the F2 and BC1 populations of TS6 x MRST9 as well as TS6 x IR68281B. Using bulked segregant analysis on an F2 population of TS6 x MRST9, an RAPD marker, OPC05(2962), was identified to be associated with TGMS in TS6.

Record 169 of 434 - AGRICOLA 1998-2004/09

AU: Li,-Z.F.; Wan,-J.M.; Xia,-J.F.; Zhai,-H.Q.; Ikehashi,-H.

TI: Identification of quantitative trait loci underlying milling quality of rice (Oryza sativa) grains.

SO: Plant breeding = Zeitschrift fèur Pflanzenzuchtung. 2004 June, v. 123, no. 3 p. 229-234.

AB: Milling quality of rice grains is important to both producers and consumers. In this study, quantitative trait loci (QTLs) controlling brown rice rate (BR), milled rice recovery (MR) and head rice recovery (HR) were analysed by composite interval mapping over 2 years using 98 backcross inbred lines (BILs). A total of 12 QTLs for the three traits were detected, of which five were for BR, four for MR and three for HR. The proportion of phenotypic variation explained by individual QTLs ranged from 7.5 to 19.9%, and additive effects contributed by a single QTL accounted for 0.46 to 2.34% of the variation. QTL-by-environment interactions were observed by comparing QTL mapping of the same population grown in two consecutive years. Three of five QTLs for BR and two of four QTLs for MR were detected in 2 years, and all three QTLs for HR were detected in 1 year only. BR was significantly correlated with MR, and all four QTLs of MR were located in the same regions as those of BR. This indicated that QTLs for highly correlated traits could often be detected in the same interval.

Record 170 of 434 - AGRICOLA 1998-2004/09

AU: Kimura,-S.; Tahira,-Y.; Ishibashi,-T.; Mori,-Y.; Mori,-T.; Hashimoto,-J.; Sakaguchi,-K.

TI: DNA repair in higher plants; photoreactivation is the major DNA repair pathway in non-proliferating cells while excision repair (

nucleotide excision repair and base excision repair) is active in proliferating cells.

SO: Nucleic acids research. 2004, v. 32, no. 9 p. 2760-2767.

Record 171 of 434 - AGRICOLA 1998-2004/09

AU: Bulgarelli,-D.; Collins,-N.C.; Tacconi,-G.; Dellaglio,-E.; Brueggeman,-R.; Kleinhofs,-A.; Stanca,-A.M.; Vale,-G.

TI: High-resolution genetic mapping of the leaf stripe resistance gene Rdg2a in barley.

SO: Theoretical and applied genetics. 2004 May, v. 108, no. 7 p. 1401-1408.

AB: The dominant gene Rdg2a of barley conferring resistance to the hemi-biotrophic seed-borne pathogen Pyrenophora graminea is located in the distal region of chromosome arm 1 (7H)S. As the first step towards isolating the gene, a high-resolution genetic map of the region was constructed using an F2 population of 1,400 plants (ThibautRdg2a x Mirco). The map included six classes of resistance gene analogues (RGAs) tightly associated with Rdg2a. Rdg2a was delimited to a genetic interval of 0.14 cM between the RGAs ssCH4 and MWG851. Additional markers were generated using the sequence from the corresponding region on rice chromosome 6, allowing delimitation of the Rdg2a syntenic interval in rice to a 115 kbp stretch of sequence. Analysis of the rice sequence failed to reveal any genes with similarity to characterized resistance genes. Therefore, either the rice-barley synteny is disrupted in this region, or Rdg2a encodes a novel type of resistance protein.

Record 172 of 434 - AGRICOLA 1998-2004/09

AU: Hayashi,-K.; Hashimoto,-N.; Daigen,-M.; Ashikawa,-I.

TI: Development of PCR-based SNP markers for rice blast resistance genes at the Piz locus.

SO: Theoretical and applied genetics. 2004 May, v. 108, no. 7 p. 1212-1220.

AB: We assessed the utility of single-nucleotide polymorphisms (SNPs) and small insertion/deletion polymorphisms (InDels) as DNA markers in genetic analysis and breeding of rice. Toward this end, we surveyed SNPs and InDels in the chromosomal region containing the Piz and Piz-t rice blast resistance genes and developed PCR-based markers for typing the SNPs. Analysis of sequences from a blast-susceptible Japanese cultivar and two cultivars each containing one of these genes revealed that SNPs are abundant in the Piz and Piz-t regions (on average, one SNP every 248 bp), but the number of InDels was much lower. The dense distribution of SNPs facilitated the generation of SNP markers in the vicinity of the genes. For typing these SNPs, we used a modified allele-specific PCR method. Of the 49 candidate allele-specific markers, 33 unambiguously and reproducibly discriminated between the two alleles. We used the markers for mapping the Piz and Piz-t genes and evaluating the size of DNA segments introgressed from the Piz donor cultivar in Japanese near-isogenic lines containing Piz. Our findings suggest that, because of its ability to generate numerous markers within a target region and its simplicity in assaying genotypes, SNP genotyping with allele-specific PCR is a valuable tool for gene mapping, map-based cloning, and marker-assisted selection in crops, especially rice.

Record 173 of 434 - AGRICOLA 1998-2004/09

AU: Yamanaka,-S.; Nakamura,-I.; Watanabe,-K.N.; Sato,-Y.

TI: Identification of SNPs in the waxy gene among glutinous rice cultivars and their evolutionary significance during the domestication process of rice.

SO: Theoretical and applied genetics. 2004 May, v. 108, no. 7 p. 1200-1204.

AB: Common non-waxy (Wx) rice cultivars contain two different alleles at the waxy locus, designated Wx a and Wx b, which encode different levels of granule-bound starch synthases and are hence involved in the control of endosperm amylose content. The Wx a allele was predominant in non-waxy indica cultivars, whereas the Wx b allele was common to the non-waxy japonica variety. Recently, some of the molecular mechanisms underlying the differentiation of Wx a from Wx b have been characterized. One structural difference between these two alleles was shown to be due to alternative splicing caused by a single-base substitution (AGGT to AGTT) at a donor site of the first intron within the Wx gene. In the case of waxy (wx) rice, it was not possible to distinguish whether the each wx allele was derived from Wx a or Wx b alleles by phenotypic analysis. However, we succeeded in developing a derived cleaved amplified polymorphic sequence (dCAPS) marker for the detection of the one-base splicing mutation without the need for sequencing. A mismatch primer was used to generate a restriction site in the Wx a allele (AGGT) but not in the Wx b allele (AGTT). Three hundred fifty-three waxy rice strains that are widely found in Asia were then employed for analysis using this dCAPS marker. Our findings suggested that waxy rice strains have both Wx a- and Wx b-derived alleles, but that the Wx b-derived allele was predominant, and its distribution was independent of indica-japonica differentiation. The wild relatives of cultivated rice all possessed the AGGT allele. It was concluded that the waxy mutations, and the corresponding rice cultivation, originated from japonica during the evolution and domestication process of rice and was preferentially selected by most Asian peoples.

Record 174 of 434 - AGRICOLA 1998-2004/09

AU: Akagi,-H.; Nakamura,-A.; Yokozeki-Misono,-Y.; Inagaki,-A.; Takahashi,-H.; Mori,-K.; Fujimura,-T.

TI: Positional cloning of the rice Rf-1 gene, a restorer of BT-type cytoplasmic male sterility that encodes a mitochondria-targeting PPR protein.

SO: Theoretical and applied genetics. 2004 May, v. 108, no. 8 p. 1449-1457.

AB: The combination of cytoplasmic male sterility (CMS) in one parent and a restorer gene (Rf) to restore fertility in another are indispensable for the development of hybrid varieties. We have found a rice Rf-1 gene that restores BT-type CMS by applying a positional cloning strategy. Using linkage analysis in combination with 6,104 BC1F3 progeny derived from a cross between two near-isogenic lines (NILs) differing only at the Rf-1 locus, we delimited the Rf-1 gene to a 22.4-kb region in the rice genome. Duplicate open reading frames (Rf-1A and Rf-1B) with a pentatricopeptide (PPR) motif were found in this region. Since several insertions and/or deletions were found in the regions corresponding to both the Rf-1A and Rf-1B genes in the maintainer's allele, they may have lost their function. Rf-1A protein had a mitochondria-targeting signal, whereas Rf-1B did not. The Rf-1B gene encoded a shorter polypeptide that was determined by a premature stop codon. Based on the function of the Rf-1 gene, its product is expected to target mitochondria and may process the transcript from an atp6/orf79 region in the mitochondrial genome. Since the Rf-1A gene encodes a 791-amino acid protein with a signal targeting mitochondria and has 16 repeats of the PPR motif, we concluded that Rf-1A is the Rf-1 gene. Nine duplications of Rf-1A homologs were found around the Rf-1 locus in the Nipponbare genome. However, while some of them encoded proteins with the PPR motif, they do not restore BT-type CMS based on the lack of co-segregation with the restoration phenotype. These duplicates may have played diversified roles in RNA processing and/or recombination in mitochondria during the co-evolution of these genes and the mitochondrial genome.

Record 175 of 434 - AGRICOLA 1998-2004/09

AU: Kono,-Y.; Kojima,-A.; Nagai,-R.; Watanabe,-M.; Kawashima,-T.; Onizawa,-T.; Teraoka,-T.; Watanab,-M.; Koshino,-H.; Uzawa,-J.

TI: Antibacterial diterpenes and their fatty acid conjugates from rice leaves.

SO: Phytochemistry. 2004 May, v. 65, no. 9 p. 1291-1298.

AB: Six structurally oryzalide-related compounds, oryzadione (1), 2, 3, 4, 5 and 6, were isolated from a neutral fraction of the extract of healthy leaves using a bacterial leaf blight-resistant cultivar of a rice plant, "Norin-27", as a group of antimicrobial substances. Their structures were determined by spectroscopic studies to be kaurane analogues and kaurane analogues conjugated with fatty acids, i.e., 1: ent-15,16-epoxy-kauran-2,3-dione (enol form: ent-15,16-epoxy-2-hydroxy-kauran-1-en-3-one), 2: ent-15,16-epoxy-3b-hydroxy-kauran-2-one, 3: ent-15,16-epoxy-3-oxa-kauran-2-one, 4: ent-15,16-epoxy-3b-myristoyloxy-kauran-2-one, 5: ent-15,16-epoxy-3a-palmitoyloxy-kauran-2-one, and 6: ent-15,16-epoxy-2b-palmitoyloxy-kauran-2-one.

Record 176 of 434 - AGRICOLA 1998-2004/09

AU: Feng,-Y.W.; Yoshinaga,-I.; Shiratani,-E.; Hitomi,-T.; Hasebe,-H.

TI: Characteristics and behavior of nutrients in a paddy field area equipped with a recycling irrigation system.

SO: Agricultural water management. 2004 July 15, v. 68, issue 1 p. 47-60.

Record 177 of 434 - AGRICOLA 1998-2004/09

AU: Park,-S.Y.; Paik,-H.Y.; Skinner,-J.D.; Spindler,-A.A.; Park,-H.R.

TI: Nutrient intake of Korean-American, Korean, and American adolescents.

SO: Journal of the American Dietetic Association. 2004 Feb., v. 104, no. 2 p. 242-245.

AB: This study compared dietary intakes of Korean, Korean-American, and American adolescents. Data were collected by 24-hour recall method from 471 Korean and 134 Korean-American adolescents. Data for American adolescents were obtained from NHANES III. Korean Americans had the lowest energy and cholesterol intakes but a higher percentage of energy from fat compared with Koreans. Korean and Korean Americans had lower intakes of calcium, iron, and zinc but higher sodium intake than Americans. Intakes of energy, folate, calcium, and iron in all three groups were below the recommended intakes for American adolescents. Korean Americans consumed cooked rice and Kimchi less often, but cookies, sweets, and soda were consumed more frequently than Koreans. These results indicate that Korean-American adolescents' dietary profiles are midway between those typical in Korea vs the United States. Nutrition education must focus on the benefits and weaknesses of Korean and western diets and how to blend the two cultures for optimal nutrition.

Record 178 of 434 - AGRICOLA 1998-2004/09

AU: Rattner,-B.A.; McGowan,-P.C.; Golden,-N.H.; Hatfield,-J.S.; Toschik,-P.C.; Lukei,-R.F.-Jr.; Hale,-R.C.; Schmitz-Afonso,-I.; Rice,-C.P.

TI: Contaminant exposure and reproductive success of ospreys (Pandion haliaetus) nesting in Chesapeake Bay regions of concern.

SO: Archives of environmental contamination and toxicology. 2004 July, v. 47, no. 1 p. 126-140.

Record 179 of 434 - AGRICOLA 1998-2004/09

AU: Bao,-J.; Sun,-M.; Zhu,-L.; Corke,-H.

TI: Analysis of quantitative trait loci for some starch properties of rice (Oryza sativa L.): thermal properties, gel texture and swelling volume.

SO: Journal of cereal science. 2004 May, v. 39, no. 3 p. 379-385.

AB: To understand the genetic basis of gelatinization temperature (GT) , gel textural traits and flour swelling volume, quantitative trait loci (QTL) were mapped for these traits using a doubled haploid (DH) population derived from a cross between indica variety Zai-Ye-Qing 8 (ZYQ8) and japonica variety Jing-Xi 17 (JX17). The results indicated that the starch property parameters were continuously distributed among the DH lines, and some DH lines showed transgressive segregation for all the parameters. A total of 16 QTLs were identified for seven traits. A major QTL, the alk gene on chromosome 6 was significant for the three GT traits, onset temperature (To), peak temperature (Tp), and completion temperature (Tc). This locus could explain 49.4, 38.9, and 28.3% of the total variance, respectively, indicating that GT parameters were substantially controlled by the alk gene which has previously been identified for alkali spreading value (ASV). The additive effects of alk on To,Tp and Tc were from ZYQ8. Another two QTLs on chromosomes 1 and 7 were also identified for the three GT parameters, whose positive effects were contributed from JX17. Another QTL on chromosome 10 with the positive effects coming from ZYQ8 was significant only for Tc. However, the enthalpy (deltaH) of gelatinization was controlled by two minor QTLs on chromosomes 1 and 7. A major QTL, the Wx gene on chromosome 6 was identified for gel hardness and flour swelling volume which explained 58.8 and 36.6% of the total variances, respectively. Another two QTLs were also detected for flour swelling volume, one of which (qSV-7) could explain 21.4% of the total variance. However, gel cohesiveness was controlled by a major QTL located between alk and Wx on chromosome 6.

Record 180 of 434 - AGRICOLA 1998-2004/09

AU: Arunachalam,-N.; Samuel,-P.P.; Hiriyan,-J.; Thenmozhi,-V.;

Gajanana,-A.
TI: Japanese encephalitis in Kerala, south India: Can Mansonia (Diptera: Culicidae) play a supplemental role in transmission.
SO: Journal of medical entomology. 2004 May, v. 41, no. 3 p. 456-461.
AB: A 2-yr entomological study was carried out in Kerala, south India, to identify the mosquito vectors of Japanese encephalitis (JE) virus and to determine their seasonal abundance and infection. In total, 150,454 mosquitoes belonging to five genera and 18 species were collected from vegetation surrounding cattle sheds and pigsties in villages at dusk. Culex tritaeniorhynchus Giles (66.7%) was the most abundant species, with increases in numbers associated with rice cultivation. JE virus isolations were made from Cx. tritaeniorhynchus and Mansonia indiana Edwards. Based on high abundance and frequent JE virus infection, Cx. tritaeniorhynchus seems to be the most important vector, whereas Ma. indiana is probably a secondary vector.

Record 181 of 434 - AGRICOLA 1998-2004/09
AU: Wei,-W.; Kakizawa,-S.; Jung,-H.Y.; Suzuki,-S.; Tanaka,-M.; Nishigawa,-H.; Miyata,-S.; Oshima,-K.; Ugaki,-M.; Hibi,-T.
TI: An antibody against the SecA membrane protein of one phytoplasma reacts with those of phylogenetically different phytoplasmas.
SO: Phytopathology. 2004 July, v. 94, no. 7 p. 683-686.
AB: Antisera raised against phloem-limited phytoplasmas generally react only with the phytoplasma strain used to produce the antigen. There is a need for an antiserum that reacts with a variety of phytoplasmas. Here, we show that an antiserum raised against the SecA membrane protein of onion yellows phytoplasma, which belongs to the aster yellows 16S-group, detected eight phytoplasma strains from four distinct 16S-groups (aster yellows, western X, rice yellow dwarf, and elm yellows). In immunoblots, an approximately = 96-kDa SecA protein was detected in plants infected with each of the eight phytoplasmas. Immunohistochemical staining of thin sections prepared from infected plants was localized in phloem tissues. This antiserum should be useful in the detection and histopathological analysis of a wide range of phytoplasmas.

Record 182 of 434 - AGRICOLA 1998-2004/09
AU: Willocquet,-L.; Elazegui,-F.A.; Castilla,-N.; Fernandez,-L.; Fischer,-K.S.; Peng,-S.B.; Teng,-P.S.; Srivastava,-R.K.; Singh,-H. M.; Zhu,-D.
TI: Research priorities for rice pest management in tropical Asia: a simulation analysis of yield losses and management efficiencies.
SO: Phytopathology. 2004 July, v. 94, no. 7 p. 672-682.
AB: A simulation study was conducted to assess the current and prospective efficiency of rice pest management and develop research priorities for lowland production situations in tropical Asia. Simulation modeling with the RICEPEST model provided the flexibility required to address varying production situations and diverse pest profiles (bacterial leaf blight, sheath blight, brown spot, leaf blast, neck blast, sheath rot, white heads, dead hearts, brown plant-hoppers, insect defoliators, and weeds). Operational definitions for management efficacy (injury reduction) and management efficiency (yield gain) were developed. This approach enabled the modeling of scenarios pertaining to different pest management strategies within the agroecological

contexts of rice production and their associated pest injuries. Rice pests could be classified into two broad research priority-setting categories with respect to simulated yield losses and management efficiencies. One group, including weeds, sheath blight, and brown spot, consists of pests for which effective pest management tools need to be developed. The second group consists of leaf blast, neck blast, bacterial leaf blight, and brown plant-hoppers, for which the efficiency of current management methods is to be maintained. Simulated yield losses in future production situations indicated that a new type of rice plant with high-harvest index and high-biomass production ("New Plant Type") was more vulnerable to pests than hybrid rice. Simulations also indicated that the impact of deployment of host resistance (e.g., through genetic engineering) was much larger when targeted against sheath blight than when targeted against stem borers. Simulated yield losses for combinations of production situations and injury profiles that dominate current lowland rice production in tropical Asia ranged from 140 to 230 g m-2. For these combinations, the simulated efficiency of current pest management methods, expressed in terms of relative yield gains, ranged from 0.38 to 0.74. Overall, the analyses indicated that 120 to 200 x 10(-6) tons of grain yield are lost yearly to pests over the 87 x 10(-6) ha of lowland rice in tropical Asia. This also amounts to the potential gain that future pest management strategies could achieve, if deployed.

Record 183 of 434 - AGRICOLA 1998-2004/09

AU: Pandey,-R.; Agarwal,-R.M.; Jeevaratnam,-K.; Sharma,-G.L.

TI: Osmotic stress-induced alterations in rice (Oryza sativa L.) and recovery on stress release.

SO: Plant growth regulation. 2004 Jan., v. 42, no. 1 p. 79-87.

AB: In laboratory experiments, rice plants cv 'Kranti' were stressed osmotically using polyethylene glycol '6000' and mannitol, whereas, in pots, plants were drought stressed by withholding water supply. Both osmotic and drought stress influenced different aspects of nitrogen metabolism, resulting in a decline in the activities of aspartate aminotransferase, alanine amino-transferase and an increase in protease activity accompanied by increased free proline and alterations in other amino acid content. An influence on alpha-amylase activity, total free sugars and starch contents was also observed, reflecting the impact of water stress on interconversion between starch and simpler sugars. Effects of polyethylene glycol '6000' as an osmotic agent were more consistent than those of mannitol during short-term (18 h) stress imposition, probably because of slight absorption of mannitol. Since the recovery for most of the parameters was substantial on release of stress, one can infer that the duration and magnitude of stress applied in the present experiments did not cause major permanent alterations in the rice cultivar 'Kranti.' The significant basic information gathered in such experiments, particularly on recovery potential, can be utilised for varietal screening.

Record 184 of 434 - AGRICOLA 1998-2004/09

AU: Tucker,-S.L.; Thornton,-C.R.; Tasker,-K.; Jacob,-C.; Giles,-G.; Egan,-M.; Talbot,-N.J.

TI: A fungal metallothionein is required for pathogenicity of

Magnaporthe grisea.
SO: Plant cell. 2004 June, v. 16, no. 6 p. 1575-1588.
AB: The causal agent of rice blast disease, the ascomycete fungus Magnaporthe grisea, infects rice (Oryza sativa) plants by means of specialized infection structures called appressoria, which are formed on the leaf surface and mechanically rupture the cuticle. We have identified a gene, Magnaporthe metallothionein 1 (MMT1), which is highly expressed throughout growth and development by M. grisea and encodes an unusual 22-amino acid metallothionein-like protein containing only six Cys residues. The MMT1-encoded protein shows a very high affinity for zinc and can act as a powerful antioxidant. Targeted gene disruption of MMT1 produced mutants that show accelerated hyphal growth rates and poor sporulation but had no effect on metal tolerance. Mmt1 mutants are incapable of causing plant disease because of an inability to bring about appressorium-mediated cuticle penetration. Mmt1 appears to be distributed in the inner side of the cell wall of the fungus. These findings indicate that Mmt1-like metallothioneins may play a novel role in fungal cell wall biochemistry that is required for fungal virulence.

Record 185 of 434 - AGRICOLA 1998-2004/09
AU: Soundararajan,-S.; Jedd,-G.; Li,-X.; Ramos-Pamplona,-M.; Chua,-N. H.; Naqvi,-N.I.
TI: Woronin body function in Magnaporthe grisea is essential for efficient pathogenesis and for survival during nitrogen starvation stress.
SO: Plant cell. 2004 June, v. 16, no. 6 p. 1564-1574.
AB: The Woronin body is a peroxisome-derived dense-core vesicle that is specific to several genera of filamentous ascomycetes, where it has been shown to seal septal pores in response to cellular damage. The Hexagonal peroxisome (Hex1) protein was recently identified as a major constituent of the Woronin body and shown to be responsible for self-assembly of the dense core of this organelle. Using a mutation in the Magnaporthe grisea HEX1 ortholog, we define a dual and essential function for Woronin bodies during the pathogenic phase of the rice blast fungus. We show that the Woronin body is initially required for proper development and function of appressoria (infection structures) and subsequently necessary for survival of infectious fungal hyphae during invasive growth and host colonization. Fungal mycelia lacking HEX1 function were unable to survive nitrogen starvation in vitro, suggesting that in planta growth defects are a consequence of the mutant's inability to cope with nutritional stress. Thus, Woronin body function provides the blast fungus with an important defense against the antagonistic and nutrient-limiting environment encountered within the host plant.

Record 186 of 434 - AGRICOLA 1998-2004/09
AU: James,-D.; Schmidt,-A.M.
TI: Use of an intron region of a chloroplast tRNA gene (trnL) as a target for PCR identification of specific food crops including sources of potential allergens.
SO: Food research international. 2004, v. 37, no. 4 p. 395-402.
AB: Simple but reliable PCR techniques were developed for the detection and identification of several food crops, including crops known to contain allergens. A single pair of

oligonucleotide primers (PL-1C and PL-2D), that target the trnL region of the chloroplast tRNA gene in polymerase chain reaction (PCR) analysis, was used to amplify crop specific fragments. The specific DNA fragments were of the following sizes; 387 bp (canola), 532 bp (corn), 571 bp (potato), 584 bp (soybean), 615 bp (white and red rice), 642 bp (peanut), and 662 bp (wheat). Each amplified fragment was reliably identified using 3% agarose gel electrophoresis. The amplified fragments were cloned, sequenced, and a variable region was used to design specific sense primers for identity confirmation of some selected crops. When combined with the antisense primer PL-2D, specific fragments of 403, 397, 343, and 304 bp were amplified for peanut, wheat, soybean, and rice, respectively. These are common crops known to contain allergens. The PCR techniques described may be easily adapted for the detection of other crops and may be modified for use in multiplex PCR detection techniques, or micro-/macro-array analysis.

Record 187 of 434 - AGRICOLA 1998-2004/09
AU: Sharma,-R.; Komatsu,-S.; Noda,-H.
TI: Proteomic analysis of brown planthopper: application to the study of carbamate toxicity.
SO: Insect biochemistry and molecular biology. 2004 May, v. 34, no. 5 p. 425-432.
AB: Toxicity to o-sec-butylphenyl methylcarbamate compound (BPMC) was analyzed in the rice brown planthopper, Nilaparvata lugens, using a differential proteomics approach of identifying proteins on two dimensional-polyacrylamide gel electrophoresis (2D-PAGE). Proteome analysis from BPMC-treated brown planthopper resulted in the modulation of 22 proteins at the expression level as compared to control samples on coomassie brilliant blue (CBB) stained gels. Out of total 22 proteins, 10 proteins showed elevated expression, eight proteins showed decreased expression and four proteins showed specific expression after insecticide treatment. The N-terminal sequences of seven out of 22 proteins were determined by a gas-phase protein sequencer. The internal amino acid sequences of the 15 proteins were determined by the sequence analyses of peptides obtained by Cleveland peptide mapping method and were compared with those of the known proteins available in public databases and the EST database of the brown planthopper in our laboratory to understand the nature of the proteins. Sequence analyses revealed that the expression of putative serine/threonine protein kinase, paramyosin, HSP 90, beta-tubulin, calreticulin, ATP synthase, actin and tropomyosin was elevated, and that of beta-mitochondrial processing peptidase, dihydrolipoamide dehydrogenase, enolase and acyl-coA dehydrogenase was reduced due to the exposure of BPMC. The differential expression of these proteins reflects the overall change in cellular structure and metabolism after insecticide treatment.

Record 188 of 434 - AGRICOLA 1998-2004/09
AU: Lupwayi,-N.Z.; Harker,-K.N.; Clayton,-G.W.; Turkington,-T.K.; Rice,-W.A.; O'Donovan,-J.T.
TI: Soil microbial biomass and diversity after herbicide application.
SO: Canadian journal of plant science = Revue Canadienne de phytotechnie. 2004 Apr., v. 84, no. 2 p. 677-685.

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Record 189 of 434 - AGRICOLA 1998-2004/09
AU:   Terada,-R.; Asao,-H.; Iida,-S.
TI:   A large-scale Agrobacterium-mediated transformation procedure
      with a strong positive-negative selection for gene targeting in
      rice (Oryza sativa L.).
SO:   Plant cell reports. 2004 Apr., v. 22, no. 9 p. 653-659.
AB:   A large-scale transformation procedure handling an adequate
      number of stable transformants with highly efficient
      positive-negative selection is a necessary prerequisite to
      successful gene targeting by homologous recombination, as the
      integration of a transgene by somatic homologous recombination in
      higher plants has been reported to be 10(-3) to 10(-5) compared
      with random integration by non-homologous end joining. We
      established an efficient and large-scale Agrobacterium-mediated
      rice transformation protocol that generated around 10(3) stable
      transformants routinely from 150 seeds and a strong
      positive-negative selection procedure that resulted in survivors
      at 10(-2) using the gene for diphtheria toxin A fragment as a
      negative marker. The established transformation procedure
      provides a basis for efficient gene targeting in rice.
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Record 190 of 434 - AGRICOLA 1998-2004/09
AU:   Luo,-H.; Hu,-Q.; Nelson,-K.; Longo,-C.; Kausch,-A.P.; Chandlee,-J.
      M.; Wipff,-J.K.; Fricker,-C.R.
TI:   Agrobacterium tumefaciens-mediated creeping bentgrass (Agrostis
      stolonifera L.) transformation using phosphinothricin selection
      results in a high frequency of single-copy transgene integration.
SO:   Plant cell reports. 2004 Apr., v. 22, no. 9 p. 645-652.
AB:   Genetic transformation of creeping bentgrass mediated by
      Agrobacterium tumefaciens has been achieved. Embryogenic callus
      initiated from seeds (cv. Penn-A-4) was infected with an A.
      tumefaciens strain (LBA4404) harboring a super-binary vector that
      contained an herbicide-resistant bar gene driven either by the
      CaMV 35S promoter or a rice ubiquitin promoter. Plants were
      regenerated from 219 independent transformation events. The
      overall stable transformation efficiency ranged from 18% to 45%.
      Southern blot and genetic analysis confirmed transgene
      integration in the creeping bentgrass genome and normal
      transmission and stable expression of the transgene in the T1
      generation. All independent transformation events carried one to
      three copies of the transgene, and a majority (60-65%) contained
      only a single copy of the foreign gene with no apparent
      rearrangements. We report here the successful use of
      Agrobacterium for the large-scale production of transgenic
      creeping bentgrass plants with a high frequency of a single-copy
      transgene insertion that exhibit stable inheritance patterns.
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Record 191 of 434 - AGRICOLA 1998-2004/09
AU:   Liu,-Q.; Feng,-Y.; Zhao,-X.; Dong,-H.; Xue,-Q.
TI:   Synonymous codon usage bias in Oryza sativa.
SO:   Plant science. 2004 July, v. 167, issue 1 p. 101-105.
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Record 192 of 434 - AGRICOLA 1998-2004/09
AU:   Yao,-S.G.; Mushika,-J.; Taketa,-S.; Ichii,-M.
TI:   The short-root mutation srt5 defines a sugar-mediated root growth
      in rice (Oryza sativa L.).
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SO: Plant science. 2004 July, v. 167, issue 1 p. 49-54.

Record 193 of 434 - AGRICOLA 1998-2004/09

AU: Zhu,-M.; Wang,-L.; Pan,-Q.

TI: Identification and characterization of a new blast resistance gene located on rice chromosome 1 through linkage and differential analyses.

SO: Phytopathology. 2004 May, v. 94, no. 5 p. 515-519.

AB: The Chinese native cv. Q14 expresses a high level of resistance to many isolates of Pyricularia grisea collected from Japan, Thailand, and China. Q14 was crossed to an indica-susceptible cultivar, Q61. To rapidly determine the chromosomal location of the major resistance gene present in the cultivar, a linkage analysis using microsatellite markers was performed in the F(2) population segregating 3R:1S (resistant/susceptible) through bulked-segregant analysis (BSA) in combination with recessive-class analysis (RCA). A total of 189 microsatellite markers selected from each chromosome equally (with approximately = 10 centimorgans) were tested with the BSA approach. Only two markers, RM151 and RM259, located on chromosome 1 showed positive and negative polymorphisms, respectively, for a resistance gene segregating in the population. To confirm the polymorphic markers, a total of 155 viable susceptible individuals were tested with the RCA approach. The markers RM151 and RM259 were found to link to the resistance gene with recombination frequencies of 11.9 « 2.8% and 9.7 « 8.0%, respectively. For further characterization of the resistance gene, 3 resistance genes mapped on chromosome 1, as well as 15 major resistance genes that might be employed in the breeding program, were selected for differential tests with 85 Chinese isolates. The resistance gene identified in this research conveys reactions distinct from those conditioned by the 18 resistance genes. This new resistance gene tentatively was designated Pi27(t).

Record 194 of 434 - AGRICOLA 1998-2004/09

AU: Tsuge,-S.; Ochiai,-H.; Inoue,-Y.; Oku,-T.; Tsuno,-K.; Kaku,-H.; Kubo,-Y.

TI: Involvement of phosphoglucose isomerase in pathogenicity of Xanthomonas oryzae pv. oryzae.

SO: Phytopathology. 2004 May, v. 94, no. 5 p. 478-483.

AB: Xanthomonas oryzae pv. oryzae, the causal agent of bacterial leaf blight of rice, was subjected to transposon mutagenesis to generate mutants defective in pathogenicity. A novel mutant 74M913 was attenuated in virulence but retained its ability to cause the hypersensitive response in leaf blight-resistant rice and tomato. Cloning and sequence analysis revealed that the transposon in 74M913 was inserted in a gene homologous to the phosphoglucose isomerase (pgi) gene of X. axonopodis pv. citri. Growth of the mutant in a synthetic medium containing fructose or xylose as a sole carbohydrate source was much reduced, indicating the transposon disrupted pgi function. The interaction between expression of pgi and hypersensitive response and pathogenicity (hrp) genes was investigated because we had demonstrated previously that expression of hrp genes of X. oryzae pv. oryzae is induced in a synthetic medium containing xylose. However, pgi and the hrp gene (hrcU) were expressed independently. This study suggests that PGI is involved in pathogenicity of X. oryzae pv.

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      oryzae.
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Record 195 of 434 - AGRICOLA 1998-2004/09
AU:   Zhang,-Z.H.; Li,-P.; Wang,-L.X.; Hu,-Z.L.; Zhu,-L.H.; Zhu,-Y.G.
TI:   Genetic dissection of the relationships of biomass production and
      partitioning with yield and yield related traits in rice.
SO:   Plant science. 2004 July, v. 167, issue 1 p. 1-8.
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Record 196 of 434 - AGRICOLA 1998-2004/09
AU:   Hirotsu,-N.; Makino,-A.; Ushio,-A.; Mae,-T.
TI:   Changes in the thermal dissipation and the electron flow in the
      water-water cycle in rice grown under conditions of
      physiologically low temperature.
SO:   Plant and cell physiology. 2004 May, v. 45, no. 5 p. 635-644.
AB:   Effects of low temperature on chlorophyll (Chl) fluorescence, gas
      exchange rate, the amounts of xanthophyll cycle pigments (Xp) and
      the activities of several antioxidant enzymes were examined in
      the 8th leaf of two rice (Oryza sativa L.) cultivars (japonica
      and indica types) and rbcS antisense rice. All plants were grown
      hydroponically at 25/20ÀC (day/night), and then exposed to 20/
      17ÀC (day/night) after full expansion of the 8th leaf, or exposed
      to either 20/17ÀC or 15/13ÀC (day/night) during the expansion of
      the 8th leaf. All plants exposed to low temperatures showed a
      decrease in CO2 assimilation rate without photoinhibition, and
      increases in the fraction of thermal dissipation in PSII, and in
      the electron flux through the water-water cycle (WWC) were
      observed. Although the increase of thermal dissipation was
      associated with increases in the ratio of carotenoids to Chl, the
      ratio of Xp to carotenoids and the de-epoxidation state of Xp,
      the increase of the electron flux of WWC was not accompanied by
      an increase in the activities of antioxidant enzymes. Such
      photoprotective responses did not differ between during and after
      full expansion of the leaf, and did not differ among the three
      genotypes. Quantitative analyses on the dissipation of excess
      light energy showed that thermal dissipation makes a larger
      contribution than WWC. Thus, although low temperature led to a
      decrease in CO2 assimilation, rice potentially coped with the
      excess light energy by increasing the thermal dissipation and the
      electron flux of WWC under low temperature irrespective of leaf
      development and genotypes.
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Record 197 of 434 - AGRICOLA 1998-2004/09
AU:   Jiang,-S.Y.; Ramachandran,-S.
TI:   Identification and molecular characterization of myosin gene
      family in Oryza sativa genome.
SO:   Plant and cell physiology. 2004 May, v. 45, no. 5 p. 590-599.
AB:   Myosins play an important role in various developmental processes
      in plants. We have identified 14 myosin genes in rice (Oryza
      sativa cv. Nipponbare) genome using sequence information
      available in public databases. Phylogenetic analysis of these
      sequences with other plant and non-plant myosins revealed that
      two of the predicted sequences belonged to class VIII and the
      others to class XI. All of these genes were distributed on seven
      chromosomes in the rice genome. Domain searches on these
      sequences indicated that a typical rice myosin consisted of
      Myosin_N, head domain, neck (IQ motifs), tail, and dilute (DIL)
      domain. Based on the sequence information obtained from predicted
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myosins, we isolated and sequenced two full-length cDNAs, OsMyoVIIIA and OsMyoXIE, representing each of the two classes of myosins. These two cDNAs isolated from different organs existed in isoforms due to differential splicing and showed minor differences from the predicted myosin in exon organization. Out of 14 myosin genes 11 were expressed in three major organs: leaves, panicles, and roots, among which three myosins exhibited different expression levels. On the other hand, three of the total myosin sequences showed organ-specific expression. The existence of different myosin genes and their isoforms in different organs or tissues indicates the diversity of myosin functions in rice.

Record 198 of 434 - AGRICOLA 1998-2004/09

AU: Hashimoto,-M.; Kisseleva,-L.; Sawa,-S.; Furukawa,-T.; Komatsu,-S.; Koshiba,-T.

TI: A novel rice PR10 protein, RSOsPR10, specifically induced in roots by biotic and abiotic stresses, possibly via the jasmonic acid signaling pathway.

SO: Plant and cell physiology. 2004 May, v. 45, no. 5 p. 550-559.

AB: Plant roots have important roles not only in absorption of water and nutrients, but also in stress tolerance such as desiccation, salt, and low temperature. We have investigated stress-response proteins from rice roots using 2-dimensional polyacrylamide-gel electrophoresis and found a rice protein, RO-292, which was induced specifically in roots when 2-week-old rice seedlings were subjected to salt and drought stress. The full-length RO-292 cDNA was cloned, and was determined to encode a protein of 160 amino acid residues (16.9 kDa, pI 4.74). The deduced amino acid sequence showed high similarity to known rice PR10 proteins, OsPR10a/PBZ1 and OsPR10b. RO-292 mRNA accumulated rapidly upon drought, NaCl, jasmonic acid and probenazole, but not by exposure to low temperature or by abscisic acid and salicylic acid. The RO-292 gene was also up-regulated by infection with rice blast fungus. Interestingly, induction was observed almost exclusively in roots, thus we named the gene RSOsPR10 (root specific rice PR10). The present results indicate that RSOsPR10 is a novel rice PR10 protein, which is rapidly induced in roots by salt, drought stresses and blast fungus infection possibly through activation of the jasmonic acid signaling pathway, but not the abscisic acid and salicylic acid signaling pathway.

Record 199 of 434 - AGRICOLA 1998-2004/09

AU: Hanba,-Y.T.; Shibasaka,-M.; Hayashi,-Y.; Hayakawa,-T.; Kasamo,-K.; Terashima,-I.; Katsuhara,-M.

TI: Overexpression of the barley aquaporin HvPIP2;1 increases internal CO2 conductance and CO2 assimilation in the leaves of transgenic rice plants.

SO: Plant and cell physiology. 2004 May, v. 45, no. 5 p. 521-529.

AB: The internal conductance for CO2 diffusion (gi) and CO2 assimilation rate were measured and the related anatomical characteristics were investigated in transgenic rice leaves that overexpressed barley aquaporin HvPIP2;1. This study was performed to test the hypothesis that aquaporin facilitates CO2 diffusion within leaves. The gi value was estimated for intact leaves by concurrent measurements of gas exchange and carbon isotope ratio. The leaves of the transgenic rice plants that expressed the highest levels of Aq-anti-HvPIP2;1 showed a 40% increase in gi as compared to gi in the leaves of wild-type rice plants. The increase in gi was accompanied by a 14% increase in CO2 assimilation rate and a 27% increase in stomatal conductance (gs). The transgenic plants that had low levels of Aq-anti-HvPIP2;1 showed decreases in gi and CO2 assimilation rate. In the plants with high levels of Aq-anti-HvPIP2;1, mesophyll cell size decreased and the cell walls of the epidermis and mesophyll cells thickened, indicating that the leaves had become xeromorphic. Although such anatomical changes could partially offset the increase in gi by the aquaporin, the increase in aquaporin content overcame such adverse effects.

Record 200 of 434 - AGRICOLA 1998-2004/09
AU: Zhang,-F.; Shen,-J.; Li,-L.; Liu,-X.
TI: An overview of rhizosphere processes related with plant nutrition in major cropping systems in China.
SO: Plant and soil. 2004 Mar., v. 260, no. 1-2 p. 89-99.