Topik : BIOTEKNOLOGI

1. Title:Tomorrow's agriculture: incentives, institutions, infrastructure and innovations. XXIV Conference of the International Association of Agricultural Economists held in Berlin, Germany 13-18 August, 2000
View Article: Agricultural Economics. 2001. 25 (2/3). 137-409
CD Volume:368
Print Article: Pages: 137-409
Author(s):Colman D
Author Affiliation:School of Economic Studies, University of Manchester, Manchester M13 9PL, UK
Document Editor:Colman-D
Conference Title:Tomorrow's agriculture: incentives, institutions, infrastructure and innovations. XXIV Conference of the International Association of Agricultural Economists held in Berlin, Germany 13-18 August, 2000
Language:English
Abstract:This issue presents a selection of 22 contributed papers and 1 plenary paper from the International Association of Agricultural Economists' conference entitled "Tomorrow's Agriculture: Incentives, Institutions, Infrastructure and Innovations". A theme joining many of the papers is the measurement of research returns, productivity and efficiency change. Other topics covered in this collection are: the analysis of market efficiency and price behaviour; the economics of reducing insecticide use; biotechnology; agricultural development; food security; and the Common Agricultural Policy
Descriptors:agricultural-development. agricultural-production. agricultural-research. biotechnology. CAP. economic-analysis. efficiency. food-security. green-revolution. insecticides. markets. prices. productivity. returns
Subject Codes:AA500. EE110. EE116. EE120. EE130. HH405. WW000
Supplementary Info:many ref
ISSN:0169-5150
Year:2001
Journal Title:Agricultural Economics
Copyright:Copyright CAB International

2. Title:An ex ante economic and policy analysis of research on genetic resistance to livestock disease: trypanosomosis in Africa
View Article: Agricultural Economics. 2001. 25 (2/3). 153-163
CD Volume:368
Print Article: Pages: 153-163
Author(s):Falconi C A Omamo S W d'Ieteren G Iraqi F
Author Affiliation:Inter-American Bank, 1300 New York Avenue NW, Washington, DC 20577, USA
Document Editor:Colman-D
Conference Title:Tomorrow's agriculture: incentives, institutions, infrastructure and innovations. XXIV Conference of the International Association of Agricultural Economists held in Berlin, Germany 13-18 August, 2000
Language:English
Abstract:This paper undertakes an ex ante economic analysis of research on how resistance to trypanosomiasis, a dominant livestock disease in Africa, can be maintained and enhanced while retaining and reinforcing characteristics of economic importance to farmers, and on how 'trypanotolerance' can be imparted to susceptible animals while retaining their other important traits. The results indicate that

potential benefits to research (historically field-based but increasingly biotechnology-driven) range from two to nine times potential costs and that the internal rate of return on investments can be six times the real interest rate. Field-based research, while exhibiting lower potential benefits on aggregate than does biotechnology research, is also less costly and, because of its more immediate payback, has higher internal rates of return. Returns to biotechnology research hinge on close links with field-based research and on strategic but relatively small incremental human and capital investments. The results also suggest that further research is needed to consistently identify and track the impacts of alternative intellectual property rights options on the levels and distributions of biotechnology research benefits
Descriptors:agricultural-research. animal-diseases. biotechnology. disease-resistance. economic-analysis. intellectual-property-rights. livestock. research-policy. returns. trypanosomiasis
Geographic Locator:Africa
Organism Descriptors:Trypanosoma. cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Trypanosomatidae. Kinetoplastida. Sarcomastigophora. Protozoa. invertebrates. animals
Subject Codes:AA500. EE110. EE117. HH600. LL822. WW000
Supplementary Info:29 ref
ISSN:0169-5150
Year:2001
Journal Title:Agricultural Economics
Copyright:Copyright CAB International

3. Title:A prospective evaluation of biotechnology in semi-subsistence agriculture
View Article: Agricultural Economics. 2001. 25 (2/3). 165-175
CD Volume:368
Print Article: Pages: 165-175
Author(s):Qaim M
Author Affiliation:Center for Development Research (ZEF), Bonn, Germany
Document Editor:Colman-D
Conference Title:Tomorrow's agriculture: incentives, institutions, infrastructure and innovations. XXIV Conference of the International Association of Agricultural Economists held in Berlin, Germany 13-18 August, 2000
Language:English
Abstract:This paper analyses ex ante the economic implications of transgenic virus- and weevil-resistant sweet potatoes in Kenya. These technologies are being developed within international projects, involving public and private organizations. It is expected that the resistant varieties will significantly reduce the crop losses in farmers' fields. Model calculations show that both innovations are likely to bring about substantial growth in economic surplus. The projected annual gross benefit is US$5.4 million for virus resistance and US$9.9 million for weevil resistance. Due to the semi-subsistence nature of sweet potato, the producing households will be the main beneficiaries. However, market consumers will also capture about one-fourth of the aggregate welfare gains. The high profitability of the projects is confirmed by significantly positive returns on research investments. The examples demonstrate the viability of successful research partnerships between the public and private sectors. As most of the basic biotechnology tools available to date are patented by private companies in the North, which often do not have sufficient market incentives to develop end-technologies for the South, more

interactions of this kind are required from a development policy perspective. Working with typical semi-subsistence crops is particularly appealing because it immediately targets the poor and avoids conflicts with the private sector's commercial interests
Descriptors:agricultural-research. biotechnology. economic-evaluation. improved-varieties. returns. sweet-potatoes. transgenic-plants. varietal-resistance. welfare-economics
Geographic Locator:Kenya
Organism Descriptors:Ipomoea-batatas. plants
Supplemental Descriptors:Ipomoea. Convolvulaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. East-Africa. Africa-South-of-Sahara. Africa. Developing-Countries. ACP-Countries. Commonwealth-of-Nations. Anglophone-Africa
Subject Codes:AA500. EE110. FF005. HH600. WW000. FF020
Supplementary Info:17 ref
ISSN:0169-5150
Year:2001
Journal Title:Agricultural Economics

4. Title:Modeling an irrigation management strategy for minimizing the leaching of atrazine
View Article: Agricultural Water Management. 2001. 48 (3). 225-238
CD Volume:354
Print Article: Pages: 225-238
Author(s):Asare D K Sammis T W Smeal D Zhang H Sitze D O
Author Affiliation:Department of Plant and Soil Sciences, Biotechnology and Nuclear Agriculture Research Institute, Ghana Atomic Energy Commission, Box LG 80 Legon-Accra, Ghana
Language:English
Abstract:Possible contamination of water resources by applied pesticides (including insecticides and herbicides) is a problem currently confronting irrigated agricultural production. Best management practices have to be adopted to minimize pesticide transport and leaching under irrigated conditions. A field capacity/mixing-cell model (IRRSCHM) and a model that uses Richard's equation and the convection-dispersion equation to describe water and contaminant dynamics in soils (LEACHP) were used to assess the leaching of atrazine (a herbicide) under maize receiving different levels of early-season irrigation at a site in New Mexico, USA. The early-season irrigation levels were 11.1, 16.8, 23.3, and 28.8 cm out of corresponding seasonal irrigation levels of 31.2, 39.6, 45.5, and 53.1 cm. The objectives were to (a) use a modelling approach to evaluate water management effects on atrazine leaching, and (b) assess the feasibility of using IRRSCHM and LEACHP to guide irrigation for minimizing atrazine leaching. IRRSCHM and LEACHP simulations deviated from the measured atrazine profile, but both models predicted reasonably well the progression in atrazine leaching with increasing water application. Additionally, atrazine pulses predicted by IRRSCHM were ahead of those by LEACHP but lagged behind those observed under the different irrigation levels. Similarly, both models underestimated atrazine leaching, with IRRSCHM leaching estimates being closer to the observed than the LEACHP estimates. For example, the atrazine profile's centre of mass position at 143 days after application, ranged from 34.2 to 49.4 cm for IRRSCHM, 23.8 to 34.7 cm for LEACHP, and 40.6 to 60.9 cm for the measured atrazine profile under irrigation levels that ranged from 31.2 to 53.1 cm of water. Based on accurate predictions of the trends in atrazine leaching in relation to different irrigation levels, IRRSCHM and LEACHP could be

used for preliminary assessment of the likely amount of atrazine leaching, resulting from targeted irrigation management strategies
Descriptors:atrazine. irrigation. leaching. maize. mathematical-models. simulation. water-management
Organism Descriptors:Zea-mays
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:JJ200. JJ800. PP200. HH430
Supplementary Info:23 ref
ISSN:0378-3774
Year:2001
Journal Title:Agricultural Water Management
Copyright:Copyright CAB International

5. Title:Aluminium toxicity in plants: a review
View Article: Agronomie. 2001. 21 (1). 3-21
CD Volume:375
Print Article: Pages: 3-21
Author(s):Rout G R Samantaray S Das P
Author Affiliation:Plant Biotechnology Division, Regional Plant Resource Centre, Bhubaneswar 751 015, Orissa, India
Language:English
Language of Summary:french
Abstract:Aluminium toxicity and problems concerning tolerance and ecological performance are discussed briefly. Differential tolerance of plant genotypes to aluminium stress is a more promising approach to increase understanding of aluminium tolerance in plants. Induction of Al tolerance and its characterization are also reviewed. The cytogenetic effects of aluminium on plants are discussed in depth. Efforts have been made to compare the relative sensitivity of various plant species including micro- and macro-flora to aluminium, and uptake and transport of aluminium are taken into account with phytotoxicity and their interactions with nutrients. Present knowledge concerning the physiology and biochemistry of aluminium with regard to phytotoxicity is discussed and offers some approaches for increasing Al tolerance. This review highlights the complexity of toxicity mechanisms of trace elements
Descriptors:aluminium. metal-tolerance. mineral-uptake. reviews. stress
Organism Descriptors:plants
Subject Codes:FF020. FF900. FF061
Supplementary Info:203 ref
ISSN:0249-5627
Year:2001
Journal Title:Agronomie
Copyright:Copyright CAB International

6. Title:Effects of inoculation with Azospirillum brasilense on chickpeas (Cicer arietinum) and faba beans (Vicia faba) under different growth conditions
View Article: Agronomie. 2001. 21 (6/7). 553-560
CD Volume:375
Print Article: Pages: 553-560
Author(s):Hamaoui B Abbadi J M Burdman S Adnan Rashid Sarig S Okon Y
Author Affiliation:Department of Plant Pathology and Microbiology, Otto Warburg Center for Agricultural Biotechnology, Faculty of Agricultural, Food and Environmental Quality Sciences, The Hebrew University of Jerusalem, Rehovot 76100, Israel
Language:English
Language of Summary:french

Abstract:The effects of the inoculation of chickpeas (Cicer arietinum) and faba beans (Vicia faba) with Azospirillum brasilense strain Cd were studied under different growth conditions. In greenhouse experiments with both legumes, inoculation with A. brasilense significantly enhanced nodulation by native rhizobia and improved root and shoot development, when compared with non-inoculated controls. Moreover, the bacterial treatment was shown to significantly reduce the negative effects on plant growth caused by irrigation with saline water. In field experiments, inoculation of chickpeas with A. brasilense peat-based inoculants also resulted in a significant increase in nodulation, root and shoot growth, and crop yield as compared with non-inoculated controls
Descriptors:chickpeas. crop-yield. faba-beans. growth. inoculation. nodulation. peat. roots. saline-water. shoots. soil-bacteria
Organism Descriptors:Azospirillum-brasilense. Cicer-arietinum. Vicia-faba
Supplemental Descriptors:Azospirillum. Rhodospirillaceae. Gracilicutes. bacteria. prokaryotes. Cicer. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Vicia
Subject Codes:FF003. FF060. FF100. JJ100
Supplementary Info:26 ref
ISSN:0249-5627
Year:2001
Journal Title:Agronomie

7. Title:The IAM-BRAIN and important notes
View Article: AMA, Agricultural Mechanization in Asia, Africa and Latin America. 2001. 32 (1). 75-82
CD Volume:356
Print Article: Pages: 75-82
Author(s):Nagasawa N Morishita A
Author Affiliation:Planning Department, Institute of Agricultural Machinery, Bio-oriented Technology Research Advancement Institution, 1-40-2 Nisshin Omiya, Saitama, Japan
Language:English
Abstract:In this article, the Japanese Institute of Agricultural Machinery (IAM)-BRAIN (Bio-oriented Technology Research Advancement Institution) and its activities on research and testing are introduced
Descriptors:biotechnology. farm-machinery. government-organizations. research. testing
Geographic Locator:Japan
Supplemental Descriptors:East-Asia. Asia. Developed-Countries. OECD-Countries
Subject Codes:DD100. NN400. AA500. WW000
Supplementary Info:6 ref
ISSN:0084-5841
Year:2001
Journal Title:AMA, Agricultural Mechanization in Asia, Africa and Latin America

8. Title:Dynamic Supply Response and Welfare Effects of Technological Change on Perennial Crops: The Case of Cocoa in Malaysia
View Article: American Journal of Agricultural Economics. 83 (2) 2001. 272-85
CD Volume:355
Print Article: Pages: 272-285
Author(s):Gotsch N Burger K
Author Affiliation:Swiss Federal Institute of Technology. Econ & Social Institute, Free U Amsterdam
Language:English

Abstract:Modern biotechnology will generate crops with higher yields and enhanced resistance to pests and diseases. In the case of perennial crops, the age composition of the present stand, the farmers' willingness to invest, and the yield profiles of old and new trees determine the speed of adoption of the new technology and the timing of the effects on supply and demand conditions. We adapt conventional welfare measures to account for these factors in the assessment of research induced supply shifts. The application to cocoa in Malaysia shows that consumers and adopting producers gain and nonadopters lose. Overall, 72% of the welfare gains go to the consumers
Descriptors:Economic Development: Agriculture; Natural Resources; Environment; Other Primary Products. Agriculture: Aggregate Supply and Demand Analysis; Prices. Agricultural R&D; Agricultural Technology; Agricultural Extension Services
Geographic Locator:Malaysia
Subject Codes:EE450. EE110
ISSN:0002-9092
Year:2001
Journal Title:American Journal of Agricultural Economics

9. Title:Public-Private Sector Linkages in Research and Development: Biotechnology and the Seed Industry in Brazil, China and India
View Article: American Journal of Agricultural Economics. 83 (3) 2001. 742-47
CD Volume:355
Print Article: Pages: 742-747
Author(s):Pray C E
Author Affiliation:Rutgers U
Language:English
Descriptors:Agricultural R&D; Agricultural Technology; Agricultural Extension Services. Management of Technological Innovation and R&D. Chemicals; Rubber; Drugs. Economic Development: Agriculture; Natural Resources; Environment; Other Primary Products
Geographic Locator:Brazil. China. India
Subject Codes:EE110. EE450. EE350. VV800
ISSN:0002-9092
Year:2001
Journal Title:American Journal of Agricultural Economics

10. Title:Integrin mobilizes intracellular Ca(2+) in renal vascular smooth muscle cells
View Article: Am J Physiol Cell Physiol 2001 Mar;280(3):C593-603
CD Volume:346
Print Article: Pages: C593-C603
Author(s):Chan WL Holstein Rathlou NH Yip KP
Author Affiliation:Department of Molecular Pharmacology, Physiology, and Biotechnology, Brown University, Providence, Rhode Island 02912, USA
Abstract:Peptides with the Arg-Gly-Asp (RGD) motif induce vasoconstriction in rat afferent arterioles by increasing the intracellular Ca(2+) concentration ([Ca(2+)](i)) in vascular smooth muscle cells (VSMC). This finding suggests that occupancy of integrins on the plasma membrane of VSMC might affect vascular tone. The purpose of this study was to determine whether occupancy of integrins by exogenous RGD peptides initiates intracellular Ca(2+) signaling in cultured renal VSMC. When smooth muscle cells were exposed to 0.1 mM hexapeptide GRGDSP, [Ca(2+)](i) rapidly increased from 91 +/- 4 to 287 +/- 37 nM

and then returned to the baseline within 20 s (P < 0.05, 34 cells/5 coverslips). In controls, the hexapeptide GRGESP did not trigger Ca(2+) mobilization. Local application of the GRGDSP induced a regional increase of cytoplasmic [Ca(2+)](i), which propagated as Ca(2+) waves traveling across the cell and induced a rapid elevation of nuclear [Ca(2+)](i). Spontaneous recurrence of smaller-amplitude Ca(2+) waves were found in 20% of cells examined after the initial response to RGD-containing peptides. Blocking dihydropyridine-sensitive Ca(2+) channels with nifedipine or removal of extracellular Ca(2+) did not inhibit the RGD-induced Ca(2+) mobilization. However, pretreatment of 20 microM ryanodine completely eliminated the RGD-induced Ca(2+) mobilization. Anti-beta(1) and anti-beta(3)-integrin antibodies with functional blocking capability simulate the effects of GRGDSP in [Ca(2+)](i). Incubation with anti-beta(1)- or beta(3)-integrin antibodies inhibited the increase in [Ca(2+)](i) induced by GRGDSP. We conclude that exogenous RGD-containing peptides induce release of Ca(2+) from ryanodine-sensitive Ca(2+) stores in renal VSMC via integrins, which can trigger cytoplasmic Ca(2+) waves propagating throughout the cell

Descriptors:Animal. Antibodies. Calcium. Calcium Channel Blockers. Calcium Channels. Cells, Cultured. Extracellular Space. Fluorescent Antibody Technique. Integrins. Intracellular Membranes. Muscle, Smooth, Vascular. Nifedipine. Oligopeptides. Osmolar Concentration. Protein Isoforms. Rats. Rats, Sprague-Dawley. Receptors, Cytoplasmic and Nuclear. Renal Circulation. Ryanodine. Support, U.S. Gov't, P.H.S.

Geographic Locator:United States

ISSN:0002-9513
Year:2001
Journal Title:American Journal of Physiology

11. Title:Pulmonary interstitial pressure and tissue matrix structure in acute hypoxia

View Article: Am J Physiol Lung Cell Mol Physiol 2001 May;280(5):L881-7
CD Volume:347
Print Article: Pages: L881-L887

Author(s):Miserocchi G Passi A Negrini D Del Fabbro M De Luca G
Author Affiliation:Department of Experimental and Environmental Medicine and Biotechnology, University of Milano-Bicocca, 20052 Monza, Italy. giuseppe.miserocchi@unimib.it

Abstract:Pulmonary interstitial pressure was measured via micropuncture in anesthetized rabbits in normoxia and after breathing 12% O(2). In normoxia [arterial PO(2) = 88 +/- 2 (SD) mmHg], pulmonary arterial pressure and pulmonary interstitial pressure were 16 +/- 8 and -9.6 +/- 2 cmH(2)O, respectively. After 6 h of hypoxia (arterial PO(2) = 39 +/- 16 mm Hg), the corresponding values were 30+/-8 and 3.5+/-2.5 cm H(2)O (P<0.05). Pulmonary interstitial proteoglycan extractability, evaluated by hexuronate assay after 0.4 M guanidinium hydrochloride extraction, was 12.3, 32.4, and 60.6 microg/g wet tissue in normoxia and after 3 and 6 h of hypoxia, respectively, indicating a weakening of the noncovalent bonds linking proteoglycans to other extracellular matrix components. Gel filtration chromatography showed an increased fragmentation of chondroitin sulfate- and heparan sulfate-proteoglycans during hypoxic exposure, accounting for a loss of extracellular matrix native architecture and basement membrane structure. Gelatin zymography demonstrated increased amounts of the proteolytically activated form of gelatinase B (matrix metalloproteinase-9) after hypoxic exposure, providing evidence that the activation of proteinases may play a role in hypoxia-induced lung injury

Descriptors:Animal. Anoxia. Blood Pressure. Chondroitin Sulfates. Chromatography, Gel. Extracellular Matrix. Extracellular Space. Gelatinase B. Heparitin Sulfate. Hexuronic Acids. Hydrostatic Pressure. Intercostal Muscles. Lung. Molecular Weight. Organ Weight. Pulmonary Artery. Rabbits. Support, Non-U.S. Gov't
Geographic Locator:United States
ISSN:0002-9513
Year:2001
Journal Title:American Journal of Physiology

12. Title:Influence of supplemental enzymes on the performance and phosphorus excretion of broilers fed wheat-based diets to 6 weeks of age
View Article: Animal Feed Science and Technology. 2001. 89 (1/2). 113-118
CD Volume:356
Print Article: Pages: 113-118
Author(s):Zyla K Koreleski J Swiatkiewicz S Ledoux D R Piironen J
Author Affiliation:Department of Food Biotechnology, University of Agriculture, 29-Listopada Avenue 46, 31-425 Krakow, Poland
Language:English
Abstract:Efficacies of phosphorolytic enzymes (phytase + acid phosphatase), and an enzymic cocktail (phytase + acid phosphatase + pectinase + citric acid), were investigated in broilers (n=600 d old chicks in 3 floor pen replicates) fed with wheat-based diets from day 1 to 43. Broilers were fed the following 4 diets: (1) a positive control diet (7.1 g total P/kg, 4.1 g non-phytate P/kg, 9.8 g Ca/kg); (2) a low P diet (4.1 g total P/kg, 1.7 g non-phytate P/kg, 6.0 g Ca/kg) supplemented with phytase (750 units/kg) and acid phosphatase (3156 units/kg); (3), a low P diet (4.1 g total P/kg, 1.7 g non-phytate P/kg, 6.0 g Ca/kg) supplemented with phytase, acid phosphatase, pectinase (1900 units/g) and citric acid (20 g/kg) and (4) a low P diet (4.1 g total P/kg, 1.7 g non-phytate P/kg, 8.0 g Ca/kg) supplemented as in diet 3. For the grower period (22-43 days), the contents of P and Ca were lowered by 0.2 and 0.3 g/kg, respectively. For the starter period, there were no differences observed among dietary treatments in terms of liveweight gains or feed efficiency. Total liveweight gains for the starter and grower periods did not differ among dietary treatments, but total feed efficiency was significantly enhanced in birds fed diet 2. At the completion of the experiment, chickens fed with phosphorolytic enzymes had the best feed efficiencies, the highest contents of ash in the toes and the highest carcass yield. Chicken receiving the cocktail of enzymes and 8 g Ca/kg (diet 4) performed as well as birds in the control treatment, but had higher yields of carcass and excreted 56% less P
Descriptors:acid-phosphatase. ash. broiler-performance. broilers. calcium. carcass-yield. citric-acid. diets. enzyme-activity. excretion. feed-additives. feed-conversion-efficiency. fowl-feeding. liveweight-gain. phosphorus. phytase. polygalacturonase. poultry
Organism Descriptors:fowls
Supplemental Descriptors:Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry
Subject Codes:LL120. LL510. LL520. QQ030. RR130
Supplementary Info:13 ref
ISSN:0377-8401
Year:2001
Journal Title:Animal Feed Science and Technology

13. Title:Binding of biotinylated legume seed lectins with glycoproteins in blotted receptor-analogs: influence of incubation pH

View Article: Animal Feed Science and Technology. 2001. 94 (3/4). 147-153
CD Volume:356
Print Article: Pages: 147-153
Author(s):Nevel C J van Rycke H de Beeckmans S Wilde R de Driessche E van
Author Variant:van-Nevel-C-J. de-Rycke-H. de-Wilde-R. van-Driessche-E
Author Affiliation:Laboratory for Protein Chemistry, Institute for Molecular Biology and Biotechnology, Vrije Universiteit Brussel, Paardenstraat 65, B-1640 Sint-Genesius-Rode, Belgium
Language:English
Abstract:The effect of incubation pH on the binding of biotinylated lectins on blotted receptor analogues was investigated. SDS-PAGE and Western blotting of lectin inhibitors (bovine and porcine plasma powder, whole egg powder and fetuin) were performed and blots were incubated with several biotinylated lectins commercially available (Phaseolus vulgaris E, Pisum sativum, Lens culinaris, Vicia faba). To study the effect of pH on the binding of the lectins to glycoproteins present in the inhibitors, identical blots were incubated in buffers with different pH values, i.e. 3-7, respectively. Binding capacity of lectins to the glycoproteins in the inhibitors was very dependent on pH condition during incubation. For all the lectins involved in this experiment, pH values lower than 4 inhibited the binding process considerably. Results are discussed taking into account the low pH values prevailing in the stomach of pigs
Descriptors:alpha-fetoprotein. binding-sites. biochemical-receptors. faba-beans. fodder-legumes. glycoproteins. inhibitors. lectins. lentils. pH. stomach
Organism Descriptors:Lens-culinaris. Phaseolus-vulgaris. pigs. Pisum-sativum. Vicia-faba
Supplemental Descriptors:Lens. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Phaseolus. Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Pisum. Vicia
Subject Codes:LL500. LL510
Supplementary Info:14 ref
ISSN:0377-8401
Year:2001
Journal Title:Animal Feed Science and Technology

14. Title:Bacteriophage therapy
View Article: Annual Review of Microbiology. 2001. 55. 437-451
CD Volume:369
Print Article: Pages: 437-451
Author(s):Summers W C
Author Affiliation:Yale University School of Medicine, New Haven, CT 06520, USA
Language:English
Abstract:In 1917, bacteriophages were recognized as epizootic infections of bacteria and were almost immediately deployed for antibacterial therapy and prophylaxis. The early trials of bacteriophage therapy for infectious diseases were confounded, however, because the biological nature of bacteriophage was poorly understood. The early literature reviewed here indicates that there are good reasons to believe that phage therapy can be effective in some circumstances. The advent of antibiotics, together with the "Soviet taint" acquired by phage therapy in the postwar period, resulted in the absence of rigorous evaluations of phage therapy until very recently. Recent laboratory and animal studies, exploiting current understanding of phage biology, suggest that phages may be useful as antibacterial agents in certain conditions

Descriptors:antibacterial-properties. antigens. bacterial-diseases. biotechnology. human-diseases. reviews. therapy
Organism Descriptors:bacteria. bacteriophages. man
Supplemental Descriptors:prokaryotes. viruses. pathogens. Homo. Hominidae. Primates. mammals. vertebrates. Chordata. animals
Subject Codes:VV210. VV710. WW000
Supplementary Info:69 ref
ISSN:0066-4227
Year:2001
Journal Title:Annual Review of Microbiology
Copyright:Copyright CAB International

15. Title:Hydrophobins: multipurpose proteins
View Article: Annual Review of Microbiology. 2001. 55. 625-646
CD Volume:369
Print Article: Pages: 625-646
Author(s):Wosten H A B
Author Affiliation:Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, 9751 NN Haren, Netherlands
Language:English
Abstract:Class I and class II hydrophobins are small secreted fungal proteins that play a role in a broad range of processes in the growth and development of filamentous fungi. For instance, they are involved in the formation of aerial structures and in the attachment of hyphae to hydrophobic surfaces. The mechanisms by which hydrophobins fulfill these functions are based on their property to self-assemble at hydrophilic-hydrophobic interfaces into a 10 nm-thin highly amphipathic film. Complementation studies have shown that class I hydrophobins belong to a closely related group of morphogenetic proteins, but that they have evolved to function at specific interfaces. Recent evidence indicates that hydrophobins do not only function by self-assembly. Monomeric hydrophobin has been implicated in cell wall assembly, but the underlying mechanism is not yet clear. In addition, hydrophobin monomers could act as toxins and elicitors
Descriptors:biological-development. cell-walls. fungal-elicitors. fungal-protein. fungal-structures. growth. mycotoxins
Subject Codes:ZZ394
Supplementary Info:102 ref
ISSN:0066-4227
Year:2001
Journal Title:Annual Review of Microbiology
Copyright:Copyright CAB International

16. Title:Cytokinin metabolism and action
View Article: Annual Review of Plant Physiology and Plant Molecular Biology. 2001. 52. 89-118
CD Volume:339
Print Article: Pages: 89-118
Author(s):Mok D W S Mok M C
Author Affiliation:Department of Horticulture, Center for Gene Research and Biotechnology, Oregon State University, Corvallis, OR 97331-7304, USA
Language:English
Abstract:Cytokinins are structurally diverse and biologically versatile plant hormones. The chemistry and physiology of cytokinins have been studied extensively, but the regulation of cytokinin biosynthesis, metabolism and signal transduction is still largely undefined. Recent advances in cloning metabolic genes and identifying putative receptors portend more rapid progress based on molecular techniques. This review

centers on cytokinin metabolism with connecting discussions on biosynthesis and signal transduction. Important findings are summarized with emphasis on metabolic enzymes and genes. Based on the information generated to date, implications and future research directions are presented
Descriptors:biosynthesis. cytokinins. DNA-cloning. enzymes. genes. metabolism. plant-growth-regulators. signal-transduction
Subject Codes:FF020. FF060
Supplementary Info:192 ref
ISSN:1040-2519
Year:2001
Journal Title:Annual Review of Plant Physiology and Plant Molecular Biology
Copyright:Copyright CAB International

17. Title:Endosperm development: cellularization and cell fate specification
View Article: Annual Review of Plant Physiology and Plant Molecular Biology. 2001. 52. 233-267
CD Volume:339
Print Article: Pages: 233-267
Author(s):Olsen O A
Author Affiliation:Department of Chemistry and Biotechnology, Agricultural University of Norway, PO. Box 5051, N-1432 Aas, Norway
Language:English
Abstract:The endosperm develops from the central cell of the megagametophyte after introduction of the second male gamete into the diploid central cell. Of the three forms of endosperm in angiosperms, the nuclear type is prevalent in economically important species, including the cereals. Landmarks in nuclear endosperm development are the coenocytic, cellularization, differentiation and maturation stages. The differentiated endosperm contains four major cell types: starchy endosperm, aleurone, transfer cells and the cells of the embryo surrounding region. Recent research has demonstrated that the first two phases of endosperm occur via mechanisms that are conserved among all groups of angiosperms, involving directed nuclear migration during the coenocytic stage and anticlinal cell wall deposition by cytoplasmic phragmoplasts formed in interzones between radial microtubular systems emanating from nuclear membranes. Complete cellularization of the endosperm coenocyte is achieved through centripetal growth of cell files, extending to the centre of the endosperm cavity. Key points in cell cycle control and control of the MT (microtubular) cytoskeletal apparatus central to endosperm development are discussed. Specification of cell fates in the cereal endosperm appears to occur via positional signalling; cells in peripheral positions, except over the main vascular tissues, assume aleurone cell fate. Cells over the main vascular tissue become transfer cells and all interior cells become starchy endosperm cells. Studies in maize have implicated Crinkly4, a protein receptor kinase-like molecule, in aleurone cell fate specification
Descriptors:cell-cycle. cereals. cytoskeleton. endosperm. maize. microtubules. plant-development. reviews
Organism Descriptors:Zea-mays
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060
Supplementary Info:193 ref
ISSN:1040-2519
Year:2001
Journal Title:Annual Review of Plant Physiology and Plant Molecular Biology
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18. Title:Function and mechanism of organic anion exudation from plant roots
View Article: Annual Review of Plant Physiology and Plant Molecular Biology. 2001. 52. 527-560
CD Volume:339
Print Article: Pages: 527-560
Author(s):Ryan P R Delhaize E Jones D L
Author Affiliation:CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Language:English
Abstract:The rhizosphere is the zone of soil immediately surrounding plant roots that is modified by root activity. In this critical zone, plants perceive and respond to their environment. As a consequence of normal growth and development, a large range of organic and inorganic substances are exchanged between the root and soil, which inevitably leads to changes in the biochemical and physical properties of the rhizosphere. Plants also modify their rhizosphere in response to certain environmental signals and stresses. Organic anions are commonly detected in this region, and their exudation from plant roots has now been associated with nutrient deficiencies and inorganic ion stresses. This review summarizes recent developments in the understanding of the function, mechanism and regulation of organic anion exudation from roots. The benefits that plants derive from the presence of organic anions in the rhizosphere are described and the potential for biotechnology to increase organic anion exudation is highlighted
Descriptors:anions. exudation. inorganic-salts. nutrient-deficiencies. reviews. rhizosphere. roots. soil. stress
Subject Codes:FF060. JJ100
Supplementary Info:193 ref
ISSN:1040-2519
Year:2001
Journal Title:Annual Review of Plant Physiology and Plant Molecular Biology

19. Title:Defensive resin biosynthesis in conifers
View Article: Annual Review of Plant Physiology and Plant Molecular Biology. 2001. 52. 689-724
CD Volume:339
Print Article: Pages: 689-724
Author(s):Trapp S Croteau R
Author Affiliation:Institute of Biological Chemistry, Washington State University, Pullman, WA 99164-6340, USA
Language:English
Abstract:Tree killing bark beetles and their vectored fungal pathogens are the most destructive agents of conifer forests worldwide. Conifers defend against attack by the constitutive and inducible production of oleoresin, a complex mixture of mono-, sesqui-, and diterpenoids that accumulates at the wound site to kill invaders and both flush and seal the injury. Although toxic to the bark beetle and fungal pathogen, oleoresin also plays a central role in the chemical ecology of these boring insects, from host selection to pheromone signalling and tritrophic level interactions. The biochemistry of oleoresin terpenoids is reviewed, and the regulation of production of this unusual plant secretion is described in the context of bark beetle infestation dynamics with respect to the function of the turpentine and rosin components. Recent advances in the molecular genetics of terpenoid biosynthesis provide evidence for the evolutionary origins of oleoresin and permit consideration of genetic engineering

strategies to improve conifer defenses as a component of modern forest biotechnology
Descriptors:biosynthesis. defence-mechanisms. defensive-secretions. forest-pests. insect-pests. oleoresins. resins. reviews. rosin. terpenoids
Organism Descriptors:insects. Pinopsida. Scolytidae
Supplemental Descriptors:gymnosperms. Spermatophyta. plants. Coleoptera. insects. arthropods. invertebrates. animals
Subject Codes:FF620. KK100. ZZ332
Supplementary Info:126 ref
ISSN:1040-2519
Year:2001
Journal Title:Annual Review of Plant Physiology and Plant Molecular Biology
Copyright:Copyright CAB International

20. Title:Cytokinesis and building of the cell plate in plants
View Article: Annual Review of Plant Physiology and Plant Molecular Biology. 2001. 52. 751-784
CD Volume:339
Print Article: Pages: 751-784
Author(s):Verma D P S
Author Affiliation:Department of Molecular Genetics, Plant Biotechnology Center, Ohio State University, Columbus, OH 43210-1002, USA
Language:English
Abstract:Cytokinesis in plant cells is more complex than in animals, as it involves building a cell plate as the final step in generating two cells. The cell plate is built in the centre of phragmoplast by fusion of Golgi-derived vesicles. This step imposes an architectural problem where ballooning of the fused structures has to be avoided to create a plate instead. This is apparently achieved by squeezing the vesicles into dumbbell-shaped vesicle-tubule-vesicle (VTV) structures with the help of phragmoplastin, a homologue of dynamin. These structures are fused at their ends in a star-shaped body creating a tubulovesicular "honeycomb-like" structure sandwiched between the positive ends of the phragmoplast microtubules. This review summarizes our current understanding of various mechanisms involved in budding-off of Golgi vesicles, delivery and fusion of vesicles to initiate cell plate, and the synthesis of polysaccharides at the forming cell plate. Little is known about the molecular mechanisms involved in determining the site, direction and the point of attachment of the growing cell plate with the parental cell wall. These gaps may be filled soon, as many genes that have been identified by mutations are analysed and functions of their products are deciphered
Descriptors:cell-division. genes. Golgi-apparatus. polysaccharides. reviews
Organism Descriptors:plants
Subject Codes:FF020. FF060. FF000
Supplementary Info:194 ref
ISSN:1040-2519
Year:2001
Journal Title:Annual Review of Plant Physiology and Plant Molecular Biology
Copyright:Copyright CAB International

21. Title:Salinity acclimation of immobilized freshwater denitrifier
View Article: Aquacultural Engineering. 24 (3). April, 2001. 169-180
CD Volume:374
Print Article: Pages: 169-180
Author(s):Park Eun Ju Seo Jae Koan Kim Mi Ryung Jung Il Hyong Kim Joong yun Kim Sung Koo
Author Affiliation:Division of Food and Biotechnology, Pukyong National University, Pusan, 608-737: skkim@mail.pknu.ac.kr

Language:English
Language of Summary:English (EN)
Abstract:To develop a marine recirculating aquarium system, the marine denitrification process was evaluated for the effects of salinity, temperature and hydraulic retention time (HRT) on marine denitrification processes. Denitrifier consortium was collected from a continuous denitrification tank operated for 120 days and was immobilized by the PVA-boric acid method. Four reactors were simultaneously operated to determine the effect of salinity. One of them, R-1, was supplied with tap water as a control and others, R- 2, R-3 and R-4 were supplied with sea water diluted with tap water by 3 steps (7.5, 15, 30 ppt), 2 steps (15, 30 ppt) and 1 step (30 ppt), respectively. The loading rate of nitrate-nitrogen averaged 20.6 g/m3/day. Salinity caused nitrite-nitrogen formation at the early stage of acclimation, even though the conversion rates of nitrate for high salinites were similar to that of the control (freshwater). Addition of salt to the system might cause a damage to denitrifiers that convert nitrate to nitrogen gas, however the activity was recovered after 10 days of operation. Also, the direct acclimation method to seawater was more efficient than the stepwise acclimation method when the freshwater denitrification system was converted to the marine system. As the HRT was reduced, the nitrate removal rate increased and denitrification efficiency decreased. The optimum HRT was 3 h with a nitrate removal rate of 34 g/m3/day. Any further decrease in HRT decreased the nitrate removal rate due to the rapid drop of nitrate removal efficiency and high flow rate
Descriptors:denitrification efficiency; freshwater habitats; hydraulic retention time; nitrate removal rate; salinity acclimation; stepwise acclimation. Freshwater Ecology (Ecology, Environmental Sciences); Methods and Techniques. nitrate
Subject Codes:Freshwater Ecology (Ecology, Environmental Sciences); Methods and Techniques
ISSN:0144-8609
Year:2001
Journal Title:Aquacultural Engineering

22. Title:Nitrification performance of nitrifiers immobilized in PVA (polyvinyl alcohol) for a marine recirculating aquarium system
View Article: Aquacultural Engineering. 24 (3). April, 2001. 181-194
CD Volume:374
Print Article: Pages: 181-194
Author(s):Seo Jae Koan Jung Il Hyong Kim Mi Ryung Kim Byong Jin Nam Soo Wan Kim Sung Koo
Author Affiliation:Department of Biotechnology and Bioengineering, Pukyong National University, Pusan, 608-737: skkim@mail.pknu.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:Characteristics of the nitrification processes with immobilized nitrifier consortium were evaluated for the development of the marine recirculating aquarium system. In order to evaluate the activity of the nitrifiers, a 45 1 airlift reactor was used for the determination of ammonia removal rate for 40 days of operation. The ammonia removal efficiency rate was 98% with 23 g ammonia-N/m3/day, respectively. The activity of immobilized nitrifiers in polyvinyl alcohol (PVA) beads treated by boric acid at the concentration of 15% was fully recovered, and the ammonia removal rate increased to 70 g ammonia-N/m3/day with 18 days of operation time. An acclimation experiment of the immobilized nitrifiers from freshwater to seawater system was carried

out for 60 days using a 2.5 1 airlift reactor with increased salt concentration. The ammonia was completely removed, and nitrite accumulated up to 6 mg/l but decreased to less than 0.1 mg/l after 30-40 days of operation. The salt concentration was related to the time to stabilize the system. Another operation was carried out to evaluate the optimum hydraulic retention time (HRT) of the marine nitrification process for 35 days. The HRT was set in the range of 6.12-0.7 h. The highest ammonia removal rate, 63 g/m3/day, was observed when the HRT was 1.0 h
Descriptors:nitrification performance; nitrifier immobilization. Aquaculture; Methods and Techniques. nitrite: accumulation; polyvinyl alcohol [PVA]
Organism Descriptors:bacteria (Bacteria): nitrifier
Supplemental Descriptors:Bacteria: Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Aquaculture; Methods and Techniques
ISSN:0144-8609
Year:2001
Journal Title:Aquacultural Engineering

23. Title:Production of Candida utilis biomass on molasses in different culture types
View Article: Aquacultural Engineering. 25 (2). September, 2001. 111-124
CD Volume:374
Print Article: Pages: 111-124
Author(s):Lee Bum Kyu Kim Joong Kyun
Author Affiliation:Division of Food Science and Biotechnology, Pukyong National University, 599-1 Daeyeon-Dong, Nam-Gu, Pusan, 608-737: junekim@pknu.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:Three different types of aerobic fermentations were performed for the mass production of C. utilis as aquafeeds. From the best fermentation result of each culture type, the biomass yield and productivity were calculated to be 0.67 and 0.24 for batch, 0.51 and 1.95 for fed-batch with sigmoidal feeding strategy, and 0.36 g g-1 and 2.15 g-1 l-1 h-1 for continuous cultures, respectively. The cultivation of C. utilis using chemicals for industrial use resulted in considerable reduction of production cost. The fed- batch fermentation was found to be the best culture type for mass production of C. utilis. The total production cost of C. utilis cultivated in the fed-batch fermentation was estimated to be USdollar sign2.76 per kg of dry cells. The total production cost is favorably comparable with the sale price of the commercial yeast product
Descriptors:aerobic fermentation; biomass; molasses. Aquaculture; Methods and Techniques
Organism Descriptors:Candida utilis (Fungi Imperfecti or Deuteromycetes): aquafeed
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Aquaculture; Methods and Techniques
ISSN:0144-8609
Year:2001
Journal Title:Aquacultural Engineering

24. Title:Recombinant expression and characterization of the Candida rugosa lip4 lipase in Pichia pastoris: comparison of glycosylation, activity, and stability
View Article: Arch Biochem Biophys 2001 Mar 1;387(1):93-8
CD Volume:380
Print Article: Pages: 93-98
Author(s):Tang SJ Shaw JF Sun KH Sun GH Chang TY Lin CK Lo YC Lee GC
Author Affiliation:Institute of Marine Biotechnology, National Taiwan Ocean University, Keelung, Republic of China. tsj@mail.ntou.edu.tw
Abstract:Although Candida rugosa utilizes a nonuniversal serine codon (CUG) for leucine, it is possible to express lipase genes (LIP) in heterologous systems. After replacing the 19 CUG codons in LIP4 with serine codons by site-directed mutagenesis, a recombinant LIP4 was functionally overexpressed in Pichia pastoris in this study. This recombinant glycosylated lipase was secreted into the culture medium with a high purity of 100 mg/liter in a culture broth. Purified recombinant LIP4 had a molecular mass of 60 kDa, showing a range similar to that of lipase in a commercial preparation. Since LIP4 has only a glycosylation site at position Asn-351, this position may also be the major glycosylation site in C. rugosa lipases. Although the thermal stability of recombinant LIP4 significantly increased from 52 to 58 degrees C after glycosylation, there were no significant differences in the catalytic properties of recombinant glycosylated lipase from P. pastoris and the unglycosylated one from Escherichia coil. These two recombinant LIP4s showed higher esterase activities toward long-chain ester (C16 and C18) and exhibited higher lipase activities toward unsaturated and long-chain lipids. In addition, LIP4 does not show interfacial activation as compared with LIP1 toward lipid substrates of tributyrin and triolein. These observations demonstrated that LIP4 shows distinguished catalytic activities with LIP1 in spite of their high sequence homology
Descriptors:Candida. Carboxylic Ester Hydrolases. Codon. Enzyme Stability. Fungal Proteins. Glycosylation. Heat. Pichia. Protein Processing, Post-Translational. Recombinant Proteins. Serine. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:United States
ISSN:0003-9861
Year:2001
Journal Title:Archives of Biochemistry and Biophysics

25. Title:Calcium- and magnesium-dependent interactions between the C-terminus of troponin I and the N-terminal, regulatory domain of troponin C
View Article: Arch Biochem Biophys 2001 Mar 15;387(2):243-9
CD Volume:380
Print Article: Pages: 243-249
Author(s):Digel J Abugo O Kobayashi T Gryczynski Z Lakowicz JR Collins JH
Author Affiliation:Medical Biotechnology Center, University of Maryland Biotechnology Institute, Baltimore 21201, USA
Abstract:The muscle thin filament protein troponin (Tn) regulates contraction of vertebrate striated muscle by conferring Ca2+ sensitivity to the interaction of actin and myosin. Troponin C (TnC), the Ca2+ binding subunit of Tn contains two homologous domains and four divalent cation binding sites. Two structural sites in the C-terminal domain of TnC bind either Ca2+ or Mg2+, and two regulatory sites in the N-terminal domain are specific for Ca2+. Interactions between TnC and the inhibitory Tn subunit troponin I (TnI) are of central importance to the Ca2+ regulation of muscle contraction and have been intensively studied. Much remains to be learned, however, due mainly to the lack of a three-dimensional structure for TnI. In particular, the role of

amino acid residues near the C-terminus of TnI is not well understood. In this report, we prepared a mutant TnC which contains a single Trp-26 residue in the N-terminal, regulatory domain. We used fluorescence lifetime and quenching measurements to monitor Ca2+- and Mg2+-dependent changes in the environment of Trp-26 in isolated TnC, as well as in binary complexes of TnC with a Trp-free mutant of TnI or a truncated form of this mutant, TnI(1-159), which lacked the C-terminal 22 amino acid residues of TnI. We found that full-length TnI and TnI(1-159) affected Trp-26 similarly when all four binding sites of TnC were occupied by Ca2+. When the regulatory Ca2+-binding sites in the N-terminal domain of TnC were vacant and the structural sites in the C-terminal domain of were occupied by Mg2+, we found significant differences between full-length TnI and TnI(1-159) in their effect on Trp-26. Our results provide the first indica- tion that the C-terminus of TnI may play an important role in the regulation of vertebrate striated muscle through Ca2+-dependent interactions with the regula- tory domain of TnC

Descriptors:Acrylamide. Amino Acid Substitution. Animal. Binding Sites. Calcium. Iodides. Magnesium. Muscle Contraction. Mutagenesis, Site-Directed. Protein Structure, Tertiary. Rabbits. Sequence Deletion. Spectrometry, Fluorescence. Support, U.S. Gov't, P.H.S.. Troponin C. Troponin I. Tryptophan

Geographic Locator:United States

ISSN:0003-9861
Year:2001
Journal Title:Archives of Biochemistry and Biophysics

26. Title:Characterization of a galactose specific adhesin of enteroaggregative Escherichia coli

View Article: Arch Biochem Biophys 2001 Jun 1;390(1):109-18
CD Volume:381
Print Article: Pages: 109-118

Author(s):Grover V Ghosh S Sharma N Chakraborti A Majumdar S Ganguly NK
Author Affiliation:Department of Experimental Medicine and Biotechnology, Postgraduate Institute of Medical Education and Research, Chandigarh, 160 012, India

Abstract:A fimbrial adhesin was identified from an enteroaggregative Escherichia coli strain. The adhesin was purified to 740-fold by sequential chromatography on an affinity matrix and gel filtration column in the FPLC system. The homogeneity of the purified protein was established by analytical isoelectrofocussing (pI 7.25). The native adhesin appeared as a high-molecular-weight aggregative protein as revealed by gel filtration chromatography on Superose 12HR10/30 column. However, in sodium dodecyl sulfate-polyacrylamide gel electrophoresis the molecular weight of the adhesin was found to be 18 kDa and this was further confirmed by gel filtration chromatography on Superose 6HR 10/30 column presence of 6 M guanidine hydrochloride. The N-terminal 15-amino-acid sequence of the adhesin did not show homology with any of the previously reported fimbrial adhesins. The purified adhesin showed adhesion to human erythrocytes in the presence of Ca(2+) (5 mM). The optimum temperature and pH for the hemadhesion activity was found to be 25 degrees C and 6.5, respectively. The inhibition study clearly suggested that the binding site of the adhesin could recognize galactose as the specific sugar. The fluorescence of 4-methylumbelliferyl-alpha-D-galactopyranoside was quenched on binding to the adhesin and maximum reversal of fluorescence quenching was observed by competitive substitution titration with raffinose. The adhesin was found to contain one binding site per monomer for its specific sugar residue. The association constant and the free energy

of binding were obtained as 3.98 x 10(5) M(-1) and -31.97 kJ/mol, respectively. The adherence of the bacteria to HEp-2 monolayer was inhibited in presence of galactose and this was further supported by a significant reduction in the bacterial adherence to the HEp-2 cells, pretreated with beta-D-galactosidase
Descriptors:Adhesins, Escherichia coli. Amino Acid Sequence. Bacterial Adhesion. Cell Line. Chromatography. Escherichia coli. Galactose. Hemagglutination Inhibition Tests. Human. Hydrogen-Ion Concentration. Isoelectric Focusing. Molecular Sequence Data. Molecular Weight. Spectrometry, Fluorescence. Support, Non-U.S. Gov't
Geographic Locator:United States
ISSN:0003-9861
Year:2001
Journal Title:Archives of Biochemistry and Biophysics

27. Title:Purification of Cajanus cajan root lectin and its interaction with rhizobial lipopolysaccharide as studied by different spectroscopic techniques
View Article: Arch Biochem Biophys 2001 Dec 1;396(1):99-105
CD Volume:381
Print Article: Pages: 99-105
Author(s):Naeem A Khan RH Vikram H Akif M
Author Affiliation:Interdisciplinary Biotechnology Unit, Aligarh Muslim University, Aligarh-202 002, India
Abstract:A lectin present in roots of Cajanus cajan seedlings was isolated and purified by affinity chromatography. Sugar specificity assayed by hemagglutination-inhibition activity indicated that lectin belongs to glucose/mannose-specific group. The root lectin was found to be mannose-specific from the second day onwards as it was reconfirmed by specific elution of different days' sample from mannose agarose matrix. The maximum interaction of lectin with goat IgM was obtained in 10-day-old sample, indicating the highest crude lectin content. Lectin (total amount of eluted protein) from different days soil sample showed a maximum amount in 10-day-old sample. For further studies, the lectin has been isolated from the roots of 10-day C. cajan seedlings and purified on mannose-CL agarose column by affinity chromatography. Lectin was found to be a dimer of 18.5-kDa subunit as revealed by SDS-PAGE. Tryptophan quenching fluorescence was studied for C. cajan root lectin. Secondary structure of C. cajan root lectin as studied by circular dichroism was found to be a typical beta-pleated sheet structure. The interaction of purified root lectin with C. cajan-specific rhizobial lipopolysaccharide and its inhibition by specific and nonspecific sugars was demonstrated by fluorescence and circular dichroism. Results discussed in this paper were studied for the first time by different spectroscopic methods, suggesting that C. cajan root lectin-lipopolysaccharide interaction is specific
Descriptors:Cell Wall. Chromatography, Affinity. Circular Dichroism. Disaccharides. Electrophoresis, Polyacrylamide Gel. Fabaceae. Immunoglobulin M. Lectins. Lipopolysaccharides. Monosaccharides. Plant Roots. Protein Binding. Rhizobium. Soil. Spectrometry, Fluorescence. Support, Non-U.S. Gov't
Geographic Locator:United States
ISSN:0003-9861
Year:2001
Journal Title:Archives of Biochemistry and Biophysics

28. Title:Cloning and expression of beta 1-adrenergic receptor genes in adipose tissues from Korean native cattle (Hanwoo)
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (1). 13-16

CD Volume:379
Print Article: Pages: 13-16
Author(s):Ha S H Chung M I Baik M G Choi Y J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Language:English
Abstract:Bovine beta 1-adrenergic receptor (AR) cDNA was cloned using degenerative primers. Bovine beta 1-AR coded for 467 amino acids and the comparison of the deduced amino acid sequence with that of sheep showed 93.4% identity. Northern blot analysis indicated that transcript size for the bovine beta 1-AR was 3.6 kb in the adipose tissue. The expression level of three beta -Ars (1, 2, and 3) in bovine abdominal, subcutaneous, and perirenal adipose tissues were examined using reverse transcription-polymerase chain reaction (RT-PCR), and the levels of beta 1- and beta 3-AR mRNA were found to be lower in the subcutaneous adipose tissue than in the abdominal and perirenal adipose tissues. These results suggest that the expression of beta -ARs mRNA are differentially regulated among the adipose tissues
Descriptors:abdominal-fat. adipose-tissue. amino-acid-sequences. biochemical-receptors. cell-cloning. genes. Korean-Native. messenger-RNA
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL700. WW000
Supplementary Info:14 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

29. Title:Genetic linkage mapping of RAPD markers segregating in Korean Ogol chicken - White Leghorn backcross population
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (3). 302-306
CD Volume:379
Print Article: Pages: 302-306
Author(s):Hwang K C Song K D Kim T H Jeong D K Sohn S H Lillehoj H S Han J Y
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea Republic
Language:English
Abstract:This study was carried out to construct mapping population and to evaluate the methods involved, including polymorphic DNA marker system and appropriate statistical analysis. As an initial step to establish chicken genome mapping project, White Leghorn (WL) and Korean Ogol chickens (KOC) were used for generating backcross population. From 8 initial parents, a total of 280 backcross progenies were obtained and 40 were used for genotyping and linkage analysis. For development of novel polymorphic markers for KOC, Random Amplified Polymorphic DNA (RAPD) markers specific for this chicken line were generated. Also included in this study were six microsatellite markers from East Lansing map as reference loci. For segregation analysis, 15 RAPD markers and 6 microsatellites were used to genotype the backcross population. Among the RAPD markers that we developed, 2 pairs of markers were identified to be linked and another 4 RAPD markers showed linkage with microsatellites of known map. In summary, this study showed that our backcross population generated from the mating of KOC to WL serves as a valuable genetic resource for genotyping.

Furthermore, RAPD markers are proved to be valuable in linkage mapping analysis
Descriptors:backcrosses. DNA-cloning. gene-mapping. genetic-markers. genetic-polymorphism. genome-analysis. linkage. microsatellites. poultry. random-amplified-polymorphic-DNA. segregation
Geographic Locator:Korea-Republic
Identifiers:fowl breeds. genotyping. Korean Ogol. White Leghorn
Organism Descriptors:fowls
Supplemental Descriptors:Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry. East-Asia. Asia. Developing-Countries. Threshold-Countries. OECD-Countries
Subject Codes:LL240. WW000
Supplementary Info:22 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

30. Title:Association of endocrine factors (insulin-like growth factor-II and binding protein-3) with litter size in pigs
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (3). 307-315
CD Volume:379
Print Article: Pages: 307-315
Author(s):Yun J S Kang W J Seo D S Park S S Hong K C Lee C Y Ko Y
Author Affiliation:Department of Animal Science, Graduate School of Biotechnology, Korea University, Seoul 136-701, Korea Republic
Language:English
Abstract:Litter size has been one of the important economic traits in porcine reproduction. The insulin-like growth factor (IGF) system has been shown to mediate actions of the steroid hormone or to synergize with other endocrine factors so that it consequently plays roles in reproductive processes, including ovulation, implantation, maintenance of pregnancy, and fetal development. However, the effect of the serum IGF system on porcine litter size has not been deeply studied. Therefore, this study was conducted to relate serum IGF-II concentration and IGF binding protein-3 (IGFBP-3) expression with porcine litter size. Moreover, the possible association of those with oestrogen receptor (ER) as a candidate gene for litter size was investigated. Swine were separated into two groups showing high and low litter sizes, and sera were collected from sows in the oestrous cycle to postnatal growth of their female progeny. Serum IGF-II concentration was measured by radioimmunoassay and IGFBP-3 expression was detected by Western ligand blotting. During the oestrous cycle, IGFBP-3 expression in both groups decreased moderately from metoestrus to oestrus, but IGF-II concentration showed a reverse pattern. Also, IGF-II concentration and IGFBP-3 expression decreased gradually as pregnancy proceeded. Unlike IGFBP-3, IGF-II decreased moderately as newborn pigs grew. Significant differences in serum IGF-II amount between the two groups were detected at 60 ($p<0.01$), 75, 90, and 105 d ($p<0.05$) of pregnancy and at 60 ($p<0.01$), 45, and 105 d ($p<0.05$) of postnatal growth. Furthermore, based on ER genotypes, a high litter size group with genotypes AB and BB showed lower IGF-II concentration than a low litter size group with a genotype AA during pregnancy. Taken together, the results indicate that the serum IGF-II and IGFBP-3 are correlated with the litter size in pigs
Descriptors:binding-proteins. gilts. insulin-like-growth-factor. litter-size. oestrogen-receptors. oestrus. ovulation. piglets. postnatal-development. pregnancy. sows

Identifiers:KoreaRepublic
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. LL250. LL600
Supplementary Info:34 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences
Copyright:Copyright CAB International

31. Title:Application of ELISA for the detection of sulfamethazine residue in live cattle
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (3). 378-381
CD Volume:379
Print Article: Pages: 378-381
Author(s):Lee H J Lee M H Han I K
Author Affiliation:School of Agricultural Biotechnology, College of Veterinary Medicine, Seoul National University, 103 Seodundong, Suwon 441-744, Korea Republic
Language:English
Abstract:Sulfamethazine has been widely used in swine for prevention or treatment of infections. Recently, the safety of the drug to consumers has been questioned because of carcinogenic effects. To prevent unwanted drug residues entering the human food chain, both government authorities and industries have established extensive control measures. The demands for reliable, simple, sensitive, rapid and low-cost methods for residue analysis of foods are increasing nowadays. In this study, we established a rapid prediction test for the detection of cattle with violative tissue residues of sulfamethazine. The recommended therapeutic dose of sulfamethazine (Sulfa-33 Injection, withdrawal time, 15 days) was administered to each of 10 cattle. Blood was sampled before drug administration and during the withdrawal period. The concentration of sulfamethazine in plasma, determined by a semi-quantitative ELISA, was compared to that of an internal standard (10 ppb). The absorbance ratio of internal standard to sample (B/Bs) was employed as an index to determine whether drug residues in cattle tissues were negative or positive. That is, a B/Bs ratio less than 1 was considered residue positive and if larger than 1 was considered negative. All 10 plasma samples from non-treated cattle showed negative to sulfamethazine. Sulfamethazine was detected in plasmas of treated cattle until Day 7 of withdrawal period. The present study showed that the semi-quantitative ELISA could be easily adapted in predicting residues of sulfamethazine in live cattle
Descriptors:drug-residues. ELISA. pharmacokinetics. sulfadimidine
Identifiers:antimicrobial agents
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:HH430. LL882. QQ200. ZZ900
Supplementary Info:19 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences
Copyright:Copyright CAB International

32. Title:Public health risks: chemical and antibiotic residues

View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (3). 402-413
CD Volume:379
Print Article: Pages: 402-413
Author(s):Lee M H Lee H J Ryu P D
Author Affiliation:Laboratory of Pharmacology, School of Agricultural Biotechnology, College of Veterinary Medicine, Seoul National University, 103 Seodundong, Suwon 441-744, Korea Republic
Language:English
Abstract:The paper reviews public health risks posed by chemical and antibiotic residues in food. It elaborates on veterinary drugs and other chemicals contaminating feed and the side effects of these, and on the concepts of withdrawal time and antibiotic residues. It also discusses the establishment and determination of tolerance levels, including no observable effect level (NOEL), acceptable daily intake (ADI), and maximum residue level (MRL). Rapid screening test methods for determining drug contamination of animal products are presented. The paper makes mention of the National Residue Program (Department of Veterinary Service, Ministry of Agriculture and Forestry) in Korea and the Food Animal Residue Avoidance Databank (FARAD). To ensure human safety, thorough enforcement of drug registration, labeling, sound use of drugs, observance of withdrawal times, development of rapid screening methods and live animal tests, extension of HACCP from farm to table, including quality assurance programs, are advised
Descriptors:antibiotic-residues. drug-residues. drug-resistance. food-contamination. food-safety. public-health. reviews. risk-assessment
Subject Codes:QQ200. HH430. LL882
Supplementary Info:27 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

33. Title:Environmental challenges of animal agriculture and the role and task of animal nutrition in environmental protection
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (3). 423-431
CD Volume:379
Print Article: Pages: 423-431
Author(s):Chen DaiWen
Author Variant:Chen-D-W
Author Affiliation:Institute of Animal Nutrition, Sichuan Agricultural University, Yaan, Sichuan, 625014, China
Language:English
Abstract:The paper provides an overview on the inevitability of environmental pollution due to intensive animal agriculture and the dependence of alleviating environmental risk on related factors, emphasizing on the role and future task of animal nutrition. The relationship between the position of animals in the food chain and animal production efficiency is discussed. Low efficiency of animal agriculture determines the inevitability of the negative impact of intensive animal agriculture on the environment, which includes the production of pollutants, inefficient consumption of existing environmental resources, and the issue of safety of animal products to human health. Water pollution, which includes contamination by nitrate, phosphorus and toxic metals, is cited as the biggest problem in animal agriculture. Strategies for alleviating environmental pollution and the potential contribution of biotechnology are discussed

Descriptors:animal-nutrition. animal-production. animal-wastes. environmental-protection. food-chains. intensive-husbandry. pollution. reviews. water-pollution
Subject Codes:PP600. VV500. XX100. LL180. LL500
Supplementary Info:22 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

34. Title:Induction of lysozyme gene expression during involution of mouse mammary gland
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (4). 462-466
CD Volume:379
Print Article: Pages: 462-466
Author(s):Lee M J Han O Back K Choi Y J Baik M G
Author Affiliation:Department of Genetic Engineering, Biotechnology Research Institute, College of Agriculture, Chonnam National University, Kwangju 500-757, Korea Republic
Language:English
Abstract:To understand molecular mechanisms of mouse mammary gland involution, clones were isolated by differential screening of a cDNA library. Partial sequences of a clone showed 100% identity to cDNA sequences of mouse lysozyme P gene. Northern analysis was performed to examine expression levels of lysozyme mRNA in mammary gland at several physiological states. Expression of lysozyme gene was induced at involution day 5 compared with lactating stage. High levels of lysozyme mRNA were also detected at virgin tissues. Two types of separate genes, P and M lysozyme, have been known in mouse, and we found that both lysozyme P and M genes were expressed in mammary tissues by reverse transcriptase-polymerase chain reaction. The lysozyme enzyme activity determined by lysoplate assay was also higher in involuted mammary tissues compared with lactating tissues, showing a similar trend to its mRNA levels. Lysozyme is an antimicrobial protein and involved in host defense mechanism. The increase in lysozyme gene expression may help to prevent microbial infection during mammary gland involution at which stage the residual milk in the mammary gland provides good nutritional sources for microbial growth
Descriptors:antiinfective-agents. enzyme-activity. gene-expression. genes. induction. involution. lysozyme. mammary-glands. messenger-RNA
Organism Descriptors:mice
Supplemental Descriptors:Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:LL040. LL240. LL650. WW000
Supplementary Info:13 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

35. Title:Effect of unsaturated fatty acids on cellulose degradation and fermentation characteristics by mixed ruminal microbes
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (4). 501-506
CD Volume:379
Print Article: Pages: 501-506
Author(s):Hwang I H Kim H D Shim S S Lee S S Ha J K

Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Language:English
Abstract:This experiment was conducted to evaluate the effects of supplemental unsaturated fatty acids (UFA) on fermentation characteristics, especially on gas production, cellulose degradation and volatile fatty acid (VFA) concentration by mixed ruminal microorganisms. In order to attain this objective, unsaturated fatty acids including oleic acid (C18:1), linoleic acid (C18:2) and arachidonic acid (C22:4) were added at varying levels. Mixed ruminal microbes used in the experiment were obtained from the rumen of a cannulated Holstein cow. Medium pH values after 7 d incubation were significantly affected by type and level of unsaturated fatty acids (P<0.01). All of UFA inhibited total gas production, and especially treatment of arachidonic acid at the levels of 0.01% gave the lowest gas production after 7 d incubation (P<0.01). Comparison of the population of protozoa revealed that UFA did not have any significant effect on the total protozoal number. The addition of UFA did not effect dry matter degradation. Volatile fatty acid (VFA) composition of the culture was influenced little by UFA, although the considerable amount of iso-type VFA were detected in UFA supplemented incubations. The ratio of acetic acids to propionic acids, however, was lower than the control in all the treatments after 7 d incubation (P<0.01)
Descriptors:acetic-acid. arachidonic-acid. cellulose. degradation. feed-supplements. linoleic-acid. methane-production. oleic-acid. pH. propionic-acid. rumen-fermentation. rumen-flora. rumen-microorganisms. rumen-protozoa. unsaturated-fatty-acids. volatile-fatty-acids
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL060. LL500. LL510
Supplementary Info:26 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

36. Title:Current status of quantitative trait locus mapping in livestock species - review -
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (4). 587-596
CD Volume:379
Print Article: Pages: 587-596
Author(s):Kim JongJoo Park Y I
Author Variant:Kim-J-J
Author Affiliation:GenomicFX, L.P., Austin, TX 78726, USA
Language:English
Abstract:In the last decade, rapid developments in molecular biotechnology and of genomic tools have enabled the creation of dense linkage maps across whole genomes of human, plant and animals. Successful development and implementation of interval mapping methodologies have allowed detection of the quantitative trait loci (QTL) responsible for economically important traits in experimental and commercial livestock populations. The candidate gene approach can be used in any general used in any general population with the availability of a large resource of candidate genes from the human or rodent genomes using comparative maps, and the validated candidate genes can be directly applied to commercial breeds. For the QTL detected from primary genome

scans, two incipient fine mapping approaches are applied by generating new recombinant over several generations or utilizing historical recombinant with identity-by-descent (IBID) and linkage disequilibrium (LAUD) mapping. The high resolution definition of QTL position from fine mapping will allow the more efficient implementation of breeding programmes such as marker-assisted selection (MAY) or marker-assisted introgression (MAI), and will provide a route toward cloning the QTL
Descriptors:gene-mapping. genes. genomes. reviews. traits
Identifiers:cloning
Subject Codes:LL240. WW000
Supplementary Info:79 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

37. Title:Cloning and expression of bovine polyadenylate binding protein 1 cDNA in mammary tissues
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (6). 771-776
CD Volume:379
Print Article: Pages: 771-776
Author(s):Kim J H Jeon D H Choi Y J Baik M G
Author Affiliation:Department of Genetic Engineering, Biotechnology Research Institute, College of Agriculture Chonnam National University, Kwangju 500-757, Korea Republic
Language:English
Abstract:A pregnancy-induced clone was identified by differential screening from a cDNA library of bovine mammary gland. The polyadenylate binding protein 1 (PABP) cDNA (EMBL, GenBank and DDBJ Accession Number AJ401269) had a total length of 1911 nucleotides coding for 636 amino acids. Its nucleotide sequence was 95 and 94% identical to those of human and mouse species, respectively, whereas the deduced amino acid sequences showed 100% identity with those of human species. Induction of the PABP mRNA was observed in bovine mammary tissues at 7 and 8 months of pregnancy, compared with unserviced, lactating and involuted states. PABP gene expression was examined in mammary epithelial HC11 cells at proliferating, differentiated and apoptotic conditions. The mRNA levels of the PABP gene were similar between proliferating and differentiated cells, but expression levels were very low in apoptotic cells, in comparison to other conditions. These results demonstrate that the PABP gene is induced during pregnancy, at which stage mammary epithelial cells are actively proliferating
Descriptors:amino-acid-sequences. binding-proteins. complementary-DNA. DNA-cloning. gene-expression. mammary-glands. mammary-tissue. messenger-RNA. pregnancy
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. WW000. LL600
Supplementary Info:15 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

38. Title:Degradation of rice straw by rumen fungi and cellulolytic bacteria through mono-, co- or sequential- cultures

View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (6). 797-802
CD Volume:379
Print Article: Pages: 797-802
Author(s):Ha J K Lee S S Kim S W Han I K Ushida K Cheng K J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Language:English
Abstract:Two strains of rumen fungi (Piromyces rhizinflata B157 and Orpinomyces joyonii SG4) and 3 strains of rumen cellulolytic bacteria (Ruminococcus albus B199, Ruminococcus flavefaciens FD1 and Fibrobacter succinogenes S85) were used as mono-, co- and sequential-cultures to assess the relative contributions and interactions between rumen fungi and cellulolytic bacteria on rice straw degradation. The rates of dry matter degradation of co-cultures were similar to those of corresponding bacterial mono-cultures. Compared to corresponding sequential-cultures, the degradation of rice straw was reduced in all co-cultures ($P<0.01$). Regardless of the microbial species, the cellulolytic bacteria seemed to inhibit the degradation of rice straw by rumen fungi
Descriptors:degradation. rice-straw. rumen. rumen-bacteria. rumen-digestion. rumen-fungi
Identifiers:Fibrobacter succinogenes. Orpinomyces joyonii. Piromyces rhizinflata. Ruminococcus flavefaciens
Organism Descriptors:Ruminococcus. Ruminococcus-albus
Supplemental Descriptors:Lachnospiraceae. Firmicutes. bacteria. prokaryotes. Ruminococcus. Peptococcaceae
Subject Codes:ZZ394. RR300
Supplementary Info:24 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

39. Title:Genetics and molecular biology in aquaculture
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (6). 894-898
CD Volume:379
Print Article: Pages: 894-898
Author(s):Lakra W S
Author Affiliation:Fish Genetics & Biotechnology Division, Central Institute of Fisheries Education, Versova, Mumbai - 400 061, India
Conference Title:3rd Joint Symposium of Japan and Korea: Rumen metabolism and physiology. 1-3 October, 2000, Miyazaki, Japan
Language:English
Abstract:This paper reviews some of the options which are now the proven genetic techniques and biotechnologies used for fish stock improvement in aquaculture. Advancement in the application of selective breeding; hybridization; chromosome and gene manipulations; sex control and sex reversal and molecular genetics in aquaculture species, for enhanced productivity, are discussed
Descriptors:aquaculture. biotechnology. fish-production. genetic-engineering. hybridization. molecular-genetics. productivity. selection. sex-control. sex-reversal
Subject Codes:LL240. MM120. LL250. WW000
Supplementary Info:32 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

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40. Title:The effect of saturated fatty acids on cellulose digestion by the rumen anaerobic fungus, Neocallimastix frontalis C5-1
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (7). 941-946
CD Volume:379
Print Article: Pages: 941-946
Author(s):Ha J K Lee S S Gao Z Kim C H Kim S W Ko J Y Cheng K J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Language:English
Abstract:The effects of various concentrations of saturated fatty acids (SFA; caprylic, capric and stearic acids) on the growth of the anaerobic fungus, Neocallimastix frontalis C5-1 isolated from the rumen of a Korean native goat were investigated. At higher concentrations of fatty acids (0.1%, w/v), the addition of SFA strongly decreased filter paper (FP) cellulose digestion and polysaccharide-degrading enzyme activity. The sensitivity of the rumen anaerobic fungus to the added fatty acids increased in the following order: caprylic (C8:0) > capric (C10:0) > stearic (C18:0) acid, although stearic acid had no significant ($p<0.05$) inhibitory effects at any of the concentrations tested. However, the addition of SFA at lower concentrations (0.01 and 0.001% levels), did not inhibit FP cellulose degradation and enzyme activity. Furthermore, although these parameters were slightly stimulated by the addition of SFA, they were not statistically different from control values. This is the first report examining the effects of fatty acids on anaerobic gut fungi. We found that the lower levels of fatty acids used in this experiment were able to stimulate the growth and specific enzyme activities of rumen anaerobic fungi, whereas the higher levels of fatty acids were inhibitory with respect to fungal cellulolysis
Descriptors:cellulase. cellulose-digestion. enzyme-activity. native-livestock. rumen-fungi. saturated-fatty-acids
Geographic Locator:Korea-Republic
Identifiers:Neocallimatix frontalis
Organism Descriptors:goats
Supplemental Descriptors:Capra. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. East-Asia. Asia. Developing-Countries. Threshold-Countries. OECD-Countries
Subject Codes:LL510. ZZ394
Supplementary Info:26 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences
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41. Title:Determination of optimal dietary sulfur amino acids ratio relative to lysine for growing barrows and gilts
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (7). 1003-1007
CD Volume:379
Print Article: Pages: 1003-1007
Author(s):Chang W H Kim J D Kim S W Xuan Z N Kim Y Y Paik I K Han I K
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Language:English
Abstract:This experiment was conducted to investigate the effects of dietary SAA (sulfur-containing amino acids) on growth performance, nutrient

digestibility and blood urea nitrogen (BUN) content, and to determine the optimal SAA:lysine ratio for growing barrows and gilts. A total of 150 pigs (75 barrows and 75 gilts, Landrace x Yorkshire x Duroc) were assigned to 6 treatments with 5 replicates of 5 pigs per pen. All pigs were fed diets containing either 1.12 (for barrows) or 1.33% (for gilts) dietary lysine with increasing SAA levels (50, 55 and 60% of dietary lysine) in a 2 x 3 factorial design. Throughout the whole experimental period (15 to 54 kg body weight), there was no interaction between sexes and SAA:lysine ratios on ADG, ADFI and FCR. However, increasing the SAA:lysine ratio from 50 to 60% in a diet showed a trend to increase ADG and ADFI of barrows. None of differences in nutrient digestibilities except for calcium and phosphorus were observed and gilts showed higher digestibility of calcium and phosphorus ($p<0.05$). Among dietary SAA:lysine ratios, there were no differences in apparent nutrient digestibility. Mean values of the essential amino acids (EAA), non-essential amino acids (NEAA) and total amino acids (TAA) digestibilities were higher in gilts than barrows ($p<0.01$). However, no differences in mean value of EAA, NEAA and TAA digestibilities were observed among dietary SAA:lysine ratios. Between sexes and among SAA:lysine ratios, no significant difference in BUN concentration was observed. This study demonstrated that the optimal inclusion ratio of SAA:lysine was 55% and below 50% in barrows and gilts, respectively

Descriptors:amino-acids. blood-chemistry. calcium. digestibility. essential-amino-acids. feed-conversion-efficiency. feed-intake. gilts. liveweight-gain. lysine. nonessential-amino-acids. phosphorus. sulfur-amino-acids. urea

Organism Descriptors:pigs

Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates

Subject Codes:RR300. LL500. LL510. LL520. RR000

Supplementary Info:21 ref

ISSN:1011-2367

Year:2001

Journal Title:Asian-Australasian Journal of Animal Sciences

42. Title:Impact of ambient temperature and dietary crude protein in wethers: nitrogen metabolism and feed efficiency

View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (9). 1221-1227

CD Volume:379

Print Article: Pages: 1221-1227

Author(s):Sun Sangsoo Christopherson R J

Author Variant:Sun-S

Author Affiliation:Department of Animal Science, Institute of Biotechnology, Chonnam National University, Kwangju 500-757, Korea Republic

Language:English

Abstract:Eighteen Suffolk wethers were housed in individual crates and exposed to controlled environmental temperatures of 1-4 deg C (cold) or 21-24 deg C (warm) during a 10-week experimental period. The sheep were fed diets containing 7, 11 or 14% CP ad libitum. A 2 x 3 factorial design with a single crossover of environment was performed. Feed intake, liveweight gain and faecal and urine N excretion were measured. Apparent digestibilities were not affected by dietary CP or temperature; however, voluntary intake per kg bodyweight was significantly ($P<0.05$) increased by dietary CP in both environments. Lambs kept in cold temperature gained weight slightly faster when N intake was above 27 g/day. N excretion and N balance were

significantly (P<0.01) affected by dietary CP, while faecal N excretion was significantly increased (P<0.05) in the animals kept in a cold environment. The ADG of the sheep fed 11% CP and kept in cold temperature was comparable to the sheep fed 14% CP and kept in warm environment. The results support the hypothesis that lambs kept in cold temperature can still utilize nutrients even with a slight reduction in dietary CP content
Descriptors:crude-protein. digestibility. environmental-temperature. faeces. feed-conversion-efficiency. feed-intake. growth-rate. liveweight-gain. nitrogen-metabolism. urine. wethers
Organism Descriptors:sheep
Supplemental Descriptors:Ovis. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL510. LL520. RR300
Supplementary Info:36 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

43. Title:Study on the development of a probiotics complex for weaned pigs
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (10). 1425-1428
CD Volume:379
Print Article: Pages: 1425-1428
Author(s):Xuan Z N Kim J D Heo K N Jung H J Lee J H Han Y K Kim Y Y Han I K
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suweon 441-744, Korea Republic
Language:English
Abstract:This study was conducted to investigate the effects of supplementation with probiotic complex on the growth performance, nutrient digestibility, diarrhoea score and microbial population in pigs weaned at 21 days of age. Treatments were: (1) 0.2% antibiotics (Avilamycin, control A); (2) 0.1% Ractocom (control B); (3) 0.1% probiotics complex; (4) 0.2% probiotics complex and (5) 0.3% probiotics complex. A total of 80 pigs were used and each treatment had 4 replicates with 4 pigs per replicate. During the phase I period (days 0 to 14), pigs fed control B diet showed higher ADG and better F/G than any other treatments, although the difference was not significant. During the later experimental period (days 15 to 28), pigs fed diet supplemented with 0.2% probiotics complex showed slightly higher ADG. Overall, the diet that contained 0.2% probiotics complex gave slightly higher ADG and ADFI than the other diets. In a metabolic trial using 20 piglets, nutrient digestibility showed the best results in pigs fed 0.2% probiotics complex diet, but not significantly different from other groups. Diarrhoea score and microbial population status in the intestines, colon and faeces were not affected by dietary treatments. In conclusion, this study suggested that a newly developed probiotics complex can replace antibiotics in weaned pigs
Descriptors:diarrhoea. digestibility. faecal-flora. feed-conversion-efficiency. feed-intake. growth. intestinal-microorganisms. nutritive-value. probiotics
Organism Descriptors:pigs
Supplemental Descriptors:Sus-scrofa. Sus. Suidae. Suiformes. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL500. LL520. RR130. RR300
Supplementary Info:12 ref
ISSN:1011-2367
Year:2001

Journal Title:Asian-Australasian Journal of Animal Sciences
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44. Title:Cloning and expression of lactate dehydrogenase H chain gene in adipose tissues of Korean cattle
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (12). 1670-1674
CD Volume:379
Print Article: Pages: 1670-1674
Author(s):Kim H H Seol M B Jeon D H Sun S S Kim K H Choi Y J Baik M G
Author Affiliation:Department of Genetic Engineering, Biotechnology Research Institute, Chonnam National University, Kwangju 500-757, Korea Republic
Language:English
Abstract:To understand molecular mechanisms that regulate deposition and release of intramuscular fat, a fasting-induced clone was identified by differential screening from cDNA library of adipose tissues of Korean cattle. The clone had a total length of 1 319 nucleotides coding for 334 amino acids. It was identified as one encoding L-lactate dehydrogenase H chain (LDH-B). Comparison of the deduced amino acid sequences of bovine LDH-B with those of pig, human, rat, and mouse showed 98, 98, 97, and 96% identity, respectively. Food deprivation for 48 h increased mRNA levels of LDH-B gene in adipose tissues of Korean cattle compared to fed- and 6 h refed- tissues. The expression of obese mRNA was examined for individual adipose tissue from several fat depots. Fasting induced expression of LDH-B gene in subcutaneous adipose tissues, but it did not affect expression levels in abdominal, perirenal and intramuscular tissues. Results demonstrate that induction of LDH-B gene during fasting may represent a metabolic shift from anaerobic state to aerobic predominance in fasted adipose tissues and that its responses to fasting are different among several adipose tissues
Descriptors:adipose-tissue. amino-acid-sequences. DNA-cloning. fasting. genes. lactate-dehydrogenase. messenger-RNA
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. LL500. LL510. WW000
Supplementary Info:16 ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences
Copyright:Copyright CAB International

45. Title:Biotechnologies for improving animal metabolism and growth - a review
View Article: Asian-Australasian Journal of Animal Sciences. 2001. 14 (12). 1794-1802
CD Volume:379
Print Article: Pages: 1794-1802
Author(s):DaiWen Chen
Author Variant:Chen-D-W
Author Affiliation:Institute of Animal Nutrition, Sichuan Agricultural University, Ya'an, Sichuan 625014, China
Language:English
Abstract:Biotechnology will play a critical role in improving animal productivity. Animal growth rate and muscle deposition potential can be greatly improved by the application of biotechnology and biotechnological products. Administration of recombinant somatotropin (ST) or other compounds such as insulin-like growth factor 1 (IGF-1)

and growth hormone-releasing peptides (GHRPs) can enhance growth rate and carcass lean percentage. Gene transfer offers a powerful approach to manipulate endocrine system and metabolic pathways toward faster growth and better feed efficiency. Biotechnology is also extensively used for improving metabolism and activity of gut microorganisms for better nutrient digestibility. Knockout of growth-inhibiting genes such as myostatin results in considerable acceleration of body weight and muscle growth. Animal growth can also be improved by the use of gene therapy. Immunomodulation is another approach for efficient growth through controlling the activity of endogenous anabolic hormones. All the above aspects will be discussed in this review
Descriptors:biotechnology. carcass-composition. gene-therapy. gene-transfer. genes. insulin-like-growth-factor. livestock. liveweight-gain. metabolism. muscles. ontogeny. peptides. reviews. somatotropin
Identifiers:myostatin
Subject Codes:LL240. WW000
Supplementary Info:many ref
ISSN:1011-2367
Year:2001
Journal Title:Asian-Australasian Journal of Animal Sciences

46. Title:The long-term ability of phosphite to control Phytophthora cinnamomi in two native plant communities of Western Australia
View Article: Australian Journal of Botany. 2001. 49 (6). 761-770
CD Volume:338
Print Article: Pages: 761-770
Author(s):Tynan K M Wilkinson C J Holmes J M Dell B Colquhoun I J McComb J A Hardy G E S J
Author Affiliation:School of Biological Sciences and Biotechnology, Murdoch University, South St, Perth, WA 6150, Australia
Language:English
Abstract:This study examined the ability of foliar applications of the fungicide phosphite (Fosject 200 or Foli-R-Fos 400) to contain colonization of P. cinnamomi in a range of plant species growing in natural plant communities in the northern sandplain and jarrah (Eucalyptus marginata) forest of southwestern Australia. Wound inoculation of plant stems with P. cinnamomi was used to determine the efficacy of phosphite over time after application. Colonization by P. cinnamomi was reduced for 5-24 months after phosphite was applied, depending on the concentration of phosphite used, plant species treated and the time of phosphite application. Plant species within and between plant communities varied considerably in their ability to take up and retain phosphite in inoculated stems and in the in planta concentrations of phosphite required to contain P. cinnamomi. As spray application rates of phosphite increased from 5 to 20 g litre-1, stem tissue concentrations increased, as did the ability of a plant species to contain P. cinnamomi. However, at application rates of phosphite above 5 g litre-1 phytotoxicity symptoms were obvious in most species, with some plants being killed. So, despite 10 and 20 g litre-1 of phosphite being more effective and persistent in controlling P. cinnamomi, these rates are not recommended for application to the plant species studied. The results of this study indicate that foliar application of phosphite has considerable potential in reducing the impact of P. cinnamomi in native plant communities in the short-term. However, in order to maintain adequate control, phosphite should be sprayed every 6-12 months, depending on the species and/or plant community

Descriptors:application-rates. chemical-control. foliar-application. fungicides. phytotoxicity. plant-communities. plant-disease-control. plant-pathogenic-fungi. plant-pathogens
Geographic Locator:Australia. Western-Australia
Identifiers:phosphite
Organism Descriptors:Eucalyptus-marginata. Phytophthora-cinnamomi
Supplemental Descriptors:Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Eucalyptus. Myrtaceae. Myrtales. dicotyledons. angiosperms. Spermatophyta. plants. Phytophthora. Peronosporales. Mastigomycotina. Eumycota. fungi. Australia
Subject Codes:FF610. HH405. KK100
Supplementary Info:28 ref
ISSN:0067-1924
Year:2001
Journal Title:Australian Journal of Botany

47. Title:Residual effect of nitrogen fixed by mungbean (Vigna radiata) and blackgram (Vigna mungo) on subsequent rice and wheat crops
View Article: Australian Journal of Experimental Agriculture. 2001. 41 (2). 245-248
CD Volume:339
Print Article: Pages: 245-248
Author(s):Ahmad T Hafeez F Y Mahmood T Malik K A
Author Affiliation:National Institute for Biotechnology and Genetic Engineering, PO Box 577, Faisalabad, Pakistan
Language:English
Abstract:Annual crop legumes, grown in rotation with cereal crops, contribute to the total pool of nitrogen in the soil and improve the yield of cereals. The present study aimed at the quantification of nitrogen fixation by mung bean and black gram using 15N isotopic dilution methodology; and the quantification of grain and nitrogen yield differences of succeeding rice and wheat crops compared with a cereal-cereal rotation in a field experiment conducted in Pakistan during 1997-98. There were 2 experiments in separate fields but with the same layout; in experiment 1, rice followed the mung bean and black gram varieties and in experiment 2, wheat followed the mung bean and black gram varieties. Nitrogen fixed ranged from 26 to 36 kg/ha in experiment 1 and from 30 to 36 kg/ha in experiment 2. Soil nitrogen spared by legume crops ranged from 2 to 26 kg/ha in experiment 1 and from 4 to 23 kg/ha in experiment 2. Rice paddy yields were 0.6-1.1 t/ha higher in the legume-cereal rotation than in the cereal-cereal sequence. Similarly, wheat grain yields were 0.5-1.1 t/ha higher in the legume-cereal rotation
Descriptors:black-gram. crop-yield. mung-beans. nitrogen-content. nitrogen-fixation. residual-effects. rice. rotations. sequential-cropping. soil-fertility. wheat
Geographic Locator:Pakistan
Organism Descriptors:Oryza. Oryza-sativa. Triticum. Triticum-aestivum. Vigna-mungo. Vigna-radiata
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations. Triticum. Vigna. Papilionoideae. Fabaceae. Fabales. dicotyledons
Subject Codes:FF005. FF100. JJ100. JJ600
Supplementary Info:23 ref
ISSN:0816-1089
Year:2001

Journal Title:Australian Journal of Experimental Agriculture

48. Title:Nutritional constraints on root nodule bacteria affecting symbiotic nitrogen fixation: a review
View Article: Australian Journal of Experimental Agriculture. 2001. 41 (3). 417-433
CD Volume:339
Print Article: Pages: 417-433
Author(s):O'Hara G W
Author Affiliation:Centre for Rhizobium Studies, School of Biological Sciences and Biotechnology, Murdoch University, Murdoch, WA 6150, Australia
Language:English
Abstract:Root nodule bacteria require access to adequate concentrations of mineral nutrients for metabolic processes to enable their survival and growth as free-living soil saprophytes, and in their symbiotic relationship with legumes. Essential nutrients with a direct requirement in metabolism of rhizobia are carbon, hydrogen, oxygen, nitrogen, phosphorus, sulfur, potassium, calcium, magnesium, iron, manganese, copper, zinc, molybdenum, nickel, cobalt and selenium. Boron does not seem to be required by rhizobia, but is essential for the establishment of effective legume symbioses. Nutrient constraints can affect both free-living and symbiotic forms of root nodule bacteria, but whether they do is a function of a complex series of events and interactions. Important physiological characteristics of rhizobia involved in, or affected by, their mineral nutrition include nutrient uptake, growth rate, gene regulation, nutrient storage, survival, genetic exchange and the viable non-culturable state. There is considerable variation between genera, species and strains of rhizobia in their response to nutrient deficiency. The effects of nutrient deficiencies on free-living rhizobia in the soil are poorly understood. Competition between strains of rhizobia for limiting phosphorus and iron in the rhizosphere may affect their ability to nodulate legumes. Processes in the development of some legume symbioses specifically require calcium, cobalt, copper, iron, potassium, molybdenum, nickel, phosphorus, selenium, zinc and boron. Limitations of phosphorus, calcium, iron and molybdenum in particular, can reduce legume productivity by affecting nodule development and function. The effects of nutrient deficiencies on rhizobia-legume signalling are not understood. The supply of essential inorganic nutrients to bacteroids in relation to nutrient partitioning in nodule tissues and nutrient transport to the symbiosome may affect effectiveness of nitrogen fixation. An integration of molecular approaches with more traditional biochemical, physiological and field-based studies is needed to improve understanding of the agricultural importance of rhizobia response to nutrient stress
Descriptors:genetics. growth-rate. legumes. mineral-uptake. nitrogen. nitrogen-fixation. nitrogen-fixing-bacteria. nodulation. nutrient-deficiencies. nutrient-requirements. nutrient-uptake. reviews. reviews. rhizosphere. survival. symbiosis
Organism Descriptors:Fabaceae. Rhizobium
Supplemental Descriptors:Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:JJ100. ZZ394. ZZ395
Supplementary Info:129 ref
ISSN:0816-1089
Year:2001
Journal Title:Australian Journal of Experimental Agriculture
Copyright:Copyright CAB International

49. Title:Acid tolerance in legume root nodule bacteria and selecting for it
View Article: Australian Journal of Experimental Agriculture. 2001. 41 (3). 435-446
CD Volume:339
Print Article: Pages: 435-446
Author(s):Dilworth M J Howieson J G Reeve W G Tiwari R P Glenn A R
Author Affiliation:Centre for Rhizobium Studies, School of Biological Sciences and Biotechnology, Murdoch University, Murdoch, WA 6150, Australia
Language:English
Abstract:Bacteria face a variety of problems in trying to survive and grow in acidic environments. These include maintaining intracellular pH (pHi) in order to protect internal cell components, modifying or abandoning those external structures inevitably exposed to acidity, and resisting stresses whose interaction with pH may be the actual determinant of survival or growth rather than H+ toxicity per se. An important aspect of acid resistance in Gram-negative bacteria (including the root nodule bacteria) is the adaptive acid tolerance response (ATR), whereby cells grown at moderately acid pH are much more resistant to being killed under strongly acidic conditions than are cells grown at neutral pH. Survival during pH shock is also markedly affected by the calcium concentration in the medium. The pH at which commercial legume inoculants are grown and supplied for inoculation into acid soils may therefore be of considerable importance for initial inoculant survival. The mechanisms of resistance to acidity in root nodule bacteria have been investigated via 3 approaches: (i) creation of acid-sensitive mutants from acid-tolerant strains, and identification of the genes involved; (ii) random insertion of reporter genes to create mutants with pH-dependent reporter expression; and (iii) proteomics and identification of proteins regulated in response to acidity. The results of the first approach, directed at genes essential for growth at acid pH, have identified a sensor-regulator gene pair (actS-actR), a copper-transporting ATPase (actP), and another gene involved in lipid metabolism (actA), inactivation of which results in sensitivity to heavy metals. While the ActS-ActR system is undoubtedly required for both acid tolerance and the ATR, it is also involved in global regulation of a wide range of cellular processes. The second approach has allowed identification of a range of acid-responsive genes, which are not themselves critical to growth at low pH. One of these (phrR) is itself a regulator gene induced by a range of stresses including acid pH, but not controlled by the ActS-ActR system. Another, lpiA, responds specifically to acidity (not to other stresses) and may well be an antiporter related to nhaB, which is involved in Na+ transport in other bacteria. The third approach indicates a number of proteins whose concentration changes with a switch from neutral to acidic growth pH; most of these seem to have no homologues in the protein databases, while the blocked N-terminal sequences of others have prevented identification. It has been common experience that strains of root nodule bacteria selected for acid tolerance in the laboratory are not necessarily successful as inoculants in acid soils. In the light of the complex interactive effects on growth and survival of H+, Ca2+ and Cu2+ concentrations in our studies, this lack of correlation is no longer surprising. It remains to be seen whether it will be possible to improve the correlation between growth on laboratory media and performance in acid soils by determining which strains show an ATR, and by screening on media with defined ranges of concentration of some of these critical metal ions, perhaps approximating those to be expected in the soils in question

Descriptors:acid-soils. adenosinetriphosphatase. genes. growth. hydrogen-ions. mutants. nitrogen-fixing-bacteria. pH. reporter-genes. soil-types. strains. survival. tolerance
Identifiers:acid tolerance
Subject Codes:JJ100. ZZ394. ZZ395. JJ200. WW000
Supplementary Info:72 ref
ISSN:0816-1089
Year:2001
Journal Title:Australian Journal of Experimental Agriculture
Copyright:Copyright CAB International

50. Title:Molecular epidemiology of infectious bronchitis virus isolates from China and Southeast Asia
View Article: Avian Diseases. 2001. 45 (1). 201-209
CD Volume:369
Print Article: Pages: 201-209
Author(s):Yu L Wang Z Jiang Y Low S Kwang J
Author Affiliation:Animal Health Biotechnology Laboratory, Institute of Molecular Agrobiology, National University of Singapore, 117604, Singapore
Language:English
Language of Summary:spanish
Abstract:In order to trace the origin and evolution of avian infectious bronchitis virus (IBV) isolates in China and Southeast Asia, genomic sequencing was used for molecular characterization of 24 IBV isolates collected from China, Malaysia, and Singapore between 1983 and 1999, and two reference strains in comparison with the published sequences. The 5' region of the S1 genes, containing hypervariable regions I and II, and 3' region of the nucleocapsid genes, containing cytotoxic T lymphocyte epitopes, were used to construct phylogenetic trees for analysis. The results showed that the 24 isolates could be divided into three distinct groups, that is, American, Asian, and European. Some isolates formed a distinct Asian phylogenetic group, suggesting that IBV has existed for some time in Asia. Our results also showed that in vivo recombination of IBV may have occurred at a rather high frequency, contributing to the diversity of these IBV isolates. Importantly, recombination events have probably occurred between vaccine strains and field strains in the natural condition
Descriptors:molecular-epidemiology. nucleotide-sequences. poultry. recombination
Geographic Locator:China. Malaysia. Singapore
Organism Descriptors:fowls. infectious-bronchitis-virus
Supplemental Descriptors:East-Asia. Asia. Developing-Countries. Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry. Coronavirus. Coronaviridae. viruses. South-East-Asia. Threshold-Countries. ASEAN-Countries. Commonwealth-of-Nations
Subject Codes:LL821. ZZ395
Supplementary Info:30 ref
ISSN:0005-2086
Year:2001
Journal Title:Avian Diseases
Copyright:Copyright CAB International

51. Title:Study of protection by recombinant fowl poxvirus expressing C-terminal nucleocapsid protein of infectious bronchitis virus against challenge
View Article: Avian Diseases. 2001. 45 (2). 340-348
CD Volume:369
Print Article: Pages: 340-348

Author(s):Yu L Liu W Schnitzlein W M Tripathy D N Kwang J
Author Affiliation:Animal Health Biotechnology Laboratory, Institute of Molecular Agrobiology, National University of Singapore, 117604, Singapore
Language:English
Language of Summary:spanish
Abstract:A stable recombinant fowl poxvirus (rFPV) expressing the C-terminal region (119 amino acids) of the nucleocapsid (N) protein of an infectious bronchitis virus (IBV) strain Ch3 was constructed by inserting the coding sequence within the thymidine kinase gene of fowl poxvirus (FPV) by homologous recombination. The N protein was expressed under control of the vaccinia virus promoter P7.5 in chicken embryo fibroblast cell cultures as seen in immunofluorescence assay and in rFPV-inoculated specific-pathogen-free (SPF) chickens by detecting antibodies with enzyme-linked immunosorbent assay (ELISA). A homologous IBV strain (Ch3) and two heterologous IBV strains (Ch5 and H4) were used to inoculate SPF chickens in a challenge to examine the protective efficacy of the rFPV. When the chickens were challenged with IBV Ch3 or Ch5, the control birds had respiratory signs of infections bronchitis, whereas all the vaccinated birds were clinically normal although low levels of the IBV infection were detected by a differential ELISA. In contrast, in the chickens challenged with IBV H4, all control birds and vaccinated birds suffered from the highly lethal IBV H4 infection. Our results suggest that the C-terminal 119 amino acid of the nucleocapsid expressed by FPV is a host-protective antigen and may induce cross-protective immunity against illness among some IBV strains
Descriptors:amino-acid-sequences. antigens. chick-embryos. homologous-recombination. immune-response. vaccination
Organism Descriptors:infectious-bronchitis-virus
Supplemental Descriptors:Coronavirus. Coronaviridae. viruses
Subject Codes:HH600. LL650. LL821
Supplementary Info:29 ref
ISSN:0005-2086
Year:2001
Journal Title:Avian Diseases
Copyright:Copyright CAB International

52. Title:Detection and screening of Salmonella enteritidis-infected chickens with recombinant flagellin
View Article: Avian Diseases. 2001. 45 (2). 410-415
CD Volume:369
Print Article: Pages: 410-415
Author(s):Yap LeeFah Low S Liu Wei Loh H Teo ThamPeng Kwang J
Author Variant:Yap-L-F. Liu-W. Teo-T-P
Author Affiliation:Animal Health Biotechnology, Institute of Molecular Agrobiology, National University of Singapore, 1 Research Link, Singapore 117604, Singapore
Language:English
Language of Summary:spanish
Abstract:Screening and identification of Salmonella enteritidis in commercial poultry flocks have assumed principal roles in preventing transmission of this pathogen to humans from hen eggs. Serologic diagnosis of S. enteritidis infection in commercial flocks currently relies on laboratory-based tests for detection of antibodies to the lipopolysaccharide, whole flagella, and bacteria. We amplified a sequence from the g,m flagellin of S. enteritidis, followed by cloning, expression, and purification of the protein. The recombinant protein was first characterized by western blot and subsequently

evaluated as enzyme-linked immunosorbent assay (ELISA) antigen for detection of S. enteritidis infection. A total number of 49 positive sera and 40 negative sera were tested for ELISA validation. A cutoff value of 0.14 was shown to be sufficient to discriminate the negative and positive sera. Results obtained by testing sera raised against different bacterial strains/serotypes further confirmed that this recombinant flagellin-based ELISA was indeed specific for the detection of S. enteritidis. Both sensitivity and specificity of the developed ELISA test were comparable with a commercially available test, indicating that it is a highly promising and reliable diagnostic tool for S. enteritidis infection
Descriptors:genes. nucleotide-sequences. poultry. recombinant-proteins. screening
Organism Descriptors:fowls. Salmonella-enteritidis
Supplemental Descriptors:Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry. Salmonella. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:LL821. ZZ395
Supplementary Info:13 ref
ISSN:0005-2086
Year:2001
Journal Title:Avian Diseases
Copyright:Copyright CAB International

53. Title:Characterization of three infectious bronchitis virus isolates from China associated with proventriculus in vaccinated chickens
View Article: Avian Diseases. 2001. 45 (2). 416-424
CD Volume:369
Print Article: Pages: 416-424
Author(s):Yu Li Jiang YiHai Low S Wang ZhiLiang Nam Seah [Nam S J] Liu Wei Kwang J
Author Variant:Yu-L. Jiang-Y-H. Wang-Z-L. Nam-S-J. Liu-W
Author Affiliation:Animal Health Biotechnology Laboratory, Institute of Molecular Agrobiology, National University of Singapore, Singapore 117604, Singapore
Language:English
Language of Summary:spanish
Abstract:Outbreaks of an avian disease in infectious bronchitis-vaccinated chickens in China have led to the characterization of coronaviral isolates Q1, J2, and T3, which were isolated from proventricular tissues of the affected young layer flocks. Serologic analysis revealed that they could induce high titers of infectious bronchitis virus (IBV) antibodies in inoculated specific-pathogen-free (SPF) chickens in indirect enzyme-linked immunosorbent assay but were not neutralized by antisera specific to the IBV serotype M41 and the Australian T strain. In a pathogenicity experiment, the clinical signs and related gross lesions resembling those of field outbreaks were reproduced in SPF chickens, and viruses were reisolated from the damaged tissues, including trachea, proventriculus, duodenum, and cecal tonsil. Sequence data demonstrated the complete S1 amino acid sequences of these isolates were almost identical despite recovery from geographically different areas in China and had 47.3%-82.3% similarity in comparison with the 47 published S1 sequences. On the basis of genotyping and limited serology, the three isolates, which were responsible for field outbreaks of the disease, might be a new IBV variant
Descriptors:amino-acid-sequences. characterization. poultry. proventriculus. vaccination
Geographic Locator:China

Identifiers:genotyping
Organism Descriptors:fowls. infectious-bronchitis-virus
Supplemental Descriptors:East-Asia. Asia. Developing-Countries. Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry. Coronavirus. Coronaviridae. viruses
Subject Codes:HH600. LL821. ZZ395
Supplementary Info:36 ref
ISSN:0005-2086
Year:2001
Journal Title:Avian Diseases
Copyright:Copyright CAB International

54. Title:Production of ethanol and xylitol from corn cobs by yeasts
View Article: Bioresource Technology. 2001. 77 (1). 57-63
CD Volume:367
Print Article: Pages: 57-63
Author(s):Farooq Latif Rajoka M I
Author Affiliation:National Institute for Biotechnology and Genetic Engineering, P.O. Box 577, Faisalabad, Pakistan
Language:English
Abstract:Saccharomyces cerevisiae and Candida tropicalis were used separately and as a coculture for simultaneous saccharification and fermentation (SSF) of 5-20% (w/v) dry maize cobs. A maximal ethanol concentration of 27, 23, 21 g/litre (w/v) from 200 g/litre (w/v) dry maize cobs was obtained by S. cerevisiae, C tropicalis and the coculture, respectively, after 96 h of fermentation. However, theoretical yields of 82%, 71% and 63% were observed from 50 g/1itre dry maize cobs for the above cultures, respectively. Maximal xylitol concentration of 21, 20 and 15 g/1itre from 200 g/1itre (w/v) dry maize cobs was obtained by C. tropicalis, the coculture, and S. cerevisiae, respectively. Maximum theoretical yields of 79%, 77% and 58% were observed from 50 g/litre of maize cobs, respectively. The volumetric productivities for ethanol and xylitol increased with the increase in substrate concentration, whereas yield decreased. Glycerol and acetic acid were formed as minor byproducts. S. cerevisiae and C. tropicalis resulted in better product yields (0.42 and 0.36 g/g) for ethanol and (0.52 and 0.71 g/g) for xylitol, respectively, whereas the coculture showed a moderate level of ethanol (0.32 g/g) and almost maximal levels of xylitol (0.69 g/g)
Descriptors:ethanol. fermentation. fermentation-products. maize-byproducts. maize-cobs. saccharification. xylitol
Organism Descriptors:Candida-tropicalis. Saccharomyces-cerevisiae. yeasts
Supplemental Descriptors:Saccharomyces. Endomycetales. Ascomycotina. Eumycota. fungi. Candida. Deuteromycotina
Subject Codes:XX100. XX700. WW000. FF003
Supplementary Info:39 ref
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology
Copyright:Copyright CAB International

55. Title:Nitrogen, carbon and phosphorus mineralization in soils from semi-arid highlands of central Mexico amended with tannery sludge
View Article: Bioresource Technology. 2001. 77 (2). 121-130
CD Volume:367
Print Article: Pages: 121-130
Author(s):Barajas Aceves M Dendooven L
Author Affiliation:Laboratory of Soil Ecology, Department of Biotechnology and Bioengineering, CINVESTAV-IPN, Avenida Instituto Politecnico Nacional

2508, Apartado Postal 14740, San Pedro Zacatenco, C.P. 07000, Mexico, DF, Mexico
Language:English
Abstract:Tannery sludge contains valuable nutrients and could be used as a fertilizer to pioneering vegetation in heavily eroded soils of the semiarid highlands of central Mexico. Soil collected under and outside the canopy of mesquite (Prosopis laevigata), huizache (Acacia tortuosa) and catclaw (Mimosa biuncifera), and cultivated with maize (Zea mays) and beans (Phaesolus vulgaris) was amended with 1.5 g tannery sludge/kg soil (or 210 kg dry sludge/ha), or left unamended. Amended and unamended soils were incubated aerobically for 70 days at 22 plus or minus 2 deg C and CO2 production, available P, and inorganic N concentrations were monitored. The CO2 production rate, total C and P, available P, biomass C and P were larger under the vegetation canopy than outside it. The soils were depleted of N as more than 50 mg N/kg soil could not be accounted for in the first days of the incubation. Nitrification showed a lag, which lasted 28 days, and the concentration of available P remained constant or increased slightly. Application of tannery sludge to soil increased CO2 production and inorganic N after 70 days, but available P did not increase. Application of tannery sludge increased C and N mineralization and could thus provide valuable nutrients to pioneer vegetation. Although no inhibitory effects on the biological functioning of the soil were found, further investigation into possible long-term environmental effects of the tannery sludge are necessary
Descriptors:beans. canopy. carbon-cycle. carbon-dioxide. eroded-soils. highlands. maize. mineralization. mineralization. nitrification. nitrogen-content. nitrogen-cycle. nutrient-availability. organic-amendments. organic-fertilizers. phosphorus. pioneer-species. rehabilitation. semiarid-zones. soil-amendments. soil-biology. soil-chemical-properties. soil-fertility. tannery-sludge. waste-utilization
Geographic Locator:Mexico
Identifiers:Phaesolus vulgaris. Prosopis laevigata
Organism Descriptors:Acacia-tortuosa. Mimosa-biuncifera. Prosopis. Zea-mays
Supplemental Descriptors:North-America. America. Developing-Countries. Threshold-Countries. Latin-America. OECD-Countries. Mimosa. Mimosoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants. Acacia. Zea. Poaceae. Cyperales. monocotyledons. Prosopis
Subject Codes:JJ700. JJ600. JJ100. JJ200. KK600. KK100. XX400
Supplementary Info:47 ref
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

56. Title:Simultaneous saccharification and fermentation of lignocellulosic wastes to ethanol using a thermotolerant yeast
View Article: Bioresource Technology. 2001. 77 (2). 193-196
CD Volume:367
Print Article: Pages: 193-196
Author(s):Krishna S H Reddy T J Chowdary G V
Author Affiliation:Biotechnology Division, Department of Chemical Engineering, Andhra University, Visakhapatnam 530 003, India
Language:English
Abstract:Simultaneous saccharification and fermentation (SSF) studies were carried out to produce ethanol from lignocellulosic wastes (sugarcane

leaves and Antigonum leptopus leaves) using Trichoderma reesei cellulase and yeast cells. The ability of a thermotolerant yeast, Kluyveromyces fragilis NCIM 3358, was compared with that of Saccharomyces cerevisiae NRRL-Y-132. K. fragilis performed better in the SSF process and gave high yields of ethanol (2.5-3.5% w/v) compared with those from S. cerevisiae (2.0-2.5% w/v). Increased ethanol yields were obtained when the cellulase was supplemented with beta -glucosidase. The conversions with K. fragilis were completed in a short time. The substrates were in the following order in terms of fast conversions: Solka floc > A. leptopus > sugarcane

Descriptors:beta-glucosidase. cellulase. ethanol-production. fermentation. leaves. lignocellulose. pretreatment. saccharification. sugarcane

Identifiers:Antigonum leptopus. Trichoderma reesei

Organism Descriptors:Kluyveromyces-fragilis. Saccharomyces-cerevisiae. Saccharum. Saccharum-officinarum. Trichoderma. Trichoderma-longibrachiatum

Supplemental Descriptors:Deuteromycotina. Eumycota. fungi. Kluyveromyces. Endomycetales. Ascomycotina. Saccharomyces. Saccharum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Trichoderma

Subject Codes:FF003. XX700. XX400. XX200

Supplementary Info:24 ref

ISSN:0960-8524

Year:2001

Journal Title:Bioresource Technology

57. Title:Production, purification and properties of microbial phytases

View Article: Bioresource Technology. 2001. 77 (3). 203-214

CD Volume:367

Print Article: Pages: 203-214

Author(s):Ashok Pandey Szakacs G Soccol C R Rodriguez Leon J A Soccol V T

Author Variant:Pandey-A

Author Affiliation:Biotechnology Division, Regional Research Laboratory, Council of Scientific and Industrial Research, Trivandrum 695-019, India

Language:English

Abstract:Phytases (myo-inositol hexakisphosphate phosphohydrolase, EC 3.1.3.8 [3-phytase]) catalyse the release of phosphate from phytate (myo-inositol hexakiphosphate). Several cereal grains, legumes and oilseeds, etc., store phosphorus as phytate. Environmental pollution due to the high-phosphate manure, resulting in the accumulation of P at various locations, has raised serious concerns. Phytases appear of significant value in effectively controlling P pollution. They can be produced from a host of sources including plants, animals and microorganisms. Microbial sources, however, are promising for their commercial exploitation. A table is included listing organisms and techniques that have been used. Strains of Aspergillus sp., chiefly A. ficuum and A. niger, have most commonly been employed for industrial purposes. Phytases are considered as a monomeric protein, generally possessing a molecular weight between 40 and 100 kDa. They show broad substrate specificity and generally have pH and temperature optima around 4.5-6.0 and 45-60 deg C. The crystal structure of phytase has been determined at 2.5 nm resolution. Immobilization of phytase has been found to enhance its thermostability. This article reviews recent trends on the production, purification and properties of microbial phytases, and briefly summarizes their molecular biology and gene expression

Descriptors:cereals. enzymes. food-quality. gene-expression. legumes. manures. oilseeds. phosphate. phytase. phytates. pollution. pollution-control. production. properties. purification. reviews
Identifiers:3-phytase. Aspergillus ficuum. Hyphomycetes. microorganismsAspergillus
Organism Descriptors:Aspergillus-niger. Fabaceae
Supplemental Descriptors:Aspergillus. Deuteromycotina. Eumycota. fungi. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:JJ700. XX100. PP600. WW000. ZZ395. XX700. FF005. QQ200
Supplementary Info:Many ref
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology
Copyright:Copyright CAB International

58. Title:Chemically modified papain for applications in detergent formulations
View Article: Bioresource Technology. 78 (1). May, 2001. 1-4
CD Volume:367
Print Article: Pages: 1-4
Author(s):Khaparde Shilpa S Singhal Rekha S
Author Affiliation:Food and Fermentation Technology Division, University Department of Chemical Technology, Matunga, Mumbai, 400 019
Language:English
Language of Summary:English (EN)
Abstract:Papain was modified using succinic anhydride, and the modified papain so obtained was compared with the native papain for its activity and stability in detergents. This study was done using commercial enzyme detergents as references. It was found that modified papain retained activity comparable to the commercial enzyme detergents. Chemically modified papain may prove to be an inexpensive alternative to alkaline proteases that are used in detergents
Descriptors:bioresource technology; biotechnology. Enzymology (Biochemistry and Molecular Biophysics). alkaline proteases: alternatives, uses; biodetergents; commercial enzyme detergents: applications; commercial enzymes: applications; detergent formulations; enzymes: applications; papain: chemically modified form, detergent formulation applications, native form; succinic anhydride: uses
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

59. Title:Yeast production from virgin grape marc
View Article: Bioresource Technology. 78 (1). May, 2001. 5-9
CD Volume:367
Print Article: Pages: 5-9
Author(s):Curto R B Lo Tripodo M M
Author Affiliation:Department of Organic and Biological Chemistry, University of Messina, Salita Sperone 31, 98166, Santa Agata, Messina: rlocurto@isengard.unime.it
Language:English
Language of Summary:English (EN)
Abstract:An alternative utilization of virgin grape marc (VGM) to produce SCP from S. cerevisiae is reported. A simple extraction method of fresh grape marc produces a sugar-rich solution; through fed-batch fermentation, a high-value yeast biomass instead of a low-value product like ethanol can be produced. Productivity and quality of yeast are similar to these obtainable from molasses. The convenience

of yeast production from VGM is briefly discussed; it appears of great interest in south Italy and generally in grape- producing countries, specially if these lack relevant sources of fermentable sugars
Descriptors:biomass; bioresource technology; biotechnology; fed-batch fermentations; single cell protein: food supplement, industrial production; virgin grape marc: alternative utilization. Bioprocess Engineering; Foods; Microbiology. sugars: fermentable
Organism Descriptors:Saccharomyces cerevisiae (Ascomycetes); grape (Vitaceae); yeasts (Fungi)
Supplemental Descriptors:Ascomycetes: Fungi, Plantae; Fungi: Plantae; Vitaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Fungi; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants
Subject Codes:Bioprocess Engineering; Foods; Microbiology
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

60. Title:Pig manure vermicompost as a component of a horticultural bedding plant medium: Effects on physicochemical properties and plant growth
View Article: Bioresource Technology. 78 (1). May, 2001. 11-20
CD Volume:367
Print Article: Pages: 11-20
Author(s):Atiyeh R M Edwards C A Subler S Metzger J D
Author Affiliation:Soil Ecology Laboratory, Ohio State University, 1735 Neil Avenue, 105 Botany and Zoology Building, Columbus, OH, 43210: atiyeh1@osu.edu
Language:English
Language of Summary:English (EN)
Abstract:This experiment was designed to characterize the physical, chemical and microbial properties of a standard commercial horticultural, greenhouse container, bedding plant medium (Metro-Mix 360), that had been substituted with a range of increasing concentrations (0%, 5%, 10%, 25%, 50% and 100% by volume) of pig manure vermicompost and to relate these properties to plant growth responses. The growth trials used tomatoes (Lycopersicon esculentum Mill.), grown in the substituted media for 31 days under glasshouse conditions, with seedling growth recorded in 20 pots for each treatment. Half of the tomato seedlings (10 pots per treatment) were watered daily with liquid inorganic fertilizer while the other half received water only. The percentage total porosity, percentage air space, pH and ammonium concentrations of the container medium all decreased significantly, after substitution of Metro-Mix 360 with equivalent amounts of pig manure vermicompost; whereas bulk density, container capacity, electrical conductivity, overall microbial activity and nitrate concentrations, all increased with increasing substitutions of vermicompost. The growth of tomato seedlings in the potting mixtures containing 100% pig manure vermicompost was reduced, possibly as a result of high soluble salt concentrations in the vermicompost and poorer porosity and aeration. The growth of tomato seedlings was greatest after substitution of Metro-Mix 360 with between 25% and 50% pig manure vermicompost, with more growth occurring in combinations of pig manure vermicompost treated regularly with a liquid fertilizer solution than in those with no fertilizer applied. Some of the growth enhancement in these mixtures seemed to be related to the combined effects of improved porosity, aeration and water retention in the medium and the high nitrate content of the substrate, which produced an increased uptake of nitrogen by the plant tissues, resulting in

increased plant growth. When the tomato seedlings were watered daily with liquid inorganic fertilizer, substitution of Metro-Mix 360 with a very small amount (5%) of pig manure vermicompost resulted in a significant increase in the growth of tomato seedlings. Such effects could not be attributed solely to the nutritional or physical properties of the pig manure vermicompost. Therefore, it seems likely that the pig manure vermicompost provided other biological inputs, such as plant growth regulators into the container medium, that still need to be identified fully

Descriptors:bioresource technology; biotechnology; pig manure vermicompost: horticultural uses, physicochemical properties; plant growth trials; plant nutrition. Horticulture (Agriculture); Waste Management (Sanitation). ammonium

Organism Descriptors:Lycopersicon esculentum [tomato] (Solanaceae): seedling; earthworms (Oligochaeta); pig (Suidae)

Supplemental Descriptors:Oligochaeta: Annelida, Invertebrata, Animalia; Solanaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Suidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Angiosperms; Animals; Annelids; Artiodactyls; Chordates; Dicots; Invertebrates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Plants; Spermatophytes; Vascular Plants; Vertebrates

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

ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

61. Title:Growth substrates made from duck excreta enriched wood shavings and source-separated municipal solid waste compost and separates: Physical and chemical characteristics

View Article: Bioresource Technology. 78 (1). May, 2001. 21-30
CD Volume:367
Print Article: Pages: 21-30

Author(s):Zoes V Dinel H Pare T Jaouich A
Author Affiliation:Eastern Cereals and Oilseeds Research Centre, Agriculture and Agri-Food Canada, 960 Carling Ave., Neatby Bldg., Ottawa, ON, K1A 0C6: paret@em.agr.ca

Language:English
Language of Summary:English (EN)

Abstract:Production and use of compost is an effective means to reduce wastes, and offers a large potential as growth substrates and source of nutrients. The objective of this study was to determine the physical and chemical characteristics of duck excreta enriched wood shavings (DMC) and source-separated municipal solid waste (MSW) composts and separates, and to assess the physical characteristics of growth substrates made from these two composts and selected substrates. MSW compost separates were the following sizes: F1 > 4 mm diameter, 2 mm < F2 < 4 mm, 1 mm < F3 < 2 mm and F4 < 1 mm. Growth substrates were prepared by mixing DMC and F2 and F3 MSW separates (M/M ratios). Growth substrates A-E consisted exclusively of 10-60% DMC and 20-60% of MSW separates F2 and F3. Growth substrates F-J, and K-O were the same as substrates A-E, with 15% M/M brick fragments or shredded plastic added as porosity agents, respectively. Growth substrates (BE/S) made of black earth (BE) and sandy loam soil (Ls) in a 1:4 (M/M) ratio, commercially available peat substrate (Pr) and an in-house sphagnum peat-based substrate (Gs) were used for comparison. Principal component analysis (PCA) showed that DMC was a better material than MSW with respect to porosity and water field capacity. MSW compost and separates differed by their relatively high levels of

water-soluble and HCl-hydrolyzable N and increased advantageous water retention capacity. PCA also showed that substrates A-E exhibited porosity and water field capacity similar to those of Pr. Substrates F-J had porosity and water field capacity similar to those of BE/S, whereas substrates K-O were more similar to Pr and to substrates A and B. The presented data indicate that DMC and MSW separates were complementary in providing good physical and chemical characteristics to the growth substrates

Descriptors:bioresource technology; biotechnology; composts: production, uses; duck excreta enriched wood shavings: preparation, uses; growth substrates: composition, physicochemical properties, preparation, uses; source-separated municipal solid waste compost: uses. Biochemistry and Molecular Biophysics; Nutrition; Waste Management (Sanitation)

Organism Descriptors:ducks (Anseriformes)

Supplemental Descriptors:Anseriformes: Aves, Vertebrata, Chordata, Animalia. Animals; Birds; Chordates; Nonhuman Vertebrates; Vertebrates

Subject Codes:Biochemistry and Molecular Biophysics; Nutrition; Waste Management (Sanitation)

ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

62. Title:Chromate tolerant bacteria isolated from tannery effluent

View Article: Bioresource Technology. 78 (1). May, 2001. 31-35
CD Volume:367
Print Article: Pages: 31-35

Author(s):Verma Tuhina Srinath T Gadpayle R U Ramteke P W Hans R K Garg S K
Author Affiliation:Environmental Microbiology Section and Photobiology Division, Industrial Toxicology Research Centre, Lucknow, 226 001: pwramteke@123india.com

Language:English
Language of Summary:English (EN)

Abstract:The occurrence of metal tolerant and antibiotic resistant organisms was investigated in tannery effluent. Seventy-seven isolates comprising heterotrophs (41) and coliforms (36) which were tolerant to chromate level of > 50 mug/ml were selected for detailed study. The majority of the coliforms were resistant to higher levels of chromate (200 mug/ml) whereas around 3% of the heterotrophs were resistant to Cr6+ at a level of > 150 mug/ml. All chromate tolerant heterotrophs were also tolerant to Cu2+ (100%) whereas only 58.53% coliforms were tolerant to Cn2+. Except in the case of Cd2+ a higher number of heterotrophs were found tolerant to other heavy metals tested. Both groups of isolates were found sensitive to mercury. Resistance to cephaloridine was more abundant ($P < 0.001$) in coliforms as compared to heterotrophs. On the other hand a significantly higher number ($P < 0.01$) of heterotrophs showed resistance to streptomycin and carbencillin. All coliforms were sensitive to chloramphenicol. Around 80% and 31.70% of coliforms and heterotrophs exhibited a relationship to the combination of metals and antibiotics. Both heterotrophs and coliforms tolerant to Hg2+ were also resistant to polymixin-B

Descriptors:bioresource technology; biotechnology; drug resistance; tannery effluents: microbial analysis. Microbiology; Waste Management (Sanitation); Toxicology. antibiotics; chromate: bacterial tolerance, toxicity; heavy metals

Geographic Locator:India (Oriental region)

Organism Descriptors:bacteria (Bacteria); coliforms (Enterobacteriaceae)

Supplemental Descriptors:Bacteria: Microorganisms; Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Microbiology; Waste Management (Sanitation); Toxicology
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

63. Title:Three-dimensional outgrowth of a wood-rotting fungus added to a contaminated soil from a former gasworks site
View Article: Bioresource Technology. 78 (1). May, 2001. 37-45
CD Volume:367
Print Article: Pages: 37-45
Author(s):Andersson B E Tornberg K Henrysson T Olsson S
Author Affiliation:Department of Biotechnology, Center for Chemistry and Chemical Engineering, Lund University, SE-221 00, Lund: erik.andersson@biotek.lu.se
Language:English
Language of Summary:English (EN)
Abstract:The capability of wood-rotting fungi (WRF) to colonise contaminated soil is an important fungal characteristic in the development of WRF-based soil bioremediation, it is also important to have methods that monitor the presence of the WRF in the soil. In this lab-scale study, it was shown that it was possible to re-capture, localise and identify a brown-rot fungus, Antrodia vaillantii, after it has been inoculated into, and grown in, a contaminated soil from a former gasworks site. The three-dimensional outgrowth of A. vaillantii was monitored by allowing it to grow into fungicide- treated wood baits, temporarily placed in the soil. After two weeks, the baits were withdrawn from the soil and surface sterilised with hydrogen peroxide to favour fungi growing inside baits, i.e., A. vaillantii. After subsequent plating of baits on selective agar medium the presence of A. vaillantii was confirmed with PCR/RFLP. A. vaillantii was found to be viable throughout the 54 days long study and exhibited a surface growth pattern similar to other well-known cord-forming basidiomycetes. Firstly, the upper part of the soil closest to the place of inoculation was colonised, however, over a period of time, the area of colonisation spread deeper into the soil. The detection method employed in the current study gave a conservative estimate of the fungal proliferation and did not require extensive sampling. Its use could be applicable in both applied research, such as soil bioremediation, and in pure microbial ecology studies
Descriptors:bioremediation; bioresource technology; biotechnology; former gasworks site; fungal growth; soil microbiology; soils. Microbiology; Pollution Assessment Control and Management; Soil Science. hydrogen peroxide
Organism Descriptors:Antrodia vaillantii (Basidiomycetes); wood-rotting fungi (Fungi): applications, soil colonization, three-dimensional outgrowth, uses
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae; Fungi: Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Microbiology; Pollution Assessment Control and Management; Soil Science
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

64. Title:Detection of catabolic genes in indigenous microbial consortia isolated from a diesel-contaminated soil
View Article: Bioresource Technology. 78 (1). May, 2001. 47-54
CD Volume:367
Print Article: Pages: 47-54
Author(s):Milcic Terzic J Lopez Vidal Y Vrvic M M Saval S
Author Affiliation:Institute of Engineering, National University of Mexico, Coyocan, Mexico, DF, 04510: ssb@pumas.iingen.unam.mx
Language:English
Language of Summary:English (EN)
Abstract:Bioremediation is often used for in situ remediation of petroleum-contaminated sites. The primary focus of this study was on understanding the indigenous microbial community which can survive in contaminated environment and is responsible for the degradation. Diesel, toluene and naphthalene-degrading microbial consortia were isolated from diesel-contaminated soil by growing on selective hydrocarbon substrates. The presence and frequency of the catabolic genes responsible for aromatic hydrocarbon biodegradation (xylE, ndoB) within the isolated consortia were screened using polymerase chain reaction PCR and DNA-DNA colony hybridization. The diesel DNA- extract possessed both the xylE catabolic gene for toluene, and the nah catabolic gene for polynuclear aromatic hydrocarbon degradation. The toluene DNA-extract possessed only the xylE catabolic gene, while the naphthalene DNA-extract only the ndoB gene. Restriction enzyme analysis with HaeIII indicated similar restriction patterns for the xylE gene fragment between toluene DNA- extract and a type strain, Pseudomonas putida ATCC 23973. A substantial proportion (74%) of the colonies from the diesel- consortium possessed the xylE gene, and the ndoB gene (78%), while a minority (29%) of the toluene-consortium harbored the xylE gene. 59% of the colonies from the naphthalene-consortium had the ndoB gene, and did not have the xylE gene. These results indicate that the microbial population has been naturally enriched in organisms carrying genes for aromatic hydrocarbon degradation and that significant aromatic biodegradative potential exists at the site. Characterization of the population genotype constitutes a molecular diagnosis which permits the determination of the catabolic potential of the site to degrade the contaminant present
Descriptors:biodegradation; bioremediation; bioresource technology; biotechnology; diesel-contaminated soils: microbial analysis; indigenous microbial consortia: analysis, isolation; microbial populations; soil pollution. Molecular Genetics (Biochemistry and Molecular Biophysics); Ecology (Environmental Sciences); Microbiology; Pollution Assessment Control and Management; Soil Science. DNA; catabolic genes: detection, functions; naphthalene; polyaromatic hydrocarbons: degradation; toluene
Organism Descriptors:bacteria (Bacteria); microorganisms (Microorganisms)
Supplemental Descriptors:Bacteria: Microorganisms; Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Ecology (Environmental Sciences); Microbiology; Pollution Assessment Control and Management; Soil Science
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

65. Title:Studies on the suitability of alginate-entrapped Chlamydomonas reinhardtii cells for sustaining nitrate consumption processes
View Article: Bioresource Technology. 78 (1). May, 2001. 55-61

CD Volume:367
Print Article: Pages: 55-61
Author(s):Vilchez Carlos Garbayo Ines Markvicheva Elena Galvan Francisco Leon Rosa
Author Affiliation:Departamento de Quimica y CC.MM, Escuela Politecnica Superior, Universidad de Huelva, 21819, Huelva: cvilchez@uhu.es
Language:English
Language of Summary:English (EN)
Abstract:Some aspects of the suitability of alginate beads entrapping Chlamydomonas reinhardtii cells for nitrate consumption from nitrate-containing waters were studied and discussed. Among 14 different metal cations tested as gel bead stabilizing agents, only calcium and barium formed beads showing nitrate-consuming activity. Pure calcium alginate cell entrapment resulted in the most suitable method for active cell immobilization compared to alginate- composite-gel beads based on poly-vinylcaprolactam (PVCL) and poly- vinylpyrrolidone (PVP). To perform a continuous nitrate consumption process, calcium alginate-entrapped cells were first grown in a 2.5 l airlift-loop reactor. A cell loading of about 150 mug Chl. g-1 gel was achieved. Afterwards, five days nitrate consumption processes were performed and three different dilution rates were applied: (i) D < mu; (ii) D = mu; (iii) D > mu, where mu is the specific growth rate (h-1). The maximum consumption rates calculated for each dilution rate were: (i) 3.8, (ii) 6.4 and (iii) 7.2 mg nitrate mg-1 Chl. h-1. For low dilution rates (D < mu) some nitrite (< 300 muM) was excreted into the culture medium. However, this concentration of nitrite was not high enough to inhibit nitrate consumption
Descriptors:bioresource technology; biotechnology; cell loading; dilution rates; pollution control. Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation). alginate: uses; nitrate: sustained nitrogen consumption processes
Organism Descriptors:Chlamydomonas reinhardtii (Chlorophyta, Flagellata): immobilized form applications
Supplemental Descriptors:Chlorophyta: Algae, Plantae; Flagellata: Protozoa, Invertebrata, Animalia. Algae; Animals; Invertebrates; Microorganisms; Nonvascular Plants; Plants; Protozoans
Subject Codes:Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

66. Title:Influence of process variables in the ethanol pulping of olive tree trimmings
View Article: Bioresource Technology. 78 (1). May, 2001. 63-69
CD Volume:367
Print Article: Pages: 63-69
Author(s):Jimenez L Perez I Garcia J C Rodriguez A
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Language:English
Language of Summary:English (EN)
Abstract:A central composition design was developed to study the influence of process variables (temperature, pulping time and ethanol concentration) on the properties of the pulp produced (yield and holocellulose, alpha-cellulose and lignin contents) and the pH of the resulting wastewater, in the ethanol pulping of olive tree trimmings.

The proposed equations reproduce the experimental results for the dependent variables with errors less than 5% for the holocellulose and alpha-cellulose contents, yield and wastewater pH, and less than 15% for the lignin content. Obtaining pulp with acceptably high yield (37.6%), high holocellulose and alpha-cellulose contents (above 88.8% and 46.9%, respectively), and low lignin contents (below 7.2%), entails operating at a pulping temperature of 200degreeC, using an ethanol concentration of 75% and a pulping time of 60 min

Descriptors:bioresource technology; biotechnology; olive tree trimmings: ethanol pulping, processing; process variables: analysis, influence. Bioprocess Engineering; Waste Management (Sanitation). celluloses; ethanol; lignins

Organism Descriptors:olive (Oleaceae)

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

Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)

ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

67. Title:Oxidation of lignin in eucalyptus kraft pulp by manganese peroxidase from Bjerkandera sp. strain BOS55

View Article: Bioresource Technology. 78 (1). May, 2001. 71-79
CD Volume:367
Print Article: Pages: 71-79

Author(s):Moreira M T Sierra Alvarez R Lema J M Feijoo G Field J A
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Language:English
Language of Summary:English (EN)

Abstract:The white rot fungus Bjerkandera sp. strain BOS55 was shown in previous studies to cause high levels of kraft pulp bleaching and delignification under culture conditions in which manganese peroxidase (MnP) occurs as the dominant oxidative enzyme. In this study, the MnP of Bjerkandera was isolated and tested in vitro with eucalyptus oxygen-delignified kraft pulp (ODKP) based on measuring the reduction in kappa number as an indicator of lignin oxidation. The MnP preparation applied at 60 U/g pulp for 6 h caused a significant decrease of 11-13% in the kappa number in the ODKP under optimal conditions compared to parallel-incubated controls lacking enzyme. The effects of MnP dosage, Mn2+ concentration, organic acid buffer selection, pH and H2O2 addition were evaluated. The optimal Mn2+ concentration range for lignin oxidation in ODKP was 100-500 muM. In the presence of low oxalate concentrations (0.3- 2 mM), the Bjerkandera MnP also significantly reduced the kappa number of ODKP by 6% without any Mn. This observation is in agreement with the fact that purified Bjerkandera MnP has Mn- independent activities. Under incubation conditions with added Mn2+, buffers composed of metal-complexing organic acids provided two-fold better kappa number reductions compared to the inert acetic acid. The optimal H2O2 dosage was found to be 0.017 mumol/min ml when added as semi-continuous pulses (every 30 min) or 0.2 mumol/min ml when generated continuously by glucose oxidase. Excess H2O2 caused severe inactivation of MnP during the incubations. Factors that improved the turnover of the enzyme, such as Mn2+ and metal-chelating acids, stabilized MnP against rapid inactivation

Descriptors:bioresource technology; biotechnology; eucalyptus kraft pulp: analysis, preparation. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering. acids; enzymes; lignin: analysis, oxidation; manganese ions; manganese peroxidase: applications
Organism Descriptors:Bjerkandera sp. (Basidiomycetes): strain-BOS55
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

68. Title:Anaerobically digested poultry slaughterhouse wastes as fertiliser in agriculture
View Article: Bioresource Technology. 78 (1). May, 2001. 81-88
CD Volume:367
Print Article: Pages: 81-88
Author(s):Salminen E Rintala J Harkonen J Kuitunen M Hogmander H Oikari A
Author Affiliation:Department of Biological and Environmental Science, University of Jyvaskyla, FIN-40351, Jyvaskyla: esa.salminen@cc.jyu.fi
Language:English
Language of Summary:English (EN)
Abstract:Chemical and physical analysis, 27-d plant growth assays with carrot (Daucus carota) and Chinese cabbage (Brassica campestris var. chinensis), and 5-d phytotoxicity assays with Chinese cabbage and perennial ryegrass (Lolium perenne) were used to investigate the suitability of anaerobically digested poultry slaughterhouse waste for fertiliser in agriculture and the effect of aerobic posttreatment on the properties of the digested material. The digested material appeared to be rich in nitrogen. In 27-d assays with digested material as nitrogen source, carrots grew almost as well as those fertilised with a commercial mineral fertiliser used as reference, whereas, the growth of Chinese cabbage was inhibited. In further 5-d phytotoxicity assays, the digested material inhibited the germination and root growth of ryegrass and Chinese cabbage, apparently because of organic acids present in it. Aerobic post-treatment of the material reduced its phytotoxicity but, probably due to the volatilisation of ammonia, resulted in loss of nitrogen
Descriptors:anaerobically digested poultry slaughterhouse wastes: agricultural uses, fertilizer uses, physicochemical properties, phytotoxicity; bioresource technology; biotechnology; food processing. Agriculture; Waste Management (Sanitation). nitrogen; organic acids
Organism Descriptors:Brassica campestris [Chinese cabbage] (Cruciferae); Daucus carota [carrot] (Umbelliferae); Lolium perenne [perennial ryegrass] (Gramineae); poultry (Aves)
Supplemental Descriptors:Aves: Vertebrata, Chordata, Animalia; Cruciferae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Umbelliferae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Birds; Chordates; Dicots; Monocots; Nonhuman Vertebrates; Plants; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Agriculture; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

69. Title:Degumming of ramie fibers by alkalophilic bacteria and their polysaccharide-degrading enzymes
View Article: Bioresource Technology. 78 (1). May, 2001. 89-94
CD Volume:367
Print Article: Pages: 89-94
Author(s):Zheng Lianshuang Du Yumin Zhang Jiayao
Author Affiliation:College of Chemistry and Environmental Science, Wuhan University, Wuhan, 430072: lszheng@whu.edu.cn
Language:English
Language of Summary:English (EN)
Abstract:Three strains of alkalophilic bacteria, Bacillus sp. NT-39, NT-53 and NT-76, were selected for the degumming of ramie fibers and production of polysaccharide-degrading enzymes. After 48 h of incubation with the strains, the loss of the gum might amount to 5.0% or more of the fibers and a number of polysaccharide-degrading enzymes were secreted to the culture supernatants. The residual gum of the fibers decreased to 9.4% after 5 h of enzymatic degumming. Analysis of gum contents and enzyme activities revealed that pectate lyase and xylanase played an important role in the degradation of residual gum. Enzymatic degumming resulted in an increment of 5.4 ISO units in fiber brightness, whereas the reduction in bundle breaking tenacity of the fibers was less than 5.0%. The results confirmed that degumming of ramie fibers by alkalophilic bacteria and their enzymes had substantial advantages
Descriptors:bioresource technology; biotechnology; ramie fibers: degumming. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Microbiology. plant gums; polysaccharide-degrading enzymes: applications, uses; polysaccharides: degradation
Organism Descriptors:Bacillus sp. (Endospore-forming Gram-Positives); bacteria (Bacteria): alkalophilic
Supplemental Descriptors:Bacteria: Microorganisms; Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Microbiology
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

70. Title:Decolourisation of synthetic and spentwash melanoidins using the white-rot fungus Phanerochaete chrysosporium JAG-40
View Article: Bioresource Technology. 78 (1). May, 2001. 95-98
CD Volume:367
Print Article: Pages: 95-98
Author(s):Dahiya Jagroop Singh Dalel Nigam Poonam
Author Affiliation:Biotechnology Research Group, University of Ulster, Coleraine, BT52 1SA: p.nigam@ulst.ac.uk
Language:English
Language of Summary:English (EN)
Abstract:Phanerochaete chrysosporium JAG-40 was isolated from the soil samples saturated with spilled molasses collected from a sugar mill. This isolate decolourised synthetic and natural melanoidins present in spentwash in liquid fermentation; up to 80% in 6 days at 30degreeC under aerobic conditions. A large inoculum size stimulated fungal biomass production, but this gave less decolourisation of pigment; 5% w/v (dry weight) mycelial suspension was found optimum for maximum decolourisation in melanoidin medium supplemented with glucose and

peptone. Gel-filtration chromatography showed that larger molecular weight fractions of melanoidin were decolourised more rapidly than small molecular weight fractions
Descriptors:biodegradation; bioresource technology; biotechnology; pollution control; soils. Biochemistry and Molecular Biophysics; Microbiology; Pollution Assessment Control and Management. enzymes; glucose; melanoidins: decolorization, spentwash, synthetic; peptone
Organism Descriptors:Phanerochaete chrysosporium (Basidiomycetes): strain-JAG-40, white- rot fungus
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Biochemistry and Molecular Biophysics; Microbiology; Pollution Assessment Control and Management
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

71. Title:Reaction coefficient (K) evaluation for full-scale facultative pond systems
View Article: Bioresource Technology. 78 (1). May, 2001. 99-102
CD Volume:367
Print Article: Pages: 99-102
Author(s):Soares S R A Bernardes R S
Author Affiliation:University of Brasilia, ENC/FT, 70.910-900, Brasilia, DF: sras@tba.com.br
Language:English
Language of Summary:English (EN)
Abstract:Facultative ponds have found application in wastewater treatment as an economical system where geographical locations are available at reasonable cost. Several design methods have been reported to describe the organic matter removal of a facultative pond and to determine the reaction coefficient (K) in general terms. Therefore, it is important to evaluate if these coefficient values can be used satisfactorily in regional cases. For this purpose the data of two full-scale facultative ponds located in Brazlandia and Samambaia, in the mid-west region of Brazil, were used. A correlation between applied COD load and reaction coefficient (K) was obtained based on a mathematical adjustment using the dispersed flow hydraulic model. The results provide a suggested regional design parameter for facultative ponds in this region in terms of domestic wastewater
Descriptors:bioresource technology; biotechnology; chemical oxygen demand; full-scale facultative pond systems: analysis, applications, evaluation, organic matter removal; waste stabilization pond systems: analysis, applications, evaluation, organic matter removal; wastewater treatment: methodology. Mathematical Biology (Computational Biology); Waste Management (Sanitation)
Geographic Locator:Brazil (South America, Neotropical region)
Subject Codes:Mathematical Biology (Computational Biology); Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

72. Title:Composted grape marc as growing medium for hypostases (Hypostases phyllostagya)
View Article: Bioresource Technology. 78 (1). May, 2001. 103-106
CD Volume:367

Print Article: Pages: 103-106
Author(s):Baran Abdullah Cayci Gokhan Kutuk Cihat Hartmann Roger
Author Affiliation:Department of Soil Science, Faculty of Agriculture, Ankara University, 06110, Ankara: abaran@agri.ankara.edu.tr
Language:English
Language of Summary:English (EN)
Abstract:The use of composted grape marc (CGM) as a plant growth medium was investigated with Hypostases (Hypostases phyllostagya). Seven media were prepared using CGM mixed, in different ratios, with native peat and perlite. The following mixtures were used: 100% CGM, 75% CGM + 25% peat, 50% CGM + 50% perlite, 25% CGM + 75% peat, 50% CGM + 25% peat + 25% perlite, 25% CGM + 50% peat + 25% perlite and 100% peat. The experiment was arranged in a randomized plot design with four replicates under greenhouse conditions. After a growing period of three months, some horticultural parameters were measured. Besides, some physical and chemical properties of the growing medium were determined. The mixtures of 50% CGM + 50% peat, 25% CGM + 75% peat and 100% peat were found to be most suitable based on the horticultural parameters. This was confirmed through the physical characteristics. Up to 50% composted grape marc can be used in mixtures with peat on account of its low cost and high nutrient content
Descriptors:bioresource technology; biotechnology; composted grape marc: horticultural parameters, plant growing medium uses; plant growth; plant nutrition. Horticulture (Agriculture); Waste Management (Sanitation)
Organism Descriptors:Hypostases phyloostagya [hypostases] (Angiospermae); grape (Vitaceae)
Supplemental Descriptors:Angiospermae: Spermatophyta, Plantae; Vitaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

73. Title:Co-composting of chestnut burr and leaf litter with solid poultry manure
View Article: Bioresource Technology. 78 (1). May, 2001. 107-109
CD Volume:367
Print Article: Pages: 107-109
Author(s):Guerra Rodriguez E Diaz Ravina M Vazquez M
Author Affiliation:Dpto. Quimica Analitica, Area Tecnologia de los Alimentos, Escuela Politecnica Superior, Universidad de Santiago de Compostela, 27002, Lugo: vazquezm@lugo.usc.es
Language:English
Language of Summary:English (EN)
Abstract:A co-composting of chestnut burr and leaf litter mixed with solid poultry manure was assessed by comparison of several chemical, physicochemical and biological parameters. The final pH of the co-compost was 8.89 and the C/N ratio was 13. The germination index (GI) obtained using the co-compost varied with the seeds used. It was 155.35% for ryegrass seeds, 56.56% for wheat seeds and 100% for barley seeds. The co-compost was mature in 103 days from a biological point of view
Descriptors:bioresource technology; biotechnology; chestnut burr/leaf litter/solid poultry manure composts: biological analysis, physicochemical analysis, preparation. Agriculture; Waste Management (Sanitation)

Organism Descriptors:Castanea sativa [chestnut] (Fagaceae); barley (Gramineae); ryegrass (Gramineae); wheat (Gramineae). seeds
Supplemental Descriptors:Fagaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agriculture; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

74. Title:Decolourisation of molasses wastewater by cells of Pseudomonas fluorescens immobilised on porous cellulose carrier
View Article: Bioresource Technology. 78 (1). May, 2001. 111-114
CD Volume:367
Print Article: Pages: 111-114
Author(s):Dahiya Jagroop Singh Dalel Nigam Poonam
Author Affiliation:Biotechnology Research Group, University of Ulster, Coleraine, BT52 1SA: p.nigam@ulst.ac.uk
Language:English
Language of Summary:English (EN)
Abstract:Pseudomonas fluorescens isolated from soil samples contaminated with molasses, decolourised molasses wastewater (MWW) samples up to 76% under non-sterile conditions in four days at 30degreeC. Immobilised cells could be reused for decolourisation activity. However, in subsequent cycles, this was found to decrease from 76% to 50% and from 50% to 24%. Decolourisation activity was regenerated from 30% to 45% by recultivating the immobilised cells in a fresh growth medium. Cellulose carrier coated with collagen was found to be most effective carrier, which produced the highest decolourisation activity of 94% in a 4-day process. This carrier could be reused with 50% of the decolourisation activity retained until the seventh day
Descriptors:bioresource technology; biotechnology; contaminated soil samples: microbial analysis; four-day process: analysis, applications; molasses. Bioprocess Engineering; Waste Management (Sanitation). porous cellulose: carrier material
Organism Descriptors:Pseudomonas fluorescens (Pseudomonadaceae): immobilized form applications
Supplemental Descriptors:Pseudomonadaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

75. Title:Production of glucose oxidase using Aspergillus niger and corn steep liquor
View Article: Bioresource Technology. 78 (2). June, 2001. 123-126
CD Volume:367
Print Article: Pages: 123-126
Author(s):Kona R P Qureshi N Pai J S
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Language:English
Language of Summary:English (EN)

Abstract:Glucose oxidase production was optimized using an isolated strain of Aspergillus niger and an economical nutrient source, corn steep liquor (CSL). The culture produced 580 +- 30 units/ml of the enzyme using 70 g/l sucrose as the carbon source. Using CSL as the sole nutrient source enzyme synthesis was increased to 640 +- 36 units/ml. None of the nitrogen sources (nitrates of calcium, sodium, ammonium, potassium and yeast extract, malt extract, and peptone) was beneficial to the enzyme synthesis. Aeration and agitation enhanced enzyme synthesis to 850 +- 45 units/ml. Glucose oxidase has numerous applications in food industry and clinical fields
Descriptors:aeration; agitation; bioresource technology; biotechnology; corn steep liquor: nutrient source, uses. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Nutrition. glucose oxidase: analysis, applications, microbial production, uses; nitrogen sources; sucrose: carbon source
Organism Descriptors:Aspergillus niger (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Nutrition
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

76. Title:Nitrogen budget in Scenedesmus obliquus cultures with artificial wastewater
View Article: Bioresource Technology. 78 (2). June, 2001. 161-164
CD Volume:367
Print Article: Pages: 161-164
Author(s):Nunez Victor J Voltolina Domenico Nieves Mario Pina Pablo Medina Alejandra Guerrero Martin
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Language:English
Language of Summary:English (EN)
Abstract:Semicontinuous cultures of Scenedesmus obliquus in artificial wastewater, recycled into proteins about 33% and 25% of the dissolved nitrogen missing from the medium 24 h after harvesting 50% and 70% of the culture, and replacing the volume harvested with fresh medium. The residual dissolved nitrogen concentrations were 25% and 43% of the initial, respectively, with an imbalance in the mass budget close to 17 and 20 mg N l-1 d-1. Most or all the nitrogen missing was found in an ammonia trap located at the air vent of the closed cultures, showing that an important role of microalgae in wastewater treatment is that of favouring NH3 stripping due to the photosynthesis-induced pH increases
Descriptors:artificial wastewaters: treatment methods; bioremediation; bioresource technology; biotechnology; pH; photosynthesis. Bioprocess Engineering; Methods and Techniques; Waste Management (Sanitation). dissolved nitrogen; proteins: recycling
Organism Descriptors:Scenedesmus obliquus (Chlorophyta)
Supplemental Descriptors:Chlorophyta: Algae, Plantae. Algae; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Methods and Techniques; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

77. Title:Regulation of cellulases and xylanases from a derepressed mutant of Cellulomonas flavigena growing on sugar-cane bagasse in continuous culture
View Article: Bioresource Technology. 78 (3). July, 2001. 285-291
CD Volume:367
Print Article: Pages: 285-291
Author(s):Ponce Noyola Teresa de la Torre Mayra
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Language:English
Language of Summary:English (EN)
Abstract:When the wild type Cellulomonas flavigena was grown on glycerol, xylose or cellobiose, it produced basal levels of carboxymethyl- cellulase (CMCase), filter-paperase (FPase) and xylanase activities. By comparison, a catabolic derepressed mutant strain of the same organism produced markedly higher levels of these enzymes when grown on the same carbon sources. Sugar-cane bagasse induced both the wild type and the mutant strain to produce three- to eight- time higher levels of FPase and xylanase than was observed with xylose or cellobiose. Continuous culture was used to determine the minimal cellobiose or glucose concentrations that repress the enzyme synthesis in both strains. 2.5 g l-1 glucose repressed FPase and xylanases from wild type, while 1.6 times more glucose was needed to repress the same activities in the PN-120 strain. In the same way, twofold more cellobiose was needed to reduce by 75% the CMCase and xylanase activities in the mutant compared to the wild type. The FPase in the presence of 4 g l-1 cellobiose did not change in the same strain. Therefore, its derepressed and feedback resistant characters of PN-120 mutant are evident. On the other hand, isoelectrofocused crude extracts of mutant and wild strains induced by sugar-cane bagasse, did not show differences in protein patterns, however, the Schiff's staining was more intense in the PN- 120 than in the wild strain. These results point out that the mutational treatment did not apparently change the extracellular proteins from mutant PN-120 and this could affect their regulation sites, since derepressed and feed-back resistant enzymes may be produced
Descriptors:sugar-cane bagasse. Enzymology (Biochemistry and Molecular Biophysics). carboxymethyl-cellulase: production; cellobiose; cellulases: regulation; filter-paperase: production; glycerol; xylanases: regulation; xylose
Organism Descriptors:Cellulomonas flavigena (Irregular Nonsporing Gram-Positive Rods): derepressed mutant, growth, strain-CDBB-531, strain-PN-120
Supplemental Descriptors:Irregular Nonsporing Gram-Positive Rods: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

78. Title:Towards maximising output from vermireactors fed with cowdung spiked paper waste
View Article: Bioresource Technology. 79 (1). August, 2001. 67-72
CD Volume:367
Print Article: Pages: 67-72

Author(s):Gajalakshmi S Ramasamy E V Abbasi S A
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Language:English
Language of Summary:English (EN)
Abstract:Paper waste, spiked with varying proportions of cowdung, was vermicomposted in 'low-rate' and 'high-rate' reactors. The former type of reactors had earthworm populations and feed loading rates similar to ones recommended by previous workers. The 'high-rate' reactors were operated with 12.5 times higher earthworm densities and feed loading rates. All the reactors were studied for six months to assess the vermicast output, survivability, growth and reproduction of the earthworms - hence the sustainability of the reactors - for long-term, continuous operation. The studies revealed the viability of the high-rate vermireactor concept. The high-rate reactors consistently produced over 6.5 times more castings per unit digester volume with no adverse effect on the earthworm population, as reflected by (a) absence of mortality, (b) consistent growth in worm zoomass, and (c) normal rate of reproduction. The studies also revealed that an increase in the cowdung fraction in the feed from 14.3% to 20%
Descriptors:bioresource technology; biotechnology; cowdung-spiked paper wastes: treatment methodologies. Bioprocess Engineering; Waste Management (Sanitation)
Organism Descriptors:earthworms (Oligochaeta): loading rates, populations, practical uses
Supplemental Descriptors:Oligochaeta: Annelida, Invertebrata, Animalia. Animals; Annelids; Invertebrates
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

79. Title:Improvement of biogas production from vinasse via covalently immobilized methanogens
View Article: Bioresource Technology. 79 (1). August, 2001. 83-85
CD Volume:367
Print Article: Pages: 83-85
Author(s):Lalov Ivo G Krysteva Milka A Phelouzat Jean Louis
Author Affiliation:Department of Biotechnology, University of Chemical Technology and Metallurgy, 8, Blvd. K1 Okhridski, 1756, Sofia: m.krysteva@mbox.cit.bg
Language:English
Language of Summary:English (EN)
Abstract:Improvement of biogas production was realized by covalent immobilization of a methanogenic consortium onto a granulated polymeric support (poly(acrylonitrile-acrylamide)). The growth kinetics of the immobilized consortium was investigated during a process of vinasse methanation, and a cell concentration increase from 12.3 mg g-1 support to 52.1 mg g-1 support was established. The methane yield reached 0.33 m3 kg-1 CODr, the maximum yield on chemical oxygen demand (COD) removal being 92%. The inhibitory effect of oxygen was reduced by immobilizing the methanogenic consortium
Descriptors:COD [chemical oxygen demand]: removal; bioresource technology; food processing wastes: uses; methanogenic consortium: immobilization; product yields; vinasse: uses. Bioprocess Engineering; Waste Management (Sanitation). biogas: improved production, yields; granulated polymers: support material; methane: improved production, yields; oxygen

Organism Descriptors:methanogen (Methanogenic Archaeobacteria): covalently immobilized form, practical uses
Supplemental Descriptors:Methanogenic Archaeobacteria: Archaeobacteria, Bacteria, Microorganisms. Archaeobacteria; Bacteria; Microorganisms
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

80. Title:Decolorization of an anthraquinone-type dye using a laccase formulation
View Article: Bioresource Technology. 79 (2). September, 2001. 171-177
CD Volume:367
Print Article: Pages: 171-177
Author(s):Soares Graca M B Costa Ferreira Maria de Amorim M T Pessoa
Author Affiliation:Bioengineering and Bioprocessing Unit, Department of Biotechnology, National Institute for Industrial Engineering and Technology (INETI), Est. Paco do Lumiar 22, Lisboa Cedex, 1649: maria.ferreira@mail.ineti.pt
Language:English
Language of Summary:English (EN)
Abstract:Decolorization of the dye Remazol Brilliant Blue R (RBBR) was studied, as it is representative of an important class of recalcitrant anthraquinone-type dyes. For this purpose a commercial laccase formulation (CLF) containing laccase, a redox mediator and a non-ionic surfactant was used. Small molecular weight components were removed from the CLF by gel filtration, which made it possible to compare the effect of its laccase alone. Apart from slightly better thermostability of the CLF as compared with the laccase alone, the pH and temperature profiles were similar regardless of the presence of the small molecular weight components. The laccase alone did not decolorize RBBR. A small molecular weight redox mediator (HBT) was necessary for decolorization to occur. A comparison of the kinetics of RBBR decolorization using the CLF and its laccase alone is reported. Provided that a redox mediator is included, it is suggested that laccase may be suitable for the wastewater treatment of similar anthraquinone dyes
Descriptors:pH; temperature. Biochemistry and Molecular Biophysics; Waste Management (Sanitation). HBT: small molecular weight redox mediator; Remazol Brilliant Blue R: decolorization; anthraquinone-type dye: decolorization; commercial laccase formulation: thermostability; laccase: activity
Subject Codes:Biochemistry and Molecular Biophysics; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

81. Title:Development of a high-temperature air-blown gasification system
View Article: Bioresource Technology. 79 (3). September, 2001. 231-241
CD Volume:367
Print Article: Pages: 231-241
Author(s):Pian Carlson C P Yoshikawa Kunio
Author Affiliation:Mechanical Engineering Division, Alfred University, Alfred, NY, 14802-1205
Language:English
Language of Summary:English (EN)

Abstract:Current status of high-temperature air-blown gasification technology development is reviewed. This advanced gasification system utilizes preheated air to convert coal and waste-derived fuels into synthetic fuel gas and value-added byproducts. A series of demonstrated, independent technologies are combined to form the core of this gasification system. A high-temperature, rapid devolatilization process is used to enhance the volatile yields from the fuel and to improve the gasification efficiency. A high- temperature pebble bed filter is used to remove the slag and particulates from the synthetic fuel gas. Finally, a novel regenerative heater is used to supply the high-temperature air for the gasifier. Component development tests have shown that higher gasification efficiencies can be obtained at more fuel-rich operating conditions when high-temperature air is used as the gasification agent. Test results also demonstrated the flex-fuel capabilities of the gasifier design. Potential uses of this technology range from large-scale integrated gasification power plants to small-scale waste-to-energy applications
Descriptors:biomass wastes: conversions, treatments; biotechnology; gasification technology: applications, development; high temperatures; high-temperature air-blown gasification systems: applications, development; waste-to-energy plants. Bioprocess Engineering; Chemistry; Waste Management (Sanitation). gases; synthetic fuel gases: production; value-added chemical by- production: production; waste-derived fuels: conversions
Subject Codes:Bioprocess Engineering; Chemistry; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

82. Title:Production of monomeric phenols by thermochemical conversion of biomass: A review
View Article: Bioresource Technology. 79 (3). September, 2001. 277-299
CD Volume:367
Print Article: Pages: 277-299
Author(s):Amen Chen Carlos Pakdel Hooshang Roy Christian
Author Affiliation:Department of Chemical Engineering, Universite Laval, Sainte-Foy, Que., G1K 7P4: croy@gch.ulaval.ca
Language:English
Language of Summary:English (EN)
Abstract:Biomass is a renewable and alternative source for the production of fuels and chemicals. This paper provides a brief survey of lignin precursors as well as thermogravimetric and pyrolysis studies of lignin with special reference to the production of phenols. Thermogravimetric analysis provides information on pyrolysis kinetics while thermogravimetry in combination with mass or infrared spectrometers allowed a rapid characterization of the vapours produced by thermal treatment. Pyrolysis enabled even greater insight into the thermal behaviour of lignin. Pyrolysis of single, dimeric and trimeric model lignin compounds can determine the thermal stability of the intermediate compounds formed and the origin of the pyrolysis products. A free radical mechanism has been suggested as a major route during the early lignin degradation stages followed by a combined free radical and concerted pathway at elevated temperatures. Pyrolysis of lignin in the presence of catalysts as additives was investigated. Significant differences in terms of yields of pyrolysis products and phenolic compounds were observed. The addition of salts resulted in a high weight loss at low temperature and yielded more char than untreated wood. Some metal catalysts such as transition metals and

metal oxides such as Fe2O3 and Cu exhibited a better activity in terms of selectivity for the degradation of lignin
Descriptors:biomass: thermochemical conversions; bioresource technology; biotechnology; methodology. Biochemistry and Molecular Biophysics; Bioprocess Engineering; Methods and Techniques. intermediate compounds: formation, molecular analysis, thermal stabilities; lignins: degradation; metal catalysts: uses; monomeric phenols: production methods
Organism Descriptors:plants (Plantae)
Supplemental Descriptors:Plantae. Plants
Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering; Methods and Techniques
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

83. Title:Pyrolytic characteristics of microalgae as renewable energy source determined by thermogravimetric analysis
View Article: Bioresource Technology. 80 (1). October, 2001. 1-7
CD Volume:368
Print Article: Pages: 1-7
Author(s):Peng Weimin Wu Qingyu Tu Pingguan Zhao Nanming
Author Affiliation:Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing, 100084: qingyu@tsinghua.edu.cn
Language:English
Language of Summary:English (EN)
Abstract:Two kinds of autotrophic microalgae, Spirulina platensis (SP) and Chlorella protothecoides (CP) were pyrolyzed at the heating rates of 15, 40, 60 and 80degreeC/min up to 800degreeC in a thermogravimetric analyzer to investigate their pyrolytic characteristics. Three stages (dehydration, devolatilization and solid decomposition) appeared in the pyrolysis process. SP and CP mainly devolatilized at 190-560degreeC and 150-540degreeC, respectively. A total volatile yield of about 71% was achieved from each microalga. As the heating rate increased, a lateral shift to higher temperatures was observed in their thermograms, and the instantaneous maximum and average reaction rates in the devolatilization stage were increased while the activation energy was decreased. The value of activation energy for CP pyrolysis was 4.22-5.25X104, lower than that of SP (7.62-9.70X104), and the char in final residue of CP was 14.00-15.14%, less than that of SP by 2- 3%. This indicated that CP is preferable for pyrolysis over SP. The experimental results may provide useful data for the design of pyrolytic processing systems using planktonic microalgae as feedstock
Descriptors:dehydration; devolatilization; feedstock; heating rate; pyrolysis; solid decomposition; temperature effects. Biochemistry and Molecular Biophysics; Bioprocess Engineering
Organism Descriptors:Chlorella protothecoides (Chlorophyta): autotrophic; Spirulina platensis (Oscillatoriales): autotrophic; microalgae (Algae): pyrolytic characteristics, renewable energy source
Supplemental Descriptors:Algae: Plantae; Chlorophyta: Algae, Plantae; Oscillatoriales: Cyanobacteria, Oxygenic Photosynthetic Bacteria, Eubacteria, Bacteria, Microorganisms. Algae; Bacteria; Cyanobacteria; Eubacteria; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

84. Title:Entrapment of white-rot fungus Trametes versicolor in Ca-alginate beads: Preparation and biosorption kinetic analysis for cadmium removal from an aqueous solution
View Article: Bioresource Technology. 80 (2). November, 2001. 121-129
CD Volume:368
Print Article: Pages: 121-129
Author(s):Arica M Yakup Kacar Yasemin Genc Omer
Author Affiliation:Department of Biology, Kirikkale University, 71450 Yahsihan, Kirikkale: arica@turkuaz.kku.edu.tr
Language:English
Language of Summary:English (EN)
Abstract:The biosorption of cadmium ions onto entrapped Trametes versicolor mycelia has been studied in a batch system. The maximum experimental biosorption capacities for entrapped live and dead fungal mycelia of T. versicolor were found as 102.3 +- 3.2 mg Cd(II) g-1 and 120.6 +- 3.8 mg Cd(II) g-1, respectively. Biosorption equilibrium was established in about 1 h and biosorption was well described by the Langmuir and Freundlich biosorption isotherms. The change in the biosorption capacity with time was found to fit the pseudo-second-order equation. Since the biosorption capacities were relatively high for both entrapped live and dead forms, those fungal forms could be considered as suitable biosorbents for the removal of cadmium in wastewater-treatment systems. The biosorbents were reused in three consecutive adsorption/desorption cycles without a significant loss in the biosorption capacity
Descriptors:bioresource technology; biotechnology; equations; wastewater treatment systems. Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation). aqueous solutions; cadmium: biosorption kinetic studies, removal methods, toxic heavy metal; calcium alginate: bead uses
Organism Descriptors:Trametes versicolor (Basidiomycetes): entrapped form applications, white rot fungus. mycelia
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

85. Title:Biodegradation of phenolic industrial wastewater in a fluidized bed bioreactor with immobilized cells of Pseudomonas putida
View Article: Bioresource Technology. 80 (2). November, 2001. 137-142
CD Volume:368
Print Article: Pages: 137-142
Author(s):Gonzalez G Herrera G Garcia Ma T Pena M
Author Affiliation:Department of Chemical Engineering, University of Valladolid, Paseo Prado de la Magdalena s/n, Valladolid, 47011: gerardo@siq.iq.cie.uva.es
Language:English
Language of Summary:English (EN)
Abstract:The paper presents the main results obtained from the study of the biodegradation of phenolic industrial wastewaters by a pure culture of immobilized cells of Pseudomonas putida ATCC 17484. The experiments were carried out in batch and continuous mode. The maximum degradation capacity and the influence of the adaptation of the microorganism to

the substrate were studied in batch mode. Industrial wastewater with a phenol concentration of 1000 mg/l was degraded when the microorganism was adapted to the toxic chemical. The presence in the wastewater of compounds other than phenol was noted and it was found that Pseudomonas putida was able to degrade these compounds. In continuous mode, a fluidized-bed bioreactor was operated and the influence of the organic loading rate on the removal efficiency of phenol was studied. The bioreactor showed phenol degradation efficiencies higher than 90%, even for a phenol loading rate of 0.5 g phenol/l d (corresponding to 0.54 g TOC/l d)

Descriptors:biodegradation; bioresource technology; biotechnology; industrial wastewaters: treatment methods; microbial adaptation mechanisms. Bioprocess Engineering; Waste Management (Sanitation). phenolic compounds: loading rates, microbial degradation

Organism Descriptors:Pseudomonas putida (Pseudomonadaceae): immobilized cell applications; microorganisms (Microorganisms)

Supplemental Descriptors:Microorganisms; Pseudomonadaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms

Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)

ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

86. Title:Biotransformation of nitrophenols in upflow anaerobic sludge blanket reactors

View Article: Bioresource Technology. 80 (3). December, 2001. 179-186
CD Volume:368
Print Article: Pages: 179-186

Author(s):Karim Khursheed Gupta S K
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Language:English
Language of Summary:English (EN)

Abstract:Four identical bench-scale upflow anaerobic sludge blanket (UASB) reactors, R1, R2, R3 and R4, were used to assess nitrophenols degradation at four different hydraulic retention times (HRT). Reactor R1 was used as control, whereas R2, R3, and R4 were fed with 2-nitrophenol (2-NP), 4-nitrophenol (4-NP), and 2,4- dinitrophenol (2,4-DNP), respectively. The concentration of each nitrophenol was gradually varied from 2 to 30 mg/l during acclimation. After acclimation reactors were operated under steady- state conditions at four different HRTs - 30, 24, 18, and 12 h, to study its effect on the removal of nitrophenols. Overall removal of 2-NP and 4-NP was always more than 99% but 2,4-DNP removal decreased from 96% to 89.7% as HRT was lowered from 30 to 12 h. 2- Aminophenol (2-AP), 4-aminophenol (4-AP) and 2-amino, 4-nitrophenol (2-A,4-NP) were found to be the major intermediates during the degradation of 2-NP,4-NP and 2,4-DNP, respectively. Out of the total input of nitrophenolic concentration (30 mg/l), on molar basis, about 41.2-48.4% of 2-NP, 59.4-68% of 4-NP, 30-26.6% of 2,4- DNP was recovered in the form of their respective amino derivatives at 30-12 h HRT. COD removal was 98-89%, 97-56%, 97-52%, and 94-46% at 30-12 h HRT for R1, R2, R3 and R4, respectively. Average cell growth was observed to be 0.15 g volatile suspended solid (VSS) per g COD consumed. Methanogenic inhibition was observed at lower HRTs (18 and 12 h), however denitrification was always more than 99% with non-detectable level of nitrite. The granules developed

inside the reactors were black in color and their average size varied between 1.9 and 2.1 mm
Descriptors:bioresource technology; biotechnology; chemical oxygen demand. Bioprocess Engineering; Metabolism; Pollution Assessment Control and Management; Waste Management (Sanitation). nitrophenols: analysis, molecular biotransformations, pollutant, removal
Organism Descriptors:microorganisms (Microorganisms)
Supplemental Descriptors:Microorganisms. Microorganisms
Subject Codes:Bioprocess Engineering; Metabolism; Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

87. Title:Solute adsorption and enzyme immobilization on chitosan beads prepared from shrimp shell wastes
View Article: Bioresource Technology. 80 (3). December, 2001. 187-193
CD Volume:368
Print Article: Pages: 187-193
Author(s):Juang Ruey Shin Wu Feng Chin Tseng Ru Ling
Author Affiliation:Department of Chemical Engineering, Yuan Ze University, Chung- Li, 320: cejuang@ce.yzu.edu.tw
Language:English
Language of Summary:English (EN)
Abstract:The equilibrium and kinetics of adsorption of reactive dye RR222 and Cu2+, and the activity of immobilization of acid phosphatase, on highly swollen chitosan beads were examined at 30degreeC. The chitosan was prepared from shrimp shell wastes and was cross-linked with different dosages of glutaraldehyde or glyoxal (100-80,000 mg/l). It was shown that the amounts of solute adsorption and the immobilization capacity of acid phosphatase on cross-linked chitosan beads were substantially affected by their degree of cross- linking. The cross-linking rate of chitosan with glutaraldehyde could be described by a pseudo-second-order equation and the cross- linking equilibrium by the Freundlich equation. This provided an experimental method to control the degree of cross-linking of chitosan beads. Finally, the activity and lifetime of the immobilized enzyme were measured to evaluate the application potential
Descriptors:bioresource technology; biotechnology; food processing wastes: treatments, utilization; shrimp cell wastes: treatments, utilization. Bioprocess Engineering; Enzymology (Biochemistry and Molecular Biophysics); Pollution Assessment Control and Management; Waste Management (Sanitation). chitosan; copper ions: adsorption equilibrium/kinetics; enzymes: immobilization; immobilized enzymes: industrial uses, preparation; reactive dyes: adsorption equilibrium/kinetics; solutes: adsorption
Subject Codes:Bioprocess Engineering; Enzymology (Biochemistry and Molecular Biophysics); Pollution Assessment Control and Management; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

88. Title:Cellulolytic activity in leachate during leach-bed anaerobic digestion of municipal solid waste
View Article: Bioresource Technology. 80 (3). December, 2001. 205-210
CD Volume:368

Print Article: Pages: 205-210
Author(s):Lai Takwai E Nopharatana Annop Pullammanappallil Pratap C Clarke William P
Author Affiliation:Department of Chemical Engineering, Advanced Wastewater Management Centre, The University of Queensland, St. Lucia, Brisbane, Qld., 4072: pratap@murdoch.edu.au
Language:English
Language of Summary:English (EN)
Abstract:The degradation of municipal solid waste (MSW) under mesophilic conditions can be enhanced by exchanging leachate between fresh waste and stabilised waste. The optimum point in time when leachate from an anaerobically digesting waste bed can be used to initiate degradation of another waste bed might occur when the leachate of the digesting waste bed is highly active with cellulolytic and methanogenic bacteria. In this study, the cellulolytic activity of the leachate was measured using the cellulose-azure assay. As products of hydrolysis are soluble compounds, the rate of generation of these compounds was estimated based on a soluble chemical oxygen demand (SCOD) balance around the fresh waste bed. It was found that once the readily soluble material present in MSW was washed out there was very little generation of SCOD without the production of methane, indicating that flushing leachate from a stabilised waste bed resulted in a balanced inoculation of the fresh waste bed. With the onset of sustained methanogenesis, the rate of SCOD generation equalled the SCOD released from the digester as methane. The experimental findings also showed that cellulolytic activities of the leachate samples closely followed the trend of SCOD generation
Descriptors:biomethanogenesis; bioresource technology; biotechnology; leachates: chemical analysis, treatments; municipal solid wastes: fresh, leach-bed anaerobic digestion, stabilized; soluble chemical oxygen demand balance. Bioprocess Engineering; Waste Management (Sanitation). celluloses: analysis, degradation; methane: production
Organism Descriptors:bacteria (Bacteria); microorganisms (Microorganisms)
Supplemental Descriptors:Bacteria: Microorganisms; Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Bioprocess Engineering; Waste Management (Sanitation)
ISSN:0960-8524
Year:2001
Journal Title:Bioresource Technology

89. Title:Analysis of phenotypic and genetic variations among populations of Oryza malampuzhaensis show evidence of altitude-dependent genetic changes
View Article: Canadian Journal of Botany. 79 (9). September, 2001. 1090-1098
CD Volume:360
Print Article: Pages: 1090-1098
Author(s):Thomas George Joseph Latha Varghese George Sreejayan Kalyanaraman K Kuriachan Philomena
Author Affiliation:Plant Molecular Biology Group, Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, 695 014, Kerala: gtpulikunnel@yahoo.com
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Oryza malampuzhaensis Krish. et Chand., one of the tetraploid taxa in the genus Oryza (Poaceae), is geographically restricted to Western Ghats, southern India. This is one of the poorly understood taxa in the genus, and not much is known about the nature and distribution of its genetic diversity. Five individuals each were selected randomly

from 11 populations of O. malampuzhaensis from different altitudinal habitats and were grown in a common-garden experiment for 3 years (1994-1997). Sixty morphological traits and 87 random amplified polymorphic DNA (RAPD) markers, generated by 14 random primers, were used to study the genetic variation among the populations. Elevation-dependent phenotypic variation was observed for a suite of metric traits. A scatterplot of mean values for these traits separated the populations from low, middle, and high altitudes into distinct groups. Cluster analysis using RAPD distance grouped the populations according to their altitudinal habitat, and a similar pattern of clustering was observed with respect to morphological distance also. The mean of both RAPD- and morphology-based pairwise genetic distance of populations belonging to similar altitudinal levels differed significantly. These estimates also depicted a significant decrease in genetic distance with increasing altitude. The results demonstrate that (i) effective isolation from gene flow coupled with natural selection governs genetic structure in O. malampuzhaensis and (ii) ecological heterogeneity associated with elevational gradient has a crucial role in the evolution of O. malampuzhaensis

Descriptors:altitude-dependent genetic change; genetic variation; phenotypic variation; population variation. Population Genetics (Population Studies)

Geographic Locator:Western Ghats (India, Asia, Oriental region)

Organism Descriptors:Oryza malampuzhaensis (Gramineae)

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

Subject Codes:Population Genetics (Population Studies)

ISSN:0008-4026

Year:2001

Journal Title:Canadian Journal of Botany

90. Title:Ultrastructure of ascus and ascospore appendages of the mangrove fungus Halosarpheia ratnagiriensis (Halosphaeriales, Ascomycota)

View Article: Canadian Journal of Botany. 79 (11). November, 2001. 1307-1317

CD Volume:360

Print Article: Pages: 1307-1317

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Language:English

Abstract:Halosarpheia Kohlm et E. Kohlm is a genus of eighteen species, all of which have septate ascospores with unfurling polar appendages. Asci and ascospores of Halosarpheia ratnagiriensis Patil et Borse were examined at the scanning (including freeze-fracture) and transmission electron microscope levels. The ascus wall has two well-defined layers and the apical apparatus comprises a refractive, electron-dense, lens-shaped disk embedded within a less electron-dense thickening. The ascospore wall comprises an episporium and a bipartite mesosporium, and the appendages are formed by extrusion of mucilaginous material through an episporial pore field. Ascospore appendage ontogeny is compared with other genera with unfurling polar appendages: Cataractispora, Diluviocola, Tunicatispora, Tirispora, and Halosarpheia aquadulcis Hsieh, H.S. Chang et E.B.G. Jones and Halosarpheia heteroguttulata S.W. Wong, K.D. Hyde et E.B.G. Jones

Descriptors:Morphology; Systematics and Taxonomy

Organism Descriptors:Cataractispora (Ascomycetes); Halosarpheia aquadulcis (Ascomycetes); Halosarpheia heteroguttulata (Ascomycetes); Halosarpheia ratnagiriensis (Ascomycetes): mangrove fungus; Halosphaeriales (Ascomycetes); Tirispora (Ascomycetes); Tunicatispora (Ascomycetes). ascospore appendage: reproductive system, ultrastructure; ascus: reproductive system, ultrastructure
Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Morphology; Systematics and Taxonomy
ISSN:0008-4026
Year:2001
Journal Title:Canadian Journal of Botany

91. Title:Isolation and 16S rRNA sequence analysis of the beneficial bacteria from the rhizosphere of rice
View Article: Canadian Journal of Microbiology. 47 (2). February, 2001. 110-117
CD Volume:365
Print Article: Pages: 110-117
Author(s):Mehnaz Samina Mirza M Sajjad Haurat Jacqueline Bally Rene Normand Philippe Bano Asghari Malik Kauser A
Author Affiliation:National Institute for Biotechnology and Genetic Engineering (NIBGE), Jhang Road, Faisalabad: sajjad_mirza@yahoo.com
Language:English
Language of Summary:English (EN); French (FR)
Abstract:The present study deals with the isolation of plant growth promoting rhizobacteria (PGPR) from rice (variety NIAB IRRI-9) and the beneficial effects of these inoculants on two Basmati rice varieties. Nitrogen-fixing activity (acetylene-reduction activity) was detected in the roots and submerged shoots of field-grown rice variety NIAB IRRI-9. Estimation of the population size of diazotrophic bacteria by ARA-based MPN (acetylene reduction assay- based most probable number) in roots and shoots indicated about 105- 106 counts/g dry weight at panicle initiation and grain filling stages. Four bacterial isolates from rice roots and shoots were obtained in pure culture which produced phytohormone indoleacetic acid (IAA) in the growth medium. Among these, three isolates S1, S4, and R3 reduced acetylene to ethylene in nitrogen-free semi- solid medium. Morphological and physiological characteristics of the isolates indicated that three nitrogen-fixing isolates S1, S4, and R3 belonged to the genus Enterobacter, while the non-fixing isolate R8 belonged to the genus Aeromonas. 16S rRNA sequence of one isolate from root (R8) and one isolate from shoot (S1) was obtained which confirmed identification of the isolates as Aeromonas veronii and Enterobacter cloacae, respectively. The 1517- nucleotide-long sequence of the isolate R8 showed 99% similarity with Aeromonas veronii (accession No. AF099023) while partial 16S rRNA sequence (two stretches of total 1271 nucleotide length) of S1 showed 97% similarity with the sequence of Enterobacter cloacae (accession No. AJ251469). The seedlings of two rice varieties Basmati 385 and Super Basmati were inoculated with the four bacterial isolates from rice and one Azospirillum brasilense strain Wb3, which was isolated from wheat. In the rice variety Basmati 385, maximum increase in root area and plant biomass was obtained in plants inoculated with Enterobacter S1 and Azospirillum Wb3, whereas in the rice variety Super Basmati, inoculation with Enterobacter R3 resulted in maximum increase of root area and plant biomass. Nitrogen fixation was quantified by using 15N isotopic dilution method. Maximum fixation was observed in Basmati 385 with the inoculants Azospirillum Wb3 and Enterobacter S1 where nearly 46% and 41% of the nitrogen was

derived from atmosphere (%Ndfa), respectively. In general, higher nitrogen fixation was observed in variety Basmati 385 than in Super Basmati, and different bacterial strains were found more effective as inoculants for the rice varieties Basmati 385 and Super Basmati
Descriptors:bacterial populations; nitrogen fixation; plant biomass; soil microbiology; soils. Molecular Genetics (Biochemistry and Molecular Biophysics); Microbiology; Soil Science. phytohormones; rRNA [ribosomal RNA]: sequencing
Organism Descriptors:bacteria (Bacteria): beneficial; rhizobacteria (Bacteria): plant growth promoting properties; rice (Gramineae): rhizosphere, seedling
Supplemental Descriptors:Bacteria: Microorganisms; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Bacteria; Eubacteria; Microorganisms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Microbiology; Soil Science
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

92. Title:Antibiotic production, accumulation of intracellular carbon reserves, and sporulation in Micromonospora echinospora (ATCC 15837)
View Article: Canadian Journal of Microbiology. 47 (2). February, 2001. 148-152
CD Volume:365
Print Article: Pages: 148-152
Author(s):Hoskisson Paul A Hobbs Glyn Sharples George P
Author Affiliation:School of Biomolecular Sciences, Liverpool John Moores University, Byrom Street, Liverpool, L3 3AF: bmsphosk@livjm.ac.uk
Language:English
Language of Summary:English (EN); French (FR)
Abstract:The physiology of the actinomycete Micromonospora echinospora was examined during growth. Biphasic accumulation of glycogen occurred, initially during the early exponential growth phase, and again following the onset of sporulation at 120 h. Lipid levels increased during growth eventually representing 25% of the cell mass. A significant proportion of the lipid was found to be in the form of triacylglycerols, which were found to accumulate markedly during the sporulation phase. The disaccharide trehalose was also found to accumulate during growth with levels rising to 5% of the dry weight during the mycelial production phase, then remaining constant during sporulation. Antibiotic was produced transiently by the cultures over the period preceding sporulation
Descriptors:bacterial growth characteristics; bacterial physiology; biotechnology; industrial microbiology; intracellular carbon reserves: analysis; sporulation. Bioprocess Engineering. antibiotics: production; glycogen: accumulation; lipids; sugars; triacylglycerols
Organism Descriptors:Micromonospora echinospora (Actinoplanetes): strain-ATCC 15837. mycelia; spores
Supplemental Descriptors:Actinoplanetes: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Bioprocess Engineering
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

93. Title:Purification, cloning, and DNA sequence analysis of a chitinase from an overproducing mutant of Streptomyces peucetius defective in daunorubicin biosynthesis
View Article: Canadian Journal of Microbiology. 47 (3). March, 2001. 179-187
CD Volume:365
Print Article: Pages: 179-187
Author(s):Vetrivel Kuzhandhaivel S Pandian Shunmugiah K Chaudhary Uma Dharmalingam Kuppamuthu
Author Affiliation:Department of Genetic Engineering, School of Biotechnology, Madurai Kamaraj University, Madurai, 625 021: kdharmalingam@vsnl.com
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Extracellular chitinases of Streptomyces peucetius and a chitinase overproducing mutant, SPVI, were purified to homogeneity by ion exchange and gel filtration chromatography. The purified enzyme has a molecular mass of 42 kDa on SDS-PAGE, and the N-terminal amino acid sequence of the protein from the wild type showed homology to catalytic domains (Domain IV) of several other Streptomyces chitinases such as S. lividans 66, S. coelicolor A3(2), S. plicatus, and S. thermoviolaceus OPC-520. Purified SPVI chitinase cross-reacted to anti-chitinase antibodies of wild-type S. peucetius chitinase. A genomic library of SPVI constructed in E. coli using lambda DASH II was probed with chiC of S. lividans 66 to screen for the chitinase gene. A 2.7 kb fragment containing the chitinase gene was subcloned from a lambda DASH II clone, and sequenced. The deduced protein had a molecular mass of 68 kDa, and showed domain organization similar to that of S. lividans 66 chiC. The N-terminal amino acid sequence of the purified S. peucetius chitinase matched with the N-terminus of the catalytic domain, indicating the proteolytic processing of 68 kDa chitinase precursor protein to 42 kDa mature chitinase containing the catalytic domain only. A putative chiR sequence of a two-component regulatory system was found upstream of the chiC sequence
Descriptors:Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics). DNA; anti-chitanase antibodies; chitinase: cloning, production, proteolytic processing, purification; daunorubicin: biosynthesis; genomic library; lambda-DASH II. Streptomyces lividans chiC gene (Streptomycetes and Related Genera); Streptomyces peucetius chiC gene (Streptomycetes and Related Genera); Streptomyces peucetius chiR gene (Streptomycetes and Related Genera)
Organism Descriptors:Escherichia coli (Enterobacteriaceae): strain-DH5-alpha; Streptomyces coelicolor (Streptomycetes and Related Genera): strain-A3(2); Streptomyces lividans (Streptomycetes and Related Genera): strain-66; Streptomyces peucetius (Streptomycetes and Related Genera): SPVI mutant, strain-ATCC 29050; Streptomyces plicatus (Streptomycetes and Related Genera); Streptomyces thermoviolaceus (Streptomycetes and Related Genera): strain-OPC-520
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Streptomycetes and Related Genera: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

94. Title:Characterization of plant growth promoting rhizobacteria isolated from polluted soils and containing 1-aminocyclopropane-1- carboxylate deaminase
View Article: Canadian Journal of Microbiology. 47 (7). July, 2001. 642-652
CD Volume:365
Print Article: Pages: 642-652
Author(s):Belimov Andrei A Safronova Vera I Sergeyeva Tatyana A Egorova Tatyana N Matveyeva Victoria A Tsyganov Viktor E Borisov Alexey Y Tikhonovich Igor A Kluge Christoph Preisfeld Angelika Dietz Karl Josef Stepanok Vitaley V
Author Affiliation:Laboratories of Biological Nitrogen and Biotechnology, All-Russia Research Institute for Agricultural Microbiology (ARRIAM), Podbelskogo Sh. 3, Pushkin 8, 196608, Saint Petersburg: belimov@rambler.ra
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Fifteen bacterial strains containing 1-aminocyclopropane-1- carboxylate (ACC) deaminase were isolated from the rhizoplane of pea (Pisum sativum L.) and Indian mustard (Brassica juncea L.) grown in different soils and a long-standing sewage sludge contaminated with heavy metals. The isolated strains were characterized and assigned to various genera and species, such as Pseudomonas brassicacearum, Pseudomonas marginalis, Pseudomonas oryzihabitans, Pseudomonas putida, Pseudomonas sp., Alcaligenes xylosoxidans, Alcaligenes sp., Variovorax paradoxus, Bacillus pumilus, and Rhodococcus sp. by determination of 16S rRNA gene sequences. The root elongation of Indian mustard and rape (Brassica napus var. oleifera L.) germinating seedlings was stimulated by inoculation with 8 and 13 isolated strains, respectively. The bacteria were tolerant to cadmium toxicity and stimulated root elongation of rape seedlings in the presence of 300 muM CdCl2 in the nutrient solution. The effect of ACC-utilising bacteria on root elongation correlated with the impact of aminoethoxyvinylglycine and silver ions, chemical inhibitors of ethylene biosynthesis. A significant improvement in the growth of rape caused by inoculation with certain selected strains was also observed in pot experiments, when the plants were cultivated in cadmium-supplemented soil. The biomass of pea cv. Sparkle and its ethylene sensitive mutant E2 (sym5), in particular, was increased through inoculation with certain strains of ACC-utilising bacteria in pot experiments in quartz sand culture. The beneficial effect of the bacteria on plant growth varied significantly depending on individual bacterial strains, plant genotype, and growth conditions. The results suggest that plant growth promoting rhizobacteria containing ACC deaminase are present in various soils and offer promise as a bacterial inoculum for improvement of plant growth, particularly under unfavourable environmental conditions
Descriptors:long-standing sewage sludge; polluted soils. Infection. 1-aminocyclopropane-1-carboxylate deaminase [ACC deaminase]; aminoethoxyvinylglycine: enzyme inhibitor; cadmium: toxicity; heavy metal: contaminant; silver ion: enzyme inhibitor. Alcaligenes sp. 16S rRNA gene (Alcaligenaceae); Alcaligenes xylosoxidans 16S rRNA gene (Alcaligenaceae); Bacillus pumilus 16S rRNA gene (Endospore- forming Gram-Positives); Pseudomonas brassicacearum 16S rRNA gene (Pseudomonadaceae); Pseudomonas marginalis 16S rRNA gene (Pseudomonadaceae); Pseudomonas oryzihabitans 16S rRNA gene (Pseudomonadaceae); Pseudomonas putida 16S rRNA gene (Pseudomonadaceae); Pseudomonas sp. 16S rRNA gene (Pseudomonadaceae); Rhodococcus sp. 16S rRNA gene (Nocardioform Actinomycetes); Variovorax paradoxus 16S rRNA gene (Gram-Negative Aerobic Rods and Cocci)

Organism Descriptors:Alcaligenes sp. (Alcaligenaceae): symbiont; Alcaligenes xylosoxidans (Alcaligenaceae): symbiont; Bacillus pumilus (Endospore-forming Gram-Positives): symbiont; Brassica juncea [Indian mustard] (Cruciferae): host; Brassica napus var. oleifera (Cruciferae): germinating, seedlings; Pisum sativum [pea] (Leguminosae): cultivar-Sparkle, ethylene sensitive mutant, host, mutant E2; Pseudomonas brassicacearum (Pseudomonadaceae): symbiont; Pseudomonas marginalis (Pseudomonadaceae): symbiont; Pseudomonas oryzihabitans (Pseudomonadaceae): symbiont; Pseudomonas putida (Pseudomonadaceae): symbiont; Pseudomonas sp. (Pseudomonadaceae): symbiont; Rhodococcus sp. (Nocardioform Actinomycetes): symbiont; Variovorax paradoxus (Gram-Negative Aerobic Rods and Cocci): symbiont; plant growth promoting rhizobacteria (Bacteria): characterization. root: elongation
Supplemental Descriptors:Alcaligenaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms; Bacteria: Microorganisms; Cruciferae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Endospore- forming Gram-Positives: Eubacteria, Bacteria, Microorganisms; Gram- Negative Aerobic Rods and Cocci: Eubacteria, Bacteria, Microorganisms; Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Nocardioform Actinomycetes: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms; Pseudomonadaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Angiosperms; Bacteria; Dicots; Eubacteria; Microorganisms; Plants; Spermatophytes; Vascular Plants
Subject Codes:Infection
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

95. Title:Extrusion of actin-positive strands from HEp-2 and Int 407 cells caused by outer membrane preparations of enteropathogenic Escherichia coli and specific attachment of wild type bacteria to the strands
View Article: Canadian Journal of Microbiology. 47 (8). August, 2001. 727-734
CD Volume:365
Print Article: Pages: 727-734
Author(s):Kumar Sukumaran Sunil Malladi Vasantha Sankaran Krishnan Haigh Richard Williams Peter Balakrishnan Arun
Author Affiliation:Centre for Biotechnology, Anna University, Chennai, 600025: arunb@annauniv.edu
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Enteropathogenic Escherichia coli (EPEC) causes persistent infantile diarrhoea. This nontoxigenic E. coli exhibits a complicated pathogenic mechanism in which its outer membrane proteins and type III secretory proteins damage intestinal epithelium and cause diarrhoea. In accordance with this, our previous study using HEp-2 cells demonstrated cytopathic effects caused by cell-free outer membrane preparations of EPEC. In this study, we report the extrusion of actin-positive strands from HEp-2 and Int 407 cells when treated with outer membrane preparations. An interesting observation of this work, perhaps relevant to the characteristic localized three-dimensional colony formation of EPEC, is the attachment of a wild type EPEC strain to these actin- positive strands
Descriptors:three-dimensional colony formation. Digestive System (Ingestion and Assimilation); Infection. diarrhea: digestive system disease. actin; actin-positive strands: extrusion; outer membrane proteins; type III secretory proteins

Organism Descriptors:Escherichia coli (Enterobacteriaceae): EPEC, enteropathogenic, nontoxigenic, pathogen, strain-CVD206, strain-DH5-alpha, strain- E2348-69, strain-JPN15, strain-UMD864, three-dimensional colony formation; HEp-2 cell line (Hominidae); Int 407 cell line (Hominidae). intestinal epithelium: digestive system; outer membrane
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia. Animals; Bacteria; Chordates; Eubacteria; Humans; Mammals; Microorganisms; Primates; Vertebrates
Subject Codes:Digestive System (Ingestion and Assimilation); Infection
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

96. Title:The effects of sequential inoculation of mixed rumen protozoa on the degradation of orchard grass cell walls by anaerobic fungus Anaeromyces mucronatus 543
View Article: Canadian Journal of Microbiology. 47 (8). August, 2001. 754-760
CD Volume:365
Print Article: Pages: 754-760
Author(s):Lee Sung S Ha Jong K Cheng K J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744: jongha@snu.ac.kr
Language:English
Language of Summary:English (EN); French (FR)
Abstract:The effects of protozoa on the degradation of plant cell walls (CW) during different growth stages of the fungus Anaeromyces mucronatus have been investigated. Since fungi show a marked lag in their in vitro cultures and many protozoa rapidly die during a prolonged incubation time, the effects of protozoa may vary according to the growth phase of the fungi. Therefore, the approach adopted was (i) to inoculate CW with fungus monoculture, (ii) to inoculate CW with fungus-protozoa coculture, or (iii) to sequentially inoculate fungal cultures that had been grown in CW for 24 (initial stage of growth), 48, and 72 h (late stage of growth) with mixed protozoa. When a fungus associated with protozoa, a growth phase dependent effect was observed. Ruminal protozoa adversely affected the growth and activity when introduced in the initial growth stage of A. mucronatus, but a synergetic interaction was detected when added to late growth stage cultures. Although there is no immediate explanation for these results, the data suggested that protozoa can engulf the fungal zoospores, which are in ruminal fluids and (or) attached to small feed particles, but cannot engulf the fungal thallus that is tightly attached to feed particles by a rhizoidal system. Our data indicated that the protozoa did not influence cellulolysis by the fungi in exponential and (or) stationary phase, but they had a marked inhibitory effect on fungi that were in lag phase. Inhibition during lag phase could result from the protozoal predation of fungal zoospores that had failed to attach to substrates
Descriptors:late growth stage cultures. Cell Biology
Organism Descriptors:Anaeromyces mucronatus (Fungi): growth stages, strain-543; mixed rumen protozoa (Protozoa): inoculation; orchard grass (Gramineae). cell wall: degradation; zoospore
Supplemental Descriptors:Fungi: Plantae; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Protozoa: Invertebrata, Animalia. Angiosperms; Animals; Fungi; Invertebrates; Microorganisms;

Monocots; Nonvascular Plants; Plants; Protozoans; Spermatophytes; Vascular Plants
Subject Codes:Cell Biology
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

97. Title:Analysis of the relationship between growth, cephalosporin C production, and fragmentation in Acremonium chrysogenum
View Article: Canadian Journal of Microbiology. 47 (9). September, 2001. 801-806
CD Volume:365
Print Article: Pages: 801-806
Author(s):Sandor Erzsebet Szentirmai Attila Paul Gopal C Thomas Colin R Pocsi Istvan Karaffa Levente
Author Affiliation:Department of Microbiology and Biotechnology, Faculty of Sciences, University of Debrecen, H-4010, Debrecen: karaffal@tigris.klte.hu
Language:English
Language of Summary:English (EN); French (FR)
Abstract:Mycelial fragmentation in submerged cultures of the cephalosporin C (CPC) producing fungus Acremonium chrysogenum was characterized by image analysis. In both fed-batch and chemostat cultures, the proportion of mycelial clumps seemed to be the most sensitive morphological indicator of fragmentation. In a fed-batch fermentation culture, this declined from roughly 60% at inoculation to less than 10% after 43 h. Subsequent additions of glucose resulted in a sharp increase back to near the initial value, an increase that reversed itself a few hours after glucose exhaustion. Meanwhile CPC production continued to decline steadily. On the other hand, the addition of soybean oil enhanced CPC production, but had no significant effect on the morphology. Although it may sometimes appear that morphology and productivity are related in batch or fed-batch cultures, this study suggests that this is because both respond simultaneously to more fundamental physiological changes, dependent on the availability of carbon. In circumstances, such as supplementary carbon source addition, the relationship is lost. Chemostat cultures supported this belief, as CPC-production rates were hardly affected by the specific growth rate, but the morphology showed significant differences, i.e., lower dilution rates resulted in a lower proportion of clumps and in smaller clumps
Descriptors:cephalosporin C production analysis; fragmentation analysis; fungal growth analysis; morphology. Metabolism; Mycology; Physiology. cephalosporin C
Organism Descriptors:Acremonium chrysogenum (Fungi Imperfecti or Deuteromycetes)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Metabolism; Mycology; Physiology
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

98. Title:Development of a method for mRNA differential display in filamentous fungi: Comparison of mRNA differential display reverse transcription polymerase chain reaction and cDNA amplified fragment length polymorphism in Leptosphaeria maculans
View Article: Canadian Journal of Microbiology. 47 (10). October, 2001. 955-960
CD Volume:365

Print Article: Pages: 955-960
Author(s):Gellatly Kevin S Ash Gavin J Taylor Janet L
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Language:English
Language of Summary:English (EN); French (FR)
Abstract:We modified a technique, cDNA-AFLP, for identifying differentially expressed genes in plants to work in the filamentous fungus Leptosphaeria maculans (Desmaz.) Ces. & De Not. The cDNA fragments generated by our method ranged in size from approximately 100 to 400 bps. On average, twice as many cDNA fragments were amplified per primer set with cDNA amplified fragment length polymorphism in comparison with mRNA differential display reverse transcription polymerase chain reaction. The DNA fragments of interest were excised from gels and analyzed by single-stranded conformation polymorphism to eliminate nondifferentially expressed cDNA contamination. The method was used to examine gene expression differences between cultures grown in the presence or absence of an analog of the Brassica phytoalexin brassinin. Eleven of the fourteen fragments examined were determined by reverse Northern blot to be differentially expressed. In examining gene expression differences between young cultures not producing sirodesmins and older cultures that were producing these phytotoxins, we found 17 of 25 fragments were differentially expressed. Northern blots with these fragments confirmed the results
Descriptors:Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics). cDNA [complementary DNA]: contamination, fragment; mRNA differential display reverse transcription polymerase chain reaction [messenger RNA differential display reverse transcription polymerase chain reaction]; phytoalexin brassinin
Organism Descriptors:Brassica (Cruciferae); Leptosphaeria maculans (Ascomycetes)
Supplemental Descriptors:Ascomycetes: Fungi, Plantae; Cruciferae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Fungi; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants
Subject Codes:Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0008-4166
Year:2001
Journal Title:Canadian Journal of Microbiology

99. Title:Improving erucic acid content in rapeseed through biotechnology: what can the Arabidopsis FAE1 and the yeast SLC1-1 genes contribute?
View Article: Crop Science. 2001. 41 (3). 739-747
CD Volume:359
Print Article: Pages: 739-747
Author(s):Katavic V Friesen W Barton D L Gossen K K Giblin E M Luciw T An Jing Zou JiTao MacKenzie S L Keller W A Males D Taylor D C
Author Variant:An-J. Zou-J-T
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Language:English
Abstract:The main goal of our research is to produce, by genetic manipulation, Brassica napus cultivars with higher amounts of 22:1 in their seed oil than in present Canadian high erucic acid rapeseed (HEAR) cultivars developed through traditional breeding, ideally with proportions of 22:1 approaching 80 mol% (828 g/kg). To probe some rate-limiting steps in the accumulation of triacylglycerols containing very long

chain fatty acids (VLCFAs), particularly erucic acid (22:1), we have taken a transgenic approach, studying the effect of expressing two target genes in HEAR B. napus cv. Hero. To study the role of the elongase complex, involved in elongation of C18 fatty acid moieties to produce VLCFAs, we expressed the A. thaliana, fatty acid elongase 1 (FAE1) gene under the control of a seed-specific promoter (napin), in Hero. This resulted in increased proportions of 22:1 in the seed oil, rising from 430 g/kg in non-transformed controls to 480 to 530 g/kg 22:1 in FAE1 transgenic Hero lines. The FAE1 lines exhibited higher elongase activity in vitro compared to control lines. These data suggest that the level of active condensing enzyme in the native elongase complex is somewhat rate limiting for synthesis of erucic acid and other VLCFAs in HEAR. In small scale field trials, the VLCFA and 22:1 content of FAE1 transgenic lines were superior to field-grown control lines. We report that in field plot trials in Saskatchewan, Canada, during 1998 and 1999, the progeny of our best T4 B. napus cv. Hero SLC1-1 transgenic lines clearly out-performed controls in terms of 22:1, oil content, and yield

Descriptors:biosynthesis. biotechnology. chemical-composition. cultivars. enzyme-activity. enzymes. erucic-acid. genes. lines. plant-composition. rape. seed-oils. transgenic-plants

Geographic Locator:Canada. Saskatchewan

Organism Descriptors:Arabidopsis-thaliana. Brassica-napus. Brassica-napus-var.-oleifera. plants

Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Brassica. North-America. America. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Canada. Brassica-napus

Subject Codes:FF005. FF020. FF040. FF060. FF500. WW000

Supplementary Info:37 ref

ISSN:0011-183X

Year:2001

Journal Title:Crop Science

100. Title:Technology Transfer: Partner Selection and Contract Design with Foreign Firms in the Indian Biotechnology Sectors

View Article: Developing Economies. 39 (1) 2001. 85-111

CD Volume:368

Print Article: Pages: 85-111

Author(s):Ramani S V El Aroui M A Audinet P

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Language:English

Abstract:Though technology transfer has been extensively studied in the economics literature, there is no distinction between the different forms of technology transfer," and few explanations on the partner selection criteria" or the "contract design" that sustain such international cooperation. In this connection, this paper attempts to contribute to the study of the strategic foundations underlying inter-firm cooperation between developed and developing countries. It develops a game theoretical model of technology transfer and tests the propositions of the model using data pertaining to India, with the biotechnology sectors as the knowledge-based industry of reference

Descriptors:Industrialization; Manufacturing and Service Industries; Choice of Technology. Technological Change: Choices and Consequences. Chemicals; Rubber; Drugs. Contracting Out; Joint Ventures

Geographic Locator:India

Subject Codes:EE450. EE350. VV800

ISSN:0012-1533
Year:2001
Journal Title:Developing Economies

101. Title:Chronic toxicity of octahydro-1,3,5,7-tetranitro-1,3,5,7- tetrazocine (HMX) in soil determined using the earthworm (Eisenia andrei) reproduction test
View Article: Environmental Pollution. 111 (2). 2001. 283-292
CD Volume:376
Print Article: Pages: 283-292
Author(s):Robidoux P Y Hawari J Thiboutot S Ampleman G Sunahara G I
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Language:English
Language of Summary:English (EN)
Abstract:The sublethal and chronic effects of the environmental contaminant and explosive octahydro-1,3,5,7-tetranitro-1,3,5,7-tetrazocine (HMX) in artificial soil were assessed using the earthworm (Eisenia andrei). Based on various reproduction parameters (total and hatched number of cocoons, number of juveniles and their biomass), fecundity was reduced at the different concentrations of HMX tested (from 280.0+-12.3 to 2502.9+-230.0 mg kg-1 dry soil) in spiked artificial soil (LOEC: 280.0+-12.3 mg kg-1 dry soil). The growth of adult E. andrei was also reduced at the different concentrations tested, though no mortality occurred, even at the highest tested concentrations. The number of juveniles produced was correlated with the number of total and hatched cocoons, and the biomass of juveniles was correlated with the number of cocoons. Pooled results of these and earlier studies on explosives (TNT, RDX) using the E. andrei reproduction test confirm that effects of HMX on cocoon production are indicative of some reproductive consequences (number of juvenile and their biomass), whereas adult growth, in general, does not correlate strongly with changes in reproduction capacity
Descriptors:biomass; chronic toxicity; cocoon production; ecological risk assessment; fecundity; reproduction; trophic level. Toxicology. ocatahydro-1,3,5,7-tetranitro-1,3,5,7-tetrazocine [HMX]: environmental contaminant, explosive, toxin
Organism Descriptors:Eisenia andrei [earthworm] (Oligochaeta): adult, juvenile
Supplemental Descriptors:Oligochaeta: Annelida, Invertebrata, Animalia. Animals; Annelids; Invertebrates
Subject Codes:Toxicology
ISSN:0269-7491
Year:2001
Journal Title:Environmental Pollution

102. Title:Biotechnology in trees: Towards improved paper pulping by lignin engineering
View Article: Euphytica. 118 (2). 2001. 185-195
CD Volume:370
Print Article: Pages: 185-195
Author(s):Chen Cuiying Baucher Marie Christensen Jorgen Holst Boerjan Wout
Author Affiliation:Vakgroep Moleculaire Genetica en Departement Plantengenetica, Vlaams Interuniversitair Instituut voor Biotechnologie, Universiteit Gent, K.L. Ledeganckstraat 35, B-9000, Gent
Language:English

Language of Summary:English (EN)
Abstract:Lignin is a heterogenous phenolic polymer that plays crucial roles in the development and physiology of vascular plants. However, it needs to be removed from cellulose by toxic and energy-requiring processes for the production of high-quality paper. Therefore, a major biotechnological challenge is to obtain transgenic trees with modified lignin to improve the quality of wood for paper making. Here, we review the results obtained by alterating the expression of genes of the monolignol biosynthesis pathway in trees and the effect of these modifications on the lignin polymer and on pulping. The data reported show that lignin engineering is a promising strategy to improve wood quality for the pulp and paper industry
Descriptors:genetic engineering; lignin engineering; plant breeding; pulping improvement; tree-related biotechnology. Forestry; Genetics. lignin; monolignol: biosynthesis
Organism Descriptors:poplar (Salicaceae): forestry crop
Supplemental Descriptors:Salicaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Forestry; Genetics
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

103. Title:Identification and classification of aromatic rices based on DNA fingerprinting
View Article: Euphytica. 118 (3). 2001. 243-251
CD Volume:370
Print Article: Pages: 243-251
Author(s):Choudhury P Ray Kohli S Srinivasan K Mohapatra T Sharma R P
Author Affiliation:National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi, 110 012
Language:English
Language of Summary:English (EN)
Abstract:Aromatic rices are preferred by the consumers all over the world due to its flavour and palatability. Although a large number of these collections are available, little systematic analysis of genetic diversity has been carried out. With the objective of identification and classification of aromatic rice genotypes, RAPD profiling was employed using 58 random decamer primers. Most of these primers (96.5%) detected polymorphism among the genotypes. Of the 465 amplified bands, 314 were polymorphic. Cluster analysis based on Jaccard's similarity coefficient using UPGMA grouped all the traditional tall, photosensitive, low yielding, long grained 'basmati' aromatics together. The short grained aromatic cultivars, formed a different cluster with high level of average similarity among themselves. The dendrogram based on 58 primers was highly similar to that based on 10 and 15 primers with matrix correlation (r) of 0.88 and 0.91, respectively. This suggested that a set of 10 primers can be employed for an initial assessment of genetic diversity in a large number of collections. All the rice genotypes included in the study could be distinguished from each other at the level of 19 to 186 polymorphic bands between individuals in pair wise comparison over all the 58 primers. Probability of identical profiles by chance suggested that about 1041 genotypes can be unambiguously differentiated by RAPD fingerprints obtained by 58 primers. A diagrammatic mode of presentation of DNA fingerprints of the aromatic rices based on 10 of the informative primers was developed

Descriptors:plant breeding. Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
Organism Descriptors:Oryza sativa [rice] (Gramineae): aromatic type, grain crop
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

104. Title:New types of major anthocyanins detected in Japanese garden iris and its wild forms
View Article: Euphytica. 118 (3). 2001. 253-256
CD Volume:370
Print Article: Pages: 253-256
Author(s):Yabuya T Imayama T Shimomura T Urushihara R Yamaguchi M
Author Affiliation:Division of Biotechnology and Biochemistry, Faculty of Agriculture, Miyazaki University, Miyazaki, 889-2192
Language:English
Language of Summary:English (EN)
Abstract:The anthocyanins of 130 cultivars, 13 lines and 3 wild forms of Iris ensata were analyzed by HPLC, and these plants were classified into 16 types of major anthocyanins. Among these types, 8 types such as petunidin 3RGac5G - delphinidin 3RGac5G, delphinidin 3RGac5G - petunidin 3RGac5G, cyanidin 3RGac5G - peonidin 3RGac5G, delphinidin 3RG - delphinidin 3RGac, petunidin 3RG5G - malvidin 3RG5G, malvidin 3RG5G - peonidin 3RG5G, peonidin 3RG5G - cyanidin 3RG5G and peonidin 3RG - cyanidin 3RG were obtained as new types. In these new types, peonidin 3RG - cyanidin 3RG and peonidin 3RG5G - cyanidin 3RG5G types were noteworthy because cyanidin 3RG and cyanidin 3RG5G are useful for the breeding of red flowers in I. ensata
Descriptors:flower color breeding: red color. Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Genetics. cyanidin: anthocyanin; delphinidin: anthocyanin; malvidin: anthocyanin; peonidin: anthocyanin; petunidin: anthocyanin
Organism Descriptors:Iris ensata [Japanese garden iris] (Iridaceae): ornamental
Supplemental Descriptors:Iridaceae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Genetics
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

105. Title:Present strategies in resistance breeding against scab (Fusarium spp.)
View Article: Euphytica. 119 (1-2). 2001. 121-127
CD Volume:370
Print Article: Pages: 121-127
Author(s):Ruckenbauer P Buerstmayr H Lemmens M
Author Affiliation:Department of Biotechnology in Plant Production, IFA-TULLN, A- 3430, Tulln
Language:English
Language of Summary:English (EN)

Abstract:No Abstract available
Descriptors:wheat breeding. Agronomy (Agriculture); Genetics; Pest Assessment Control and Management. scab: fungal disease, resistance breeding
Organism Descriptors:Fusarium avenaceum (Fungi Imperfecti or Deuteromycetes): pathogen; Fusarium culmorum (Fungi Imperfecti or Deuteromycetes): pathogen; Fusarium graminearum (Fungi Imperfecti or Deuteromycetes): pathogen; wheat (Gramineae)
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Fungi; Microorganisms; Monocots; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Genetics; Pest Assessment Control and Management
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

106. Title:Transgenic wheat plants: A powerful breeding source
View Article: Euphytica. 119 (1-2). 2001. 133-136
CD Volume:370
Print Article: Pages: 133-136
Author(s):Pellegrineschi A McLean S Salgado M Velazquez L Hernandez R Brito R M Noguera M Medhurst A Hoisington D
Author Affiliation:International Maize and Wheat Improvement Center (CIMMYT), Mexico, DF
Language:English
Language of Summary:English (EN)
Abstract:Plant breeders are always interested in new genetic resources. In the past, the sources have been limited to existing germplasm. Genetic engineering now provides the opportunity for almost unlimited strategies to create novel resources. As a first stage, the Applied Biotechnology Center (ABC) at CIMMYT developed a method for the mass production of fertile transgenic wheat (Triticum aestivum L.) that yields plants ready for transfer to soil in 13-14 weeks after the initiation of cultures, and, over the course of a year, an average production of 5-6 transgenic plants per day. CIMMYT elite cultivars are co-bombarded with marker gene and a gene of interest with co-transformation efficiencies around 25-30%. The reliability of this method opens the possibility for the routine introduction of novel genes that may induce resistance to diseases and abiotic stresses, allow the modification of dough quality, and increase the levels of micronutrients such as iron, zinc, and vitamins. The first group of genes being evaluated by the ABC are the pathogenesis related (PR) proteins, such as the thaumatin-like protein (TLP) from barley, chitinase, and 1-3 beta-glucanase. Stable integration of the genes in the genome and inheritance in the progeny were determined by phenotypical analyses that challenged the plants against a wide range of pathogens. Using these genes, we have recovered more than 1200 independent events (confirmed by PCR and Southern blot analyses) that show responses to the pathogens that range from tolerance to hypersensitive reactions. The quantity and anti-fungal activity of the endogenous thaumatin-like proteins were analyzed in T1 and T2 progeny plants. Western blot analyses showed different protein patterns of the wheat endogenous TLPs. Preliminary results indicated that some patterns increased the resistance of transgenic wheat plants to Alternaria triticina. This relationship is being further investigated
Descriptors:genetic engineering; wheat breeding. Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)

Organism Descriptors:Alternaria alternata (Fungi Imperfecti or Deuteromycetes): pathogen; Triticum aestivum (Gramineae): grain crop, transgenic plants
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae; Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Fungi; Microorganisms; Monocots; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

107. Title:Resistance to Tomato spotted wilt virus introgressed from Lycopersicon peruvianum in line UPV 1 may be allelic to Sw-5 and can be used to enhance the resistance of hybrids cultivars
View Article: Euphytica. 119 (3). 2001. 357-367
CD Volume:370
Print Article: Pages: 357-367
Author(s):Rosello Salvador Ricarte Beatriz Diez Maria Jose Nuez Fernando
Author Affiliation:Biotechnology Dept., Universidad Politecnica de Valencia (UPV), Cno. Vera, 14, 46022, Valencia
Language:English
Language of Summary:English (EN)
Abstract:The breeding line UPV 1 developed from the PE-18 accession of Lycopersicon peruvianum collected in Huallanca, Ancash, Peru, shows resistance to TSWV. Mechanical inoculation and thrips transmission were used to study the inheritance of TSWV resistance of this line. UPV 1 resistance is controlled by a dominant gene. The penetrance of this resistance gene was complete in mechanical inoculation and incomplete when thrips transmission was used. Linkage tests between the resistance genes of lines UPV 1 and RDD (Sw-5), indicated allelism. A molecular analysis using a SCAR marker tightly linked to Sw-5 also supported this hypothesis. In heterozygotes the level of resistance expressed in UPV 1 is higher than that expressed in RDD (Sw-5), indicating that the resistance from UPV 1 may be of higher value for the development of commercial hybrids
Descriptors:allelism; breeding line UPV 1 development; disease resistance; hybrid cultivar resistance; hybridization; plant breeding. Horticulture (Agriculture); Genetics; Infection; Pest Assessment Control and Management. Lycopersicon resistance genes (Solanaceae)
Geographic Locator:Huallanca (Peru, South America, Neotropical region)
Organism Descriptors:Frankliniella occidentalis (Thysanoptera): vector; Lycopersicon peruvianum (Solanaceae): PE-18 accession; tomato spotted wilt virus (Bunyaviridae (plant host only)): phytopathogen
Supplemental Descriptors:Bunyaviridae (plant host only): Plant Viruses, Viruses, Microorganisms; Solanaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Thysanoptera: Insecta, Arthropoda, Invertebrata, Animalia. Angiosperms; Animals; Arthropods; Dicots; Insects; Invertebrates; Microorganisms; Plant Viruses; Plants; Spermatophytes; Vascular Plants; Viruses
Subject Codes:Horticulture (Agriculture); Genetics; Infection; Pest Assessment Control and Management
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

108. Title:The Cassava Biotechnology Network: 10 years in action

View Article: Euphytica. 120 (1). 2001. vii
CD Volume:370
Print Article: Pages: vii
Author(s):Raemakers Krit Carvalho Luiz Visser Richard
Language:English
Language of Summary:English (EN)
Abstract:No Abstract available
Descriptors:plant breeding. Horticulture (Agriculture)
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

109. Title:Somatic embryogenesis from floral tissue of cassava (Manihot esculenta Crantz)
View Article: Euphytica. 120 (1). 2001. 1-6
CD Volume:370
Print Article: Pages: 1-6
Author(s):Woodward Barbara Puonti Kaerlas Johanna
Author Affiliation:John Innes Centre, Norwich Research Park, Colney, Norwich, NR4 7UH
Language:English
Language of Summary:English (EN)
Abstract:The aim of this study was to examine the embryogenic potential of floral material of the cassava cultivar MCOL 1505. Macerated immature inflorescences were found to be highly embryogenic, with almost 78% of the explants producing somatic embryos. Somatic embryos were also produced from whole male florets and half florets although at much lower rates. No regeneration was obtained from anther, microspore or floret wall tissue. Somatic embryos derived from immature inflorescences were regenerated via organogenesis and the plants derived from this process were assessed in terms of phenotype and ploidy level. If haploid plants could be produced by this method, this would have significant implications in assisting traditional cassava breeding, as this would allow homozygosity to be reached more rapidly. In a crop such as cassava, which is highly heterozygous in nature, the use of haploids in a breeding programme could considerably shorten the time taken to produce new desirable cultivars. This is the first report on plant regeneration through somatic embryogenesis from floral tissue of cassava
Descriptors:biotechnology; plant breeding; regeneration; somatic embryogenesis. Horticulture (Agriculture); Development; Methods and Techniques
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): cultivar-MCOL 1505, vegetable crop. flower: reproductive system
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Development; Methods and Techniques
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

110. Title:Linamarin content and genetic stability of cassava plants derived by somatic embryogenesis
View Article: Euphytica. 120 (1). 2001. 7-13
CD Volume:370
Print Article: Pages: 7-13
Author(s):Joseph Tessy Yeoh Hock Hin Loh Chiang Shiong
Author Affiliation:Department of Biological Sciences, National University of Singapore, 10 Kent Ridge Crescent, Singapore, 119260
Language:English
Language of Summary:English (EN)
Abstract:A protocol was established for high frequency cyclic somatic embryogenesis for different varieties of cassava. An efficient plant regeneration system was developed for the high cyanogenic variety PRC 60a. Linamarin content and linamarase activity were determined in various tissues of secondary somatic embryos and regenerated plants of PRC 60a. Both linamarin and linamarase activity were not detected in embryogenic callus, roots induced from callus and somatic embryo tissues. The stems and leaves of regenerated plants (in vitro) and storage roots and leaves of mature plants (in vivo), however, contained variable amounts of linamarin and linamarase activity whereas in the nonstorage root tissues (in vitro) only linamarin was detected. The present study suggested that the linamarin biosynthetic pathway may be absent or not switched on in the embryogenic callus and somatic embryos. The ploidy level and somatic chromosome number of the regenerated plants were found to be same as the source plants. The availability of this regeneration system would be useful not only for investigating cyanogenesis but also for genetic manipulation in cassava
Descriptors:biosynthetic pathway; biotechnology; chromosome number; cyanogenesis; genetic stability; plant breeding; ploidy level; regeneration; somatic embryogenesis. Horticulture (Agriculture); Development; Metabolism; Methods and Techniques. cyanide; linamarase; linamarin: content
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): cultivar-PRC 60a, vegetable crop. nonstorage root tissue; storage root
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Development; Metabolism; Methods and Techniques
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

111. Title:Progress made in FEC transformation of cassava
View Article: Euphytica. 120 (1). 2001. 15-24
CD Volume:370
Print Article: Pages: 15-24
Author(s):Raemakers Krit Schreuder Marianne Pereira Isolde Munyikwa Tichafa Jacobsen Evert Visser Richard
Author Affiliation:Laboratory of Plant Breeding, Graduate School Experimental Plant Sciences, Wageningen University, 6700 AJ, Wageningen
Language:English
Language of Summary:English (EN)
Abstract:In cassava friable embryogenic callus (FEC) has been used to obtain transgenic plants using particle bombardment, electroporation, and Agrobacterium tumefaciens. FEC cultures have been obtained in 6 of the 10 tested genotypes. In all genotypes FEC could be regenerated into

plants, however the efficiency differed between the genotypes. Almost all plants regenerated from 6 months old FEC cultures of TMS604444, Adira 4, Thai 5 and M7 were morphological similar to control plants. However, in R60 and R90 a large number of plants were not identical to control plants. Older FEC lines of TMS60444 have a reduced ability to regenerate plants and the plants show somaclonal variation. Somaclonal variation is observed in the same extend in transgenic and non-transgenic plants. The origin of this variation is both genetic and epigenetic. Luciferase based selection is less efficient in producing transgenic lines than chemical selection. Furthermore Agrobacterium tumefaciens mediated transformation is much more efficient than particle bombardment with respect to the production of transgenic lines. A tentative model is introduced which best describes the effect of different selection regimes on the time period required to produce transgenic plants. Kanamycin and stringent luciferase selection required a shorter period of time than selection based on hygromycin, phosphinothricin or non-stringent luciferase. However, a more significant reduction of time was obtained if young instead of old FEC lines of genotype TMS60444 were used for genetic modification. In accordance to the model these young FEC lines of TMS60444 produced transgenic plants within 4 months with both Agrobacterium tumefaciens combined with kanamycin selection and particle bombardment combined with stringent luciferase selection

Descriptors:biotechnology; genotype variation; plant breeding; somaclonal variation. Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques. luciferase

Organism Descriptors:Agrobacterium tumefaciens (Rhizobiaceae): transformation vector; Manihot esculenta [cassava] (Euphorbiaceae): transgenic, vegetable crop

Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Rhizobiaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Angiosperms; Bacteria; Dicots; Eubacteria; Microorganisms; Plants; Spermatophytes; Vascular Plants

Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques

ISSN:0014-2336
Year:2001
Journal Title:Euphytica

112. Title:Production of embryogenic tissues and regeneration of transgenic plants in cassava (Manihot esculenta Crantz)

View Article: Euphytica. 120 (1). 2001. 25-34
CD Volume:370
Print Article: Pages: 25-34

Author(s):Taylor Nigel J Masona Munyaradzi V Carcamo Rosa Ho Thao Schopke Christian Fauquet Claude M

Author Affiliation:International Laboratory for Tropical Agricultural Biotechnology, ILTAB/Danforth Plant Science Center, Center for Molecular, Electronics, University of Missouri, St. Louis, MO, 63121: iltab@danforthcenter.org

Language:English
Language of Summary:English (EN)

Abstract:Disorganised embryogenic tissues have been utilised as target tissues for transgene insertion and transgenic plant regeneration in cassava (Manihot esculenta). The production of friable embryogenic callus in fourteen geographically diverse cassava cultivars, from which eleven

were established as embryogenic suspension cultures, is reported. Embryogenic tissues were similar in nature in all cultivars tested although there was variation in the time required to generate friable callus and the growth rates of suspension cultures. Regeneration of plants has been achieved from eight cultivars but varied significantly in efficiency, with cv. TMS 60444 and Line 2 from Zimbabwe being the most responsive. Tissues from the remaining eight cultivars became arrested at globular and torpedo stages of regeneration indicating that they most likely process an inherent ability to produce plants but require further research to allow this to be realised. Significant numbers of transgenic plants containing transgenes for putative resistance to important viral diseases of cassava in addition to visual marker genes have been regenerated. Transgenic plants from three the cultivars TMS 60444, Bonoua Rouge and M.Col 1505 were recovered after particle bombardment of embryogenic suspension cultures. Correlation's have been made between abnormal leaf morphology and plant vigour with the use of embryogenic suspension cultures for transgene insertion. As an result friable embryogenic callus is now being successfully utilised as the target tissue for genetic transformation and plant regeneration at ILTAB

Descriptors:biotechnology; plant breeding; regeneration. Horticulture (Agriculture); Development; Methods and Techniques

Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): cultivar-Bonoua Rouge, cultivar-M.Col 1505, cultivar-TMS 60444, vegetable crop

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

Subject Codes:Horticulture (Agriculture); Development; Methods and Techniques

ISSN:0014-2336
Year:2001
Journal Title:Euphytica

113. Title:Efficient production of transgenic plants by Agrobacterium-mediated transformation of cassava (Manihot esculenta Crantz)

View Article: Euphytica. 120 (1). 2001. 35-42
CD Volume:370
Print Article: Pages: 35-42

Author(s):Schreuder M M Raemakers C J J M Jacobsen E Visser R G F
Author Affiliation:The Graduate School of Experimental Plant Sciences, Laboratory of Plant Breeding, Wageningen University and Research Center, 6700 AJ, Wageningen

Language:English
Language of Summary:English (EN)

Abstract:An efficient and reproducible method was developed for Agrobacterium-mediated transformation of embryogenic suspension cultures of cassava. LBA4404(pTOK233), containing the nptII, hph and gus marker genes, was used in the experiments. Chemical selection by means of kanamycin was used to establish 1037 antibiotic resistant callus lines, of which 526 showed GUS expression. Of the 241 callus lines that were transferred to maturation medium 219 formed somatic embryos. Thirty-seven of the 38 lines that were transferred to germination medium produced plants. GUS-positive plants could be obtained from 31 lines; in 14 of those lines 100% of the produced plants were GUS-positive, the remaining 17 lines yielded GUS-positive plants at an average of 72%. The transgenic nature of these plants was confirmed by Southern blot analysis

Descriptors:biotechnology; chemical selection; plant breeding. Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Development; Methods and Techniques. GUS [beta-

glucuronidase]. gus gene: transgene; hph gene: transgene; nptII gene: transgene
Organism Descriptors:Agrobacterium tumefaciens (Rhizobiaceae): transformation vector; Manihot esculenta [cassava] (Euphorbiaceae): transgenic, vegetable crop
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Rhizobiaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Angiosperms; Bacteria; Dicots; Eubacteria; Microorganisms; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics); Development; Methods and Techniques
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

114. Title:Transferring a cassava (Manihot esculenta Crantz) genetic engineering capability to the African environment: Progress and prospects
View Article: Euphytica. 120 (1). 2001. 43-48
CD Volume:370
Print Article: Pages: 43-48
Author(s):Masona Munyaradzi V Taylor Nigel J Robertson A Ian Fauquet Claude M
Author Affiliation:Center for Molecular Electronics, ILTAB/Donald Danforth Plant Science Center, St Louis, MO, 63121: iltab@danforthcenter.org
Language:English
Language of Summary:English (EN)
Abstract:The procedures required to produce genetically transformed cassava were developed and are now in place in three laboratories in the USA and Europe. Future implementation and sustainability of transgenic technologies for the agronomic improvement of cassava will depend, however, on transferring these capabilities to locations where cassava has an important socioeconomic niche. If successful, such countries can apply the technology towards their particular needs. Training scientists from the developing countries in the transgenic biotechnologies is of primary importance in this effort. There are, however, many other factors including the availability of laboratory supplies, equipment, suitably experienced support staff, sufficient funding levels and biosafety considerations, which must be addressed and put in place before a transgenic program can be fully implemented in a given country. A transgenic capability is being transferred from the International Laboratory for Tropical Agricultural Biotechnology (ILTAB), USA, to the University of Zimbabwe. Three southern African cassava varieties were induced to form embryogenic suspension cultures at ILTAB and have been transferred to Zimbabwe. These tissues are presently being used as the basis of genetic transformation programs in both laboratories. Problems encountered in the transfer process as well as possible solutions aimed at adapting the available protocols will be presented
Descriptors:biotechnology; environmental conditions; genetic engineering capability; intellectual property rights; laboratory requirements; plant breeding; scientist training. Horticulture (Agriculture). African cassava mosaic disease: viral disease
Geographic Locator:Africa (Ethiopian region); Zimbabwe (Ethiopian region)
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): transgenic, vegetable crop
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants

Subject Codes:Horticulture (Agriculture)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

115. Title:Expression and structure of an elongation factor-1alpha gene (MeEF1) from cassava (Manihot esculenta Crantz)
View Article: Euphytica. 120 (1). 2001. 49-58
CD Volume:370
Print Article: Pages: 49-58
Author(s):Suhandono S Hughes J Brown K Hughes M A
Author Affiliation:Dept. Biochemistry and Genetics, Newcastle University, Newcastle Upon Tyne, NE2 4HH
Language:English
Language of Summary:English (EN)
Abstract:In order to isolate an elongation factor-1alpha (EF-1alpha) gene from cassava, a lambda EMBL3 genomic library, made from a single cassava genotype (MBRA 534, from the CIAT cassava germplasm collection), was screened with a full length EF-1alpha cDNA clone (blt63) from barley. Six positive clones were isolated from an amplified library and 4866 bp from one clone (MeEF1) were subcloned into pGEM3zf(-) and pGEM5zf(-). The sequence has 2709 bp 5' of the translation start site, 1347 bp of coding sequence split into two exons by an intron (374 bp) and 435 bp 3' of the stop codon. A 657 bp intron was also found 5' of the translation start site. The coding sequence is very similar, with 86% DNA sequence identity and 95% deduced amino acid sequence identity, to an EF-1alpha gene from Arabidopsis thaliana. The promoter region of MeEF1 contains 3 putative control elements that are located upstream of the transcription start site. These control elements include a TEF1 box, a TELO box and two TATA boxes. The gene is expressed in early stages of development and in young tissue. Transient expression using particle bombardment shows that the promoter drives uidA gene expression in leaves of cassava and Arabidopsis. An interesting feature of the MeEF1 gene is that the presence of the 5'UTR intron affects the level of expression
Descriptors:biotechnology; plant breeding. Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics). elongation factor-1alpha. Manihot esculenta MeEF1 gene [Manihot esculenta elongation factor-1alpha gene] (Euphorbiaceae): expression, structure
Organism Descriptors:Arabidopsis thaliana (Cruciferae); Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop
Supplemental Descriptors:Cruciferae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

116. Title:Hydroxyproline-rich glycoproteins expressed during stress responses in cassava
View Article: Euphytica. 120 (1). 2001. 59-70
CD Volume:370
Print Article: Pages: 59-70

Author(s):Han Yuanhuai Gomez Vasquez Rocio Reilly Kim Li Hongying Tohme Joe Cooper Richard M Beeching John R
Author Affiliation:Department of Biology and Biochemistry, University of Bath, Bath, BA2 7AY
Language:English
Language of Summary:English (EN)
Abstract:The storage roots of cassava (Manihot esculenta Crantz) suffer from a rapid post-harvest deterioration that is a major constraint to their increased exploitation. In many ways this deterioration resembles wound responses in other better studied plant systems, though it appears to lack an adequate wound repair response. A cDNA clone (cMeHRGP1) for a hydroxyproline-rich glycoprotein expressed during the deterioration response was isolated and characterised. This clone proved to be an antisense pairing, coding for part of phosphoserine aminotransferase on its complementary strand. Messenger RNA corresponding to cMeHRGP1 accumulated in deteriorating cassava roots from day three after harvest, by which time the deterioration response was well advanced. Thereby confirming that aspects of the wound repair response were inadequate in harvested cassava roots
Descriptors:antisense pairing; biotechnology; plant breeding; post-harvest deterioration; stress response; wound response. Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Foods. hydroxyproline-rich glycoprotein: expression
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop. storage root
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Foods
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

117. Title:Isolation and characterisation of cDNAs encoding the large and small subunits of ADP-glucose pyrophosphorylase from cassava (Manihot esculenta Crantz)
View Article: Euphytica. 120 (1). 2001. 71-83
CD Volume:370
Print Article: Pages: 71-83
Author(s):Munyikwa Tichafa R I Kreuze Jan Fregene Martin Suurs Luc Jacobsen Evert Visser Richard G F
Author Affiliation:Laboratory of Plant Breeding, Graduate School Experimental Plant Sciences, Wageningen University, 6700 AJ, Wageningen
Language:English
Language of Summary:English (EN)
Abstract:Screening of a tuber specific cassava cDNA library resulted in the isolation of full length cDNA clones with homology to the genes encoding the small and large subunits of ADP glucose pyrophosphorylase. Sequence analysis revealed that AGPase B the clone with homology to the small subunit shared 54% homology at amino acid level with the AGPase S clone that is more closely related to the large subunit. Segregation analysis of a cross between the cassava cultivars TMS 30572 and CM 2177-2 revealed that AGPase S is a single copy gene that is localised on the female derived linkage group E of the cassava genetic map. AGPase B is a low copy gene of which one member is localised on the female derived linkage group P. The two genes are expressed in all cassava tissues but AGPase B exhibits a

higher steady state mRNA level than AGPase S and is highly expressed in leaf and tuber tissue. The AGPase enzyme activity was much higher in young cassava leaves as compared to older leaves and tubers. Cassava AGPase was activated by 3-PGA and inhibited by up to 90% in the presence of inorganic phosphate (Pi). The tuber enzyme was relatively unaffected by 3PGA but was highly inhibited by Pi. Transformation of potato (Solanum tuberosum) plants with an antisense AGPase B construct resulted in 10 out of 134 antisense AGPase B plants having on average 3.5 times more tubers than the control non transgenic plants. Analysis of these transgenic plants revealed they had greatly reduced levels of AGPase B mRNA, 1.5 to 3 times less starch, and five times higher levels of soluble sugars, sucrose, glucose and fructose, to those found in control plants

Descriptors:biotechnology; plant breeding. Horticulture (Agriculture); Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics). ADP-glucose; ADP-glucose pyrophosphorylase: large subunits, small subunits; ADP-glucose pyrophosphorylase-encoding complementary DNA: characterization, isolation; AGPase [ADP glucose pyrophosphorylase]; ATP; glucose-1-phosphate; inorganic phosphate

Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop; Solanum tuberosum [potato] (Solanaceae): transgenic

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

Subject Codes:Horticulture (Agriculture); Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics)

ISSN:0014-2336
Year:2001
Journal Title:Euphytica

118. Title:Molecular analysis of differentially expressed genes during postharvest deterioration in cassava (Manihot esculenta Crantz) tuberous roots

View Article: Euphytica. 120 (1). 2001. 85-93
CD Volume:370
Print Article: Pages: 85-93

Author(s):Huang Jiang Bachem Christian Jacobsen Evert Visser Richard G F
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Language:English
Language of Summary:English (EN)

Abstract:One of the major problems for cassava is the rapid deterioration after harvesting cassava tuberous roots, which limits the possibilities for production and distribution of cassava in the world. Postharvest deterioration is an inherent problem for cassava since wounding and mechanical damage of the tuberous roots cannot be prevented during harvesting, which includes postharvest physiological deterioration (PPD) and secondary deterioration. To date, the molecular mechanism and biochemical pathways of PPD are poorly understood. The aim of this project, which is focusing on the early stages (first 72 hrs), is to gain molecular insight and identify important metabolic pathways during the process of PPD in cassava tuberous roots. Finally by reverse genetic approaches to delay or even prevent the process of PPD in cassava tuberous roots. By using a new RNA fingerprinting method,

called cDNA-AFLP, we have screened more than 6,000 TDFs (Transcript Derived Fragments) via up to 100 primer combinations during the early process of PPD in cassava. Only 10% of the TDFs are developmentally regulated, while the other 90% are expressed throughout the process of PPD in cassava tuberous roots. Furthermore, in order to set up a functional catalogue of differentially expressed genes during PPD, 70 TDFs were selected and isolated based on their expression patterns, which were either up-regulated, down-regulated or transiently induced. Around 40 of these TDFs were found to be similar with known genes in databases. The other 30 TDFs were present mostly genes without known function. Through data analysis, it is shown that important biochemical and physiological processes, such as notably oxygen stress, carbohydrate metabolism, protein metabolism and phenolic compounds synthesis, are involved in PPD in cassava tuberous roots

Descriptors:biotechnology; cassava: postharvest deterioration, vegetable; genetic expression; oxygen stress; plant breeding. Horticulture (Agriculture); Foods; Genetics; Metabolism. carbohydrate: metabolism; phenolic compound: biosynthesis; protein: metabolism

Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop. tuberous root

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

Subject Codes:Horticulture (Agriculture); Foods; Genetics; Metabolism

ISSN:0014-2336
Year:2001
Journal Title:Euphytica

119. Title:Environmental conditions during root development: Drought constraint on cassava starch quality

View Article: Euphytica. 120 (1). 2001. 95-101
CD Volume:370
Print Article: Pages: 95-101

Author(s):Sriroth Klanarong Piyachomkwan Kuakoon Santisopasri Vilai Oates Christopher G
Author Affiliation:Department of Biotechnology, Kasetsart University, Bangkok: aapkrs@ku.ac.th

Language:English
Language of Summary:English (EN)

Abstract:Cassava has the reputation of being a drought tolerant crop, however, when deprived of water, plant and root development are affected. This ultimately will translate to an altered starch synthesis expressed by variation of starch quality. The magnitude of which, is influenced by the severity of stress conditions and stage of plant maturity. During early plant development, water stress retards growth, which will only be resumed after the immature plant has received sufficient water. Despite of an increased starch yield, the effect of initial water stress on starch quality is still sustained. In mature plants, starch quality is affected by environmental conditions prior to root harvest, especially the onset of rain after a stress period as indicated by a reduced starch paste. This paper presents the argument for extending the scope of traditional breeding programs beyond selecting for plant growth under drought conditions, to strategies that place greater emphasis on stabilizing starch quality

Descriptors:biotechnology; drought; environmental conditions; plant breeding; water stress. Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Foods. starch: peak viscosity, quality, swelling power

Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop. root: development
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Foods
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

120. Title:Methods for detecting the cassava bacterial blight pathogen: A practical approach for managing the disease
View Article: Euphytica. 120 (1). 2001. 103-107
CD Volume:370
Print Article: Pages: 103-107
Author(s):Verdier Valerie Ojeda Sandra Mosquera Gloria
Author Affiliation:Biotechnology Research Unit, Centro Internacional de Agricultura Tropical (C.I.A.T.) and Institut de Recherche pour le Developpement (I.R.D.), A.A. 6713, Cali: v.verdier@cgiar.org
Language:English
Language of Summary:English (EN)
Abstract:Cassava bacterial blight (CBB), caused by Xanthomonas axonopodis pv. manihotis (Xam), is a particularly destructive disease in South America and Africa. The movement of infected asymptomatic stems is a major means of pathogen dispersal as well as infected seeds. The success of a cassava-seed certification program depends on the availability of reliable tests to detect the pathogen in vegetative planting materials and true seeds. We report here the different methods that permitted to detect the pathogen in cassava tissues. A polymerase chain reaction (PCR) test was developed for this pathogen. The PCR assay worked well for pathogen detection in extracts from leaf and stem lesions and the minimum number of cells that could be detected ranged from 3 X 102 to 104 CFU per ml. Nested-PCR worked well for Xam detection from naturally infected seeds. This technique was specific, sensitive, and rapid for detecting Xam in cassava true seeds. The highest detection level found was 1-2 viable cells per reaction. A dot-blot assay was developed by evaluating a 898 bp DNA fragment unique to Xam strains as a diagnostic DNA probe. The probe detected Xam strains in crude extracts of leaf and stem lesions, cassava fruits and sexual seeds that were naturally infected. Overall sensitivity of the dot-blot method was about 103 CFU per reaction. The dot-blot hybridization technique can be easily used for culture indexing. A monoclonal antibody (MAb) was also used for an enzyme-linked immunosorbent assay (ELISA) and tested with various infected tissues. Overall sensitivity of the method was about 103CFU per reaction
Descriptors:biotechnology; plant breeding; seed transmission. Horticulture (Agriculture); Infection; Methods and Techniques; Pest Assessment Control and Management. cassava bacterial blight [CBB]: bacterial disease, detection, management
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): host, vegetable crop; Xanthomonas axonopodis (Pseudomonadaceae): pathovar-manihotis, phytopathogen
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Pseudomonadaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Angiosperms;

Bacteria; Dicots; Eubacteria; Microorganisms; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Infection; Methods and Techniques; Pest Assessment Control and Management
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

121. Title:The response of cassava cultivars to root-knot nematode infestation: An in vitro method
View Article: Euphytica. 120 (1). 2001. 109-113
CD Volume:370
Print Article: Pages: 109-113
Author(s):van Vuuren Rosan Jansen Woodward Barbara
Author Affiliation:John Innes Centre, Norwich Research Park, Colney, Norwich, NR4 7UH: barbara.woodward@bbsrc.ac.uk
Language:English
Language of Summary:English (EN)
Abstract:The aim of this study was to obtain information on the response of cassava (Manihot esculenta Crantz) to root-knot nematode infestation. To achieve this aim, a novel in vitro dual root/nematode culture method was used, where root cultures of several cassava cultivars were inoculated with axenic Meloidogyne javanica eggs. Following an incubation period, cassava roots were stained, weighed and dissected to determine the number of galls produced on the roots, as well as the number of mature females embedded in the galls. The number of eggs and larvae produced during this time were also determined. Results indicated that the modified in vitro nematode culture medium used was suitable for most root cultures of cassava cultivars. It was found that some cassava cultivars were highly susceptible to root-knot nematode infestation, with some cultivars showing very high numbers of galls and up to 50 mature females inside each gall. Some cassava cultivars screened, however, showed low numbers of galls and mature females, even though the presence of larvae was high. Some of these cultivars formed callus-like structures instead of galls, and this may be a resistance mechanism. This method may be useful as a screening tool, to determine the response and resistance or susceptibility of cassava cultivars to root-knot nematode infestation
Descriptors:biotechnology; cultivar response; host response; plant breeding. Horticulture (Agriculture); Parasitology; Pest Assessment Control and Management
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop; Meloidogyne javanica [root-knot nematode] (Nematoda): phytoparasite
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Nematoda: Aschelminthes, Helminthes, Invertebrata, Animalia. Angiosperms; Animals; Aschelminths; Dicots; Helminths; Invertebrates; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Parasitology; Pest Assessment Control and Management
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

122. Title:Genomic and biological diversity of the African cassava geminiviruses
View Article: Euphytica. 120 (1). 2001. 115-125
CD Volume:370

Print Article: Pages: 115-125
Author(s):Pita J S Fondong V N Sangare A Kokora R N N Fauquet C M
Author Affiliation:International Laboratory for Tropical Agricultural Biotechnology (ILTAB), Donald Danforth Plant Science Center, UMSL/CME-M308, St Louis, MO, 63121-4499: iltab@danforthcenter.org
Language:English
Language of Summary:English (EN)
Abstract:The virological situation of cassava in Africa is increasing in complexity due to the number and types of viruses isolated from different locations within the continent. Here, we report the complete nucleotide sequences of both A and B components of two geminivirus species infecting cassava in the Ivory Coast and review the current knowledge of the molecular and biological diversity of the African cassava geminiviruses. As a whole, newly obtained sequences are compared with those of the African cassava mosaic geminiviruses identified to date. Results indicate that all isolates of African cassava mosaic virus (ACMV), irrespective of their geographical origin are clustered together with little or no variation in their genomic sequence. On the contrary, the genomes of the East African cassava mosaic virus (EACMV) are more genetically diverse due to the frequent occurrence of recombinations within their two components. Indeed, the EACMV-like viruses vary so much that their classification is becoming problematic. In addition, there is also a large range of phenotypic symptom variation for each of these virus species, irrespective of the location of isolation. Furthermore, it has been shown that ACMV and EACMV can be synergistic in cassava, resulting in a greater DNA accumulation and consequently inducing severe symptoms. For all these reasons, this paper initiates a discussion concerning the species demarcation for cassava geminivirus
Descriptors:biotechnology; plant breeding; synergism; transreplication; viral biological diversity; viral genomic diversity. Horticulture (Agriculture); Genetics; Infection; Pest Assessment Control and Management
Geographic Locator:Africa (Ethiopian region)
Organism Descriptors:African cassava mosaic virus (Geminivirus): phytopathogen; East African cassava mosaic virus (Geminivirus): phytopathogen; Manihot esculenta [cassava] (Euphorbiaceae): host, vegetable crop
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Geminivirus: Plant Viruses, Viruses, Microorganisms. Angiosperms; Dicots; Microorganisms; Plant Viruses; Plants; Spermatophytes; Vascular Plants; Viruses
Subject Codes:Horticulture (Agriculture); Genetics; Infection; Pest Assessment Control and Management
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

123. Title:The primary gene pool of cassava (Manihot esculenta Crantz subspecies esculenta, Euphorbiaceae)
View Article: Euphytica. 120 (1). 2001. 127-132
CD Volume:370
Print Article: Pages: 127-132
Author(s):Allem A C Mendes R A Salomao A N Burle M L
Author Affiliation:Embrapa Recursos Geneticos e Biotecnologia, 70849-970, Brasilia, DF
Language:English
Language of Summary:English (EN)

Abstract:The primary gene pool (GP-1) of a crop is composed of gene reservoirs that cross easily with the domesticated, while the crosses regularly produce fertile offspring. The GP-1 is further subdivided into cultivated and wild gene pools. The cultivated gene pool encompasses commercial stocks of the crop, as well as landraces. The wild GP-1 of the crop comprises putative ancestors and closely related species that show a fair degree of fertile relationships with the domesticate. Two South American wild subspecies of cassava (M. flabellifolia and M. peruviana) were proposed as natural members of the wild GP-1 of the crop. Another Brazilian species (M. pruinosa) is morphologically so close to both wild subspecies that it may turn out as another member of the wild GP-1
Descriptors:ancestry; biotechnology; cultivated gene pool; domestication; plant breeding; primary gene pool; wild gene pool. Horticulture (Agriculture); Evolution and Adaptation
Organism Descriptors:Manihot esculenta ssp. esculenta [cassava] (Euphorbiaceae): vegetable crop; Manihot flabellifolia (Euphorbiaceae); Manihot peruviana (Euphorbiaceae); Manihot pruinosa (Euphorbiaceae)
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Evolution and Adaptation
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

124. Title:Assessing genetic diversity in the cassava (Manihot esculenta Crantz) germplasm collection in Brazil using PCR-based markers
View Article: Euphytica. 120 (1). 2001. 133-142
CD Volume:370
Print Article: Pages: 133-142
Author(s):Carvalho Luiz Joaquim Castelo Branco Schaal Barbara Anna
Author Affiliation:Genetic Resources and Biotechnology, EMBRAPA, Brasilia, DF, 70770-900: carvalho@cenargen.embrapa.br
Language:English
Language of Summary:English (EN)
Abstract:Knowledge of the origin, organization and nature of the cassava (Manihot esculenta Crantz) germplasm collection in Brazil is incomplete due to lack of critical information on several aspects of the collection. This study verifies the utility of SSR-primed PCR markers for germplasm assessment and then utilizes these markers as well as RAPD's to characterize the Brazilian collection. We specifically address the following questions: 1) what is the relationship of morphologically closely related species to cultivated cassava? 2) What is the genetic diversity of cultivars within and between different habitats in Brazil? 3) Do agronomic traits and molecular markers reveal the same relationship among cassava accessions? 4) How complete is the Brazilian cassava collection and how well is it represented in the Word Core Collection of cassava, maintained by CIAT? Results of the interspecific studies of cassava and its wild relatives confirms the close relationship of cassava, Manihot esculenta ssp. esculenta to Manihot esculenta ssp. flabellifolia as well identifying several other closely related wild species. Next, PCR-based markers indicate a strong grouping of varieties related to the region of cultivation in Brazil. Moreover, important regions such as Cerrados and Amazon are relatively poorly represented in germplasm collections. Interestingly, the relationships of accessions based on agronomic traits are not fully congruent with

relationships revealed with RAPD markers. Finally, the genetic diversity of the Brazilian cassava collection is not fully represented in the Core of the Word Core Collection of CIAT
Descriptors:biotechnology; genetic diversity; germplasm collection; plant breeding. Horticulture (Agriculture); Conservation; Population Genetics (Population Studies). RAPD [random amplified polymorphic DNA]; SSR
Geographic Locator:Brazil (South America, Neotropical region)
Organism Descriptors:Manihot esculenta ssp. esculenta [cassava] (Euphorbiaceae): vegetable crop; Manihot esculenta ssp. flabellifolia (Euphorbiaceae)
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Conservation; Population Genetics (Population Studies)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

125. Title:Traditional management of cassava morphological and genetic diversity by the Makushi Amerindians (Guyana, South America): Perspectives for on-farm conservation of crop genetic resources
View Article: Euphytica. 120 (1). 2001. 143-157
CD Volume:370
Print Article: Pages: 143-157
Author(s):Elias Marianne McKey Doyle Panaud Olivier Anstett Marie Charlotte Robert Thierry
Author Affiliation:Centre d'Ecologie Fonctionnelle et Evolutive (CEFE), CNRS, 1919 route de Mende, 34293, Montpellier Cedex, 5
Language:English
Language of Summary:English (EN)
Abstract:In this paper we present original data on morphological and genetic diversity of cassava managed by the Makushi Amerindians from Guyana. Although they propagate cassava exclusively vegetatively by means of stem cuttings, many Amerindian farmers also use and multiply volunteer plants grown from seeds produced by sexual reproduction. Morphological characters were recorded for 29 varieties cultivated by the Makushi and two populations of plants originating from volunteer cassava seedlings. Genetic characterisation with AFLP markers was available for 21 of the examined varieties. The morphological and agronomic characters were highly variable among varieties. Every variety could be differentiated from any other one, except for one pair of varieties. However, high intra-varietal variability existed, which might lead to confusions between phenotypically similar varieties by the Makushi. Seedlings were on average different from the pool of the varieties studied, but 67% were found to resemble closely enough one of the varieties to be liable to be assigned to it. Confusion between very similar varieties, as well as assignment of seedlings to a variety, should generate genetic variability within varieties, which was detected with AFLP markers. As in other sites in Amazonia, there was only a weak correlation between inter- varietal distances assessed with molecular and with morphological markers, suggesting that diversification of morphological characters has taken place repeatedly and independently across the Amazonian range of the crop. Diversifying selection, exchanges of varieties between farmers, and incorporation of sexually produced volunteer plants are key mechanisms responsible for the high diversity observed. Strategies of conservation of genetic resources should take these dynamic processes into account

Descriptors:biotechnology; crop genetic resource management; diversity management; genetic diversity; morphological diversity; on-farm conservation perspectives; plant breeding; traditional agroecosystem; traditional management system. Horticulture (Agriculture); Conservation; Genetics; Sociology (Population Studies)
Geographic Locator:Guyana (South America, Neotropical region)
Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop; human (Hominidae): Makushi Amerindian
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia. Angiosperms; Animals; Chordates; Dicots; Humans; Mammals; Plants; Primates; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Horticulture (Agriculture); Conservation; Genetics; Sociology (Population Studies)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

126. Title:Genome mapping in cassava improvement: Challenges, achievements and opportunities
View Article: Euphytica. 120 (1). 2001. 159-165
CD Volume:370
Print Article: Pages: 159-165
Author(s):Fregene M Okogbenin E Mba C Angel F Suarez Maria Christina Janneth Guitierez Chavarriaga P Roca W Bonierbale M Tohme J
Author Affiliation:Centro Internacional de Agricultura Tropical (CIAT), Cali
Language:English
Language of Summary:English (EN)
Abstract:Breeding goals of yield increases, root quality improvement, and disease resistance in cassava are considerably slowed down by biological characteristics of the crop, which includes a long growth cycle, a heterozygous genetic background and a poor knowledge of the organization of crop diversity. These factors severely hamper the speed and ease of moving around useful genes in cassava. The consequences are that cassava production fails to keep up with demand, especially in regions where over 90% of yield is consumed as food, leading to an increase in acreage of cassava fields mostly into marginal lands. The advent of molecular markers, genome studies and plant genetic transformation holds promise of providing ways around breeding obstacles in long growth cycle and heterozygous crops. A number of these new tools, including a molecular genetic map, markers linked to disease resistance genes, and marker-aided studies of complex traits now exist or are being developed for cassava at CIAT. Large scale sequencing and mapping of expressed sequence tags (ESTs) have been initiated, towards a transcript map of cassava and the implementation of the candidate- gene approach to complex trait mapping. A cassava bacterial artificial chromosome (BAC) library has also been constructed to expedite positional cloning of genes, known only by their phenotypes and their position relative to markers on a molecular genetic map and complementation studies of candidate loci. Studies of genes that control traits of agronomic importance, and their allelic diversity in nature, provides powerful tools for understanding the basis of crop performance and improvement
Descriptors:biotechnology; crop diversity; crop improvement; crop performance; phenotype; plant breeding; root quality. Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics). BAC [bacterial artificial chromosome]; EST [expressed sequence tag]

Organism Descriptors:Manihot esculenta [cassava] (Euphorbiaceae): vegetable crop
Supplemental Descriptors:Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

127. Title:Random amplified polymorphic DNA (RAPD) markers variability among cultivars and landraces of common beans (Phaseolus vulgaris L.) of south-Brazil
View Article: Euphytica. 120 (2). 2001. 257-263
CD Volume:370
Print Article: Pages: 257-263
Author(s):Maciel F L Gerald L T S Echeverrigaray S
Author Affiliation:Institute of Biotechnology, University of Caxias do Sul, Caxias do Sul, RS
Language:English
Language of Summary:English (EN)
Abstract:To evaluate the variability among cultivars and landraces of common bean (Phaseolus vulgaris L.), 15 cultivars and 18 landraces of common bean (Phaseolus vulgaris L.), a undefined species of Phaseolus, two landraces of Vigna angularis L., and a landrace of soybean (Glycine max L.), were screened with fifteen oligonucleotide primers in PCR reactions. An average of 20.3 RAPD bands were scored per primer. A total of 304 amplification products were scored of which 88.8% were polymorphic among Phaseolus genotypes. Based on the RAPD markers, four major clusters were formed. Three clusters corresponded to the soybean, to the two Vigna angularis landraces, and to the Phaseolus sp. landrace, respectively. The fourth cluster include all the landraces and cultivars of Phaseolus vulgaris. This large group could be separated into three subgroups that were correlated with the phaseolin patterns and the average seed weight of the genotypes. The analysis shows that most of the landraces collected in South Brazil (17 out of 18) belong to the Andean gene pool, and most of the cultivars (13 out of 15) belong to the Middle American gene pool
Descriptors:plant breeding. Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
Organism Descriptors:Glycine max [soybean] (Leguminosae): landrace; Phaseolus vulgaris [common bean] (Leguminosae): cultivars, landraces, vegetable crop; Vigna angularis (Leguminosae): landrace
Supplemental Descriptors:Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

128. Title:An improved in vitro technique for isolated microspore culture of barley
View Article: Euphytica. 120 (3). 2001. 379-385
CD Volume:370
Print Article: Pages: 379-385

Author(s):Kasha K J Simion E Oro R Yao Q A Hu T C Carlson A R
Author Affiliation:Dept. of Plant Agriculture, Biotechnology Division, University of Guelph, Guelph, ON, N1G 2W1
Language:English
Language of Summary:English (EN)
Abstract:A detailed procedure for isolated microspore culture of barley is presented along with examples of response across genotypes. Over 30 genotypes, including winter and spring growth habit and 2-row and 6-row genotypes, have shown an essentially genotype independent response, averaging about 10,000 embryos per 5 cm petri culture plate. The regeneration frequency, checked on samples of 500 embryos per plate ranged from 36 to 97% with most genotypes being in the range of 70 to 90%. About 70 to 80% of the plants regenerated have been completely fertile doubled haploids, thus eliminating the need to double the chromosome number of plants. Many little details are critical to success of the microspore procedure and while it saves much time compared to anther culture, greater attention to details and cleanliness is essential
Descriptors:regeneration frequency. Agronomy (Agriculture); Methods and Techniques
Organism Descriptors:barley (Gramineae): fertile double haploids, grain crop, spring growth habit, winter growth habit
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Methods and Techniques
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

129. Title:Tolerance to paraquat is correlated with the traits associated with water stress tolerance in segregating F2 populations of barley and wheat
View Article: Euphytica. 121 (1). 2001. 81-86
CD Volume:370
Print Article: Pages: 81-86
Author(s):Altinkut Ahu Kazan Kemal Ipekci Zeliha Gozukirmizi Nermin
Author Affiliation:Tubitak, Marmara Research Center, Research Institute for Genetic Engineering and Biotechnology, 41470, Gebze-Kocaeli
Language:English
Language of Summary:English (EN)
Abstract:To identify scorable marker traits that can be used in cereal breeding programs for selecting drought tolerant individuals, we investigated the correlation among the drought-associated traits in two F2 populations derived from the crosses made between drought tolerant and sensitive barley and wheat parental genotypes. The parental genotypes of these crosses also differed by at least three other traits - paraquat tolerance, leaf size, and the relative water content. These three traits were scored in two F2 populations of 80 individuals for each barley and wheat cross. Analysis of results indicated that the enhanced tolerance to paraquat was correlated with reduced leaf size and increased relative water content, two traits associated with water stress phenotypes of the drought tolerant barley and wheat parents. Our results suggested that the selection based on paraquat tolerance is technically less demanding and thus useful for rapid screening of individuals for enhanced drought tolerance in segregating populations

Descriptors:drought tolerance; plant breeding; segregating F-2 population characteristics; selection; water stress tolerance traits. Agronomy (Agriculture); Genetics; Physiology. paraquat: tolerance
Organism Descriptors:Hordeum vulgare [barley] (Gramineae): grain crop; Triticum aestivum [wheat] (Gramineae): grain crop
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Genetics; Physiology
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

130. Title:RAPD variability in rice (Oryza sativa L.) plants derived from desiccation-tolerant calli
View Article: Euphytica. 121 (3). 2001. 297-303
CD Volume:370
Print Article: Pages: 297-303
Author(s):Phong Dinh Thi Muoi Le Thi Binh Le Tran
Author Affiliation:Institute of Biotechnology (IBT), National Center for Natural Science and Technology (NCST), Hoang Quoc Viet Street, Cau Giay, Hanoi
Language:English
Abstract:Genetic modification from selfed progenies of 18 rice (Oryza sativa L.) plants regenerated from callus tissues which survived desiccation, were investigated at the DNA level using the random amplified polymorphic DNA (RAPD) method. Twelve 10-mer random primers were used to amplify DNA of progenies from the regenerated plants, and a total of 228 PCR products and 1780 DNA fragments were obtained by primers, generating between four to thirteen major bands. The size of the amplified fragments ranged from 0.2 to 2.55 kb. The results showed that 10 out of 12 primers produced polymorphic bands, two primers (RA31 and RA185) showed no polymorphism among plants tested. A dendrogram of the genetic distance was constructed based on their polymorphism, demonstrating that somaclonal variation exists in rice plants regenerated from callus which survived the desiccation treatment. Part of this variation can be useful in rice breeding
Descriptors:genetic distance; plant breeding; somaclonal variation. Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics). RAPD [random amplified polymorphic DNA]: variability
Organism Descriptors:Oryza sativa [rice] (Gramineae): grain crop
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

131. Title:Bulked AFLP analysis for the assessment of genetic diversity in white clover (Trifolium repens L.)
View Article: Euphytica. 121 (3). 2001. 305-315
CD Volume:370
Print Article: Pages: 305-315
Author(s):Kolliker R Jones E S Jahufer M Z Z Forster J W
Author Affiliation:Plant Biotechnology Centre, Agriculture Victoria, La Trobe University, Bundoora, VIC, 3083

Language:English
Abstract:The use of bulked leaf samples from individual plants for amplified fragment length polymorphism (AFLP) analysis was evaluated as a tool for assessment of genetic diversity in white clover (Trifolium repens L.). Bulking of leaf samples produced slightly simpler AFLP profiles compared to the combined profiles of individual plants from the same cultivar. Approximately 90% of bands which were present in individual plants were present in bulked samples of the same cultivar. The majority of those absent were rare bands, shared by less than 25% of individual plants. Replicate bulk samples gave almost identical banding patterns, demonstrating the robustness of the bulked AFLP technique. Cluster analysis of AFLP data derived from individual plants resulted in a phenogram similar to that produced from data derived from bulked samples of the same plants. AFLP analysis of bulked samples detected significant amounts of genetic variability among 52 cultivars and accessions with genetic similarity values ranging from 0.42 to 0.92. However, cluster analysis of AFLP data only partially reflected the geographic origin of cultivars and accessions and was not congruent with cluster analysis based on variation for morphophysiological characters. Bulked AFLP analysis provides a powerful tool for rapid assessment of genetic variability in white clover and may also be used for cultivar identification
Descriptors:genetic diversity; plant breeding. Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
Organism Descriptors:Trifolium repens [white clover] (Leguminosae): forage crop
Supplemental Descriptors:Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

132. Title:Discrimination between Oryza malampuzhaensis Krish. et Chand. and Oryza officinalis Wall ex Watt based on RAPD markers and morphological traits
View Article: Euphytica. 122 (1). 2001. 181-189
CD Volume:370
Print Article: Pages: 181-189
Author(s):Thomas George Joseph Latha Varghese George Kalyanaraman K Kuriachan Philomena Das M R
Author Affiliation:Plant Molecular Biology Group, Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, KER, 695 014; E-Mail: gtpulikunnel@yahoo.com
Language:English
Abstract:Oryza malampuzhaensis, one of the tetraploid taxa of the genus Oryza, is geographically restricted to Western Ghats of South India. Its taxonomic status is not well established and is generally treated as a tetraploid race of O. officinalis. Sixty- three morphological traits and 262 random amplified polymorphic DNA (RAPD) markers generated by 23 random decamer primers were used to assess the genetic relationship between O. malampuzhaensis and O. officinalis. Pair wise comparisons based on both RAPDs and morphological traits revealed 60% genetic distance between the two taxa and was significantly higher ($p<0.01$) than the corresponding intra-specific distances. Cluster and principal component analysis (PCA) of genetic distance estimations based on RAPDs and morphological traits clearly differentiated the two taxa.

High frequency of discrete O. malampuzhaensis specific RAPDs (21%) and the significantly higher ($p<0.05$) mean number of amplification products per individual in O. malampuzhaensis observed in the study reflect its allopolyploid nature. Low genetic diversity within O. malampuzhaensis revealed by RAPD analysis indicates the recent origin of this taxa. The RAPD analysis further revealed the possibility that the putative 'C' genome progenitor of O. malampuzhaensis is a close relative of O. officinalis. In addition, amplification products diagnostic to O. malampuzhaensis were identified. The results of the present study clearly demonstrated that the O. malampuzhaensis is a distinct entity, and support the recent conclusion that O. malampuzhaensis has diverged enough to deserve species status

Descriptors:plant breeding. Molecular Genetics (Biochemistry and Molecular Biophysics); Systematics and Taxonomy

Geographic Locator:India (Asia, Oriental region)

Organism Descriptors:Oryza malampuzhaensis (Gramineae): identification, tetraploid; Oryza officinalis (Gramineae): identification

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

Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Systematics and Taxonomy

ISSN:0014-2336

Year:2001

Journal Title:Euphytica

133. Title:AFLP analysis of genetic diversity within and between populations of perennial ryegrass (Lolium perenne L.)

View Article: Euphytica. 122 (1). 2001. 191-201

CD Volume:370

Print Article: Pages: 191-201

Author(s):Guthridge K M Dupal M P Kolliker R Jones E S Smith K F Forster J W

Author Affiliation:Plant Biotechnology Centre, Agriculture Victoria, La Trobe University, Bundoora, VIC, 3089

Language:English

Abstract:Amplified fragment length polymorphism (AFLP) analysis has been used to measure genetic diversity in perennial ryegrass (Lolium perenne L.) and to relate intra- and interpopulation variation to breeding history. Cluster analysis of AFLP data from contrasting populations showed features consistent with the origins of these varieties. Significant differences in intrapopulation diversity were detected and partial separation of different cultivars was observed. Restricted base cultivars, derived from small numbers of foundation clones, were suitable for this type of study, allowing near complete discrimination of closely related cultivars. Analysis of bulked samples was based on the pooling of genomic DNA from 20 individuals from 6 selected populations. Cluster analysis of AFLP data from bulked samples produced a phenogram showing relationships consistent with the results of individual analysis. AFLP profiling provides an important tool for the detection and quantification of genetic variation in perennial ryegrass

Descriptors:plant breeding. Agronomy (Agriculture); Population Genetics (Population Studies)

Organism Descriptors:Lolium perenne [perennial ryegrass] (Gramineae): forage crop

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

Subject Codes:Agronomy (Agriculture); Population Genetics (Population Studies)
ISSN:0014-2336
Year:2001
Journal Title:Euphytica

134. Title:Immobilization of recombinant strains of Saccharomyces cerevisiae for the hydrolysis of lactose in salted Domiati cheese whey
View Article: European Food Research and Technology. 212 (2). 2001. 225-227
CD Volume:357
Print Article: Pages: 225-227
Author(s):El Nemr Tarek M
Author Affiliation:Dairy Science and Technology Department, Faculty of Agriculture (El-Shatby), Alexandria University, Alexandria
Language:English
Language of Summary:English (EN)
Abstract:Intergeneric protoplast fusants SK-26 and SK-35 between Saccharomyces cerevisiae ATCC 4126 and Kluyveromyces lactis CBS 683 produced 2.70 ml dl-1 and 1.52 ml dl-1 (v/v) of ethanol during fermentation of lactose at 25 degreeC in salted Domiati cheese whey containing 6.1 g dl-1 (w/v) NaCl when entrapped in alginate spheres, whereas the free recombinant cells produced 2.36 ml dl-1 and 1.09 ml dl-1 (v/v) of ethanol. Yeast hybrids spheres can be used nine times with accumulated increases of ethanol production of 9.1 ml dl-1 and 8.98 ml dl-1 (v/v), respectively
Descriptors:Domiati cheese: cheese; Foods; biotechnology; fermentations; industrial alcohol production; salted cheese whey: disposal/management. Bioprocess Engineering; Microbiology; Waste Management (Sanitation). ethanol: production; lactose: hydrolysis
Organism Descriptors:Saccharomyces cerevisiae (Ascomycetes): recombinant strain immobilization, uses
Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Microbiology; Waste Management (Sanitation)
ISSN:1438-2377
Year:2001
Journal Title:European Food Research and Technology

135. Title:Characterisation of the Roundup Ready soybean insert
View Article: European Food Research and Technology. 213 (2). August, 2001. 107-112
CD Volume:357
Print Article: Pages: 107-112
Author(s):Windels Pieter Taverniers Isabel Depicker Ann Van Bockstaele Erik De Loose Marc
Author Affiliation:Department for Plant Genetics and Breeding, Centre for Agricultural Research, Caritasstraat 21, 9090, Melle: m.deloose@clo.fgov.be
Language:English
Language of Summary:English (EN)
Abstract:In this article we describe the isolation and characterisation of the junction between insert DNA and plant DNA in the transgenic Roundup Ready soybean line event 40-3-2. Our results establish that during integration of the insert DNA several rearrangements occurred at the 3' NOS junction and that the genomic plant DNA at the pre-integration site may have been rearranged. These findings highlight the utility of characterising junction regions to fulfil the request for information

regarding which DNA sequences have been incorporated in commercialised transgenic lines. Furthermore, the characterisation of junction regions is, in our opinion, the method of choice to support method development for detection and identification of plant biotechnology-derived products
Descriptors:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics). DNA junction regions: characterization, isolation; genomic plant DNA; insert DNA. soybean 3'NOS gene (Leguminosae)
Organism Descriptors:soybean (Leguminosae): Roundup Ready, transgenic, vegetable crop
Supplemental Descriptors:Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:1438-2377
Year:2001
Journal Title:European Food Research and Technology

136. Title:Use of response surface methodology to investigate the effects of processing conditions on frozen dough quality and stability
View Article: European Food Research and Technology. 213 (4-5). October, 2001. 323-328
CD Volume:357
Print Article: Pages: 323-328
Author(s):Kenny S Grau H Arendt E K
Author Affiliation:Department of Food Technology and National Food Biotechnology Centre, University College Cork, National University of Ireland, Cork: e.arendt@ucc.ie
Language:English
Language of Summary:English (EN)
Abstract:Processing conditions used in frozen dough production have a major effect on frozen dough quality and stability. A short-time straight dough baking procedure was used and the effects of dough temperature after mixing, rest time and thaw time were investigated using response surface methodology. A central composite design was constructed to study the effects of these processing conditions on baking performance. Dough temperature was studied between 15 and 30degreeC. Rest time was varied from 0 to 45 min. Thawing was carried out in a retarder/proofer using a dough conditioning programme, and thaw time was varied from 3.75 to 8.25 h. Response variables measured were; proof time, specific volume, crumb firmness, crumb gumminess and crumb chewiness. Baking performance was evaluated after 1, 10 and 20 weeks of frozen storage and optimisation was carried out using desirability (a multiple response method). After one week of frozen storage, optimum processing conditions were; dough temperature, 27.7degreeC; rest time, 30 min and thaw time, 7.2 h. After ten weeks of frozen storage optimum processing conditions were; dough temperature, 23.8degreeC; rest time, 14 min and thaw time, 7.1 h. After 20 weeks of frozen storage, optimum processing conditions were; dough temperature, 22.1degreeC; rest time, 4 min and thaw time, 7.9 h
Descriptors:baking; breadmaking; food chemistry; food processing; food technology; frozen doughs: analysis, baking performance, food product, processing conditions, quality, stability; methodology; temperatures; wheat bread: analysis, bakery product, preparation, quality. Foods; Methods and Techniques
Subject Codes:Foods; Methods and Techniques

ISSN:1438-2377
Year:2001
Journal Title:European Food Research and Technology

137. Title:Fast characterisation of selected beta-casein and beta- lactoglobulin variants using specific single nucleotide polymorphisms derived from milk cell DNA: A novel real-time PCR approach
View Article: European Food Research and Technology. 213 (4-5). October, 2001. 356-360
CD Volume:357
Print Article: Pages: 356-360
Author(s):Einspanier Ralf Klotz Andreas Buchberger Johann Krause Ingolf
Author Affiliation:Institut fuer Physiologie, FML-Weihenstephan, Technische Universitaet Muenchen, Freising: einspani@weihenstephan.de
Language:English
Language of Summary:English (EN)
Abstract:The determination of genetic variants of beta-casein (beta-CN A1, A2, B) and beta-lactoglobulin (beta-LG A, B, C, D) directly from milk is described by means of detection of distinct mutations in the nucleotide sequence and verified using isoelectric focusing of the corresponding proteins. With the inherent positive effect of certain genetic variants on cheese-making properties, the information derived by the new technique is of interest for the dairy technology as well as for the milk production. Based on the protein sequence information available from databases, deduced gene fragments containing the variant-specific mutations were generated using PCR. A partial nucleotide sequence of the beta-LG-gene fragment D, containing allele-specific point mutations, could be determined. For beta-CN those mutations occur at amino acid residues 67 and 122 (beta-CN gene locus 8101+8267) whereas for the beta-LG variants specific mutations occur at amino acid residues 45, 59, 64+118 (beta-LG gene locus 3662, 3706, 4581+4583). Additionally, seven mutations were found in intron 2 of the beta-LG gene. Based on specific PCR fragments generated from milk cell DNA, genotyping of alleles of beta-CN and beta-LG or admixtures becomes efficient and simultaneous. Hence, a real-time PCR approach was established specifically distinguishing three important beta-CN milk protein variants with remarkable benefits when compared to other DNA-based mutation detection systems
Descriptors:biotechnology; cheese-making; food chemistry; food technology; gene mutations: detection; introns; methodology. Foods; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics). DNA: molecular analysis, nucleotide polymorphisms; amino acids: analysis; beta-casein: molecular analysis, molecular variants; beta- lactoglobulins: molecular analysis, molecular variants; food proteins: molecular analysis, molecular variants; gene fragments: detection
Organism Descriptors:dairy cattle (Bovidae)
Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Foods; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:1438-2377
Year:2001
Journal Title:European Food Research and Technology

138. Title:PCR-ELISA for the CaMV-35S promoter as a screening method for genetically modified Roundup Ready soybeans
View Article: European Food Research and Technology. 213 (4-5). October, 2001. 366-371
CD Volume:357
Print Article: Pages: 366-371
Author(s):Brunnert Hans Josef Spener Friedrich Boerchers Torsten
Author Affiliation:Institut fuer Chemo- und Biosensorik, Mendelstrasse 7, 48149, Muenster: t.boerchers@icb-online.de
Language:English
Language of Summary:English (EN)
Abstract:Screening of food components using a polymerase chain reaction (PCR) for the presence of genetic elements, such as the widespread cauliflower mosaic virus 35S promoter introduced into genetically modified organisms (GMOs), has become a routine method in modern food analysis. With the aim of developing a high throughput method suitable for automation we established a PCR-enzyme-linked immunosorbent assay (PCR-ELISA). It is based on specific hybridization of an immobilized, biotinylated PCR product with a digoxigenin-labelled internal probe; the label then serves in colorimetric immunodetection. With this fast and convenient method laborious blotting procedures and the use of hazardous ethidium bromide in gel staining are avoided. The optimized protocol for this PCR-ELISA allows the detection of as little as 0.1 ng amplicon in only 2 h. With this new technique we analyzed whole Roundup Ready soybeans as well as soybean flour with GMO contents ranging from 0.1% to 2%
Descriptors:CaMV-35S promoter: detection methods; amplicons; automation; food components: screening methodologies; food technology; methodology; plant biotechnology; soybean flour: analysis, food product, preparation. Agronomy (Agriculture); Foods; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
Organism Descriptors:cauliflower mosaic virus (Caulimovirus): phytopathogen; soybeans (Leguminosae): cultivar-Roundup Ready, oil crop
Supplemental Descriptors:Caulimovirus: Plant Viruses, Viruses, Microorganisms; Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Microorganisms; Plant Viruses; Plants; Spermatophytes; Vascular Plants; Viruses
Subject Codes:Agronomy (Agriculture); Foods; Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
ISSN:1438-2377
Year:2001
Journal Title:European Food Research and Technology

139. Title:Efficacy testing of commercial disinfectants against foodborne pathogenic and spoilage microbes in biofilm-constructs
View Article: European Food Research and Technology. 213 (4-5). October, 2001. 409-414
CD Volume:357
Print Article: Pages: 409-414
Author(s):Wirtanen Gun Aalto Mervi Harkonen Paivi Gilbert Peter Mattila Sandholm Tiina
Author Affiliation:VTT Biotechnology, Tietotie 2, Espoo: gun.wirtanen@vtt.fi
Language:English
Language of Summary:English (EN)
Abstract:This paper describes the evaluation of poloxamer-hydrogel biofilm-constructs for the routine efficacy testing of disinfectants at normal use strength. Aqueous solutions of poloxamer Pluronic F127 show thermo-reversible gelation, being liquid at temperatures <15degreeC

but firm gels at temperatures >15degreeC. Chilled poloxamer solutions (30% w/v) were made up in a tryptone soy broth and inoculated with stationary-phase cultures of 14 foodborne spoilage microbes, including Pseudomonas, Bacillus, Staphylococcus, Micrococcus, enterobacteria and a yeast, as well as pathogen test- strains, including Listeria and Salmonella. Drops (either 200 mul or 100 mul) were placed onto pre-warmed, sterile, stainless steel discs held in sealed Petri dishes. The constructs were incubated for 5 h at 30degreeC and all strains grew well in the poloxamer hydrogel. Incubated poloxamer gels and their discs were transferred to solutions of commercial disinfectant formulations containing either amphoteric surfactants, hydrogen peroxide with peracetic acid or silver ions, sodium hypochlorite, or alcohols with and without additives. After 5 min at 25degreeC the test pieces were removed from the disinfectant solution and transferred to a neutraliser at 10-15degreeC. These tests were carried out in triplicate. The gels dispersed rapidly, releasing the cells and enabling a count of the viable cells. All formulations effected a >5-log kill of planktonic challenges within 5 min. An effective killing of microbial cells within the biofilm-constructs was shown when the reduction was at least 0.3 log units. The results were highly reproducible, with patterns of susceptibility varying as a function of the organism, disinfectant type, and concentration. The experiments support the view that poloxamer hydrogels can be used for testing the disinfectant efficacy of various formulations against contaminants isolated from food and drink processes

Descriptors:bacterial food contamination: analysis, detection, prevention; bacterial food spoilage: analysis, detection, prevention; biofilms; disinfection; food processing; food technology; temperatures. Foods; Microbiology; Sanitation. commercial disinfectants: efficacy testing methods, uses

Organism Descriptors:bacteria (Bacteria)

Supplemental Descriptors:Bacteria: Microorganisms. Bacteria; Eubacteria; Microorganisms

Subject Codes:Foods; Microbiology; Sanitation

ISSN:1438-2377

Year:2001

Journal Title:European Food Research and Technology

140. Title:Consumer attitudes to genetically modified organisms in food in the UK

View Article: European Review of Agricultural Economics. 2001. 28 (4). 479-498

CD Volume:361

Print Article: Pages: 479-498

Author(s):Burton M Rigby D Young T James S

Author Affiliation:University of Western Australia, Perth, Western Australia, Australia

Language:English

Abstract:This paper reports a year 2000 study of UK consumer attitudes (n=228) to genetically modified organisms (GMOs) in food and the extent to which these attitudes translate into willingness to pay to avoid these products. The results indicate the relative importance of different aspects of the food system in forming food preferences, and that GM food is only one of a number of concerns, albeit a significant one. Attitudes towards organic food are found to be a useful indicator of attitudes towards GM technology, as the preference structure that underlies the former also appears to inform the latter. Significant differences are found between attitudes to GM food in which plants are modified by the introduction of genes from other plants and those in

which plants are modified by the introduction of genes from animals and plants
Descriptors:biotechnology. consumer-attitudes. consumer-surveys. food-preferences. food-safety. organic-foods. willingness-to-pay
Geographic Locator:UK
Identifiers:genetically modified organisms
Supplemental Descriptors:British-Isles. Western-Europe. Europe. Developed-Countries. Commonwealth-of-Nations. European-Union-Countries. OECD-Countries
Subject Codes:EE116. EE720. QQ000. QQ200. WW000
Supplementary Info:32 ref
ISSN:0165-1587
Year:2001
Journal Title:European Review of Agricultural Economics
Copyright:Copyright CAB International

141. Title:Chloride binding by the AML1/Runx1 transcription factor studied by NMR
View Article: FEBS Lett 2001 Jan 12,;488(1-2):81-4
CD Volume:363
Print Article: Pages: 81-84
Author(s):Wolf Watz M Backstrom S Grundstrom T Sauer U Hard T
Author Affiliation:Department of Biotechnology, Royal Institute of Technology, Center for Structural Biochemistry, Novum, Huddinge, Sweden
Abstract:It is known that the DNA binding Runt domain of the AML1/Runx1 transcription factor coordinates Cl(-) ions. In this paper we have determined Cl(-) binding affinities of AML1 by (35)Cl nuclear magnetic resonance (NMR) linewidth analysis. The Runt domain binds Cl(-) with a dissociation constant (K(d,Cl)) of 34 mM. If CBFbeta is added to form a 1:1 complex, the K(d,Cl) value increases to 56 mM. Homology modeling suggests that a high occupancy Cl(-) binding site overlaps with the DNA binding surface. NMR data show that DNA displaces this Cl(-) ion. Possible biological roles of Cl(-) binding are discussed based on these findings
Descriptors:Amino Acid Sequence. Binding, Competitive. Chlorides. DNA. DNA-Binding Proteins. *Magnetic Resonance Spectroscopy. Models, Molecular. Molecular Sequence Data. Protein Binding. Protein Structure, Tertiary. Sequence Alignment. Support, Non-U.S. Gov't. Thermodynamics. Transcription Factors
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

142. Title:Hydroxyl radical-induced apoptosis in human tumor cells is associated with telomere shortening but not telomerase inhibition and caspase activation
View Article: FEBS Lett 2001 Jan 19;488(3):123-32
CD Volume:363
Print Article: Pages: 123-132
Author(s):Ren JG Xia HL Just T Dai YR
Author Affiliation:Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing, PR China
Abstract:Reactive oxygen species (ROS) have been found to trigger apoptosis in tumor cells. At the same time, telomerase is found to be associated with malignancy and reduced apoptosis. However little is known about the linkage between ROS such as *OH and telomerase/telomere. To address the interrelations between *OH and telomerase/telomere in tumor cell killing, HeLa, 293 and MW451 cells were induced to undergo

apoptosis with *OH radicals generated via Fe(2+)-mediated Fenton reactions (0.1 mM FeSO(4) plus 0.3-0.9 mM H2O2) and telomerase activity, telomere length were measured during apoptosis. We found that during *OH-induced apoptosis, telomere shortening took place while no changes in telomerase activity were observed. Our results suggest that *OH-induced telomere shortening is not through telomerase inhibition but possibly a direct effect of *OH on telomeres themselves indicating that telomere shortening but not telomerase inhibition is the primary event during *OH-induced apoptosis. Strikingly, we also found that *OH-induced apoptosis in HeLa cells is caspase-3-independent but is associated with reduction of mitochondrial transmembrane potential. Our results indicate that *OH triggers apoptotic tumor cell death through a telomere-related, caspase-independent pathway

Descriptors:Apoptosis. Caspases. Cell Line. DNA Fragmentation. Enzyme Activation. Flow Cytometry. Glutathione. Hela Cells. Human. Hydrogen Peroxide. Hydroxyl Radical. In Situ Nick-End Labeling. Membrane Potentials. Microscopy, Electron. Mitochondria. Reactive Oxygen Species. Telomerase. Telomere

Geographic Locator:Netherlands

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Journal Title:FEBS Letters

143. Title:Expression of telomerase inhibits hydroxyl radical-induced apoptosis in normal telomerase negative human lung fibroblasts

View Article: FEBS Lett 2001 Jan 19;488(3):133-8

CD Volume:363

Print Article: Pages: 133-138

Author(s):Ren JG Xia HL Tian YM Just T Cai GP Dai YR

Author Affiliation:Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing, PR China

Abstract:In tumor cells telomerase activity is associated with resistance to apoptosis and the introduction of the human telomerase reverse transcriptase (hTERT) subunit into normal human cells is associated with life span extension of the cells. To determine the role of telomerase in regulating apoptosis, telomerase negative human embryo lung fibroblasts were transfected with the hTERT gene. Unlike the control fibroblasts, the telomerase-expressing cells had elongated telomeres and were resistant to apoptosis induced by hydroxyl radicals. The results indicate that expression of telomerase and, thus, the maintenance of telomere length in normal human somatic cells caused resistance to not only cellular senescence but also apoptosis. Moreover, we found that hydroxyl radical-induced apoptosis in telomerase-expressing and control fibroblasts was caspase-3 independent. These findings have revealed a new type of interrelation between telomerase and caspase-3, which may indicate that in this case the expressed telomerase may inhibit apoptosis at a site not related to the caspase-3 cascade

Descriptors:*Apoptosis. Caspases. Clone Cells. Dose-Response Relationship, Drug. Fibroblasts. *Gene Deletion. Human. Hydroxyl Radical. Lung. Telomerase. Telomere. Transfection

Geographic Locator:Netherlands

ISSN:0014-5793

Year:2001

Journal Title:FEBS Letters

144. Title:Pathogen-induced expression of plant ATP: citrate lyase

View Article: FEBS Letters. 2001. 488 (3). 211-212

CD Volume:363
Print Article: Pages: 211-212
Author(s):Suh MiChung Yi SoYoung Lee SanghYeob Sim WoongSeop Pai HyunSook Choi Doil
Author Variant:Suh-M-C. Yi-S-Y. Lee-S-Y. Sim-W-S. Pai-H-S. Choi-D
Author Affiliation:Graduate School of Biotechnology, Korea University, Seoul 136-701, Korea Republic
Language:English
Abstract:In order to better understand the molecular and cellular defence mechanisms during the hypersensitive response (HR) that results from the interaction between a plant pathogen and its non-host, 8-week-old Capsicum annuum cv. Pukang leaves were inoculated with the soyabean pathogen Xanthomonas campestris pv. glycines [X. axonopodis pv. glycines] (5 x 107 CFU). A pool of genes induced or repressed by infection was isolated using differential display PCR, and one of the DNA fragments was found to have significant sequence homology with ATP:citrate lyase (ACL). A cDNA library was constructed and screened using a cDNA fragment of ACL as a probe. A cDNA clone with an open reading frame containing 608 amino acids was isolated and designated Ca-ACL1 (GenBank accession number AF290958). Deduced amino acid sequences have significant sequence homology with the C-terminal part of known animal ACLs. Expression kinetics of the Ca-ACL1 transcripts during inoculation with X. campestris pv. glycines was studied using northern blot analysis of infected hot pepper leaves. HR cell death appeared approx equal to 15 h post-infiltration. In further tests, significant accumulation of the transcript was observed in resistant but not in susceptible Capsicum lines
Descriptors:amino-acid-sequences. chillies. disease-resistance. DNA-libraries. enzyme-activity. enzymes. gene-expression. host-parasite-relationships. nucleotide-sequences. open-reading-frames. plant-diseases. plant-pathogenic-bacteria. plant-pathogens. polymerase-chain-reaction. varietal-reactions
Identifiers:ATP:citrate lyase
Organism Descriptors:Capsicum. Capsicum-annuum. Xanthomonas-axonopodis-pv.-glycines
Supplemental Descriptors:Capsicum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Xanthomonas-axonopodis. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF020. FF003. FF610. HH600. WW000
Supplementary Info:5 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

145. Title:Enzymatic synthesis of a novel trehalose derivative, 3,3'-diketotrehalose, and its potential application as the trehalase enzyme inhibitor
View Article: FEBS Lett 2001 Jan 26;489(1):42-5
CD Volume:363
Print Article: Pages: 42-45
Author(s):Sode K Akaike E Sugiura H Tsugawa W
Author Affiliation:Department of Biotechnology, Tokyo University of Agriculture and Technology, 2-24-16 Nakamachi, Koganei, 184-8588, Tokyo, Japan. sode@cc.tuat.ac.jp
Abstract:We reported the preparation of a novel trehalose derivative based on enzymatic oxidation of trehalose by water-soluble glucose-3-dehydrogenase (G3DH) from marine bacterium Halomonas sp. alpha-15 cells. The product of G3DH enzymatic conversion was 3,3'-

diketotrehalose (3,3'dkT), a novel trehalose derivative of which both third hydroxy groups of glucopyranosides were oxidized. 3,3'dkT was revealed to show an inhibitory effect toward pig-kidney and Bombyx mori trehalases. The IC(50) values of 3,3'dkT were 0.8 and 2.5 mM and K(i) values were 0.2 and 0.6 mM for pig-kidney and for B. mori trehalases, respectively. In addition, 3,3'dkT did not show any inhibitory effect on both maltase and mannosidase activities. Therefore, 3,3'dkT was a specific inhibitor of trehalases
Descriptors:Animal. Binding, Competitive. Catalysis. Enzyme Inhibitors. Glucose Dehydrogenases. Halomonas. Kinetics. Silkworms. Trehalase. Trehalose
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

146. Title:Intermolecular interactions between the SH3 domain and the proline-rich TH region of Bruton's tyrosine kinase
View Article: FEBS Lett 2001 Jan 26;489(1):67-70
CD Volume:363
Print Article: Pages: 67-70
Author(s):Hansson H Okoh MP Smith CI Vihinen M Hard T
Author Affiliation:Department of Biotechnology, Royal Institute of Technology, Center for Structural Biochemistry, Novum, Sweden
Abstract:The SH3 domain of Bruton's tyrosine kinase (Btk) is preceded by the Tec homology (TH) region containing proline-rich sequences. We have studied a protein fragment containing both the Btk SH3 domain and the proline-rich sequences of the TH region (PRR-SH3). Intermolecular NMR cross-relaxation measurements, gel permeation chromatography profiles, titrations with proline-rich peptides, and (15)N NMR relaxation measurements are all consistent with a monomer-dimer equilibrium with a dissociation constant on the order of 60 microM. The intermolecular interactions do, at least in part, involve proline-rich sequences in the TH region. This behavior of Btk PRR-SH3 may have implications for the functional action of Btk
Descriptors:Chromatography, Gel. DNA-Binding Proteins. Dimerization. Human. Magnetic Resonance Spectroscopy. Nuclear Proteins. Proline. Protein-Tyrosine Kinase. Signal Transduction. Support, Non-U.S. Gov't. Time Factors. src Homology Domains
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

147. Title:Early signaling components in ultraviolet-B responses: distinct roles for different reactive oxygen species and nitric oxide
View Article: FEBS Lett 2001 Feb 2;489(2-3):237-42
CD Volume:363
Print Article: Pages: 237-242
Author(s):A H Mackerness S John CF Jordan B Thomas B
Author Affiliation:Department of Plant Genetics and Biotechnology, Horticulture Research International, Wellesbourne, Warwick, UK. s.amin-hanjani@maff.gsi.gov.uk
Abstract:The nature and origin of the reactive oxygen species (ROS) involved in the early part of Ultraviolet-B (UV-B)-induced signaling pathways were investigated in Arabidopsis thaliana using a range of enzyme inhibitors and free radical scavengers. The increase in PR-1 transcript and decrease in Lhcb transcript in response to UV-B exposure was shown to be mediated through pathways involving hydrogen peroxide (H(2)O(2)) derived from superoxide (O(2)(&z.rad;-)). In

contrast, the up-regulation of PDF1.2 transcript was mediated through a pathway involving O(2)(&z.rad;-) directly. The origins of the ROS were also shown to be distinct and to involve NADPH oxidase and peroxidase(s). The up-regulation of Chs by UV-B was not affected by ROS scavengers, but was reduced by inhibitors of nitric oxide synthase (NOS) or NO scavengers. Together these results suggest that UV-B exposure leads to the generation of ROS, from multiple sources, and NO, through increased NOS activity, giving rise to parallel signaling pathways mediating responses of specific genes to UV-B radiation
Descriptors:Acyltransferases. Arabidopsis. Catalase. Dose-Response Relationship, Drug. Free Radical Scavengers. Gene Expression Regulation, Plant. Glutathione. Hydrogen Peroxide. NG-Nitroarginine Methyl Ester. Nitric Oxide. Nitroso Compounds. Photosynthetic Reaction Center, Plant. Plant Proteins. RNA, Ribosomal, 18S. Reactive Oxygen Species. S-Nitrosoglutathione. Salicylamides. Signal Transduction. Superoxide Dismutase. Superoxides. Support, Non-U.S. Gov't. *Ultraviolet Rays
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

148. Title:Guide DNA technique reveals that the protein component of bacterial ribonuclease P is a modifier for substrate recognition
View Article: FEBS Lett 2001 Feb 23;491(1-2):94-8
CD Volume:363
Print Article: Pages: 94-98
Author(s):Tanaka T Baba H Hori Y Kikuchi Y
Author Affiliation:Division of Bioscience and Biotechnology, Department of Ecological Engineering, Toyohashi University of Technology, Tempaku-cho, Toyohashi, 441-8580, Aichi, Japan. tanakat@eco.tut.ac.jp
Abstract:We developed a guide DNA technique with which the cleavage efficiency of pre-tRNA substrate raised in the RNase P reaction. The 20-mer guide DNAs hybridizing to the upstream region of the cleaving site enhanced the cleavage reactions of RNA substrates by Escherichia coli RNase P. This guide DNA technique was also applicable to cleavage site selection by choosing the DNA-hybridizing site. Results showed that RNase P accepts DNA/RNA double-stranded 5'-leader region with high catalytic efficiency as well as single-stranded RNA region in pre-tRNAs as substrates, which suggests that the protein component of bacterial RNase P prefers bulky nucleotides. The protein component did not affect the normal 5'-processing reaction of pre-tRNAs, but enhanced the mis-cleaving (hyperprocessing) reactions of tRNA in non-cloverleaf folding. Our results suggested that the protein component of RNase P is a modifier for substrate recognition
Descriptors:Bacterial Proteins. Base Sequence. Endoribonucleases. Escherichia coli. Molecular Sequence Data. *Nucleic Acid Conformation. Nucleic Acid Hybridization. Oligonucleotide Probes. RNA Precursors. RNA, Bacterial. RNA, Catalytic. RNA, Transfer. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

149. Title:Oncostatin M and hepatocyte growth factor induce hepatic maturation via distinct signaling pathways
View Article: FEBS Lett 2001 Mar 9;492(1-2):90-4
CD Volume:363
Print Article: Pages: 90-94

Author(s):Kamiya A Kinoshita T Miyajima A
Author Affiliation:Stem Cell Regulation, Kanagawa Academy of Science and Technology, Teikyo University Biotechnology Research Center 1F, Kawasaki, Japan. kamiya@stem.kast.or.jp
Abstract:Liver development is regulated by soluble factors as well as cell-cell contacts. We previously reported that oncostatin M (OSM) induced hepatic maturation in a primary culture of embryonic day 14 liver cells. While OSM expression in the liver starts in mid gestation and decreases in postnatal stages, hepatocyte growth factor (HGF) is mainly expressed in the liver in the first few days after birth. In this study, we compared the effect of OSM and HGF on the differentiation of fetal hepatic cells in vitro. Like OSM, HGF in the presence of dexamethasone induced expression of glucose-6-phosphatase, tyrosine amino transferase and carbamoyl-phosphate synthase, and accumulation of glycogen in fetal hepatic cells, although to a lesser extent than OSM. Interestingly, while both OSM and HGF up-regulated production of albumin, secretion of albumin occurred only in response to OSM. In addition, although hepatic maturation induced by OSM depends on STAT3, HGF failed to activate STAT3 and HGF-induced differentiation was independent of STAT3. These results indicate that OSM and HGF induce hepatic maturation through different signaling pathways
Descriptors:Animal. Cell Differentiation. DNA-Binding Proteins. Fetus. Hepatocyte Growth Factor. Liver. Mice. Mice, Inbred C57BL. Peptides. Serum Albumin. Signal Transduction. Support, Non-U.S. Gov't. Trans-Activators
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

150. Title:The structure of glutamate transporters shows channel-like features
View Article: FEBS Lett 2001 Mar 16;492(3):183-6
CD Volume:363
Print Article: Pages: 183-186
Author(s):Slotboom DJ Konings WN Lolkema JS
Author Affiliation:Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Kerklaan 30, 9751 NN, Haren, The Netherlands
Abstract:Neuronal and glial glutamate transporters remove the excitatory neurotransmitter glutamate from the synaptic cleft and thus prevent neurotoxicity. The proteins belong to a large family of secondary transporters, which includes transporters from a variety of bacterial, archaeal and eukaryotic organisms. The transporters consist of eight membrane-spanning alpha-helices and two pore-loop structures, which are unique among secondary transporters but may resemble pore-loops found in ion channels. Another distinctive structural feature is the presence of a highly amphipathic membrane-spanning alpha-helix that provides a hydrophilic path through the membrane. The unusual structural features of the transporters are discussed in relation to their function
Descriptors:ATP-Binding Cassette Transporters. Amino Acid Transport System X-AG. Animal. Human. Membrane Proteins. Models, Biological. Neurons. Protein Conformation. Sequence Analysis, Protein. Synaptic Transmission
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

151. Title:A new family of small, palmitoylated, membrane-associated proteins, characterized by the presence of a cysteine-rich hydrophobic motif
View Article: FEBS Lett 2001 Mar 16;492(3):204-9
CD Volume:363
Print Article: Pages: 204-209
Author(s):Cools J Mentens N Marynen P
Author Affiliation:The Human Genome Laboratory, Center for Human Genetics, University of Leuven, Flanders Interuniversity Institute for Biotechnology (VIB), Herestraat 49, B-3000, Leuven, Belgium
Abstract:We recently cloned the CHIC2 gene (previously BTL) by virtue of its involvement in a chromosomal translocation t(4;12)(q11;p13) occurring in acute myeloid leukemias. In this study we show that CHIC2 is a member of a highly conserved family of proteins characterized by the presence of a striking cysteine-rich hydrophobic (CHIC) motif. Our data illustrate that cysteines in this central CHIC motif are palmitoylated and that CHIC2 is associated with vesicular structures and the plasma membrane. The CHIC proteins thus resemble the cysteine string proteins, which function in regulated exocytosis
Descriptors:Amino Acid Motifs. Amino Acid Sequence. Animal. Cell Membrane. Cysteine. DNA-Binding Proteins. Human. K562 Cells. Luminescent Proteins. Membrane Proteins. Mice. Molecular Sequence Data. Proto-Oncogene Proteins c-myc. Rats. Sequence Homology, Amino Acid. Subcellular Fractions. Transcription Factors. Transport Vesicles
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

152. Title:Substitution of a conserved aspartate allows cation-induced polymerization of FtsZ
View Article: FEBS Lett 2001 Apr 6;494(1-2):34-7
CD Volume:363
Print Article: Pages: 34-37
Author(s):Scheffers DJ de Wit JG den Blaauwen T Driessen AJ
Author Affiliation:Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Kerklaan, The Netherlands
Abstract:The prokaryotic tubulin homologue FtsZ polymerizes in vitro in a nucleotide dependent fashion. Here we report that replacement of the strictly conserved Asp212 residue of Escherichia coli FtsZ by a Cys or Asn, but not by a Glu residue results in FtsZ that polymerizes with divalent cations in the absence of added GTP. FtsZ D212C and D212N mutants co-purify with GTP as bound nucleotide, providing an explanation for the unusual phenotype. We conclude that D212 plays a critical role in the coordination of a metal ion and the nucleotide at the interface of two FtsZ monomers
Descriptors:Amino Acid Substitution. Aspartic Acid. Bacterial Proteins. Cations, Divalent. Guanosine Triphosphate. Mutagenesis, Site-Directed. *Polymers. Support, Non-U.S. Gov't
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

153. Title:The second cysteine-rich domain of Mac1p is a potent transactivator that modulates DNA binding efficiency and functionality of the protein
View Article: FEBS Lett 2001 Apr 6;494(1-2):38-43
CD Volume:363

Print Article: Pages: 38-43
Author(s):Voutsina A Fragiadakis GS Boutla A Alexandraki D
Author Affiliation:Foundation for Research and Technology-HELLAS, Institute of Molecular Biology and Biotechnology, Heraklion, Crete, Greece
Abstract:Mac1p is a Saccharomyces cerevisiae DNA binding transcription factor that activates genes involved in copper uptake. A copper-induced N-C-terminal intramolecular interaction and copper-independent homodimerization affect its function. Here, we present a functional analysis of Mac1p deletion derivatives that attributes new roles to the second cysteine-rich (REPII) domain of the protein. This domain exhibits the copper-responsive potent transactivation function when assayed independently and, in the context of the entire protein, modulates the efficiency of Mac1p binding to DNA. The efficiency of binding to both copper-response promoter elements can determine the in vivo functionality of Mac1p independent of homodimerization
Descriptors:Binding Sites. Copper. Cysteine. DNA. Dimerization. Fungal Proteins. Nuclear Proteins. Saccharomyces cerevisiae. Support, Non-U.S. Gov't. Trans-Activation (Genetics). Trans-Activators. Transcription Factors
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

154. Title:An Arabidopsis mutant cex1 exhibits constant accumulation of jasmonate-regulated AtVSP, Thi2.1 and PDF1.2
View Article: FEBS Letters. 2001. 494 (3). 161-164
CD Volume:363
Print Article: Pages: 161-164
Author(s):Xu LingHui Liu FuQuan Wang ZhiLong Peng Wen Huang RongFeng Huang DaFang Xie DaoXin
Author Variant:Xu-L-H. Liu-F-Q. Wang-Z-L. Peng-W. Huang-R-F. Huang-D-F. Xie-D-X
Author Affiliation:Institute of Biotechnology Research, Chinese Academy of Agricultural Sciences, Beijing 100081, China
Language:English
Abstract:Jasmonates (JA) act as a regulator in plant growth as well as a signal in plant defence. The Arabidopsis vegetative storage protein (AtVSP) and plant defence-related proteins, thionin (Thi2.1) and defensin (PDF1.2), have previously been shown to accumulate in response to JA induction. In this report, we isolated and characterized a novel recessive mutant, cex1, conferring constitutive JA-responsive phenotypes including JA-inhibitory growth and constitutive expression of JA-regulated AtVSP, Thi2.1 and PDF1.2. The plant morphology and the gene expression pattern of the cex1 mutant could be phenocopied by treatment of wild-type plants with exogenous JA, indicating that CEX1 might be a negative regulator of the JA response pathway
Descriptors:jasmonic-acid. methyl-jasmonate. mutants. plant-growth-regulators. plant-physiology. plant-proteins. recessive-genes. signal-transduction
Identifiers:defensins
Organism Descriptors:Arabidopsis
Supplemental Descriptors:Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF060
Supplementary Info:27 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

155. Title:A synaptojanin-homologous region of Salmonella typhimurium SigD is essential for inositol phosphatase activity and Akt activation
View Article: FEBS Lett 2001 Apr 13;494(3):201-7
CD Volume:363
Print Article: Pages: 201-207
Author(s):Marcus SL Wenk MR Steele Mortimer O Finlay BB
Author Affiliation:Biotechnology Laboratory, University of British Columbia, Wesbrook Building 237, 6174 University Boulevard, Vancouver, BC, Canada V6T 1Z3
Abstract:The Ser-Thr kinase Akt is activated in epithelial cells by Salmonella enterica serovar typhimurium. The bacterial effector SigD, which is translocated into host cells via the specialized type III secretion system, is essential for Akt activation. Here, we investigated the inositol phospholipid substrate preferences of SigD. Recombinant SigD preferentially dephosphorylated phosphatidylinositol 3,5-biphosphate and phosphatidylinositol 3,4,5-triphosphate over other phosphatidylinositol lipids. Phosphatidylinositol 3-phosphate was not a substrate, suggesting the 5' phosphate moiety is one of the preferred substrates. Database searches revealed that SigD bears a small region of homology to the mammalian type II inositol 5-phosphatase synaptojanin. Mutation of two conserved residues in this region, Lys527 and Lys530, decreased or abrogated phosphatase activity, respectively. The Shigella flexneri SigD homologue, IpgD, displayed a similar activity in vitro and also activated Akt when used to complement a DeltasigD Salmonella strain. A mutation in IpgD at Lys507, analogous to Lys530 of SigD, also failed to activate Akt. Thus, we have characterized a region near the carboxyl-terminus of SigD which is important for phosphatase activity. We discuss how dephosphorylation of inositol phospholipids by SigD in vivo might contribute to the activation of Akt
Descriptors:Amino Acid Sequence. Animal. Bacterial Proteins. Conserved Sequence. Enzyme Activation. Genetic Complementation Test. Hela Cells. Human. Lysine. Molecular Sequence Data. Mutation. Nerve Tissue Proteins. Phosphatidylinositols. Phosphoric Monoester Hydrolases. Phosphorylation. Proto-Oncogene Proteins. Rats. Salmonella typhimurium. Sequence Alignment. Shigella flexneri. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

156. Title:Stereochemistry of family 52 glycosyl hydrolases: a beta-xylosidase from Bacillus stearothermophilus T-6 is a retaining enzyme
View Article: FEBS Lett 2001 Apr 20;495(1-2):39-43
CD Volume:363
Print Article: Pages: 39-43
Author(s):Bravman T Zolotnitsky G Shulami S Belakhov V Solomon D Baasov T Shoham G Shoham Y
Author Affiliation:Department of Food Engineering and Biotechnology, Technion Israel Institute of Technology, Haifa 32000, Israel
Abstract:A beta-xylosidase from Bacillus stearothermophilus T-6 assigned to the uncharacterized glycosyl hydrolase family 52 was cloned, overexpressed in Escherichia coli and purified. The enzyme showed maximum activity at 65 degrees C and pH 5.6-6.3. The stereochemistry of the hydrolysis of p-nitrophenyl beta-D-xylopyranoside was followed by 1H-nuclear magnetic resonance. Time dependent spectrum analysis showed that the configuration of the anomeric carbon was retained, indicating that a retaining mechanism prevails in family 52 glycosyl hydrolases.

Sequence alignment and site-directed mutagenesis enabled the identification of functionally important amino acid residues of which Glu337 and Glu413 are likely to be the two key catalytic residues involved in enzyme catalysis
Descriptors:Bacillus stearothermophilus. Catalysis. Cloning, Molecular. Consensus Sequence. Escherichia coli. Glycosides. Hydrogen-Ion Concentration. Hydrolysis. Magnetic Resonance Spectroscopy. Molecular Conformation. Molecular Sequence Data. Multigene Family. Mutagenesis, Site-Directed. Sequence Analysis, DNA. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't. Support, U.S. Gov't, Non-P.H.S.. Xylosidases
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

157. Title:Glutamic acid 160 is the acid-base catalyst of beta-xylosidase from Bacillus stearothermophilus T-6: a family 39 glycoside hydrolase
View Article: FEBS Lett 2001 Apr 20;495(1-2):115-9
CD Volume:363
Print Article: Pages: 115-119
Author(s):Bravman T Mechaly A Shulami S Belakhov V Baasov T Shoham G Shoham Y
Author Affiliation:Department of Food Engineering and Biotechnology, Technion Isreal Institute of Technology, Haifa 32000, Israel
Abstract:A beta-xylosidase from Bacillus stearothermophilus T-6 was cloned, overexpressed in Escherichia coli and purified to homogeneity. Based on sequence alignment, the enzyme belongs to family 39 glycoside hydrolases, which itself forms part of the wider GH-A clan. The conserved Glu160 was proposed as the acid-base catalyst. An E160A mutant was constructed and subjected to steady state and pre-steady state kinetic analysis together with azide rescue and pH activity profiles. The observed results support the assignment of Glu160 as the acid-base catalytic residue
Descriptors:Azides. Bacillus stearothermophilus. Binding Sites. Catalysis. Cloning, Molecular. Dose-Response Relationship, Drug. Escherichia coli. Glutamic Acid. Glycosides. Hydrolysis. Molecular Sequence Data. Sequence Analysis, DNA. Sequence Homology, Amino Acid. Substrate Specificity. Support, Non-U.S. Gov't. Support, U.S. Gov't, Non-P.H.S.. Xylosidases
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

158. Title:The human and murine protocadherin-beta one-exon gene families show high evolutionary conservation, despite the difference in gene number
View Article: FEBS Lett 2001 Apr 20;495(1-2):120-5
CD Volume:363
Print Article: Pages: 120-125
Author(s):Vanhalst K Kools P Vanden Eynde E van Roy F
Author Affiliation:Molecular Cell Biology Unit, Department of Molecular Biology, Flanders Interuniversity Institute for Biotechnology (VIB), Ghent University, Ledeganckstraat 35, B-9000, Ghent, Belgium
Abstract:Extensive cDNA analysis demonstrated that all human and mouse protocadherin-beta genes are one-exon genes. The protein sequences of these genes are highly conserved, especially the three most membrane-proximal extracellular domains. Phylogenetic analysis suggested that this unique gene family evolved by duplication of one single protocadherin-beta gene to 15 copies. The final difference in the number of protocadherin-beta genes in man (#19) and mouse (#22) is

probably caused by duplications later in evolution. The complex relationship between human and mouse genes and the lack of pseudogenes in the mouse protocadherin-beta gene cluster suggest a species-specific evolutionary pressure for maintenance of numerous protocadherin-beta genes
Descriptors:Amino Acid Sequence. Animal. Cadherins. Conserved Sequence. *Evolution, Molecular. Exons. Gene Dosage. Gene Duplication. Human. Mice. Molecular Sequence Data. Multigene Family. Phylogeny. Protein Precursors. Sequence Alignment. Support, Non-U.S. Gov't
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

159. Title:Inhibition of cytokine-induced vascular cell adhesion molecule-1 expression; possible mechanism for anti-atherogenic effect of Agastache rugosa
View Article: FEBS Letters. 2001. 495 (3). 142-147
CD Volume:363
Print Article: Pages: 142-147
Author(s):Hong JungJoo Choi JaeHoon Oh SeiRyang Lee HyeongKyu Park JaeHak Lee KunYeong Kim JungJae Jeong TaeSook Oh GooTaeg
Author Variant:Hong-J-J. Choi-J-H. Oh-S-R. Lee-H-K. Park-J-H. Lee-K-Y. Kim-J-J. Jeong-T-S. Oh-G-T
Author Affiliation:Genetic Resources Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), P.O. Box 115, Yusong, Taejon 305-600, Korea Republic
Language:English
Abstract:Adhesion molecules such as vascular cell adhesion molecule-1 (VCAM-1) play an important role during the early stages of atherogenesis. Agastache rugosa has an anti-atherogenic effect in low density lipoprotein receptor -/- mice. Moreover, A. rugosa reduced macrophage infiltration and VCAM-1 expression has been localized in aortic endothelium that overlies early foam cell lesions. This study ascertained that tilianin (100 micro M), a major component of A. rugosa, inhibits the tumour necrotic factor- alpha (TNF- alpha)-induced expression of VCAM-1 by 74% in cultured human umbilical vein endothelial cells (HUVECs). Also, tilianin (100 micro M) reduced TNF-alpha -induced activation of nuclear factor- kappa B in HUVECs
Descriptors:aorta. atherogenesis. cytoadherence. cytokines. endothelium. macrophages. plant-extracts. tumour-necrosis-factor. umbilicus
Identifiers:Agastache rugosa. Saxifragales
Organism Descriptors:Agastache. mice
Supplemental Descriptors:Lamiaceae. Lamiales. dicotyledons. angiosperms. Spermatophyta. plants. Agastache. Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals. Crassulaceae
Subject Codes:SS200. VV450. VV600
Supplementary Info:29 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

160. Title:A novel dual-specificity protein kinase targeted to the chloroplast in tobacco
View Article: FEBS Lett 2001 May 25;497(2-3):124-30
CD Volume:363
Print Article: Pages: 124-130
Author(s):Cho HS Yoon GM Lee SS Kim YA Hwang I Choi D Pai HS

Author Affiliation:Plant Cell Biochemistry Labouratory, Korea Research Institute of Bioscience and Biotechnology, South Korea
Abstract:The NtDSK1 cDNA encoding a novel chloroplast-targeted protein kinase was identified in Nicotiana tabacum. It contains the kinase domain at the C-terminus and a putative regulatory domain at the N-terminus. The recombinant NtDSK1 underwent autophosphorylation of serine, threonine, and tyrosine residues, indicating that NtDSK1 encodes a functional dual-specificity protein kinase. The NtDSK1-green fluorescent protein fusion protein was targeted to chloroplasts. Furthermore, the NtDSK1 protein was immunodetected in chloroplast fractions isolated from tobacco seedlings. The NtDSK1 mRNA expression was developmentally regulated in different tissues, including anthers and germinating seeds, and strongly stimulated by gibberellin. The mRNA was rapidly light responsive during seedling growth. NtDSK1 may play a role in a light-regulated signaling process in tobacco
Descriptors:Chloroplasts. DNA, Complementary. Gene Expression Regulation, Plant. Genomic Library. Gibberellins. Light. Molecular Sequence Data. Phosphorylation. Plant Components. *Plants, Toxic. Protein Kinases. Protein-Serine-Threonine Kinases. Protein-Tyrosine Kinase. RNA, Messenger. Sequence Analysis, DNA. Sequence Homology, Amino Acid. Substrate Specificity. Support, Non-U.S. Gov't. Tobacco
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

161. Title:Differential inheritance modes of DNA methylation between euchromatic and heterochromatic DNA sequences in ageing fetal bovine fibroblasts
View Article: FEBS Letters. 2001. 498 (1). 1-5
CD Volume:363
Print Article: Pages: 1-5
Author(s):Kang YongKook Koo DeogBon Park JungSun Choi YoungHee Lee KyungKwang Han YongMahn
Author Variant:Kang-Y-K. Koo-D-B. Park-J-S. Choi-Y-H. Lee-K-K. Han-Y-M
Author Affiliation:Animal Developmental Biotechnology Laboratory, Korea Research Institute of Bioscience and Biotechnology (KRIBB), P.O. Box 115, Yusong, Taejon 305-600, Korea Republic
Language:English
Abstract:To elucidate overall changes in DNA methylation occurring by inappropriate epigenetic control during ageing, we compared fetal bovine fibroblasts and their aged neomycin-resistant versions using bisulfite-PCR technology. Reduction in DNA methylation was observed in euchromatic repeats (18S-rRNAlart2) and promoter regions of single-copy genes (the cytokeratin/ beta -lactoglobulin/interleukin-13 genes). Contrastingly, a stable maintenance of DNA methylation was revealed in various heterochromatic sequences (satellite I/II/alphoid and Bov-B). The differential inheritance mode of DNA methylation was confirmed through the analysis of individual neomycin-resistant clones. These global, multi-locus analyses provide evidence on the tendency of differential epigenetic modification between genomic DNA regions during ageing
Descriptors:aging. beta-lactoglobulin. bisulfites. DNA-methylation. epigenetics. genes. interleukins. neomycin. nucleotide-sequences. polymerase-chain-reaction
Identifiers:cytokeratin. interleukin 13
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. WW000

Supplementary Info:27 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

162. Title:Binding and regulation of HIF-1alpha by a subunit of the proteasome complex, PSMA7
View Article: FEBS Lett 2001 Jun 1;498(1):62-6
CD Volume:363
Print Article: Pages: 62-66
Author(s):Cho S Choi YJ Kim JM Jeong ST Kim JH Kim SH Ryu SE
Author Affiliation:Center for Cellular Switch Protein Structure, Korea Research Institute of Bioscience and Biotechnology, Yusong, Taejon, South Korea. scho@mail.kribb.re.kr
Abstract:The hypoxia-inducible factor-1alpha (HIF-1alpha) is an important transcription factor for cellular responses to oxygen tension. It is rapidly degraded under normoxic conditions by the ubiquitin-dependent proteasome pathway. Here we report a critical role of the 20S proteasome subunit PSMA7 in HIF-1alpha regulation. PSMA7 was found to interact specifically with two subdomains of HIF-1alpha. PSMA7 inhibited the transactivation function of HIF-1alpha under both normoxic and hypoxia-mimicking conditions. In addition, we show that the PSMA7-mediated regulation of HIF-1alpha activity is associated with the proteasome pathway
Descriptors:Binding Sites. Cells, Cultured. Cysteine Endopeptidases. DNA-Binding Proteins. Human. Multienzyme Complexes. Nuclear Proteins. Protein Structure, Tertiary. Support, Non-U.S. Gov't. Trans-Activation (Genetics). Transfection
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

163. Title:Functional redundancy of the zinc fingers of A20 for inhibition of NF-kappaB activation and protein-protein interactions
View Article: FEBS Lett 2001 Jun 1;498(1):93-7
CD Volume:363
Print Article: Pages: 93-97
Author(s):Klinkenberg M Van Huffel S Heyninck K Beyaert R
Author Affiliation:Department of Molecular Biology, Unit for Molecular Signal Transduction in Inflammation, University of Ghent, Flanders Interuniversity Institute for Biotechnology, K.L. Ledeganckstraat 35, B-9000 Ghent, Belgium
Abstract:The tumor necrosis factor (TNF) inducible protein A20 is a potent inhibitor of nuclear factor-kappaB (IkappaB)-mediated gene expression in response to TNF and several other stimuli. The C-terminal domain of A20 is characterized by seven zinc finger structures. Here, we show that a minimum of four zinc fingers is required to inhibit TNF-induced nuclear factor-kappaB (NF-kappaB) activation to a level that is comparable to that obtained with the wild-type A20 protein. However, there was no strict requirement for a particular zinc finger structure, since a mutant A20 protein containing only the first four zinc fingers was as potent as a mutant protein containing only the last four zinc fingers. A similar functional redundancy of the A20 zinc fingers was also observed for binding of A20 to a number of other proteins, including two novel NF-kappaB inhibitory proteins (ABIN-1, ABIN-2), A20 itself, the anti-apoptotic protein TXBP151, and a regulatory component of the IkappaB kinase complex, IKKgamma.

Moreover, we demonstrate that complete loss of binding of any of these proteins correlates with complete loss of A20's ability to inhibit TNF-induced NF-kappaB activation. However, binding of IKKgamma as such is not sufficient for inhibition of NF-kappaB dependent gene expression in response to TNF
Descriptors:Amino Acid Sequence. Cells, Cultured. Human. Molecular Sequence Data. NF-kappa B. Protein-Serine-Threonine Kinases. Proteins. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't. Zinc Fingers
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

164. Title:Functions of the conserved anionic amino acids and those interacting with the substrate phosphate group of phosphoglucose isomerase
View Article: FEBS Lett 2001 Jun 15;499(1-2):11-4
CD Volume:363
Print Article: Pages: 11-14
Author(s):Meng M Lin HY Hsieh CJ Chen YT
Author Affiliation:Graduate Institute of Agricultural Biotechnology, National Chung Hsing University, 250 Kuo-Kuang Road, 40227, Taichung, Taiwan. mhmeng@dragon.nchu.edu.tw
Abstract:Phosphoglucose isomerase catalyzes the isomerization between glucose 6-phosphate and fructose 6-phosphate in cytoplasm, and functions as autocrine motility factor and neuroleukin outside the cells. A phosphoglucose isomerase from Bacillus stearothermophilus (pgiA) was subjected to mutagenesis study to address the catalytic function of the conserved anionic residues and those probably interacting with the phosphate group of substrates. The results suggest that Glu290 works concertedly with His311 as a general acid-base pair to initiate the isomerization step, and Glu150 assists the base function of His311. The conserved loop structure consisting of Gly205-Gly206-Arg207 plays a critical role for the recognition of substrates
Descriptors:Amino Acid Substitution. Bacillus stearothermophilus. Binding Sites. Catalysis. Conserved Sequence. Electrostatics. Glucose-6-Phosphate Isomerase. Hydrogen Bonding. Hydrogen-Ion Concentration. Kinetics. Models, Molecular. Mutation. Phosphates. Protein Conformation. Substrate Specificity. Support, Non-U.S. Gov't. Thermodynamics
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

165. Title:Influence of oocyte nuclei on demethylation of donor genome in cloned bovine embryos
View Article: FEBS Lett 2001 Jun 15;499(1-2):55-8
CD Volume:363
Print Article: Pages: 55-58
Author(s):Kang YK Koo DB Park JS Choi YH Lee KK Han YM
Author Affiliation:Animal Developmental Biotechnology Laboratory, Korea Research Institute of Bioscience and Biotechnology (KRIBB), P.O. Box 115, Yusong, 305-600, Taejon, South Korea
Abstract:We recently demonstrated that satellite regions exhibit an aberrant DNA methylation in cloned bovine embryos. Here, we examined, using bisulfite-sequencing technology, whether the inefficient demethylation of cloned donor genomes could be rescued by the presence of oocytic nuclei. Both AciI digestion and sequencing analyses showed that satellite sequence was demethylated more efficiently in cloned tetraploid blastocysts than in diploid clones. When methyl-CpG density

(the number of methyl-CpG sites per string) was scored, a significant decrease was observed in tetraploids (P<0.001). These results suggest that unknown mechanisms provided by oocytic nuclei could assist the demethylation of satellite sequences in tetraploid clones
Descriptors:Animal. Blastocyst. Cattle. Cell Nucleus. Clone Cells. *Cloning, Organism. CpG Islands. *DNA Methylation. DNA, Satellite. Deoxyribonucleases, Type II Site-Specific. Diploidy. Embryo. Fibroblasts. *Genome. Male. Oocytes. Polymerase Chain Reaction. Polyploidy. Restriction Mapping. Sulfites. Support, Non-U.S. Gov't
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

166. Title:An interplay between the TOM complex and porin isoforms in the yeast Saccharomyces cerevisiae mitochondria
View Article: FEBS Lett 2001 Jun 29;500(1-2):12-6
CD Volume:368
Print Article: Pages: 12-16
Author(s):Antos N Budzinska M Kmita H
Author Affiliation:Institute of Molecular Biology and Biotechnology, Department of Bioenergetics, Adam Mickiewicz University, Fredry 10, 61-701 Poznan, Poland
Abstract:The outer mitochondrial membrane of Saccharomyces cerevisiae contains two isoforms of mitochondrial porin, known also as the voltage-dependent anion channel. The isoform termed here porin1 displays channel-forming activity enabling metabolite transport whereas the second one, termed here porin2, does not form a channel and its function is still not clear. We have shown recently that in the absence of porin1, the channel within the protein import machinery (the TOM complex) is essential for metabolite transport across the outer membrane [Kmita and Budzinska, Biochim. Biophys. Acta 1509 (2000) 6044-6050]. Here, we report that the TOM complex channel may also serve as a supplementary pathway for metabolites in the presence of porin1 when the permeability of the latter is limited and the role of the TOM complex seems to increase when porin2 is depleted
Descriptors:Biological Transport. Carrier Proteins. Gene Deletion. Intracellular Membranes. Mitochondria. NAD. Oxidation-Reduction. Porins. Protein Isoforms. Saccharomyces cerevisiae. Tetrahydrofolate Dehydrogenase. Up-Regulation
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

167. Title:Down modulation of IL-18 expression by human papillomavirus type 16 E6 oncogene via binding to IL-18
View Article: FEBS Lett 2001 Jul 20;501(2-3):139-45
CD Volume:364
Print Article: Pages: 139-145
Author(s):Cho YS Kang JW Cho M Cho CW Lee S Choe YK Kim Y Choi I Park SN Kim S Dinarello CA Yoon DY
Author Affiliation:Korea Research Institute of Bioscience and Biotechnology, Taejon, South Korea
Abstract:To understand modulation of a novel immune-related cytokine, interleukin-18, by human papillomavirus type (HPV) 16 oncogenes, HaCaT, normal keratinocyte cell line, and C-33A, HPV-negative cervical cancer cell line, were prepared to establish stable cell lines expressing E6, E6 mutant (E6m), E6E7, or E7 constitutively.

Expressions of various HPV oncogene transcripts were identified by RT-PCR. Expression of HPV oncogene E6 was reversely correlated to the expression of interleukin-18, a novel pro-inflammatory cytokine. The expression of E6 in C-33A, independent of E6 splicing, resulted in decreased IL-18 expression and that of IL-18 was also significantly reduced in HaCaT cells expressing E6. The level of p53 was reduced in C-33A cells expressing E6 whereas not altered in HaCaT cells expressing E6, suggesting that E6 downregulated IL-18 expression via an independent pathway of p53 degradation in HaCaT cells which have a mutated p53 form. However, E7 did not affect IL-18 expression significantly in both C-33A and HaCaT cells. Cotransfection experiments showed that E6 oncogene did not inhibit the activities of IL-18 promoter P1 and P2, suggesting that E6 oncogene indirectly inhibited IL-18 expression. Taken together, E6, E6m and E6/E7 inhibited IL-18 expression with some variation, assuming that cells expressing E6 oncogene can evade immune surveillance by downregulating the expression of immune stimulating cytokine gene, IL-18, and inhibiting the cascade of downstream effects that follow activation of the IL-18 receptor

Descriptors:Binding, Competitive. Down-Regulation. Hela Cells. Human. Interferon Type II. Interleukin-18. Leukocytes, Mononuclear. Oncogene Proteins, Viral. *Papillomavirus, Human. Promoter Regions (Genetics). Protein p53. Support, Non-U.S. Gov't. Support, U.S. Gov't, P.H.S.. Transfection. Tumor Cells, Cultured

Geographic Locator:Netherlands

ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

168. Title:The nuclear localization signal of zebrafish terra is located within the DM domain

View Article: FEBS Lett 2001 Aug 10;503(1):25-9
CD Volume:364
Print Article: Pages: 25-29

Author(s):Zhang L Hua Z Ren J Meng A
Author Affiliation:Institute of Cellular and Developmental Biology, Department of Biological Sciences and Biotechnology, National Laboratory of Protein Sciences of MOE, Tsinghua University, 100084, Beijing, China

Abstract:Zebrafish Terra is a member of the DM domain-containing transcription factor family and is involved in somitogenesis. The other known members of this family play a role in sex differentiation across species from Caenorhabditis elegans to human. Using the green fluorescence protein-Terra fusion constructs, we have identified the nuclear localization signal (NLS) of terra by transfecting human HeLa cells. The terra NLS is located between the two intertwined zinc-binding sites of the DNA-binding domain. However, the nuclear translocation of terra is independent of the structure required for DNA binding. Mutational analysis demonstrates that basic residues K77 and R78 within the DM domain are absolutely required for the translocation of Terra into the nuclei. Sequence comparison discloses that the NLS of Terra is also present in the other known members of the DM family, indicating the conservative nature of the NLS of this family during evolution

Descriptors:Amino Acid Sequence. Animal. Base Sequence. Binding Sites. Cell Nucleus. DNA Primers. DNA-Binding Proteins. Hela Cells. Human. Luminescent Proteins. Microscopy, Fluorescence. Molecular Sequence Data. *Nuclear Localization Signal. Protein Transport. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't. Zebrafish. Zinc

Geographic Locator:Netherlands

ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

169. Title:E3 ligase activity of RING finger proteins that interact with Hip-2, a human ubiquitin-conjugating enzyme
View Article: FEBS Lett 2001 Aug 10;503(1):61-4
CD Volume:364
Print Article: Pages: 61-64
Author(s):Lee SJ Choi JY Sung YM Park H Rhim H Kang S
Author Affiliation:Graduate School of Biotechnology, Korea University, Seoul, South Korea
Abstract:To identify proteins that interact with Huntingtin-interacting protein-2 (Hip-2), a ubiquitin-conjugating enzyme, a yeast two-hybrid screen system was used to isolate five positive clones. Sequence analyses showed that, with one exception, all Hip-2-interacting proteins contained the RING finger motifs. The interaction of Hip-2 with RNF2, one of the clones, was further confirmed through in vitro and in vivo experiments. Mutations in the RING domain of RNF2 prevented the clone from binding to Hip-2, an indication that the RING domain is the binding determinant. RNF2 showed a ubiquitin ligase (E3) activity in the presence of Hip-2, suggesting that a subset of RING finger proteins may have roles as E3s
Descriptors:Amino Acid Sequence. DNA-Binding Proteins. Ligases. Molecular Sequence Data. Protein Binding. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't. Two-Hybrid System Techniques
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

170. Title:The protease inhibitor chagasin of Trypanosoma cruzi adopts an immunoglobulin-type fold and may have arisen by horizontal gene transfer
View Article: FEBS Lett 2001 Aug 24;504(1-2):41-4
CD Volume:364
Print Article: Pages: 41-44
Author(s):Rigden DJ Monteiro AC Grossi de Sa MF
Author Affiliation:National Centre of Genetic Resources and Biotechnology, Cenargen/Embrapa, S.A.I.N. Parque Rural, Final W5 Norte, 70770-900, Brasilia, Brazil. daniel@cenargen.embrapa.br
Abstract:Chagasin, a protein from Trypanosoma cruzi, is the first member of a new family of tight binding cysteine protease inhibitors [Monteiro, A.C.S., Abrahamson, M., Lima, A.P.C., Vannier-Santos, M.A. and Scharfstein, J. (2001) J. Cell Sci., in press] [corrected]. Despite its lack of significant sequence identity with known proteins, convincing structural models, using variable light chain templates, could be constructed on the basis of threading results. Experimental support for the final structure came from inhibition data for overlapping oligopeptides spanning the chagasin sequence. Chagasin therefore exemplifies a new protease inhibitor structural class and a new natural use for an immunoglobulin-like domain. Limited sequence resemblance suggests that chagasin may represent the result of a rare horizontal gene transfer from host to parasite
Descriptors:Amino Acid Sequence. Animal. Cysteine Proteinase Inhibitors. *Gene Transfer, Horizontal. Immunoglobulins. Models, Molecular. Molecular Sequence Data. *Protein Folding. Protozoan Proteins. Sequence Homology, Amino Acid. Support, Non-U.S. Gov't. Trypanosoma cruzi
Geographic Locator:Netherlands

ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

171. Title:Semliki Forest virus vectors: efficient vehicles for in vitro and in vivo gene delivery
View Article: FEBS Letters. 2001. 504 (3). 99-103
CD Volume:364
Print Article: Pages: 99-103
Author(s):Lundstrom K Schweitzer C Rotmann D Hermann D Schneider E M Ehrengruber M U
Author Affiliation:F. Hoffmann-La Roche, CNS Department, CH-4070 Basel, Switzerland
Conference Title:Structure, dynamics and function of proteins in biological membranes. Proceedings of a conference, Ascona, Switzerland, 13-17 March 2001
Language:English
Abstract:Rapidly generated high-titre Semliki Forest virus (SFV) vectors can infect numerous mammalian cell lines and primary cell cultures, and result in high levels of transgene expression. SFV-based expression of transmembrane receptors has been characterized by specific ligand-binding activity and functional responses. Adaptation of the SFV technology for mammalian suspension cultures has allowed the production of hundreds of milligrams of recombinant receptor for purification and structural studies. The same SFV-stock solutions used for the infection of mammalian cells in culture have also been successfully applied for efficient transgene expression in organotypic hippocampal slices, as well as in vivo in rodent brain
Descriptors:biotechnology. disease-vectors. gene-expression. genetic-engineering. genetic-vectors. hippocampus. recombinant-proteins. transgenics
Organism Descriptors:Semliki-Forest-virus
Supplemental Descriptors:Alphavirus. Togaviridae. viruses
Subject Codes:WW000
Supplementary Info:32 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters
Copyright:Copyright CAB International

172. Title:Activation of the MKK4-JNK pathway during erythroid differentiation of K562 cells is inhibited by the heat shock factor 2-beta isoform
View Article: FEBS Lett 2001 Sep 7;505(1):168-72
CD Volume:364
Print Article: Pages: 168-172
Author(s):Hietakangas V Elo I Rosenstrom H Coffey ET Kyriakis JM Eriksson JE Sistonen L
Author Affiliation:Turku Centre for Biotechnology, University of Turku, Abo Akademi University, Finland
Abstract:In this study we report the activation of c-Jun N-terminal kinase (JNK) in human K562 erythroleukemia cells undergoing hemin-mediated erythroid differentiation, which occurs concomitantly with activation of heat shock factor 2 (HSF2) and leads to a simultaneous in vivo phosphorylation of c-Jun. The activation of JNK occurs through activation of mitogen-activated protein kinase kinase (MKK) 4 and not by activation of MKK7 or inhibition of JNK-directed phosphatases. We have previously shown that overexpression of the HSF2-beta isoform inhibits the activation of HSF2 upon hemin-induced erythroid differentiation. Here we demonstrate that HSF2-beta overexpression

blocks the hemin-induced activation of the MKK4-JNK pathway, suggesting an erythroid lineage-specific JNK activation likely to be regulated by HSF2
Descriptors:Anisomycin. *Cell Differentiation. Enzyme Activation. Enzyme Inhibitors. Erythroid Progenitor Cells. Heat-Shock Proteins. Hemin. Human. Leukemia, Erythroblastic, Acute. Mitogen-Activated Protein Kinase Kinases. Mitogen-Activated Protein Kinases. Protein Isoforms. Proto-Oncogene Proteins c-jun. Staurosporine. Support, Non-U.S. Gov't. Transcription Factors. Tumor Cells, Cultured
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

173. Title:Slotoxin, alphaKTx1.11, a new scorpion peptide blocker of MaxiK channels that differentiates between alpha and alpha+beta (beta1 or beta4) complexes
View Article: FEBS Lett 2001 Sep 21;505(3):369-73
CD Volume:364
Print Article: Pages: 369-373
Author(s):Garcia Valdes J Zamudio FZ Toro L Possani LD Possan LD
Author Affiliation:Department of Molecular Recognition and Structural Biology, Institute of Biotechnology, National Autonomous University of Mexico, Cuernavaca, Mexico
Abstract:A novel peptide from Centruroides noxius Hoffmann scorpion venom was isolated and sequenced. The 37 amino acid peptide belongs to the charybdotoxin sub-family (alphaKTx1) and was numbered member 11. alphaKTx1.11 has 75% sequence identity with iberiotoxin and 54% with charybdotoxin. alphaKTx1.11 revealed specificity for mammalian MaxiK channels (hSlo), thus, was named slotoxin. Slotoxin blocks the MaxiK pore-forming alpha subunit reversibly (K(d)=1.5 nM). Slotoxin association with alpha+beta (beta1 or beta4) channels was approximately 10 times slower than iberiotoxin and charybdotoxin, leading to a lack of effect on alpha+beta4 when tested at 100 nM for 5 min. Thus, slotoxin is a better tool to distinguish MaxiK alpha+beta complexes
Descriptors:Amino Acid Sequence. Chromatography, High Pressure Liquid. Molecular Sequence Data. *Potassium Channel Blockers. Potassium Channels. Scorpion Venoms. Sequence Homology, Amino Acid. Substrate Specificity. Support, Non-U.S. Gov't. Support, U.S. Gov't, Non-P.H.S.. Support, U.S. Gov't, P.H.S.
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

174. Title:AS-48: a circular protein with an extremely stable globular structure
View Article: FEBS Lett 2001 Sep 21;505(3):379-82
CD Volume:364
Print Article: Pages: 379-382
Author(s):Cobos ES Filimonov VV Galvez A Maqueda M Valdivia E Martinez JC Mateo PL
Author Affiliation:Department of Physical Chemistry and Institute of Biotechnology, Faculty of Sciences, University of Ganada, Spain
Abstract:The unfolding thermodynamics of the circular enterocin protein AS-48, produced by Enterococcus faecalis, has been characterized by differential scanning calorimetry. The native structure of the 70-residue protein is extremely thermally stable. Thus, at pH 2.5 and low ionic strength thermal denaturation occurs under equilibrium at 102

degrees C, while the unfolded state irreversibly aggregates at neutral and alkaline pH. Calorimetric data analysis shows that the specific enthalpy change upon unfolding is unusually small and the heat capacity change is quite normal for a protein of this size, whereas the Gibbs energy change at 25 degrees C is relatively high. At least part of this high stability might be put down to entropic constraints induced by the circular organization of the polypeptide chain
Descriptors:Antibiotics, Peptide. Calorimetry, Differential Scanning. Hydrogen-Ion Concentration. Osmolar Concentration. Protein Conformation. Protein Denaturation. Support, Non-U.S. Gov't
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

175. Title:The polymerization mechanism of the bacterial cell division protein FtsZ
View Article: FEBS Lett 2001 Sep 28;506(1):6-10
CD Volume:364
Print Article: Pages: 6-10
Author(s):Scheffers D Driessen AJ
Author Affiliation:Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Kerklaan 30, 9751 NN Haren, The Netherlands
Abstract:Bacteria and archaea usually divide symmetrically by formation of a septum in the middle of the cell. A key event in cell division is the assembly of the FtsZ ring. FtsZ is the prokaryotic homolog of tubulin and forms polymers in the presence of guanine nucleotides. Here, we specifically address the polymerization of FtsZ and the role of nucleotide hydrolysis in polymer formation and stabilization. Recent structural and biochemical results are discussed and a model for FtsZ polymerization, similar to that for tubulin, is presented
Descriptors:Bacterial Proteins. Biopolymers. Guanosine Triphosphate. Hydrolysis. Models, Molecular. Protein Conformation. Support, Non-U.S. Gov't. Tubulin
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

176. Title:Genetic evidence that antibacterial activity of lysozyme is independent of its catalytic function
View Article: FEBS Lett 2001 Sep 28;506(1):27-32
CD Volume:364
Print Article: Pages: 27-32
Author(s):Ibrahim HR Matsuzaki T Aoki T
Author Affiliation:Department of Biochemistry and Biotechnology, Faculty of Agriculture, Kagoshima University, 1-21-24 Korimoto, Kagoshima, 890-0065, Japan. hishamri@chem.agri.kagoshima-u.ac.jp
Abstract:A catalytically inactive mutant of hen egg white lysozyme was constructed by site-directed mutagenesis to elucidate the role of enzymatic activity on its antimicrobial activity against Gram-positive bacteria. The catalytic residue aspartic acid at position 52 of lysozyme was substituted with serine (D52S-Lz) and the mutant cDNA was inserted into a yeast expression vector, pYES-2. Western blot analysis indicated that the mutation did not affect secretion of the D52S-Lz lysozyme into the medium of the expressing Saccharomyces cerevisiae, INVSC1. In addition, circular dichroism and fluorescence spectral analysis revealed no change in the structure of D52S-Lz compared to

that of wild-type (Wt-Lz) lysozyme. The mutation (D52S) abolished the catalytic activity of lysozyme. Antimicrobial tests against Staphylococcus aureus and Bacillus subtilis revealed that the catalytically inactive D52S-Lz was as bactericidal as the Wt-Lz lysozyme. Heat treatment leading to enzyme inactivation had no effect on the bactericidal activity of either wild-type or the mutant D52S-Lz lysozyme. The binding affinity of D52S-Lz to the isolated peptidoglycan of S. aureus was unaffected. Our results provide the first demonstration of direct genetic evidence that the antimicrobial activity of lysozyme is operationally independent of its muramidase activity, and strongly suggest the antimicrobial action of lysozyme is due to structural factors

Descriptors:Anti-Infective Agents. Bacillus subtilis. Base Sequence. Blotting, Western. Catalytic Domain. DNA Primers. Microbial Sensitivity Tests. Muramidase. Mutagenesis, Site-Directed. Staphylococcus aureus. Support, Non-U.S. Gov't

Geographic Locator:Netherlands

ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

177. Title:Two distinct isopentenyl diphosphate isomerases in cytosol and plastid are differentially induced by environmental stresses in tobacco

View Article: FEBS Letters. 2001. 506 (1). 61-64
CD Volume:364
Print Article: Pages: 61-64

Author(s):Nakamura A Shimada H Masuda T Ohta H Takamiya K
Author Affiliation:Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, Midori-ku, Yokohama 226-8501, Japan

Language:English

Abstract:Two distinct cDNA clones encoding isopentenyl diphosphate isomerase (IPI1 and IPI2) were isolated from Nicotiana tabacum. In situ expression of IPI1- and IPI2-green fluorescent protein fusion constructs revealed that IPI1 and IPI2 were localized in chloroplast and cytosol, respectively. The level of IPI1 mRNA was increased under high-salt and high-light stress conditions, while that of IPI2 mRNA was increased under high-salt and cold stress conditions. Both IPI transcripts were increased in an abscisic acid-independent manner. This is the first report of a cytosolic IPI. The results indicated that two distinct IPIs are differentially induced in response to stress. The nucleotide sequence data in this paper have been submitted to the DDBJ database (IPI1, accession number AB049815; IPI2, AB049816)

Descriptors:chloroplasts. clones. cold-stress. complementary-DNA. cytosol. environmental-factors. enzymes. gene-expression. genes. isoprenoids. light. localization. messenger-RNA. nucleotide-sequences. plastids. salinity. stress. stress-response. tobacco

Identifiers:isopentenyl-diphosphate delta-isomerase

Organism Descriptors:Nicotiana. Nicotiana-tabacum

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

Subject Codes:FF005. FF020. FF060. WW000. FF900

Supplementary Info:16 ref

ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

178. Title:TAK1 activation of the mouse JunB promoter is mediated through a CCAAT box and NF-Y
View Article: FEBS Lett 2001 Oct 12;506(3):267-71
CD Volume:364
Print Article: Pages: 267-271
Author(s):Eggen BJ Benus GF Folkertsma S Jonk LJ Kruijer W
Author Affiliation:Developmental Genetics, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Kerklaan 30, 9751 NN, Haren, The Netherlands. b.j.l.eggen@biol.rug.nl
Abstract:The JunB gene is activated by many stimuli including transforming growth factor beta (TGFbeta) family members and interleukin-6 (IL-6). Here the effect of TGFbeta activated kinase 1 (TAK1), a mitogen activated protein kinase kinase kinase (MAPKKK) implicated in TGFbeta, bone morphogenetic protein (BMP) and interleukin-1 (IL-1) signaling, on JunB promoter activity was investigated. Promoter analysis led to the identification of a CCAAT motif in the JunB gene, essential for activation by TAK1. Transfer of this CCAAT element to a heterologous minimal promoter conferred TAK1-responsiveness. The CCAAT-binding transcription factor, nuclear factor Y (NF-Y), activated the JunB promoter and a dominant negative NF-YA construct inhibited TAK1 activation of JunB. Our results demonstrate that JunB gene activation by TAK1 is mediated by the CCAAT-binding factor NF-Y
Descriptors:Animal. Base Sequence. CCAAT-Binding Factor. Cell Line. DNA. DNA Primers. Gene Expression Regulation. Genes, Reporter. Human. Interleukin-1. Luciferase. MAP Kinase Kinase Kinases. Mice. *Promoter Regions (Genetics). Proto-Oncogene Proteins c-jun. Reverse Transcriptase Polymerase Chain Reaction. Support, Non-U.S. Gov't. Transforming Growth Factor beta
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

179. Title:A non-natural amino acid for efficient incorporation into proteins as a sensitive fluorescent probe
View Article: FEBS Lett 2001 Oct 19;507(1):35-8
CD Volume:364
Print Article: Pages: 35-38
Author(s):Taki M Hohsaka T Murakami H Taira K Sisido M
Author Affiliation:Department of Bioscience and Biotechnology, Faculty of Engineering, Okayama University, Okayama, Japan
Abstract:A small and highly fluorescent non-natural amino acid that contains an anthraniloyl group (atnDap) was incorporated into various positions of streptavidin. The positions were directed by a CGGG/CCCG four-base codon/anticodon pair. The non-natural mutants were obtained in excellent yields and some of them retained strong biotin-binding activity. The fluorescence wavelength as well as the intensity of the anthraniloyl group at position 120 were sensitive to biotin binding. These unique properties indicate that the atnDap is the most suitable non-natural amino acid for a position-specific fluorescent labeling of proteins that is highly sensitive to microenvironmental changes
Descriptors:Amino Acids. Anthranilic Acids. Binding Sites. Biotin. Escherichia coli. Fluorescent Dyes. Mutagenesis, Site-Directed. Proteins. Recombinant Proteins. Spectrometry, Fluorescence. Streptavidin. Support, Non-U.S. Gov't
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

180. Title:Involvement of B-Raf in Ras-induced Raf-1 activation
View Article: FEBS Lett 2001 Nov 2;507(3):295-8
CD Volume:364
Print Article: Pages: 295-298
Author(s):Mizutani S Inouye K Koide H Kaziro Y
Author Affiliation:Faculty of Bioscience and Biotechnology, Tokyo Institute of Technology, 4259 Nagatsuta-cho, Midori-ku, 226-8501, Yokohama, Japan
Abstract:The mechanism of Ras-induced Raf-1 activation is not fully understood. Previously, we identified a 400-kDa protein complex as a Ras-dependent Raf-1 activator. In this study, we identified B-Raf as a component of this complex. B-Raf was concentrated during the purification of the activator. Immunodepletion of B-Raf abolished the effect of the activator on Raf-1. Furthermore, B-Raf and Ras-activated Raf-1 co-operatively, when co-transfected into human embryonic kidney 293 cells. On the other hand, Ras-dependent extracellular signal-regulated kinase/mitogen-activated protein kinase kinase stimulator (a complex of B-Raf and 14-3-3) failed to activate Raf-1 in our cell-free system. These results suggest that B-Raf is an essential component of the Ras-dependent Raf-1 activator
Descriptors:Cells, Cultured. Human. Proto-Oncogene Proteins c-raf. Support, Non-U.S. Gov't. Transfection. ras Proteins
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

181. Title:Both proline-rich sequences in the TH region of Bruton's tyrosine kinase stabilize intermolecular interactions with the SH3 domain
View Article: FEBS Lett 2001 Nov 9;508(1):11-5
CD Volume:364
Print Article: Pages: 11-15
Author(s):Hansson H Smith CI Hard T
Author Affiliation:Department of Biotechnology, Royal Institute of Technology (KTH), SCFAB, S-106 91 Stockholm, Sweden
Abstract:The Tec homology (TH) region located N-terminal to the Src homology 3 (SH3) domain of Bruton's tyrosine kinase (Btk) contains two proline-rich SH3-binding sequences (PRRs). We have previously demonstrated that the TH region acts to stabilize intermolecular interactions in N-terminally extended SH3 (PRR-SH3) fragments. Here, we analyze six PRR-SH3 fragments with different proline-to-alanine substitutions in the two PRRs. Gel permeation chromatography and nuclear magnetic resonance spectroscopy show that both PRRs can stabilize self-association. This observation provides an explanation to why the TH region of Btk makes intermolecular interactions, whereas the corresponding interaction in the related Itk kinase with only one PRR, is intramolecular
Descriptors:Chromatography, Gel. Human. Mutagenesis, Site-Directed. Nuclear Magnetic Resonance, Biomolecular. Peptide Fragments. Protein-Tyrosine Kinase. Recombinant Fusion Proteins. Support, Non-U.S. Gov't. *src Homology Domains
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

182. Title:SecDFyajC is not required for the maintenance of the proton motive force
View Article: FEBS Lett 2001 Nov 9;508(1):103-6
CD Volume:364

Print Article: Pages: 103-106
Author(s):Nouwen N van der Laan M Driessen AJ
Author Affiliation:Department of Microbiology, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Kerklaan 30, 9751 NN Haren, The Netherlands. n.nouwen@biol.rug.nl
Abstract:SecDFyajC of Escherichia coli is required for efficient export of proteins in vivo. However, the functional role of SecDFyajC in protein translocation is unclear. We evaluated the postulated function of SecDFyajC in the maintenance of the proton motive force. As previously reported, inner membrane vesicles (IMVs) lacking SecDFyajC are defective in the generation of a stable proton motive force when energized with succinate. This phenomenon is, however, not observed when NADH is used as an electron donor. Moreover, the proton motive force generated in SecDFyajC-depleted vesicles stimulated translocation to the same extent as seen with IMVs containing SecDFyajC. Further analysis demonstrates that the reduced proton motive force with succinate in IMVs lacking SecDFyajC is due to a lower amount of the enzyme succinate dehydrogenase. The expression of this enzyme complex is repressed by growth on glucose media, the condition used to deplete SecDFyajC. These results demonstrate that SecDFyajC is not required for proton motive force-driven protein translocation
Descriptors:Bacterial Proteins. Cell Membrane. Escherichia coli. Macromolecular Systems. Membrane Proteins. Protein Precursors. *Protein Transport. *Proton-Motive Force. Succinate Dehydrogenase. Support, Non-U.S. Gov't. Transport Vesicles
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

183. Title:A naturally occurring non-coding fusion transcript derived from scorpion venom gland: implication for the regulation of scorpion toxin gene expression
View Article: FEBS Letters. 2001. 508 (2). 241-244
CD Volume:364
Print Article: Pages: 241-244
Author(s):Zhu ShunYi Li WenXin Cao ZhiJian
Author Variant:Zhu-S-Y. Li-W-X. Cao-Z-J
Author Affiliation:Department of Biotechnology, College of Life Sciences, Wuhan University 430072, Wuhan, Hubei Province, China
Language:English
Abstract:Scorpion venom glands synthesize and secrete a great number of low molecular mass toxic peptides for prey and defence. Many cDNAs and genomic genes encoding these toxins have been isolated and sequenced. However, their expression regulation mechanism is not yet known at present. During screening of a cDNA library prepared from venom glands of the scorpion Buthus martensii, we isolated a natural fusion cDNA composed of the 5'-untranslated region (UTR) and upstream coding sequence of a long-chain toxin transcript and the downstream coding sequence and 3'-UTR of a short-chain toxin transcript. The junction site is just the overlapping region of 11 nucleotides (GGCAAGGAAAT) between the 2 wild transcripts, and thus leads to the formation of an early stop codon, which will cause premature translation. Based on the above observations, combined with the genomic data, we proposed a characteristic regulation mechanism of scorpion toxin genes, in which trans-splicing and nonsense mediated mRNA decay are involved

Descriptors:codons. complementary-DNA. gene-expression. genetic-regulation. messenger-RNA. nucleotide-sequences. nucleotides. toxins. venom-glands. venoms
Identifiers:Buthus martensii
Organism Descriptors:Buthus
Supplemental Descriptors:Buthidae. Scorpiones. Arachnida. arthropods. invertebrates. animals. Buthus
Subject Codes:VV820
Supplementary Info:19 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters
Copyright:Copyright CAB International

184. Title:Human monkeypox and smallpox viruses: genomic comparison
View Article: FEBS Letters. 2001. 509 (1). 66-70
CD Volume:364
Print Article: Pages: 66-70
Author(s):Shchelkunov S N Totmenin A V Babkin I V Safronov P F Ryazankina O I Petrov N A Gutorov V V Uvarova E A Mikheev M V Sisler J R Esposito J J Jahrling P B Moss B Sandakhchiev L S
Author Affiliation:State Research Center of Virology and Biotechnology 'Vector', Koltsovo, Novosibirsk Region 630559, Russia
Language:English
Abstract:Monkeypox virus (MPV) causes a human disease which resembles smallpox but with a lower person-to-person transmission rate. To determine the genetic relationship between the orthopoxviruses causing these two diseases, we sequenced the 197-kb genome of MPV isolated from a patient during a large human monkeypox outbreak in Zaire in 1996. The nucleotide sequence within the central region of the MPV genome, which encodes essential enzymes and structural proteins, was 96.3% identical with that of variola (smallpox) virus (VAR). In contrast, there were considerable differences between MPV and VAR in the regions encoding virulence and host-range factors near the ends of the genome. Our data indicate that MPV is not the direct ancestor of VAR and is unlikely to naturally acquire all properties of VAR
Descriptors:amino-acid-sequences. genes. genetic-correlation. genetic-variation. genome-analysis. genomes. human-diseases. molecular-genetics. monkeypox. nucleotide-sequences. smallpox
Geographic Locator:Congo-Democratic-Republic
Identifiers:monkeypox virus
Organism Descriptors:man. variola-virus
Supplemental Descriptors:Central-Africa. Africa-South-of-Sahara. Africa. ACP-Countries. Francophone-Africa. Least-Developed-Countries. Developing-Countries. Homo. Hominidae. Primates. mammals. vertebrates. Chordata. animals. Orthopoxvirus. Chordopoxvirinae. Poxviridae. viruses
Subject Codes:VV210. ZZ395
Supplementary Info:41 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters
Copyright:Copyright CAB International

185. Title:Identification of mouse trp homologs and lipid rafts from spermatogenic cells and sperm
View Article: FEBS Lett 2001 Nov 30;509(1):119-25
CD Volume:364
Print Article: Pages: 119-125

Author(s):Trevino CL Serrano CJ Beltran C Felix R Darszon A
Author Affiliation:Department of Genetics and Molecular Physiology, Institute of Biotechnology, UNAM, Cuernavaca, Mexico
Abstract:Intracellular Ca(2+) has an important regulatory role in the control of sperm motility, capacitation, and the acrosome reaction (AR). However, little is known about the molecular identity of the membrane systems that regulate Ca(2+) in sperm. In this report, we provide evidence for the expression of seven Drosophila transient receptor potential homolog genes (trp1-7) and three of their protein products (Trp1, Trp3 and Trp6) in mouse sperm. Allegedly some trps encode capacitative Ca(2+) channels. Immunoconfocal images showed that while Trp6 was present in the postacrosomal region and could be involved in sperm AR, expression of Trp1 and Trp3 was confined to the flagellum, suggesting that they may serve sperm to regulate important Ca(2+)-dependent events in addition to the AR. Likewise, one of these proteins (Trp1) co-immunolocalized with caveolin-1, a major component of caveolae, a subset of lipid rafts potentially important for signaling events and Ca(2+) flux. Furthermore, by using fluorescein-coupled cholera toxin B subunit, which specifically binds to the raft component ganglioside GM1, we identified caveolin- and Trp-independent lipid rafts residing in the plasma membrane of mature sperm. Notably, the distribution of GM1 changes drastically upon completion of the AR
Descriptors:Acrosome Reaction. Animal. Blotting, Western. Calcium. Calcium Channels. Cholera Toxin. Insect Proteins. Male. Membrane Microdomains. Mice. Microscopy, Confocal. RNA. Reverse Transcriptase Polymerase Chain Reaction. Signal Transduction. Spermatocytes. Spermatogenesis. Spermatozoa. Support, Non-U.S. Gov't. Transduction, Genetic
Geographic Locator:Netherlands
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

186. Title:A novel type 2C protein phosphatase from the human fungal pathogen Candida albicans
View Article: FEBS Letters. 2001. 509 (1). 142-144
CD Volume:364
Print Article: Pages: 142-144
Author(s):Jiang LingHuo Whiteway M Shen ShiHsiang
Author Variant:Jiang-L-H. Shen-S-H
Author Affiliation:Mammalian Cells Genetics Group, Health Sector, Biotechnology Research Institute, National Research Council of Canada, Montreal, QC H4P 2R2, Canada
Language:English
Abstract:This paper describes the identification and characterization of the CaPTC7p, the first PP2C phosphatase in C. albicans, encoded by the YHR76 gene. Results suggest that the CaPTC7p possesses the characteristics of classical PP2C enzymes. The interesting structural features of CaPTC7p and its high conservation in the eukaryotic organisms make it a novel member of the PP2C superfamily
Descriptors:amino-acid-sequences. genes. molecular-genetics. nucleotide-sequences. phosphoric-monoester-hydrolases
Organism Descriptors:Candida-albicans
Supplemental Descriptors:Candida. Deuteromycotina. Eumycota. fungi
Subject Codes:VV210. ZZ394. ZZ395
Supplementary Info:5 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

Copyright:Copyright CAB International

187. Title:Rubiscolin, a delta selective opioid peptide derived from plant Rubisco
View Article: FEBS Letters. 2001. 509 (2). 213-217
CD Volume:364
Print Article: Pages: 213-217
Author(s):Yang ShuZhang Yunden J Sonoda S Doyama N Lipkowski A W Kawamura Y Yoshikawa M
Author Variant:Yang-S-Z
Author Affiliation:Division of Food Bioscience and Biotechnology, Graduate School of Agriculture, Kyoto University, Uji, Kyoto 611-0011, Japan
Language:English
Abstract:We found that the sequences YPLDL and YPLDLF in the large subunit of spinach D-ribulose-1,5-bisphosphate carboxylase/oxygenase [ribulose-bisphosphate carboxylase] (Rubisco) met the structure YP-aliphatic amino acid which might have opioid activity. We then synthesized these peptides to test their opioid activity. The IC50 of these peptides in mouse vas deferens assay were 51.0 and 24.4 micro M, respectively, and those in delta receptor binding assay using [3H]deltorphin II as radioligand were 2.09 and 0.93 micro M, respectively. Both peptides were selective for delta receptor. We named them rubiscolin-5 and -6, respectively. Rubiscolin-5 and -6 have antinociceptive activity in mice after i.c.v. or oral administration. The enzymatic conditions to release rubiscolin were investigated using both spinach Rubisco and synthetic fragment peptides. This is the first example of bioactive peptides derived from plant Rubisco
Descriptors:amino-acid-sequences. ductus-deferens. enzymes. ileum. opioid-peptides. ribulose-bisphosphate-carboxylase. spinach
Organism Descriptors:guineapigs. mice. Spinacia-oleracea
Supplemental Descriptors:Cavia. Caviidae. rodents. mammals. vertebrates. Chordata. animals. Muridae. small-mammals. Spinacia. Chenopodiaceae. Caryophyllales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. SS200. VV450
Supplementary Info:27 ref
ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters
Copyright:Copyright CAB International

188. Title:Clusterin/apolipoprotein J is a novel biomarker of cellular senescence that does not affect the proliferative capacity of human diploid fibroblasts
View Article: FEBS Lett 2001 Dec 7;509(2):287-97
CD Volume:364
Print Article: Pages: 287-297
Author(s):Petropoulou C Trougakos IP Kolettas E Toussaint O Gonos ES
Author Affiliation:Laboratory of Molecular and Cellular Aging, Institute of Biological Research and Biotechnology, National Hellenic Research Foundation, 48 Vas. Constantinou Ave., 116 35 Athens, Greece
Abstract:Normal human fibroblasts have a limited replicative potential in culture and eventually reach a state of irreversible growth arrest, termed senescence. In a previous study aiming to identify genes that are differentially regulated during cellular senescence we have cloned clusterin/apolipoprotein J (Apo J), a 80 kDa secreted glycoprotein. In the current report we pursue our studies and show that senescence of human diploid fibroblasts is accompanied by up-regulation of both Apo J mRNA and protein levels, but with no altered biogenesis, binding partner profile or intracellular distribution of the two Apo J forms

detected. To analyze the causal relationship between senescence and Apo J protein accumulation, we stably overexpressed the Apo J gene in primary as well as in SV40 T antigen-immortalized human fibroblasts and we showed no alteration of the proliferative capacity of the transduced cells. Despite previous reports on tumor-derived cell lines, overexpression of Apo J in human fibroblasts did not provide protection against apoptosis or growth arrest induced by hydrogen peroxide. Overall, our results suggest that Apo J overexpression does not induce senescence but it is rather a secondary consequence of the senescence phenotype. To our knowledge this is the first report that provides a functional analysis of human Apo J during replicative senescence

Descriptors:Antigens, Differentiation. Cell Aging. Diploidy. Fibroblasts. Glycoproteins. Human. Molecular Chaperones. Oxidative Stress. Recombinant Proteins. Support, Non-U.S. Gov't. Up-Regulation

Geographic Locator:Netherlands

ISSN:0014-5793
Year:2001
Journal Title:FEBS Letters

189. Title:Partial purification and characterisation of a xylanase enzyme produced by a micro-organism isolated from selected indigenous fruits of Zimbabwe

View Article: Food Chemistry. 72 (2). 1 February, 2001. 179-185
CD Volume:377
Print Article: Pages: 179-185

Author(s):Chivero Ernest T Mutukumira Anthony N Zvauya Remigio
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Language:English
Language of Summary:English (EN)

Abstract:Aerobic bacteria and fungi isolated from Ziziphus mauritiana, Scierocarya birrea fruits and a cattle compost were screened for production of endo-xylanase enzyme. Xylanolytic activity was found in 10 of the 88 isolates obtained. Two best endo-xylanase enzyme producers (SB-9a and TC-17d) were selected for further investigations. The two isolates were classified as belonging to the genus Bacillus. The endo-xylanase enzymes from both isolates were optimically active at pH 8 and stable over a pH range of 6.0- 9.0. The optimum temperature for xylanase activity, assayed at pH 8 was 60degreeC. The endo-xylanase from isolate SB-9a was stable at 50degreeC, maintaining over 50% of its activity for 1 h at pH 8. The endo-xylanase from isolate TC-17d was less stable, maintaining about 20% of its activity for 20 mm at 50degreeC and pH 8. Endo- xylanase activity for isolate SB-9a was inhibited by Hg2+, Ag+ and Mn2+ ions while Fe3+, K+, Nat, Ca2+, and Cu2+ ions stimulated xylanase activity. The endo-xylanase enzyme from isolate SB-9a was partially purified by ammonium sulphate precipitation, and gel filtration chromatography. It had a specific activity of 308 nkat/mg protein. This enzyme could have potential uses in biotechnological applications such as in pulp, paper and food manufacture due to its high specific activity and alkaline pH optima

Descriptors:biotechnology; cattle compost; food chemistry; food processing; fruits: fruit, indigenous; paper manufacture. Enzymology (Biochemistry and Molecular Biophysics); Foods; Microbiology. metal ions: enzyme inhibitor; xylanases: analysis, applications, characterization, inhibitors, pH, production, purification, temperature, uses

Geographic Locator:Zimbabwe (Ethiopian region)

Organism Descriptors:Bacillus spp. (Endospore-forming Gram-Positives); Ziziphus mauritiana (Rhamnaceae); bacteria (Bacteria); fungi (Fungi); microorganisms (Microorganisms); plants (Plantae)
Supplemental Descriptors:Bacteria: Microorganisms; Endospore-forming Gram-Positives: Eubacteria, Bacteria, Microorganisms; Fungi: Plantae; Microorganisms; Plantae; Rhamnaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Bacteria; Dicots; Eubacteria; Fungi; Microorganisms; Nonvascular Plants; Plants; Spermatophytes; Vascular Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Foods; Microbiology
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

190. Title:The effect of sugars and pectin on flavour release from a soft drink-related model system
View Article: Food Chemistry. 72 (3). 15 February, 2001. 363-368
CD Volume:377
Print Article: Pages: 363-368
Author(s):Hansson A Andersson J Leufven A
Author Affiliation:The Swedish Institute for Food and Biotechnology (SIK), S-402 29, Goteborg: ahn@sik.se
Language:English
Language of Summary:English (EN)
Abstract:Three types of sugar and high-methoxyl pectin at different concentrations were added to a soft drink-related model system consisting of water and six flavour compounds. The addition of these ingredients contributes to changes in viscosity and water activity, which in turn affects the release of the flavour compounds to the gas phase above the soft drink. In the study, a higher concentration of sucrose and invert sugar increased the release of five flavour compounds, probably owing to a so-called "salting-out" effect. Starch syrup at a concentration of 60% increased the amount of three of the flavour compounds released and would probably increase the release of more compounds at a higher concentration. When pectin was added to the system, it was seen that viscosity does not influence release of the flavour molecules, but that the kind of stabiliser used is more important
Descriptors:flavor release; soft drink-related model system. Foods. L-menthone: flavor compound; cis-3-hexenyl acetate: flavor compound; ethyl hexanoate: flavor compound; glucose: sweetener; high-methoxyl pectin: sweetener; invert sugar: sweetener; isopentyl acetate: flavor compound; limonene: flavor compound; linalool: flavor compound; sucrose: sweetener
Subject Codes:Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

191. Title:Physical properties of palm kernel olein-anhydrous milk fat mixtures transesterified using mycelium-bound lipase from Rhizomucor miehei
View Article: Food Chemistry. 72 (4). March, 2001. 447-454
CD Volume:377
Print Article: Pages: 447-454
Author(s):Liew Margaret Y B Ghazali H M Long K Lai O M Yazid A M

Author Affiliation:Faculty of Food Science and Biotechnology, University Putra Malaysia, UPM, 43400, Serdang, Selangor: hasanah@fsb.upm.edu.my
Language:English
Language of Summary:English (EN)
Abstract:The transesterification activity of mycelium-bound lipase from Rhizomucor miehei on palm kernel olein:anhydrous milk fat (PKO:AMF) blends was investigated. Commercial immobilised R. miehei lipase preparation, Lipozyme IM60 (Novo Nordisk), was used as a comparison. Mixtures of PKO:AMF, at ratios of 100:0, 70:30, 60:40, 50:50 and 0:100, were transesterified using either enzyme in a solvent-free system. The triglyceride (TG) profile, slip melting point, solid fat content, melting thermogram and the polymorphic form of the unreacted and transesterified mixtures were evaluated. Results indicated that transesterification by either enzyme was able to produce an oil mixture with new TG profiles, generally lower slip melting points and solid fat contents. The melting thermograms from differential scanning calorimetry analysis indicated changes in the triglyceride's crystalline composition and an overall shift to lower melting TG. Although the catalytic activities were similar for both lipases, Lipozyme-catalysed mixtures produced higher degrees of transesterification (43-51%) than mycelium-bound lipase-catalysed (22-34%) mixtures. This study also demonstrated that the transesterified PKO:AMF mixture at 70:30 ratio completely melted at 25C, and this meets the melting criteria for fat used in ice cream formulation
Descriptors:biotechnology; edible fats and oils: analysis, fats and oils, treatment; food chemistry; food processing; ice cream: dairy product, formulations. Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Foods. fungal lipases: applications, immobilized forms, mycelium-bond, transesterification activity; palm kernel olein-anhydrous milk fat mixtures: enzymatic treatment; triglycerides: analysis
Organism Descriptors:Rhizomucor miehei (Phycomycetes). mycelium
Supplemental Descriptors:Phycomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Bioprocess Engineering; Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

192. Title:Effect of storage temperature on texture, polymorphic structure, bloom formation and sensory attributes of filled dark chocolate
View Article: Food Chemistry. 72 (4). March, 2001. 491-497
CD Volume:377
Print Article: Pages: 491-497
Author(s):Ali A Selamat J Che Man Y B Suria A M
Author Affiliation:Faculty of Food Science and Biotechnology, Universiti Putra Malaysia, 43400, Serdang, Selangor: jinap@tpu.upm.edu.my
Language:English
Language of Summary:English (EN)
Abstract:The effects of 18 and 30degreeC storage temperatures on texture, polymorphic structure, bloom formation and sensory attributes of dark chocolate, stored for 8 weeks were studied. Results showed that storage at 18degreeC for 8 weeks, significantly retarded changes in filled chocolates; the chocolates were free from bloom during the storage period. In contrast, at 30degreeC there was an increase in the rate of fat migration and rate of change of C36 and C50, and also a decrease in texture and the polymorph structure in the coating changed

to beta and beta' polymorphs. However, the chocolates bloomed in the third week of storage (2 cycles). Sensory evaluation indicated that, storage at 18degreeC is better than 30degreeC, and desiccated coconut gives a pleasant flavour to the chocolate
Descriptors:filled dark chocolate: analysis, bloom formation, candy, flavor, polymorphic structure, sensory attributes, storage temperature, texture; food chemistry; food flavor; food processing; food quality; food texture. Foods
Subject Codes:Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

193. Title:Effect of processing on available carbohydrate content and starch digestibility of kidney beans (Phaseolus vulgaris L.)
View Article: Food Chemistry. 73 (3). May, 2001. 351-355
CD Volume:377
Print Article: Pages: 351-355
Author(s):Rehman Zia ur Salariya A M Zafar S I
Author Affiliation:Biotechnology and Food Research Centre, P.C.S.I.R. Laboratories Complex, Ferozepur Road, Lahore, 54600: ampl@nexlinx.net.pk
Language:English
Language of Summary:English (EN)
Abstract:The effects of different soaking and cooking methods were investigated on available carbohydrate content and starch digestibility of red and white kidney beans. Total soluble sugars, reducing sugars, non-reducing sugars and starch contents of red and white kidney beans were 9.95 and 11.3%, 0.82 and 0.96%, 9.13 and 10.3%, and 44.4 and 47.8%, respectively. All these available carbohydrate components decreased to various extents as a result of soaking and cooking. From 2.51 to 13.6% and 7.03 to 28.0% of total soluble sugars were lost on soaking kidney beans in tap water and sodium bicarbonate solution, respectively. However, losses in total soluble sugars were maximum (19.9-60.9%) on cooking pre-soaked kidney beans. Losses in starch contents were 4.27 to 24.7% and 30.4 to 70.7% as a result of the soaking and cooking processes, respectively. Besides these losses, starch digestibility of kidney beans was also markedly improved as a result of cooking. However, no appreciable improvement in starch digestibility was observed after soaking kidney beans in water or alkaline solution
Descriptors:food chemistry; food nutritional quality; food processing; kidney beans: analysis, chemical aspects, cooking, nutritional aspects, processing, soaking, vegetable. Foods. carbohydrates: nutritional analysis; starches: digestibility analysis; sugars: analysis
Organism Descriptors:Phaseolus vulgaris [kidney bean] (Leguminosae)
Supplemental Descriptors:Leguminosae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

194. Title:Performance of a lipase-catalyzed transesterified palm kernel olein and palm stearin blend in frying banana chips
View Article: Food Chemistry. 74 (1). July, 2001. 21-33
CD Volume:377

Print Article: Pages: 21-33
Author(s):Chu B S Ghazali H M Lai O M Man Y B Che Yusof S Yusoff M S A
Author Affiliation:Faculty of Food Science and Biotechnology, Universiti Putra Malaysia, 43400 UPM, Serdang, Selangor DE: lom@fsb.upm.edu.my
Language:English
Language of Summary:English (EN)
Abstract:The frying performance of an enzymatically transesterified palm stearin and palm kernel olein (1:1 by weight) blend was compared with its control (physical mixture or no enzyme added) and a commercial plastic frying shortening (CS). The samples were used as deep-fat frying media at 180degreeC for banana chips for seven consecutive days. The samples were then analysed for iodine value (IV), free fatty acid (FFA) content, peroxide value (PV), thiobarbituric acid (TBA) value, p-anisidine value (AV), total polar compounds (TPC), fatty acid composition, specific extinction, E1cm1% at 233 and 269 nm, polymer contents, viscosity and colour indices. The fried banana chips were analysed for acceptability by sensory evaluations. Storage properties of the banana chips were also evaluated by trained sensory panellists and a modified TBA test. The transesterified blend was found to have significantly (P<0.05) higher IV, FFA, PV, TBA value, AV, TPC, E1cm1% at 233 and 269 nm values, polymer content, viscosity and colour indices compared to the control, indicating that the transesterified blend was more susceptible to oxidative deterioration during deep-fat frying. CS generally showed the largest changes in most of the parameters, basically due to its high polyunsaturated fatty acid levels. There was no significant difference (P>0.05; for all the attributes tested) between the acceptability of the banana chips fried by the transesterified and control blends. However, the banana chips fried in CS had significantly (P<0.05) lower scores in terms of flavour, aftertaste and overall acceptability. This might be due to the typical hydrogenation flavour of CS. In the storage stability study of the banana chips, it was found that the banana chips fried in the transesterified blend were significantly (P<0.05) more rancid (lower score in sensory evaluations) and had a higher TBA value at the end of the storage time than the control
Descriptors:banana chips: sensory properties, snack food, storage properties; commercial plastic frying shortening: fats and oils; palm kernel olein-palm stearin blend: fats and oils, frying performance. Foods
Subject Codes:Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

195. Title:Nutrient contents of some traditional Kuwaiti dishes: Proximate composition, and phytate content
View Article: Food Chemistry. 74 (2). August, 2001. 169-175
CD Volume:377
Print Article: Pages: 169-175
Author(s):Dashti B H Al Awadi F Khalafawi M S Al Zenki S Sawaya W
Author Affiliation:Biotechnology Department, Kuwait Institute for Scientific Research, 13109, Safat: bdashti@safat.kisr.edu.kw
Language:English
Language of Summary:English (EN)
Abstract:Thirty-two Kuwaiti composite dishes were analyzed for their proximate composition and phytate content. The moisture content ranged from 89.5% in vegetable soup to 0.89% in rahash (a traditional sweet). The fat content varied from 0.99 to 29.2%. Fish dishes showed the highest protein content (20.9%) while vegetable soup had the lowest (1.19%).

Carbohydrate content of the 32 dishes varied from 3.5% in fried fish to 53.3% in rahash. The ash content ranged from 5.1% in hallomi cheese to as low as 0.39% in legemat (sweet dumpling). Phytate content, ranged from 2835 mg/100 g in rahash to 32.6 mg/100 g in labnah (strained yoghurt)
Descriptors:ash content; fish: fish; hallomi cheese: dairy product; labnah: dairy product; legemat: ethnic food; moisture content; rahash: candy; traditional Kuwaiti foods: ethnic food, nutrient content, proximate composition; vegetable soup: soup. Foods. carbohydrate; fat; phytate; protein
Subject Codes:Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

196. Title:Effect of changes in pH on the release of flavour compounds from a soft drink-related model system
View Article: Food Chemistry. 74 (4). September, 2001. 429-435
CD Volume:377
Print Article: Pages: 429-435
Author(s):Hansson A Andersson J Leufven A Pehrson K
Author Affiliation:SIK, Swedish Institute for Food and Biotechnology (SIK), S-402 29, Goteborg: ahn@sik.se
Language:English
Language of Summary:English (EN)
Abstract:Citric acid and phosphoric acid were added in variable amounts to a soft drink model system to show their effect on the release of six flavour compounds. High concentrations of the acids decreased the release of esters, probably because of the presence of large amounts of the dissociated form of the acids. However, the same amounts of added citric acid had no effect on flavour release when pH was regulated with sodium hydroxide. Changes in pH values achieved by adding hydrochloric acid also had no effect on flavour release. These results indicate that pH values used in soft drinks do not affect the release of flavour molecules. It is more likely the citric acid and the phosphoric acid, particularly their dissociated forms, which decrease the release of the esters. The other flavour compounds were not affected
Descriptors:food chemistry; pH; soft drink-related model system: analysis, preparation. Foods. citric acid; esters: analysis, release studies; flavor compounds: analysis, release studies; phosphoric acid
Subject Codes:Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

197. Title:Physico-chemical changes in sugarcane (Saccharum officinarum var yellow cane) and the extracted juice at different portions of the stem during development and maturation
View Article: Food Chemistry. 75 (2). November, 2001. 131-137
CD Volume:377
Print Article: Pages: 131-137
Author(s):Qudsieh Hanan Yassin M Yusof Salmah Osman Azizah Rahman Russly Abdul
Author Affiliation:Department of Food Technology, Faculty of Food Science and Biotechnology, University Putra Malaysia, 43400 UPM, Serdang, Selangor DE: salmah@fsb.edu.my
Language:English

Language of Summary:English (EN)
Abstract:A study was conducted to determine the physicochemical differences between portions (top, middle, and bottom) of sugarcane at different maturation stages (between 3 and 10 months from planting). The variety used was Saccharum officinarum var. Yellow cane. The parameters analysed were weight, diameter, yield, total soluble solids (TSS), pH, titratable acidity, sugar content (sucrose, glucose, fructose). The weight, diameter, total soluble solids (TSS) and sucrose content increased significantly ($P < 0.01$) in all portions (top, middle and bottom) up to the end of maturity. On the other hand, titratable acidity (TA), pH, juice yield, glucose and fructose contents decreased significantly ($P < 0.01$) during maturation. However, significant differences were also detected in weight, diameter, TSS, sugar content, pH, TA and juice yield between the different portions during maturation. Sucrose content, juice yield and TSS were found to be the most suitable indicators of maturity, while TA, glucose and fructose contents were found to be poor maturity indicators. A suitable harvesting stage was found to be between 7 and 8 months after planting
Descriptors:Agronomy (Agriculture); Foods. fructose; glucose; sucrose; sugarcane juice extract: pH, sugar content, time of extraction, titratable acidity, total soluble solids, weight
Organism Descriptors:Saccharum officinarum [sugarcane] (Gramineae): cultivar-yellow cane, harvesting stage, maturity, phsyico-chemical changes. sugarcane stem: bottom, middle, physicochemical differences, top
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Agronomy (Agriculture); Foods
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

198. Title:Antioxidant effects of Origanum majorana L. on superoxide anion radicals
View Article: Food Chemistry. 75 (4). December, 2001. 439-444
CD Volume:377
Print Article: Pages: 439-444
Author(s):Jun Woo Jin Han Bok Kyung Yu Kwang Won Kim Moo Sung Chang Ih Seop Kim Hee Yun Cho Hong Yon
Author Affiliation:Graduate School of Biotechnology, Korea University, No. 1, 5-Ga, Anam-Dong, Sungbuk-Gu, Seoul, 136-701; E-Mail: hycho@mail.korea.ac.kr
Language:English
Abstract:A purified compound with antioxidant properties (28 mg), T3b, was isolated from a methanol extract (10 g) of Origanum majorana L. by sequential procedures, with silica gel column, thin-layer, and LH- 20 Sephadex gel column chromatographies. The in vitro scavenging activity of T3b on superoxide anion radical (O_2^{-}.) was investigated and compared to those of seven commercially available synthetic or natural antioxidants. Of those, the strongest scavenging action was observed in T3b with an IC50 of 1.44 mug/ml. The T3b also exhibited significant inhibitory effects on 12-O-tetradecanolyphorbol-13- acetate (TPA)-induced O_2^{-}. generation and hydrogen peroxide formation in differentiated HL-60 cells, indicating that the isolated compound is a potent chemopreventer. The purified compound from O. majorana L. was shown to possess both O_2^{-}. scavenging activity and an inhibitory effect against TPA-induced O_2^{-}. generation

Descriptors:marjoram: herbs and spices. Foods; Pharmacognosy (Pharmacology). Origanum majorana methanol extract: antioxidant effects, chemopreventor, free radical scavenger, isolation, pharmacodynamics; hydrogen peroxide; superoxide anion radical
Organism Descriptors:HL-60 cell line (Hominidae); Origanum majorana [marjoram] (Labiatae)
Supplemental Descriptors:Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Labiatae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Chordates; Dicots; Humans; Mammals; Plants; Primates; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Foods; Pharmacognosy (Pharmacology)
ISSN:0308-8146
Year:2001
Journal Title:Food Chemistry

199. Title:Can biotechnology reach the poor? The adequacy of information and seed delivery
View Article: Food Policy. 2001. 26 (3). 249-264
CD Volume:355
Print Article: Pages: 249-264
Author(s):Tripp R
Author Affiliation:Overseas Development Institute, 111 Westminster Bridge Road, London SE1 7JD, UK
Language:English
Abstract:The paper examines the expectation that biotechnology can provide significant benefits for smallholder farmers. It uses evidence from current seed systems and variety choice in developing countries. In particular, it examines the adequacy of information flow and the performance of seed markets. Many of the biotechnology innovations proposed for use by smallholders feature qualities that may not be immediately obvious to farmers; implications are drawn for the potential demand for these transgenic varieties. The adequacy of seed systems is also examined, including the characteristics of local seed diffusion and the experience of commercial seed enterprises. The paper concludes that investments in public biotechnology must be accompanied by policies that encourage commercial seed system development and that empower farmers to be able to take full advantage of new technology
Descriptors:agricultural-policy. biotechnology. diffusion-of-information. farmers. improved-varieties. seed-industry. seeds. transgenic-plants
Geographic Locator:Developing-Countries
Organism Descriptors:plants
Subject Codes:CC300. EE110. EE120. EE140. WW000
Supplementary Info:32 ref
ISSN:0306-9192
Year:2001
Journal Title:Food Policy

200. Title:Spatial distribution patterns of riverine forest taxa in Brasilia, Brazil
View Article: Forest Ecology and Management. 2001. 140 (2/3). 257-264
CD Volume:378
Print Article: Pages: 257-264
Author(s):Leite E J
Author Affiliation:Embrapa Genetic Resources and Biotechnology, CP 02372, 70849-970 Brasilia DF, Brazil
Language:English

Abstract:The spatial distribution of adult individuals (more than or equal to 15 cm diameter at breast height) was investigated in a gallery forest of the Brasilia National Park, Brazil. Four wood species, important to the Brazilian national genetic conservation programme, were chosen: Astronium fraxinifolium, (Anacardiaceae); Cariniana estrellensis, (Lecythidaceae); Didymopanax morototoni [Schefflera morototoni], (Araliaceae) and Hymenaea courbaril var. stilbocarpa, (Leguminosae-Caesalpinioideae). While distribution was uneven, no relationship with gradient or topographic position could be detected, but aggregation was perceived. Stocking levels were typically low, from 0.15 to 3.31 individuals ha-1
Descriptors:forest-trees. forests. geographical-distribution. nature-conservation. plant-genetic-resources. riparian-forests. spatial-distribution. trees. tropical-forests
Geographic Locator:Brazil. Distrito-Federal
Identifiers:Araliales. Astronium fraxinifolium. Schefflera morototoni
Organism Descriptors:Astronium. Cariniana-estrellensis. Hymenaea-courbaril. Schefflera
Supplemental Descriptors:Anacardiaceae. Sapindales. dicotyledons. angiosperms. Spermatophyta. plants. South-America. America. Developing-Countries. Threshold-Countries. Latin-America. Cariniana. Lecythidaceae. Lecythidales. Brazil. Hymenaea. Caesalpinioideae. Fabaceae. Fabales. Schefflera. Araliaceae. Apiales
Subject Codes:KK100. KK110. PP720
Supplementary Info:24 ref
ISSN:0378-1127
Year:2001
Journal Title:Forest Ecology and Management

201. Title:Induction of gene expression in sheepshead minnows (Cyprinodon variegatus) treated with 17 beta -estradiol, diethylstilbestrol, or ethinylestradiol: the use of mRNA fingerprints as an indicator of gene regulation
View Article: General and Comparative Endocrinology. 2001. 121 (3). 250-260
CD Volume:353
Print Article: Pages: 250-260
Author(s):Denslow N D Bowman C J Ferguson R J Lee H S Hemmer M J Folmar L C
Author Affiliation:Department of Biochemistry and Molecular Biology, Center for Biotechnology, University of Florida, PO Box 100156 HC, Gainesville, Florida 32610, USA
Language:English
Abstract:The differential display reverse transcriptase polymerase chain reaction (DD-RTPCR) procedure was utilized to evaluate gene expression in male sheepshead minnows (n=35) injected with a single high dose of 17 beta -estradiol (E2; 5 mg/kg) or exposed to environmentally relevant concentrations (nominally 200 ng/litre) of E2 and 17 alpha -ethynyl estradiol. Upregulated messages for 2 genes that encode the zona radiata proteins ZP2 and ZP3 and a gene for vitellogenin were identified. Two genes were downregulated by estradiol, including transferrin and ribosomal protein S26. It is suggested that DD-RTPCR may be valuable in examining the potential effects of environmental contaminants on other endocrine-mediated pathways of reproduction, growth and development
Descriptors:diethylstilbestrol. estradiol. ethinylestradiol. gene-expression. laboratory-methods
Identifiers:Cyprinodon. Cyprinodon variegatus
Organism Descriptors:Cyprinodontidae

Supplemental Descriptors:Cyprinodontidae. Cyprinodontiformes. Osteichthyes. fishes. vertebrates. Chordata. animals. aquatic-animals. aquatic-organisms
Subject Codes:YY300. ZZ900
Supplementary Info:40 ref
ISSN:0016-6480
Year:2001
Journal Title:General and Comparative Endocrinology
Copyright:Copyright CAB International

202. Title:Evidence for a hyperglycemic effect of methionine-enkephalin in the prawns Penaeus indicus and Metapenaeus monocerus
View Article: Gen Comp Endocrinol 2001 Jul;123(1):90-9
CD Volume:353
Print Article: Pages: 90-99
Author(s):Kishori B Premasheela B Ramamurthi R Reddy PS
Author Affiliation:Department of Biotechnology, Sri Venkatestwara University, Tirupati, India
Abstract:The influence of methionine-enkephalin on carbohydrate metabolism of the prawns Penaeus indicus and Metapenaeus monocerus was studied. Injection of the opioid methionine-enkephalin into intact prawns induced significant hyperglycemia in a dose-dependent manner. Total tissue (midgut gland and muscle) carbohydrate and glycogen levels decreased following methionine-enkephalin injection, with a significant activation of phosphorylase in intact prawns, indicating glycogenolysis leading to hyperglycemia. In contrast, injection of methionine-enkephalin into eyestalk-ablated crabs did not affect the levels of hemolymph glucose, total tissue carbohydrates and glycogen, and activity of phosphorylase. These results support an earlier hypothesis for crabs which proposed that methionine-enkephalin acts as a neurotransmitter in crustaceans and stimulates the release of hyperglycemic hormone in inducing hyperglycemia
Descriptors:Animal. Blood Glucose. Carbohydrates. Dose-Response Relationship, Drug. Enkephalin, Methionine. Eye. Glycogen. Hemolymph. Phosphorylases. Shrimp. Support, Non-U.S. Gov't. Tissue Extracts
Geographic Locator:United States
ISSN:0016-6480
Year:2001
Journal Title:General and Comparative Endocrinology

203. Title:Molecular cloning and expression analysis of the turkey vasoactive intestinal peptide receptor
View Article: General and Comparative Endocrinology. 2001. 124 (1). 53-65
CD Volume:353
Print Article: Pages: 53-65
Author(s):You Seungkwon Hsu C C Kim H Kho Yoonjung Choi YunJaie El Halawani M E Farris J Foster D N
Author Variant:You-S. Kho-Y. Choi-Y-J
Author Affiliation:School of Agricultural Biotechnology, Seoul National University, Suwon 441-744, Korea Republic
Language:English
Abstract:Adult large white Nicholas turkey hens were grouped into nonphotostimulated, photostimulated, laying, incubating, photorefractory and vasoactive intestinal peptide (VIP)-immunized layers after which they were sacrificed and RNA was extracted from their tissues for reverse transcription-polymerase chain reaction (RT-PCR), cDNA amplification and Northern blot analysis. A 2347 bp turkey VIP-receptor (tVIP-R) cDNA was cloned that encodes a protein with a 52 kDa predicted Mr and shares similarities with rat lung (72%) and human

(70%) VIP-Rs as well as mouse glucagon (45%) and rat secretin (55%) receptors. Northern blot analysis revealed a 2.7 kb transcript in the pituitaries of laying hens. The steady-state tVIP-R mRNA levels were markedly diminished in the pituitary of VIP-immunized turkeys while mRNA expression in other tissues were not affected. Sequence data for tVIP-R has been deposited with the EMBL/GenBank Data Libraries under Accession Number U31991

Descriptors:complementary-DNA. gene-expression. hens. hormone-receptors. messenger-RNA. pituitary. poultry. vasoactive-intestinal-peptide

Organism Descriptors:fowls. turkeys

Supplemental Descriptors:Meleagris. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry. Gallus-gallus. Gallus

Subject Codes:LL240. WW000. LL600

Supplementary Info:46 ref

ISSN:0016-6480

Year:2001

Journal Title:General and Comparative Endocrinology

204. Title:Requirement for three novel protein complexes in the absence of the Sgs1 DNA helicase in Saccharomyces cerevisiae

View Article: Genetics 2001 Jan;157(1):103-18

CD Volume:366

Print Article: Pages: 103-118

Author(s):Mullen JR Kaliraman V Ibrahim SS Brill SJ

Author Affiliation:Department of Molecular Biology and Biochemistry, Center for Advanced Biotechnology and Medicine, Rutgers University, Piscataway, New Jersey 08855, USA

Abstract:The Saccharomyces cerevisiae Sgs1 protein is a member of the RecQ family of DNA helicases and is required for genome stability, but not cell viability. To identify proteins that function in the absence of Sgs1, a synthetic-lethal screen was performed. We obtained mutations in six complementation groups that we refer to as SLX genes. Most of the SLX genes encode uncharacterized open reading frames that are conserved in other species. None of these genes is required for viability and all SLX null mutations are synthetically lethal with mutations in TOP3, encoding the SGS1-interacting DNA topoisomerase. Analysis of the null mutants identified a pair of genes in each of three phenotypic classes. Mutations in MMS4 (SLX2) and SLX3 generate identical phenotypes, including weak UV and strong MMS hypersensitivity, complete loss of sporulation, and synthetic growth defects with mutations in TOP1. Mms4 and Slx3 proteins coimmunoprecipitate from cell extracts, suggesting that they function in a complex. Mutations in SLX5 and SLX8 generate hydroxyurea sensitivity, reduced sporulation efficiency, and a slow-growth phenotype characterized by heterogeneous colony morphology. The Slx5 and Slx8 proteins contain RING finger domains and coimmunoprecipitate from cell extracts. The SLX1 and SLX4 genes are required for viability in the presence of an sgs1 temperature-sensitive allele at the restrictive temperature and Slx1 and Slx4 proteins are similarly associated in cell extracts. We propose that the MMS4/SLX3, SLX5/8, and SLX1/4 gene pairs encode heterodimeric complexes and speculate that these complexes are required to resolve recombination intermediates that arise in response to DNA damage, during meiosis, and in the absence of SGS1/TOP3

Descriptors:Alleles. Amino Acid Sequence. DNA Helicases. Fungal Proteins. Gene Deletion. Genes, Fungal. Genetic Complementation Test. Molecular Sequence Data. Mutation. Phenotype. Recombination, Genetic.

Saccharomyces cerevisiae. Sequence Homology, Amino Acid. Support, U.S. Gov't, P.H.S.. Trans-Activators
Geographic Locator:United States
ISSN:0016-6731
Year:2001
Journal Title:Genetics

205. Title:Analysis of expressed sequence tags from two starvation, time-of-day-specific libraries of Neurospora crassa reveals novel clock-controlled genes
View Article: Genetics 2001 Mar;157(3):1057-65
CD Volume:366
Print Article: Pages: 1057-1065
Author(s):Zhu H Nowrousian M Kupfer D Colot HV Berrocal Tito G Lai H Bell Pedersen D Roe BA Loros JJ Dunlap JC
Author Affiliation:Department of Chemistry and Biochemistry, Advanced Center for Genome Technology, University of Oklahoma, Norman, Oklahoma 73019, USA
Abstract:In an effort to determine genes that are expressed in mycelial cultures of Neurospora crassa over the course of the circadian day, we have sequenced 13,000 cDNA clones from two time-of-day-specific libraries (morning and evening library) generating approximately 20,000 sequences. Contig analysis allowed the identification of 445 unique expressed sequence tags (ESTs) and 986 ESTs present in multiple cDNA clones. For approximately 50% of the sequences (710 of 1431), significant matches to sequences in the National Center for Biotechnology Information database (of known or unknown function) were detected. About 50% of the ESTs (721 of 1431) showed no similarity to previously identified genes. We hybridized Northern blots with probes derived from 26 clones chosen from contigs identified by multiple cDNA clones and EST sequences. Using these sequences, the representation of genes among the morning and evening sequences, respectively, in most cases does not reflect their expression patterns over the course of the day. Nevertheless, we were able to identify four new clock-controlled genes. On the basis of these data we predict that a significant proportion of the expressed Neurospora genes may be regulated by the circadian clock. The mRNA levels of all four genes peak in the subjective morning as is the case with previously identified ccgs
Descriptors:Blotting, Northern. Circadian Rhythm. Contig Mapping. DNA, Complementary. Databases, Factual. *Expressed Sequence Tags. *Gene Library. Models, Genetic. Molecular Sequence Data. Neurospora crassa. Sequence Analysis, DNA. Software. Support, Non-U.S. Gov't. Support, U.S. Gov't, Non-P.H.S.. Support, U.S. Gov't, P.H.S.. Time Factors
Geographic Locator:United States
ISSN:0016-6731
Year:2001
Journal Title:Genetics

206. Title:Complete replacement of the mitochondrial genotype in a Bos indicus calf reconstructed by nuclear transfer to a Bos taurus oocyte
View Article: Genetics. 2001. 158 (1). 351-356
CD Volume:366
Print Article: Pages: 351-356
Author(s):Meirelles F V Bordignon V Watanabe Y Watanabe M Dayan A Lobo R B Garcia J M Smith L C
Author Affiliation:Departamento de Genetica, Faculdade de Medicina-USP, Ribeirao Preto, SP 14049-900, Brazil
Language:English

Abstract:Due to the exclusively maternal inheritance of mitochondria, mitochondrial genotypes can be coupled to a particular nuclear genotype by continuous mating of founder females and their female offspring to males of the desired nuclear genotype. However, backcrossing is a gradual procedure that, apart from being lengthy, cannot ascertain that genetic and epigenetic changes will modify the original nuclear genotype. Animal cloning by nuclear transfer using host ooplasm carrying polymorphic mitochondrial genomes allows, among other biotechnology applications, the coupling of nuclear and mitochondrial genotypes of diverse origin within a single generation. Previous attempts to use Bos taurus oocytes as hosts to transfer nuclei from unrelated species led to the development to the blastocyst stage but none supported gestation to term. Our aim in this study was to determine whether B. taurus oocytes support development of nuclei from the closely related B. indicus cattle and to examine the fate of their mitochondrial genotypes throughout development. We show that indicus:taurus reconstructed oocytes develop to the blastocyst stage and produce live offspring after transfer to surrogate cows. We also demonstrate that, in reconstructed embryos, donor cell-derived mitochondria undergo a stringent genetic drift during early development leading, in most cases, to a reduction or complete elimination of B. indicus mtDNA. These results demonstrate that cross-subspecies animal cloning is a viable approach both for matching diverse nuclear and cytoplasmic genes to create novel breeds of cattle and for rescuing closely related endangered cattle
Descriptors:animal-cloning. blastocyst. calves. cows. epigenetics. genetic-change. genetic-drift. genotypes. mitochondria. mitochondrial-DNA. nuclei. oocyte-maturation. oocytes
Identifiers:nuclear transfer
Organism Descriptors:cattle. zebu
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL240. LL250. WW000
Supplementary Info:25 ref
ISSN:0016-6731
Year:2001
Journal Title:Genetics

207. Title:Bacterial artificial chromosome-based physical map of the rice genome constructed by restriction fingerprint analysis
View Article: Genetics 2001 Aug;158(4):1711-24
CD Volume:366
Print Article: Pages: 1711-1724
Author(s):Tao Q Chang YL Wang J Chen H Islam Faridi MN Scheuring C Wang B Stelly DM Zhang HB
Author Affiliation:Department of Soil and Crop Sciences and Crop Biotechnology Center, Texas A&M University, College Station, TX 77843-2123, USA
Abstract:Genome-wide physical mapping with bacteria-based large-insert clones (e.g., BACs, PACs, and PBCs) promises to revolutionize genomics of large, complex genomes. To accelerate rice and other grass species genome research, we developed a genome-wide BAC-based map of the rice genome. The map consists of 298 BAC contigs and covers 419 Mb of the 430-Mb rice genome. Subsequent analysis indicated that the contigs constituting the map are accurate and reliable. Particularly important to proficiency were (1) a high-resolution, high-throughput DNA sequencing gel-based electrophoretic method for BAC fingerprinting, (2) the use of several complementary large-insert BAC libraries, and (3) computer-aided contig assembly. It has been demonstrated that the

fingerprinting method is not significantly influenced by repeated sequences, genome size, and genome complexity. Use of several complementary libraries developed with different restriction enzymes minimized the "gaps" in the physical map. In contrast to previous estimates, a clonal coverage of 6.0-8.0 genome equivalents seems to be sufficient for development of a genome-wide physical map of approximately 95% genome coverage. This study indicates that genome-wide BAC-based physical maps can be developed quickly and economically for a variety of plant and animal species by restriction fingerprint analysis via DNA sequencing gel-based electrophoresis

Descriptors:Chromosomes, Artificial, Bacterial. Contig Mapping. DNA. Gene Library. Genetic Markers. *Genome, Plant. Models, Genetic. *Physical Chromosome Mapping. *Restriction Mapping. Rice. Support, Non-U.S. Gov't

Geographic Locator:United States

ISSN:0016-6731
Year:2001
Journal Title:Genetics

208. Title:Drosophila immunity: genes on the third chromosome required for the response to bacterial infection

View Article: Genetics. 2001. 159 (1). 189-199
CD Volume:368
Print Article: Pages: 189-199

Author(s):Wu L P Choe K M Lu Y Anderson K V
Author Affiliation:Center for Agricultural Biotechnology, University of Maryland Biotechnology Institute, College Park, MD 20742, USA

Language:English

Abstract:We screened the third chromosome of D. melanogaster for mutations that prevent the normal immune response. We identified mutant lines based on their failure to induce transcription of an antibacterial peptide gene in response to infection or their failure to form melanized clots at the site of wounding. These mutations define 14 immune response deficient genes (ird) that have distinct roles in the immune response. We have identified the molecular basis of several ird phenotypes. Two genes, scribble and kurtz/modulo, affect the cellular organization of the fat body, the tissue responsible for antimicrobial peptide production. Two ird genes encode components of the signalling pathways that mediate responses to bacterial infection, a Drosophila gene encoding a homologue of I kappa B kinase (DmIkk beta) and Relish, a Rel-family transcription factor. These genetic studies should provide a basis for a comprehensive understanding of the genetic control of immune responses in Drosophila

Descriptors:bacterial-diseases. biochemical-pathways. chromosomes. enzymes. fat-body. gene-expression. genes. genetic-regulation. immunity. kinases. mutants. mutations. phenotypes. transcription-factors

Organism Descriptors:Drosophila-melanogaster

Supplemental Descriptors:Drosophila. Drosophilidae. Diptera. insects. arthropods. invertebrates. animals

Subject Codes:WW000. YY300. YY400. YY700

Supplementary Info:many ref

ISSN:0016-6731
Year:2001
Journal Title:Genetics

209. Title:An integrated map of Arabidopsis thaliana for functional analysis of its genome sequence

View Article: Genetics 2001 Nov;159(3):1231-42

CD Volume:368
Print Article: Pages: 1231-1242
Author(s):Chang YL Tao Q Scheuring C Ding K Meksem K Zhang HB
Author Affiliation:Department of Soil and Crop Sciences and Crop Biotechnology Center, Texas A&M University, College Station, Texas 77843-2123, USA
Abstract:The genome of the model plant species Arabidopsis thaliana has recently been sequenced. To accelerate its current genome research, we developed a whole-genome, BAC/BIBAC-based, integrated physical, genetic, and sequence map of the A. thaliana ecotype Columbia. This new map was constructed from the clones of a new plant-transformation-competent BIBAC library and is integrated with the existing sequence map. The clones were restriction fingerprinted by DNA sequencing gel-based electrophoresis, assembled into contigs, and anchored to an existing genetic map. The map consists of 194 BAC/BIBAC contigs, spanning 126 Mb of the 130-Mb Arabidopsis genome. A total of 120 contigs, spanning 114 Mb, were anchored to the chromosomes of Arabidopsis. Accuracy of the integrated map was verified using the existing physical and sequence maps and numerous DNA markers. Integration of the new map with the sequence map has enabled gap closure of the sequence map and will facilitate functional analysis of the genome sequence. The method used here has been demonstrated to be sufficient for whole-genome physical mapping from large-insert random bacterial clones and thus is applicable to rapid development of whole-genome physical maps for other species
Descriptors:Arabidopsis. *Chromosome Mapping. Contig Mapping. Gene Library. Genome. *Genome, Plant. Models, Genetic. Physical Chromosome Mapping. Support, Non-U.S. Gov't
Geographic Locator:United States
ISSN:0016-6731
Year:2001
Journal Title:Genetics

210. Title:Arabidopsis genes essential for seedling viability: isolation of insertional mutants and molecular cloning
View Article: Genetics 2001 Dec;159(4):1765-78
CD Volume:368
Print Article: Pages: 1765-1778
Author(s):Budziszewski GJ Lewis SP Glover LW Reineke J Jones G Ziemnik LS Lonowski J Nyfeler B Aux G Zhou Q McElver J Patton DA Martienssen R Grossniklaus U Ma H Law M Levin JZ
Author Affiliation:Syngenta Biotechnology, Inc., Research Triangle Park, North Carolina 27709, USA
Abstract:We have undertaken a large-scale genetic screen to identify genes with a seedling-lethal mutant phenotype. From screening approximately 38,000 insertional mutant lines, we identified >500 seedling-lethal mutants, completed cosegregation analysis of the insertion and the lethal phenotype for >200 mutants, molecularly characterized 54 mutants, and provided a detailed description for 22 of them. Most of the seedling-lethal mutants seem to affect chloroplast function because they display altered pigmentation and affect genes encoding proteins predicted to have chloroplast localization. Although a high level of functional redundancy in Arabidopsis might be expected because 65% of genes are members of gene families, we found that 41% of the essential genes found in this study are members of Arabidopsis gene families. In addition, we isolated several interesting classes of mutants and genes. We found three mutants in the recently discovered nonmevalonate isoprenoid biosynthetic pathway and mutants disrupting genes similar to Tic40 and tatC, which are likely to be involved in chloroplast protein translocation. Finally, we directly compared T-DNA

and Ac/Ds transposon mutagenesis methods in Arabidopsis on a genome scale. In each population, we found only about one-third of the insertion mutations cosegregated with a mutant phenotype
Descriptors:Arabidopsis. Cell Survival. Chloroplasts. *Cloning, Molecular. DNA Transposable Elements. Models, Genetic. Multigene Family. *Mutagenesis, Insertional. *Mutation. Phenotype. Plasmids. Polymerase Chain Reaction. Seeds
Geographic Locator:United States
ISSN:0016-6731
Year:2001
Journal Title:Genetics

211. Title:Effect of tuftsin on excretion pattern of virulent Newcastle disease virus following challenge of chicken
View Article: Indian Veterinary Journal. 2001. 78 (3). 181-183
CD Volume:356
Print Article: Pages: 181-183
Author(s):Saravanabava K Nachimuthu K Padmanaban V D
Author Affiliation:Department of Animal Biotechnology, Madras Veterinary College, Chennai - 600 007, India
Language:English
Abstract:240 White Leghorn chicks were grouped into 4 wherein: group 1, was vaccinated with Newcastle disease vaccine (NDV) and tuftsin; group 2, given vaccine alone; group 3, tuftsin alone and group 4, was unvaccinated. There was a significant increase in antibody titres in birds vaccinated with tuftsin as compared to those without tuftsin. Bird having serum antibody titres from 2.66 to 9.33 excreted the virus for 3-9 days post-challenge, while those with 11.16 titres and above did not. Tuftsin produced significant increase in serum antibody level to NDV vaccination which reduced virus shedding depending on the antibody titre. It is concluded that tuftsin can be used safely and effectively as an immunopotentiator in regular NDV control programme
Descriptors:antibodies. chicks. excretion. immune-response. Newcastle-disease. poultry. serum. vaccination. vaccines. virulence
Organism Descriptors:fowls. Newcastle-disease-virus
Supplemental Descriptors:Gallus-gallus. Gallus. Phasianidae. Galliformes. birds. vertebrates. Chordata. animals. poultry. avian-paramyxovirus. Paramyxovirus. Paramyxoviridae. viruses
Subject Codes:HH600. LL650. LL821
Supplementary Info:6 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal

212. Title:Rapid detection of rabies virus by one-tube and one-buffer reverse-transcription polymerase chain reaction
View Article: Indian Veterinary Journal. 2001. 78 (4). 275-277
CD Volume:356
Print Article: Pages: 275-277
Author(s):Gupta P K Singh R K De S N Rao Y U B Butchaiah G
Author Affiliation:National Biotechnology Centre, Indian Veterinary Research Institute, Izatnagar - 243 122, U.P., India
Language:English
Descriptors:assays. genes. polymerase-chain-reaction. reverse-transcription
Organism Descriptors:dogs. rabies-virus
Supplemental Descriptors:Canis. Canidae. Fissipeda. carnivores. mammals. vertebrates. Chordata. animals. small-mammals. Lyssavirus. Rhabdoviridae. viruses

Subject Codes:LL886. ZZ900
Supplementary Info:5 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

213. Title:Human placental extract for treatment of cystic ovarian condition - a case report
View Article: Indian Veterinary Journal. 2001. 78 (4). 339-340
CD Volume:356
Print Article: Pages: 339-340
Author(s):Tamuli M K
Author Affiliation:Department of Gynaecology, Obstetrics and Artificial Insemination, College of Veterinary Science, Assam Agricultural University, Khanapara Campus, Guwahati-781 022, India
Language:English
Descriptors:biotechnology. case-reports. clinical-aspects. cows. diagnosis. insemination. ovarian-cysts. placenta
Organism Descriptors:cattle
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL860. LL886. WW000
Supplementary Info:11 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

214. Title:Conception in goats and improvement of fertility with human placental extract
View Article: Indian Veterinary Journal. 2001. 78 (4). 341-342
CD Volume:356
Print Article: Pages: 341-342
Author(s):Tamuli M K
Author Affiliation:Department of Gynaecology, Obstetrics & Artificial Insemination, College of Veterinary Science, Assam Agricultural University, Khanapara Campus, Guwahati-781022, India
Language:English
Abstract:361 does between zero to fifth lactation were inseminated with good quality frozen semen having more than 65% motility. The overall conception rate was 86.14% to first insemination. The rest of the goats conceived within third insemination as they repeated the oestrus cycles at regular interval of 20-21 days. The conception rate was 100% (N=39); 96.87% (N=64); 88.35% (N=189); 64.51% (N=31) and 62.96% (N=27) during insemination between 31 to 36 hours, 37 to 42 hours, 24 to 30 hours, between 24 hours and after 42 hours from the onset of estrus respectively
Descriptors:biotechnology. conception. conception-rate. fertility. frozen-semen. GnRH. insemination. kidding-rate. lactation
Identifiers:human placental extract
Organism Descriptors:goats
Supplemental Descriptors:Capra. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. LL600. WW000
Supplementary Info:11 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal

Copyright:Copyright CAB International

215. Title:Sequential variation in aminotransferase activity during foetal development in ruminant
View Article: Indian Veterinary Journal. 2001. 78 (9). 857-858
CD Volume:356
Print Article: Pages: 857-858
Author(s):Dhanotiya R S Gupta R S Dixit N K
Author Affiliation:Department of Animal Biochemistry and Biotechnology, College of Veterinary Science & A.H. Mhow (M.P.), India
Language:English
Descriptors:alanine-aminotransferase. aspartate-aminotransferase. enzyme-activity. fetal-development. fetus. gluconeogenesis
Organism Descriptors:goats
Supplemental Descriptors:Capra. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates
Subject Codes:LL250. LL600
Supplementary Info:6 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

216. Title:Dot enzyme immunoassay for detection of canine distemper virus
View Article: Indian Veterinary Journal. 2001. 78 (11). 981-983
CD Volume:356
Print Article: Pages: 981-983
Author(s):Ramadass P Latha D
Author Affiliation:Department of Animal Biotechnology, Madras Veterinary College, Chennai - 600 007, Tamil Nadu, India
Language:English
Abstract:In this study, dot enzyme immunoassay (DIA) was standardized for the detection of canine distemper (CD) virus from conjunctival swab suspensions obtained from dogs suspected for CD. The results were then compared with the results of immunofluorescence assay. A total of 322 conjunctival swabs were collected from dogs during a period of 1 year, from July 1999, at a veterinary hospital in Chennai (Tamil Nadu, India). DIA detected 112 positive cases (34.8%) with the development of brown colouration at the site of application of sample dot on the nitrocellulose membrane (NCM). The intensities of the reaction varied in different samples. On visual examination, the colour intensity of dots increased as the antigen concentration increased. The results were assessed semi-quantitatively from dark brown (4+) to lighter brown (1+), to no colour (-ve). Immunofluoresence assay detected 105 samples (32.6%), which is slightly less than that detected by DIA. The DIA method described in the paper was rapidly performed; its simplicity and rapidity means that it can be used in the field for testing large number of samples. The coloured dots in a positive reaction can easily be seen, and does not require the use of any instrumentation
Descriptors:conjunctiva. diagnosis. diagnostic-techniques. disease-prevalence. enzyme-immunoassay. epidemiology
Geographic Locator:India. Tamil-Nadu
Identifiers:canine distemper virus
Organism Descriptors:distemper-virus. dogs
Supplemental Descriptors:Morbillivirus. Paramyxoviridae. viruses. Canis. Canidae. Fissipeda. carnivores. mammals. vertebrates. Chordata. animals. small-mammals. South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations. India

Subject Codes:LL070. LL821. LL886. ZZ900
Supplementary Info:14 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

217. Title:Variation and repeatability in ascorbic acid concentration in bovine and bubaline semen
View Article: Indian Veterinary Journal. 2001. 78 (11). 1021-1023
CD Volume:356
Print Article: Pages: 1021-1023
Author(s):Jain M C Arora N Arora J S
Author Affiliation:Department of Biochemistry and Biotechnology, College of Veterinary Science and Animal Husbandry, Jabalpur (M.P.), 482 001, India
Language:English
Abstract:The heritability of ascorbic acid concentration in the semen of bovines was studied. Semen samples from 6 healthy Murrah buffalo bulls, 2 Tharparkar, 2 Red Dane, three 1/2 Holstein x 1/2 Tharparkar, two 3/4 Holstein x 1/4 Tharparkar bulls. Results show that species difference had no significant effect on the ascorbic acid concentration of semen. Hence, the data were poooled for the species, and anlaysis of variance was estimated. Intra-class correlation was estimated to obtain the repeatability of the trait. The Tharparkar breed had the highest ascorbic acid concentration in semen, followed by Red Dane. Ignoring the breed differences, when all the data were pooled, the mean ascorbic acid value was higher than the mean bubaline ascorbic acid value. This difference in the 2 species was not significant
Descriptors:ascorbic-acid. breed-differences. heritability. semen. species-differences. traits
Organism Descriptors:buffaloes. cattle
Supplemental Descriptors:Bubalus. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Bos
Subject Codes:LL250. LL600
Supplementary Info:13 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal
Copyright:Copyright CAB International

218. Title:Use of polymerase chain reaction for the detection of leptospires in clinical samples
View Article: Indian Veterinary Journal. 2001. 78 (12). 1087-1090
CD Volume:356
Print Article: Pages: 1087-1090
Author(s):Kumar A S Ramadass P Nachimuthu K
Author Affiliation:Dept. of Animal Biotechnology, Madras Veterinary College, Chennai - 600 007, India
Language:English
Abstract:The diagnostic value of polymerase chain reaction (PCR) was tested on different types of clinical samples. Blood, urine cerebrospinal fluid (CSF) and milk samples from dogs and cattle were obtained from Madras Veterinary College Hospital in Chennai (Tamil Nadu, India). Human samples were obtained from patients suspected of having leptospirosis. Of the 46 human blood samples, an 85% positivity was observed when PCR was used; urine samples showed 50% positivity and CSF showed 75% positivity. On the other hand, blood, urine and CSF collected from dogs showed positivity of 50, 82 and 67%, respectively when diagnosed

using PCR. Cattle blood samples showed 75% positivity when PCR was used. Results indicate that the PCR assay is a highly sensitive and specific method for the detection of leptospira infection. Also, that PCR can be used, not only for blood and urine, but also for other samples like CSF and milk, for the quick diagnosis of leptospirosis
Descriptors:blood. diagnosis. diagnostic-techniques. human-diseases. leptospirosis. milk. polymerase-chain-reaction. urine
Geographic Locator:India. Tamil-Nadu
Organism Descriptors:cattle. dogs. Leptospira. man
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Canis. Canidae. Fissipeda. carnivores. small-mammals. South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations. Leptospiraceae. Spirochaetales. Gracilicutes. bacteria. prokaryotes. Homo. Hominidae. Primates. India
Subject Codes:LL070. LL821. LL886. VV210. VV720. ZZ900
Supplementary Info:6 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal

219. Title:Biological control of Haemonchus contortus in sheep by nematophagous fungus, Duddingtonia flagrans
View Article: Indian Veterinary Journal. 2001. 78 (12). 1091-1094
CD Volume:356
Print Article: Pages: 1091-1094
Author(s):Sanyal P K
Author Affiliation:Biotechnology Laboratory, National Dairy Development Board, Anand - 388 001, Gujarat, India
Language:English
Abstract:The study determined if chlamydospores of Duddingtonia flagrans can survive sheep gut passage, climatic conditions on pasture and can reduce the number of infective larvae of Haemonchus contortus in pasture and in faeces. After acclimatization of 10 male lambs to a specified diet for 15 days, the animals were each experimentally infected with 10 000 live infective larvae of H. contortus, and divided into 2 groups. At 15 days post-infection, one group (n=5) was fed with chlamydospores of D. flagrans at 0.5 million spores/kg body weight, twice daily, for 30 days; whereas the other group was not. Results show that daily feeding with the microfungus led to lowered herbage infectivity. Also, recovery of infective third stage larvae was considerably reduced in in vitro faecal cultures
Descriptors:animal-parasitic-nematodes. biological-control. chlamydospores. nematophagous-fungi. survival
Identifiers:Duddingtonia flagrans. lamb
Organism Descriptors:Deuteromycotina. Haemonchus-contortus. sheep
Supplemental Descriptors:Eumycota. fungi. Haemonchus. Trichostrongylidae. Nematoda. invertebrates. animals. Ovis. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. ungulates
Subject Codes:HH100. LL822. ZZ394
Supplementary Info:10 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal

220. Title:Rapid DNA isolation from the leptospiral cultures using high salt method

View Article: Indian Veterinary Journal. 2001. 78 (12). 1158-1159
CD Volume:356
Print Article: Pages: 1158-1159
Author(s):Senthil Kumar Ramadass P
Author Variant:Kumar-S
Author Affiliation:Dept. of Animal Biotechnology, Madras Veterinary College, Chennai - 600 007, Tamil Nadu, India
Language:English
Abstract:A simple, rapid, and cost-effective method of isolation of good quality DNA from leptospiral cultures was developed. Leptospiral cultures (2 ml) were centrifuged at 10 000 rpm for 20 min, and the resulting pellet was washed twice with solution I. The final pellet was resuspended in 0.5 ml of solution II. 50 micro l of lysozyme was added and kept at 37 deg C water bath for 15 min, and at the end of incubation, 50 ml of 10% sodium dodecyl sulfate was added. 250 micro l of 6 M NaCl was added and mixed well. The mixture was then centrifuged at 12 000 rpm for 5 min at 4 deg C, and the DNA pellet obtained was washed with 70% ethanol. The DNA preparation was checked for purity and concentration by measuring the optical densities (OD) at 260 and 280 nm. Lysozyme was included in the procedure to lyse the bacterial cell wall, and sodium chloride replaced the use of protease and phenol in salting out the protein contaminants. The whole procedure can be completed within one hour. The DNA prepared can be directly used for restriction enzyme digestion, hybridization, PCR and RAPD methods
Descriptors:absorbance. DNA. isolation. isolation-techniques. lysozyme. methodology. purity. sodium-chloride
Organism Descriptors:Leptospira
Supplemental Descriptors:Leptospiraceae. Spirochaetales. Gracilicutes. bacteria. prokaryotes
Subject Codes:LL821. WW000. ZZ395. ZZ900
Supplementary Info:3 ref
ISSN:0019-6479
Year:2001
Journal Title:Indian Veterinary Journal

221. Title:Certification of genetically modified forest plantations
View Article: International Forestry Review. 2001. 3 (2). 87-104, 169-170
CD Volume:362
Print Article: Pages: 87-104,169-170
Author(s):Strauss S H Coventry P Campbell M M Pryor S N Burley J
Author Affiliation:Department of Plant Sciences, Oxford Forestry Institute, South Parks Road, Oxford OX1 3RB, UK
Language:English
Language of Summary:spanish. french
Abstract:The use of recombinant DNA and asexual gene transfer methods to genetically modify (GM) plantation trees, also called genetic engineering, has been treated variably by the diverse systems that certify forest management practices. Only one system, the Forest Stewardship Council (FSC), bans all uses, including contained field research, and this prohibition applies regardless of whether genes derive from the same or different species, or whether the trait imparted is a small modification to physiology or a novel property. In contrast, FSC allows consideration of benefit versus risk for other practices of intensive plantation management that may have complex or irreversible ecological consequences, including the uses of exotic populations or tree species, hybrids, or clones; biological control organisms; and fertilizers, herbicides, and pesticides. We review FSC's stated concerns about GM plantations and show that all of them

are likely to be soluble given research and monitoring of GM plantations during early stages of development. We argue that the FSC ban makes it very difficult for certified companies to participate in the very field research required to resolve the concerns, and forgoes an opportunity to direct research toward desired applications of GM. It also severely constrains the ability to use the rapidly growing knowledge of genomes to attain a number of environmental benefits - themselves often requirements of certification standards. These might include production of more wood from less plantation land, wood that results in less pollution during pulping or energy generation, means for containment of highly bred or exotic species, reduced use of undesirable pesticides and herbicides, and mitigation of damage to soils as a result of mechanical weed control
Descriptors:biotechnology. certification. forest-management. forest-plantations. forests. gene-transfer. genetic-engineering. recombinant-DNA. sustainability. transgenic-plants. tree-breeding
Organism Descriptors:plants
Subject Codes:FF020. KK110. WW000
Supplementary Info:84 ref
ISSN:1465-5489
Year:2001
Journal Title:International Forestry Review

222. Title:Low-temperature brewing by freeze-dried immobilized cells on gluten pellets
View Article: Journal of Agricultural and Food Chemistry. 49 (1). January, 2001. 373-377
CD Volume:367
Print Article: Pages: 373-377
Author(s):Bekatorou A Koutinas A A Psarianos K Kanellaki M
Author Affiliation:Food Biotechnology Group, Department of Chemistry, University of Patras, GR-26500, Patras
Language:English
Language of Summary:English (EN)
Abstract:A biocatalyst, prepared by the immobilization of a cryotolerant strain of Saccharomyces cerevisiae on gluten pellets, was freeze- dried without any protecting medium and used for repeated batch fermentations of wort for each of the temperatures 15, 10, 5, and 0 degreeC. The fermentation time for freeze-dried immobilized cells was about 2-fold that of the corresponding time for wet immobilized cells on gluten pellets, and lower than the corresponding time for freeze-dried free cells, especially at 5 and 0 degreeC. Beers produced by freeze-dried immobilized cells contained alcohol levels in the range of 5.0-5.5% v/v, diacetyl concentrations lower than 0.5 mg/L, polyphenol concentrations lower than 145.5 mg/L, and free cell concentrations lower than 3 g/L. As a result, they had a very good clarity after the end of primary fermentation. The amounts of amyl alcohols were lower than 129.1 mg/L and reduced as the temperature was decreased. Ethyl acetate concentrations were found in the range of 22.1-29.2 mg/L, giving a very good aroma and taste in the produced beers
Descriptors:beer: alcoholic beverage, aroma, taste. Foods. amyl alcohols; diacetyl; ethyl acetate; gluten; polyphenol
Organism Descriptors:Saccharomyces cerevisiae (Ascomycetes): biocatalyst, cryotolerant strain, freeze-dried immobilized cells
Supplemental Descriptors:Ascomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Foods

ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

223. Title:Methyleugenol in Ocimum basilicum L. Cv. Genovese Gigante
View Article: Journal of Agricultural and Food Chemistry. 49 (1). January, 2001. 517-521
CD Volume:367
Print Article: Pages: 517-521
Author(s):Miele Mariangela Dondero Ramona Ciarallo Giovanni Mazzei Mauro
Author Affiliation:Pharmaceutical Biotechnology Laboratory, Department of Pharmaceutical Sciences, University of Genova, Viale Benedetto XV 3, 16132, Genova: mazzei@ermes.cba.unige.it
Language:English
Language of Summary:English (EN)
Abstract:Ocimum basilicum cv. Genovese Gigante is the basil cultivar used the most in the production of a typical Italian sauce called pesto. The aromatic composition of plants at different growth stages was determined. Plants from different areas of northwestern Italy were analyzed at 4 and 6 weeks after sowing and showed methyleugenol and eugenol as the main components. The content of these compounds was correlated with plant height rather than plant age. Particularly, methyleugenol was predominant in plants up to 10 cm in height, whereas eugenol was prevalent in taller plants. These results are important in the evaluation of risk to human health posed by dietary ingestion of methyleugenol contained in pesto
Descriptors:basil: herbs and spices; pesto: sauces and condiments. Foods; Toxicology. eugenol; methyleugenol: toxin
Geographic Locator:northwestern Italy (Italy, Europe, Palearctic region)
Organism Descriptors:Ocimum basilicum [basil] (Labiatae): cultivar-Genovese Gigante
Supplemental Descriptors:Labiatae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods; Toxicology
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

224. Title:Control of enzymatic browning in potato (Solanum tuberosum L.) by sense and antisense RNA from tomato polyphenol oxidase
View Article: Journal of Agricultural and Food Chemistry. 49 (2). February, 2001. 652-657
CD Volume:367
Print Article: Pages: 652-657
Author(s):Coetzer Chris Corsini Dennis Love Steve Pavek Joe Tumer Nilgun
Author Affiliation:Biotechnology Center for Agriculture and the Environment and Department of Plant Pathology, Rutgers University, Cook College, New Brunswick, NJ, 08903-0231: tumer@aesop.rutgers.edu
Language:English
Language of Summary:English (EN)
Abstract:Polyphenol oxidase (PPO) activity of Russet Burbank potato was inhibited by sense and antisense PPO RNAs expressed from a tomato PPO cDNA under the control of the 35S promoter from the cauliflower mosaic virus. Transgenic Russet Burbank potato plants from 37 different lines were grown in the field. PPO activity and the level of enzymatic browning were measured in the tubers harvested from the field. Of the tubers from 28 transgenic lines that were sampled, tubers from 5 lines

exhibited reduced browning. The level of PPO activity correlated with the reduction in enzymatic browning in these lines. These results indicate that expression of tomato PPO RNA in sense or antisense orientation inhibits PPO activity and enzymatic browning in the major commercial potato cultivar. Expression of tomato PPO RNA in sense orientation led to the greatest decrease in PPO activity and enzymatic browning, possibly due to cosuppression. These results suggest that expression of closely related heterologous genes can be used to prevent enzymatic browning in a wide variety of food crops without the application of various food additives

Descriptors:enzymatic browning; potato: vegetable. Molecular Genetics (Biochemistry and Molecular Biophysics); Foods. antisense RNA; cDNA [complementary DNA]; polyphenol oxidase; sense RNA. tomato PPO gene [tomato polyphenol oxidase gene] (Solanaceae): transgene

Organism Descriptors:Solanum tuberosum [potato] (Solanaceae): cultivar-Russet Burbank, transgenic

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

Subject Codes:Molecular Genetics (Biochemistry and Molecular Biophysics); Foods

ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

225. Title:Effect of carbohydrate substrate on fermentation by kefir yeast supported on delignified cellulosic materials

View Article: Journal of Agricultural and Food Chemistry. 49 (2). February, 2001. 658-663
CD Volume:367
Print Article: Pages: 658-663

Author(s):Athanasiadis I Boskou D Kanellaki M Koutinas A A
Author Affiliation:Food Biotechnology Group, Department of Chemistry, University of Patras, Patras: A.A.Koutinas@upatras.gr

Language:English
Language of Summary:English (EN)

Abstract:The suitability of delignified cellulosic (DC) material supported kefir yeast to ferment raw materials that contain various single carbohydrates, for the production of potable alcohol and alcoholic drinks, is examined in this investigation. Results are reported of fermentations carried out with sucrose, fructose, and glucose in synthetic media. Repeated batch fermentations at various initial sugar concentrations of sucrose, fructose, and glucose were performed at 30 degreeC in the presence of the aforementioned biocatalyst. The results clearly show feasible yields in the range of 0.38-0.41 g/g, alcohol concentrations of 7.6-8.2% v/v, fermentation time of 90-115 h, and conversion of 92-96%. DC material supported kefir fermented 11-fold more rapidly than free cells and 9-fold more rapidly in comparison to kissiris supported kefir. The main volatile byproducts such as amyl alcohols (mixture of 2-methyl-1-butanol and 3-methyl-1-butanol), ethanal, and ethyl acetate were formed in all sugar fermentation products. The formation of 65-110 ppm of ethyl acetate is as high and even higher than that obtained with traditional wine yeasts. The increase of the initial concentration of sugar in the fermentation media resulted in an increase in contents of volatiles. The fine aroma that was obtained in the product of fructose could be attributed to the high percentage of ethyl acetate on total volatiles. The efficiency of DC material supported kefir was the same for the fermentations of individual sugars or a mixture of fructose, sucrose,

and glucose. When whey with raisin extracts was fermented, lower yields were obtained but the aroma of the product was even better
Descriptors:kefir: beverage; wine: alcoholic beverage. Bioprocess Engineering; Foods. 2-methyl-1-butanol; 3-methyl-1-butanol; delignified cellulosic materials; ethanal; ethyl acetate; fructose; glucose; sucrose
Organism Descriptors:yeast (Fungi): fermentation agent
Supplemental Descriptors:Fungi: Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Bioprocess Engineering; Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

226. Title:Combined effect of ascorbic acid and gamma irradiation on microbial and sensorial characteristics of beef patties during refrigerated storage
View Article: Journal of Agricultural and Food Chemistry. 49 (2). February, 2001. 919-925
CD Volume:367
Print Article: Pages: 919-925
Author(s):Giroux M Ouattara B Yefsah R Smoragiewicz W Saucier L Lacroix M
Author Affiliation:Canadian Irradiation Center, Research Center in Microbiology and Biotechnology, INRS - Institut Armand-Frappier, 531 Boulevard des Prairies, Laval, Quebec, H7V 1B7: monique.lacroix@inrs- iaf.uquebec.ca
Language:English
Language of Summary:English (EN)
Abstract:The present study was undertaken to evaluate the effect of ascorbic acid concentrations (0.03 to 0.5%) and irradiation doses (0.5 to 4 kGy) on microbial growth, color coordinates (L*, a*, and b*), and sensory characteristics (taste and odor) of beef patties during storage at 4 +- 1 degreeC. Ascorbic acid was also compared to citric acid at a similar pH value in order to differentiate the effects of ascorbic acid from those of pH reduction. Results showed significant reduction (p ltoreq 0.05) of aerobic plate counts (APCs) and total coliforms, and a significant interaction (p ltoreq 0.05) between ascorbic acid and irradiation dose was observed. The irradiation treatment had detrimental effects on redness, yellowness, and hue angle values of meat. However, incorporation of ascorbic acid into the meat before irradiation resulted in significant (p ltoreq 0.05) stabilization of color parameters. The color improvement obtained with ascorbic acid was not related to the pH reduction. Also, no significant detrimental effect on taste or odor was found in irradiated samples containing ascorbic acid
Descriptors:aerobic plate counts; beef patties: color, meat product, microbial characteristics, sensorial characteristics. Foods. ascorbic acid: food preservative
Organism Descriptors:coliform (Enterobacteriaceae)
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

227. Title:Aging of whey protein films and the effect on mechanical and barrier properties

View Article: Journal of Agricultural and Food Chemistry. 49 (2). February, 2001. 989-995
CD Volume:367
Print Article: Pages: 989-995
Author(s):Anker Martin Stading Mats Hermansson Anne Marie
Author Affiliation:SIK-The Swedish Institute for Food and Biotechnology, SE-402 29, Goteborg: mats.stading@sik.se
Language:English
Language of Summary:English (EN)
Abstract:This work focuses on the aging of whey protein isolate (WPI) films plasticized with glycerol (G) and sorbitol (S). The films were cast from heated aqueous solutions at pH 7 and dried at 23 degreeC and 50% relative humidity (RH) for 16 h. They were stored in a climate room (23 degreeC, 50% RH) for 120 days, and the film properties were measured at regular intervals. The moisture content (MC) of the WPI/G films decreased from 22% (2 days) to 15% (45 days) and was thereafter constant at 15% (up to 120 days). This affected the mechanical properties and caused an increased stress at break (from 2.7 to 8.3 MPa), a decreased strain at break (from 33 to 4%), and an increased glass transition temperature (Tg) (from -56 to -45 degreeC). The barrier properties were, however, unaffected, with constant water vapor permeability and a uniform film thickness. The MC of the WPI/S films was constant at apprx9%, which gave no change in film properties
Descriptors:moisture content; whey protein isolate films: aging, barrier properties, food packaging, mechanical properties. Foods. glycerol: plasticizer; sorbitol: plasticizer; whey protein isolate
Subject Codes:Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

228. Title:Use of methanolysis for the determination of total ellagic and gallic acid contents of wood and food products
View Article: Journal of Agricultural and Food Chemistry. 49 (3). March, 2001. 1165-1168
CD Volume:367
Print Article: Pages: 1165-1168
Author(s):Lei Zhentian Jervis Judith Helm Richard F
Author Affiliation:Department of Wood Science and Forest Products, Fralin Biotechnology Center, Virginia Polytechnic Institute and State University, Blacksburg, VA, 24061-0346: helmrf@vt.edu
Language:English
Language of Summary:English (EN)
Abstract:Anhydrous methanolic HCl has been found to be an excellent reagent for releasing ellagic acid and gallic acid (as methyl gallate) from biomass substrates. Optimization of both the reaction conditions and the gradient HPLC analysis has led to the development of a new protocol. The method provides ellagic acid yields significantly higher than those obtained previously, indicating total ellagic acid contents of several substrates have previously been underestimated
Descriptors:fire products; wood products. Biochemistry and Molecular Biophysics; Methods and Techniques. anhydrous methanolic hydrochloric acid; ellagic acid; gallic acid
Subject Codes:Biochemistry and Molecular Biophysics; Methods and Techniques
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

229. Title:Biotechnology and the journal of agricultural and food chemistry
View Article: Journal of Agricultural and Food Chemistry. 49 (4). April, 2001. 1667-1668
CD Volume:367
Print Article: Pages: 1667-1668
Author(s):Seiber James N
Language:English
Language of Summary:English (EN)
Abstract:No Abstract available
Descriptors:Journal of Agricultural and Food Chemistry; agricultural biotechnology; food biotechnology; genetic engineering. Foods
Subject Codes:Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

230. Title:alpha -Glucosidase inhibitory action of natural acylated anthocyanins. 1. Survey of natural pigments with potent inhibitory activity
View Article: Journal of Agricultural and Food Chemistry. 2001. 49 (4). 1948-1951
CD Volume:367
Print Article: Pages: 1948-1951
Author(s):Matsui T Ueda T Oki T Sugita K Terahara N Matsumoto K
Author Affiliation:Department of Bioscience and Biotechnology, Division of Bioresource and Bioenvironmental Sciences, Faculty of Agriculture, Graduate School, Kyushu University, 6-10-1 Hakozaki, Higashi-ku, Fukuoka 812-8581, Japan
Language:English
Abstract:alpha -Glucosidase (AGH) inhibitory study by natural anthocyanin extracts was done. As the result of a free AGH assay system, 12 anthocyanin extracts were found to have a potent AGH inhibitory activity; in particular, Pharbitis nil (SOA) extract showed the strongest maltase inhibitory activity, with an IC50 value of 0.35 mg/mL, as great as that of Ipomoea batatas (YGM) extract (IC50 = 0.36 mg/mL). Interestingly, neither extract inhibited the sucrase activity at all. For the immobilized assay system, which may reflect the pharmacokinetics of AGH at the small intestine, SOA and YGM extracts gave more potent maltase inhibitory activities than those of the free AGH assay, with IC50 values of 0.17 and 0.26 mg/mL, respectively. Both extracts also inhibited alpha -amylase action, indicating that anthocyanins would have a potential function to suppress the increase in postprandial glucose level from starch
Descriptors:alpha-amylase. alpha-glucosidase. anthocyanins. glucosidase-inhibitors. pigments. sweet-potatoes
Identifiers:sucrase
Organism Descriptors:Ipomoea-batatas. Pharbitis-nil
Supplemental Descriptors:Ipomoea. Convolvulaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Pharbitis
Subject Codes:FF005. FF060
Supplementary Info:25 ref
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

231. Title:alpha -Glucosidase inhibitory action of natural acylated anthocyanins. 2. alpha -Glucosidase inhibition by isolated acylated anthocyanins
View Article: Journal of Agricultural and Food Chemistry. 2001. 49 (4). 1952-1956
CD Volume:367
Print Article: Pages: 1952-1956
Author(s):Matsui T Ueda T Oki T Sugita K Terahara N Matsumoto K
Author Affiliation:Department of Bioscience and Biotechnology, Division of Bioresource and Bioenvironmental Sciences, Faculty of Agriculture, Graduate School, Kyushu University, 6-10-1 Hakozaki, Higashi-ku, Fukuoka 812-8581, Japan
Language:English
Abstract:Four diacylated pelargonidin (Pg: SOA-4 and SOA-6), cyanidin (Cy: YGM-3), and peonidin (Pn: YGM-6) 3-sophoroside-5-glucosides isolated from the red flowers of the morning glory, Pharbitis nil cv. Scarlett O'Hara (SOA), and the storage roots of purple sweet potato, Ipomoea batatas cv. Ayamurasaki (YGM), were subjected to an alpha -glucosidase (AGH) inhibitory assay, in which the assay was performed with the immobilized AGH (iAGH) system to mimic the membrane-bound-AGH at the small intestine. As a result, the acylated anthocyanins showed strong maltase inhibitory activities with IC50 values of <200 micro M, whereas no sucrase inhibition was observed. Of these, SOA-4 [Pg 3-O-(2-O-(6-O-(E-3-O-(beta -D-glucopyranosyl)caffeyl)- beta -D-glucopyranosyl)-6-O-E-caffeyl- beta -D-glucopyranoside)-5-O- beta -D-glucopyranoside] possessed the most potent maltase inhibitory activity (IC50 = 60 micro M). As a result of a marked reduction of iAGH inhibitory activity by deacylating the anthocyanins, that is, Pg (or Cy or Pn) sophoroside-5-glucoside, acylation of anthocyanin with caffeic (Caf) or ferulic (Fer) acid was found to be important in the expression of iAGH (maltase) inhibition. In addition, the result that Pg-based anthocyanins showed the most potent maltase inhibition, with an IC50 value of 4.6 mM, and the effect being in the descending order of potency of Pg > Pn = Cy strongly suggested that no replacement at the 3'(5')-position of the aglycon B-ring may be essential for inhibiting iAGH action
Descriptors:alpha-glucosidase. anthocyanins. cyanidin. flowers. inhibition. pelargonidin. roots. sweet-potatoes
Identifiers:peonidin. sucrase
Organism Descriptors:Ipomoea-batatas. Pharbitis-nil
Supplemental Descriptors:Ipomoea. Convolvulaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. Pharbitis
Subject Codes:FF003. FF005. FF060
Supplementary Info:17 ref
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry
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232. Title:Effect of preslaughter feed withdrawal period on longissimus tenderness and the expression of calpains in the ovine
View Article: Journal of Agricultural and Food Chemistry. 49 (4). April, 2001. 1990-1998
CD Volume:367
Print Article: Pages: 1990-1998
Author(s):Ilian Mohammad A Morton James D Bekhit Alaa El Din Roberts Noelle Palmer Barry Sorimachi Hiroyuki Bickerstaffe Roy
Author Affiliation:Molecular Biotechnology Group, Animal and Food Sciences Division, Lincoln University, Canterbury: alayanm@whio.lincoln.ac.nz

Language:English
Language of Summary:English (EN)
Abstract:The objective was to study the role of calpains in meat tenderness. Lambs were fasted for various periods of time to generate differences in meat tenderness and to determine in tandem the expression of calpain 1, calpain 2, calpain 3, and calpastatin. The assumption has been that increased calpain expression associated with an increase in tenderness indicates a role for calpain in the tenderization process and vice versa. Fasting lambs for 1 day caused a significant improvement in longissimus (LD) tenderness compared to the control. Correlations between the tenderness of the LD and the expression of the calpains and calpastatin were significant for calpains 1 and 3 but not for calpain 2 or calpastatin. Consequently, this study supports a role for calpains 1 and 3, but not for calpain 2, in the tenderization of the LD from fasted lambs during post-mortem aging
Descriptors:longissimus meat: meat, tenderness; preslaughter feed withdrawal. Animal Husbandry (Agriculture); Foods. calpain 1; calpain 2; calpain 3; calpastatin
Organism Descriptors:ovine (Bovidae): lamb
Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Animal Husbandry (Agriculture); Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

233. Title:Thermal inactivation kinetics and application of phospho- and galactolipid-degrading enzymes for evaluation of quality changes in frozen vegetables
View Article: Journal of Agricultural and Food Chemistry. 49 (5). May, 2001. 2241- 2248
CD Volume:367
Print Article: Pages: 2241-2248
Author(s):Kim Myo Jeong Oh Jae Myung Cheon Sang Hee Cheong Tae Kyou Lee Sang Hwa Choi Eun Ok Lee Hyeon Gyu Park Cheon Seok Park Kwan Hwa
Author Affiliation:Department of Food Science and Technology and Research Center for New Bio-Materials in Agriculture, School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744: parkkh@plaza.snu.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:Lipid-acyl hydrolases (LAHases) play significant roles in lipid degradation during the storage of vegetables. In particular, spinach contains a large portion of galactolipids (59.5%) and phospholipids (22.4%) among its fat-soluble components, which are used as substrates for LAHases. Thermal inactivation of various LAHases, including phospholipases A, C, and D, phosphatase, and galactolipase, from spinach and carrot was investigated to optimize the blanching process prior to the frozen storage of vegetables. Thermostability of phospholipase C or galactolipase was greatest among the LAHases from both spinach and carrot. Galactolipase from spinach exhibited a D value of 3.39 X 102 s at 80 degreeC and a z value of 8.21 degreeC, whereas phospholipase C from spinach showed D80 of 1.72 X 102 s with a z value of 9.26 degreeC. In the case of LAHases from carrot, the D65 and z values of galactolipase were 6.66 X 102 s and 8.69 degreeC, respectively, whereas phospholipase C displayed D85 of 3.12 X 102 s and a z value of 15.8 degreeC. Highly active and thermostable

galactolipase and phospholipase C in spinach and carrot made it possible for them to be used as indicator enzymes for the determination of quality deterioration of the stored vegetables
Descriptors:carrot: quality, vegetable; spinach: quality, vegetable. Enzymology (Biochemistry and Molecular Biophysics); Foods. galactolipase: thermal inactivation kinetics; lipid-acyl hydrolases: thermal inactivation kinetics; phosphatase: thermal inactivation kinetics; phospholipase A: thermal inactivation kinetics; phospholipase C: thermal inactivation kinetics; phospholipase D: thermal inactivation kinetics
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

234. Title:Effects of pretreatments on the diffusion kinetics and some quality parameters of osmotically dehydrated apple slices
View Article: Journal of Agricultural and Food Chemistry. 49 (6). June, 2001. 2804-2811
CD Volume:367
Print Article: Pages: 2804-2811
Author(s):Taiwo Kehinde A Angersbach Alexander Ade Omowaye Beatrice I O Knorr Dietrich
Author Affiliation:Department of Food Biotechnology and Process Engineering, Berlin University of Technology, Koenigin-Luise Strasse 22, D- 14195, Berlin: foodtech@mailszrz.zrz.tu-berlin.de
Language:English
Language of Summary:English (EN)
Abstract:This study compared mass transfer during osmotic dehydration (OD) and some quality indices of untreated apple slices to those of apple slices pretreated by either blanching, freezing, or applying high-intensity electric field pulses (HELP) or high pressure (HP). HP, HELP, and blanching increased water loss. Untreated and HELP- treated samples had comparable solids gains, which were lower ($P < 0.05$) than in the other samples. Apple slices turned brown after pretreatment but the L values of these samples increased with OD. The breaking force of dried samples increased with OD time, and pretreated samples had firmer dried texture than the untreated. Vitamin C content decreased with OD time, but HP- and HELP-treated apples had better retention of vitamin C
Descriptors:apple slices: fruit, quality. Foods. vitamin C: retention
Subject Codes:Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

235. Title:His-His-Leu, an angiotensin I converting enzyme inhibitory peptide derived from Korean soybean paste, exerts antihypertensive activity in vivo
View Article: Journal of Agricultural and Food Chemistry. 49 (6). June, 2001. 3004-3009
CD Volume:367
Print Article: Pages: 3004-3009
Author(s):Shin Zae Ik Yu Rina Park Soo Ah Chung Dae Kyun Ahn Chang Won Nam Hee Sop Kim Kil Soo Lee Hyong Joo

Author Affiliation:Department of Food Science and Technology, School of Agricultural Biotechnology, Seoul National University, Suwon, 441-744: leehyjo@snu.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:It has been reported that soybean peptide fractions isolated from Korean fermented soybean paste exert angiotensin I converting enzyme (ACE) inhibitory activity in vitro. In this study, further purification and identification of the most active fraction inhibiting ACE activity were performed, and its antihypertensive activity in vivo was confirmed. Subsequently, a novel ACE inhibitory peptide was isolated by preparative HPLC. The amino acid sequence of the isolated peptide was identified as His-His-Leu (HHL) by Edman degradation. The IC50 value of the HHL for ACE activity was 2.2 mug/mL in vitro. Moreover, the synthetic tripeptide HHL (spHHL) resulted in a significant decrease of ACE activity in the aorta and led to lowered systolic blood pressure (SBP) in spontaneously hypertensive (SH) rats compared to control. Triple injections of spHHL, 5 mg/kg of body weight/injection resulted in a significant decrease of SBP by 61 mmHg ($p < 0.01$) after the third injection. These results demonstrated that the ACE inhibitory peptide HHL derived from Korean fermented soybean paste exerted antihypertensive activity in vivo
Descriptors:Korean fermented soybean paste: vegetable product; systolic blood pressure. Foods; Cardiovascular System (Transport and Circulation). hypertension: vascular disease. angiotensin I converting enzyme [EC 3.4.15.1]; histidyl-histidyl- leucine: angiotensin I converting enzyme inhibitory peptide, antihypertensive activity
Organism Descriptors:rat (Muridae): animal model, spontaneously hypertensive. aorta: circulatory system
Supplemental Descriptors:Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia. Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
Subject Codes:Foods; Cardiovascular System (Transport and Circulation)
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

236. Title:Alpha-tocopherol content in 62 edible tropical plants
View Article: Journal of Agricultural and Food Chemistry. 49 (6). June, 2001. 3101-3105
CD Volume:367
Print Article: Pages: 3101-3105
Author(s):Ching Ling Soon Mohamed Suhaila
Author Affiliation:Faculty of Food Science and Biotechnology, Universiti Putra Malaysia, 43400, Serdang, Selangor
Language:English
Language of Summary:English (EN)
Abstract:Vitamin E was determined by the high-performance liquid chromatography (HPLC) method. All the plants tested showed differences in their alpha-tocopherol content and the differences were significant ($p < 0.05$). The highest alpha-tocopherol content was in Sauropus androgynus leaves (426.8 mg/kg edible portion), followed by Citrus hystrix leaves (398.3 mg/kg), Calamus scipronum (193.8 mg/kg), starfruit leaves Averrhoa belimbi (168.3 mg/kg), red pepper Capsicum annum (155.4 mg/kg), local celery Apium graveolens (136.4 mg/kg), sweet potato shoots Ipomoea batatas (130.1 mg/kg), Pandanus odorus (131.5 mg/kg), Oenanthe javanica (146.8 mg/kg), black tea Camelia chinensis (183.3 mg/kg), papaya Carica papaya shoots (111.3 mg/kg), wolfberry leaves

Lycium chinense (94.4 mg/kg), bird chili Capsicum frutescens leaves (95.4 mg/kg), drumstick Moringa oleifera leaves (90.0 mg/kg), green chili Capsicum annum (87 mg/kg), Allium fistulosum leaves (74.6 mg/kg), and bell pepper Capsicum annum (71.0 mg/kg). alpha-Tocopherol was not detected in Brassica oleracea, Phaeomeria speciosa, Pachyrrhizus speciosa, Pleurotus sajor-caju, and Solanum melongena
Descriptors:edible plants: vegetable. Foods. alpha-tocopherol
Organism Descriptors:Allium fistulosum (Liliaceae); Apium graveolens [celery] (Umbelliferae); Averrhoa belimbi [starfruit] (Oxalidaceae); Calamus scipronum (Palmae); Camelia chinensis [Camellia chinesis, black tea] (Theaceae); Capsicum annum [red pepper] (Solanaceae); Capsicum frutescens [bird chili] (Solanaceae); Carica papaya [papaya] (Caricaceae); Citrus hystrix (Rutaceae); Ipomoea batatas [sweet potato] (Convolvulaceae); Lycium chinense [wolfberry] (Solanaceae); Moringa oleifera [drumstick] (Moringaceae); Oenanthe javanica (Umbelliferae); Pandanus odorus (Pandanaceae); Sauropus androgynus (Euphorbiaceae)
Supplemental Descriptors:Caricaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Convolvulaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Euphorbiaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Liliaceae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Moringaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Oxalidaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Palmae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Pandanaceae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Rutaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Solanaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Theaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Umbelliferae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

237. Title:Flavonoid (myricetin, quercetin, kaempferol, luteolin, and apigenin) content of edible tropical plants
View Article: Journal of Agricultural and Food Chemistry. 49 (6). June, 2001. 3106-3112
CD Volume:367
Print Article: Pages: 3106-3112
Author(s):Miean Koo Hui Mohamed Suhaila
Author Affiliation:Faculty of Food Science and Biotechnology, University Putra Malaysia, 43400, Serdang, Selangor
Language:English
Language of Summary:English (EN)
Abstract:Studies were conducted on the flavonoids (myricetin, quercetin, kaempferol, luteolin, and apigenin) contents of 62 edible tropical plants. The highest total flavonoids content was in onion leaves (1497.5 mg/kg quercetin, 391.0 mg/kg luteolin, and 832.0 mg/kg kaempferol), followed by Semambu leaves (2041.0 mg/kg), bird chili (1663.0 mg/kg), black tea (1491.0 mg/kg), papaya shoots (1264.0 mg/kg), and guava (1128.5 mg/kg). The major flavonoid in these plant extracts is quercetin, followed by myricetin and kaempferol. Luteolin could be detected only in broccoli (74.5 mg/kg dry weight), green chili (33.0 mg/kg), bird chili (1035.0 mg/kg), onion leaves (391.0 mg/kg), belimbi fruit (202.0 mg/kg), belimbi leaves (464.5 mg/kg),

French bean (11.0 mg/kg), carrot (37.5 mg/kg), white radish (9.0 mg/kg), local celery (80.5 mg/kg), limau purut leaves (30.5 mg/kg), and dried asam gelugur (107.5 mg/kg). Apigenin was found only in Chinese cabbage (187.0 mg/kg), bell pepper (272.0 mg/kg), garlic (217.0 mg/kg), belimbi fruit (458.0 mg/kg), French peas (176.0 mg/kg), snake gourd (42.4 mg/kg), guava (579.0 mg/kg), wolfberry leaves (547.0 mg/kg), local celery (338.5 mg/kg), daun turi (39.5 mg/kg), and kadok (34.5 mg/kg). In vegetables, quercetin glycosides predominate, but glycosides of kaempferol, luteolin, and apigenin are also present. Fruits contain almost exclusively quercetin glycosides, whereas kaempferol and myricetin glycosides are found only in trace quantities

Descriptors:edible tropical plants: vegetable; fruits: fruit; vegetables: vegetable. Foods. apigenin; flavonoids; kaempferol; luteolin; myricetin; quercetin

Subject Codes:Foods

ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

238. Title:Enzyme-assisted extraction of antioxidative phenols from black currant juice press residues (Ribes nigrum)

View Article: Journal of Agricultural and Food Chemistry. 49 (7). July, 2001. 3169-3177
CD Volume:369
Print Article: Pages: 3169-3177

Author(s):Landbo Anne Katrine Meyer Anne S
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Language:English
Language of Summary:English (EN)

Abstract:Enzymatic release of phenolic compounds from pomace remaining from black currant (Ribes nigrum) juice production was examined. Treatment with each of the commercial pectinolytic enzyme preparations Grindamyl pectinase, Macer8 FJ, Macer8 R, and Pectinex BE, as well as treatment with Novozym 89 protease, significantly increased plant cell wall breakdown of the pomace. Each of the tested enzyme preparations except Grindamyl pectinase also significantly enhanced the amount of phenols extracted from the pomace. Macer8 FJ and Macer8 R decreased the extraction yields of anthocyanins, whereas Pectinex BE and Novozym 89 protease showed no effect. A decrease in pomace particle sizes from 500-1000 mum to <125 mum increased the phenol yields 1.6-5 times. Black currant pomace devoid of seeds gave significantly higher yields of phenols than pomace with seeds and seedless wine pomace. Four selected black currant pomace extracts all exerted a pronounced antioxidant activity against human LDL oxidation in vitro when tested at equimolar phenol concentrations of 7.5-10 muM

Descriptors:black currant juice: beverage, preparation, press residue chemical analysis. Biochemistry and Molecular Biophysics; Foods; Nutrition. LDL [low density lipoprotein]: oxidation inhibition analysis; anthocyanins: analysis; industrial enzyme preparations: uses; phenols: antioxidative properties, extraction, molecular analysis

Organism Descriptors:Ribes nigrum [black currant] (Saxifragaceae); human (Hominidae)

Supplemental Descriptors:Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Saxifragaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Animals; Chordates; Dicots; Humans; Mammals; Plants; Primates; Spermatophytes; Vascular Plants; Vertebrates

Subject Codes:Biochemistry and Molecular Biophysics; Foods; Nutrition
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

239. Title:Effects of dietary supplementation with Yucca schidigera Roezl ex Ortgies and its saponin and non-saponin fractions on rat metabolism
View Article: Journal of Agricultural and Food Chemistry. 49 (7). July, 2001. 3408-3413
CD Volume:369
Print Article: Pages: 3408-3413
Author(s):Duffy Cepta F Killeen Gerry F Connolly Cathal D Power Ronan F
Author Affiliation:Alltech Biotechnology Center, Sarney, Summerhill Road, Dunboyne, Co. Meath: cduffy@alltech-bio.com
Language:English
Language of Summary:English (EN)
Abstract:Yucca schidigera Roezl ex Ortgies, family Lillaceae, was fractionated with butan-1-ol to yield a butanol extractable fraction (BE; saponin fraction) and a non-butanol fraction (NBE; non-saponin fraction). Four groups of eight male rats were allowed ad libitum access to diets supplemented with water (control) or 200 mg kg-1 total Y. schidigera (TOT) or 200 mg kg-1 of each of the fractions (NBE or BE). The effects of dietary supplementation with the fractions and their interactions in TOT were analyzed according to the factorial experimental design by two-way analysis of variance. All three supplementation groups displayed significantly reduced serum urea levels ($P<0.05$). The TOT and NBE fractions were found to significantly increase serum insulin levels ($P<0.01$) in the absence of any fluctuations in serum glucose levels. Urea cycle enzyme activities, namely, arginase (EC 3.5.3.1) and argininosuccinate lyase (EC 4.3.2.1), were significantly decreased ($P<0.05$) in vivo, although no effect was observed in vitro. Both fractions displayed effects, indicating that the active constituents are present in both fractions
Descriptors:animal feeding studies; animal feedstuffs: supplementation; diets. Biochemistry and Molecular Biophysics; Metabolism; Nutrition. enzymes; non-saponin fractions: analysis; saponin fractions: analysis
Organism Descriptors:Yucca schidigera (Agavaceae); rat (Muridae). blood serum: biochemical analysis, blood and lymphatics
Supplemental Descriptors:Agavaceae: Monocotyledones, Angiospermae, Spermatophyta, Plantae; Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia. Angiosperms; Animals; Chordates; Mammals; Monocots; Nonhuman Mammals; Nonhuman Vertebrates; Plants; Rodents; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Biochemistry and Molecular Biophysics; Metabolism; Nutrition
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

240. Title:Electron spin resonance studies of free radicals in gamma- irradiated soybean paste
View Article: Journal of Agricultural and Food Chemistry. 49 (7). July, 2001. 3457-3462
CD Volume:369
Print Article: Pages: 3457-3462
Author(s):Lee Eun Joo Volkov Vitaly I Lee Cherl Ho
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Language:English
Language of Summary:English (EN)
Abstract:Free radicals in gamma-irradiated soybean paste were investigated by electron spin resonance (ESR) spectroscopy to determine the effect of temperature (77-296 K) and moisture content (1-54%) of samples irradiated at high dose (1-40 kGy). The samples were kept in liquid nitrogen (77 K) during irradiation and subsequent ESR measurements. The spectra shown at 77 K consisted of the hydrogen atom lines at low and high field and complicated symmetric spectrum. By increasing the microwave power, the line shape of ESR spectra altered, which indicated the detection of different paramagnetic centers at different microwave powers. In saturation curves, it was possible to select four types of spectra components which were different in their relaxation times. By the different irradiation doses, the change in free radical concentration showed a curvilinearaly increasing relationship with irradiation dose in wet samples, whereas a proportional relationship was observed with dried samples. This might indicate that the indirect process of free radical formation was involved with the existence of free water radicals in the wet samples
Descriptors:food chemistry; gamma-irradiation: chemical effects; soybean paste: chemical analysis, irradiated, preparation, sauces and condiments. Biochemistry and Molecular Biophysics; Foods; Radiation Biology; Toxicology. free radicals: analysis, detection
Subject Codes:Biochemistry and Molecular Biophysics; Foods; Radiation Biology; Toxicology
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

241. Title:Efficiency of enzymatic and other alternative clarification and fining treatments on turbidity and haze in cherry juice
View Article: Journal of Agricultural and Food Chemistry. 49 (8). August, 2001. 3644-3650
CD Volume:369
Print Article: Pages: 3644-3650
Author(s):Meyer Anne S Koser Christian Adler Nissen Jens
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Language:English
Language of Summary:English (EN)
Abstract:Several alternative strategies were examined for improving conventional juice fining procedures for cherry juice clarification and fining in laboratory-scale experiments: Centrifugation of freshly pressed juice from 1000g to 35000g induced decreased turbidity according to a steep, negative power function. Individual and interactive effects on turbidity and haze formation in precentrifuged and uncentrifuged cherry juice of treatments with pectinase, acid protease, bromelain, gallic acid, and gelatin- silica sol were investigated in a factorial experimental design with 32 different parameter combinations. Gelatin-silica sol consistently had the best effect on juice clarity. Centrifugation of cherry juice (10000g for 15 min) prior to clarification treatment significantly improved juice clarity and diminished the rate of haze formation during cold storage of juice. Both treatment of precentrifuged cherry juice with Novozym 89L protease and co- addition of pectinase and gallic acid improved cherry juice clarity and diminished haze levels. None of the alternative treatments produced the unwieldy colloids notorious to gelatin-silica

sol treatment. The data suggest that several alternative clarification strategies deserve further consideration in large-scale cherry juice processing. Precentrifugation of juice before clarification and fining is immediately recommended
Descriptors:cherry juice: fruit juice, haze, turbidity. Foods. acid protease; bromelain; gallic acid; gelatin-silica sol; pectinase
Subject Codes:Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

242. Title:Isoflavone transformation during soybean koji preparation and subsequent miso fermentation supplemented with ethanol and NaCl
View Article: Journal of Agricultural and Food Chemistry. 49 (8). August, 2001. 3656-3660
CD Volume:369
Print Article: Pages: 3656-3660
Author(s):Chiou Robin Y Y Cheng S L
Author Affiliation:Graduate Institute of Biotechnology, National Chiayi University, Chiayi: rychiou@mail.ncyu.edu.tw
Language:English
Language of Summary:English (EN)
Abstract:Soybeans were soaked with water for 4 h, steam-cooked, inoculated with the conidia of Aspergillus oryzae, and incubated for 3 days for koji preparation. The koji was then mixed with water-soaked and steam-cooked soybeans (1:2, w/w), ground into paste, and supplemented with 15% ethanol and 12.5% NaCl or 3% ethanol and 6% NaCl for miso fermentation at 30 degreeC. Daidzin, genistin, daidzein, and genistein contents were extracted from the lyophilized and pulverized soybean powder or from the miso homogenate by a developed one-tube procedure and analyzed with an HPLC. After water soaking, daidzein and genistein contents increased markedly, whereas daidzin and genistin contents decreased. Further increases of daidzein and genistein contents and decreases of daidzin and genistin contents were observed after koji mold growth. During fermentation, fungal and lactic acid bacterial (LAB) growth in the miso products was inhibited, whereas soluble protein contents increased much more rapidly in the low-salt miso products supplemented with 3% ethanol and 6% NaCl than the other products. When the 4- and 8-week-fermented miso products were cooked with tofu for sensory evaluation, flavor ratings of the low- salt products were higher than that of a popular commercial product. In both products, the most daidzins and genistins were hydrolyzed after 4 weeks of fermentation. The hydrolytic enzymes contributing to isoflavone transformation originated from soybeans after water soaking and from koji with mold growth. It was of merit that the low-salt fermented products were fairly acceptable in flavor rating and rich in daidzein and genistein contents after 4 weeks of fermentation
Descriptors:miso: flavor, vegetable product; soybean koji: vegetable product; tofu: vegetable product. Foods. daidzein; daidzin; ethanol; genistein; genistin; hydrolytic enzymes; isoflavone: transformation; sodium chloride; soluble protein
Organism Descriptors:Aspergillus oryzae (Fungi Imperfecti or Deuteromycetes): fermentation agent
Supplemental Descriptors:Fungi Imperfecti or Deuteromycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Foods
ISSN:0021-8561
Year:2001

Journal Title:Journal of Agricultural and Food Chemistry

243. Title:Aroma compounds in the production of liquid beet sugar
View Article: Journal of Agricultural and Food Chemistry. 49 (8). August, 2001. 3875-3880
CD Volume:369
Print Article: Pages: 3875-3880
Author(s):Pihlsgard Per Leufven Anders Lingnert Hans
Author Affiliation:Swedish Institute for Food and Biotechnology (SIK), SE-402 29, Goteborg: anders.leufven@sik.se
Language:English
Language of Summary:English (EN)
Abstract:Samples of in-process liquid beet sugar were collected from three different parts of a beet sugar factory and a refinery. The samples were analyzed with respect to aroma compounds by means of both liquid-liquid extraction and gas-phase (headspace) extraction followed by gas chromatography-olfactometry (GC-O) and GC-mass spectrometry (GC-MS). The aromas of the eluted compounds were evaluated qualitatively and quantitatively for the different samples. In general, earthy and sour aromas were often present in the raw juice sample, whereas caramel aromas were mainly present in the samples taken further downstream in the process. For fruity, floral, and solvent-like aromas, different parallel trends were noted. Some aromas were present only at the beginning of the process, whereas others developed toward the end of the process
Descriptors:liquid beet sugar: aroma, sugar product. Foods; Methods and Techniques. caramel aroma compounds; earthy aroma compounds; floral aroma compounds; fruity aroma compounds; solvent-like aroma compounds; sour aroma compounds
Subject Codes:Foods; Methods and Techniques
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

244. Title:Protein-enriched spaghetti fortified with corn gluten meal
View Article: Journal of Agricultural and Food Chemistry. 49 (8). August, 2001. 3906-3910
CD Volume:369
Print Article: Pages: 3906-3910
Author(s):Wu Y Victor Hareland Gary A Warner Kathleen
Author Affiliation:Fermentation Biotechnology Research Unit, National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL, 61604: wuyv@mail.ncaur.usda.gov
Language:English
Language of Summary:English (EN)
Abstract:Spaghetti was prepared by replacing either 5 or 10% semolina or farina with corn gluten meal, a high-protein fraction from the wet milling of corn, to increase the protein content of pasta. Spaghetti fortified with corn gluten meal had a similar cooked weight and cooking loss but was less firm compared with the control. The overall flavor quality score of the spaghetti decreased with the increasing additions of either water-washed, water/ethanol-washed or regular corn gluten meal because of the higher intensity of the fermented flavor. Spaghetti with acceptable quality can be prepared with 5% water/ethanol-washed corn gluten meal, thereby improving its nutritional value while providing an additional market for corn gluten meal

Descriptors:corn gluten meal: grain product, pasta ingredient; farina: grain product, pasta ingredient; semolina: grain product, pasta ingredient; spaghetti: flavor, fortification, pasta, protein- enriched, quality. Foods
Subject Codes:Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

245. Title:Pressure-induced denaturation of monomer beta-lactoglobulin is partially irreversible: Comparison of monomer form (highly acidic pH) with dimer form (neutral pH)
View Article: Journal of Agricultural and Food Chemistry. 49 (8). August, 2001. 4052-4059
CD Volume:369
Print Article: Pages: 4052-4059
Author(s):Ikeuchi Y Nakagawa K Endo T Suzuki A Hayashi T Ito T
Author Affiliation:Laboratory of Chemistry and Technology of Animal Products, Department of Bioscience and Biotechnology, Graduate School of Agriculture, Kyushu University, Fukuoka, 812-8581: ikeuchiy@agr.kyushu-u.ac.jp
Language:English
Language of Summary:English (EN)
Abstract:This study was conducted to assess the effect of high hydrostatic pressure on monomer beta-lactoglobulin (BLg) at acid pH by fluorescence spectroscopy under pressure and by circular dichroism (CD) and 1H NMR spectroscopies after release of pressure. The intrinsic (tryptophan) fluorescence measurement and the study of 8-anilinonaphthalene-1-sulfonate (ANS) binding to BLg indicated that at pH 2.0 the recovery of center of spectral mass or ANS fluorescence was almost complete upon pressure release. No difference in 1H NMR spectra was observed between pressurized and unpressurized BLg. In addition, NMR detection of the H/D exchange of aromatic protein indicated that the conformation of the vicinity of tryptophan residues could be refolded almost completely after release of pressure. These results seemingly confirm that the pressure-induced denaturation of BLg at pH 2.0 is reversible. However, cis-parinaric acid binding ability of pressurized BLg was largely lost, although its retinol binding ability was the same as its unpressurized one. Furthermore, CD spectra of the far-UV region and 2D NMR spectra evidently revealed the difference in the conformation of the molecule between unpressurized and pressurized BLg. These results are interpreted as an existence of partially fragile structure in the BLg molecule by high pressure
Descriptors:pH effect. Biochemistry and Molecular Biophysics; Foods. 8-anilinonaphthalene-1-sulfonate; beta-lactoglobulin: dimer form, food additive, monomer form, pressure-induced denaturation, tryptophan residues; cis-parinaric acid; retinol
Subject Codes:Biochemistry and Molecular Biophysics; Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

246. Title:Correlation between the chemical and genetic relationships among commercial thyme cultivars
View Article: Journal of Agricultural and Food Chemistry. 49 (9). September, 2001. 4220-4223
CD Volume:367

Print Article: Pages: 4220-4223
Author(s):Echeverrigaray S Agostini G Atti Serfini L Paroul N Pauletti G F dos Santos A C Atti
Author Affiliation:Institute of Biotechnology, University of Caxias do Sul, Caxias do Sul, RS: selaguna@yahoo.com
Language:English
Language of Summary:English (EN)
Abstract:The essential oil composition and genetic variability of six commercial cultivars of thyme (Thymus vulgaris L.), a Mediterranean medicinal and aromatic plant, were analyzed by GC-MS and randomly amplified polymorphic DNA (RAPD), respectively. All evaluated cultivars belong to the thymol chemotype, with differences in the concentrations of thymol, gamma-terpinene, p-cymene, and other minor components. The comparison of the oil components concentration by multivariate analysis allowed separation of the cultivars into two groups. All of the cultivars exhibited characteristic RAPD patterns that allowed their identification. On the basis of the RAPD patterns, the cultivars could be divided into two clusters, which coincides with results obtained by oil GS-MS analysis, with a correlation coefficient of -0.779
Descriptors:chemical composition; chemical relationship; cultivar chemical relationship; cultivar genetic relationship; genetic relationship; genetic variability; plant breeding. Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Genetics. essential oil: composition; gamma-terpinene; p-cymene; thymol
Organism Descriptors:Thymus vulgaris [thyme] (Labiatae): aromatic crop, cultivar-Batlle, cultivar-Blumen, cultivar-Burpee, cultivar-Isla, cultivar-SEM, cultivar-Tropical, medicinal plant
Supplemental Descriptors:Labiatae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Horticulture (Agriculture); Biochemistry and Molecular Biophysics; Genetics
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

247. Title:Identification and antioxidant activity of novel chlorogenic acid derivatives from bamboo (Phyllostachys edulis)
View Article: Journal of Agricultural and Food Chemistry. 49 (10). October, 2001. 4646-4655
CD Volume:369
Print Article: Pages: 4646-4655
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Language:English
Language of Summary:English (EN)
Abstract:One known and two novel antioxidant compounds have been isolated from bamboo (Phyllostachys edulis). The butanol-soluble extract of the bamboo leaves was found to have a significant antioxidant activity, as measured by scavenging the stable 1,1-diphenyl-2- picrylhydrazyl (DPPH) free radical and the superoxide anion radical (O2-) in the xanthine/xanthine oxidase assay system. Antioxidant activity-directed fractionation of the extract led to the isolation and characterization of three structural isomeric chlorogenic acid derivatives: 3-O-(3'-methylcaffeoyl)quinic acid (1), 5-O-caffeoyl-4- methylquinic acid (2), and 3-O-caffeoyl-1-methylquinic acid (3). Compounds 2 and 3 were isolated and characterized for the first rime from the natural

products. In the DPPH scavenging assay as well as in the iron-induced rat microsomal lipid peroxidation system, compounds 2 (IC50=8.8 and 19.2 muM) and 3 (IC50=6.9 and 14.6 muM) showed apprx2-4 times higher antioxidant activity than did chlorogenic acid (IC50=12.3 and 28.3 muM) and other related hydroxycinnamates such as caffeic acid (IC50=13.7 and 25.5 muM) and ferulic acid (IC50=36.5 and 56.9 muM). Among the three compounds, compound 1 yielded the weakest antioxidant activity, and the DPPH scavenging and lipid peroxidation inhibitory activity (IC50=16.0 and 29.8 muM) was lower than those of chlorogenic and caffeic acids. All three compounds exhibited both superoxide scavenging activities and inhibitory effects on xanthine oxidase. Their superoxide anion (O2-) scavenging activities (IC50=1, 4.3 muM; 2, 2.8 muM; and 3, 1.2 muM) were markedly stronger than those of ascorbic acid (IC50=56.0 muM), alpha-tocopherol (IC50>100 muM), and other test compounds, although their inhibition effects on xanthine oxidase may contribute to the potent scavenging activity, alpha-Tocopherol exerted a signicant inhibitory effect (65.5% of the control) on superoxide generation in 12-O-tetradecanoylphorbol-13-acetate-induced human promyelocytic leukemia HL-60 cells, and compound 3 showed moderate activity (36.0%). On the other hand, other compounds including 1, 2, chlorogenic acid, and other antioxidants were weakly active (24.8-10.1%) in the suppression of superoxide generation
Descriptors:Biochemistry and Molecular Biophysics; Foods. chlorogenic acid derivatives: antioxidant activity, identification, novel structures; superoxide; xanthine oxidase
Organism Descriptors:Phyllostachys edulis [bamboo] (Gramineae)
Supplemental Descriptors:Gramineae: Monocotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Monocots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Biochemistry and Molecular Biophysics; Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

248. Title:Sweetness and enzymatic activity of lysozyme
View Article: Journal of Agricultural and Food Chemistry. 49 (10). October, 2001. 4937-4941
CD Volume:369
Print Article: Pages: 4937-4941
Author(s):Masuda Tetsuya Ueno Yuki Kitabatake Naofumi
Author Affiliation:Division of Food Science and Biotechnology, Graduate School of Agriculture, Kyoto University, Uji, Kyoto, 611-0011: kitabata@food2.food.kyoto-u.ac.jp
Language:English
Language of Summary:English (EN)
Abstract:Hen egg lysozyme elicits a sweet taste sensation for human beings. Effects of reduction of disulfide bonds, heat treatment, and chemical modification of hen egg lysozyme on both sweetness and hydrolytic activity were investigated. Both the sweetness and enzymatic activities were lost when the intradisulfide linkage in a lysozyme molecule was reduced and S-3-(trimethylated amino) propylated. The sweetness and enzymatic activity of lysozyme were lost on heating at 95degreeC for 18 h. These facts suggest that tertiary structures of lysozyme are indispensable for eliciting a sweet taste as well as enzymatic activity. Although the modification of carboxyl residues in a lysozyme by glycine methylester or aminomethansulfonic acid resulted in the loss of enzymatic activity by blocking the catalytic residues, the sweetness was fully retained. These results indicate that the

sweetness of lysozyme was independent of its enzymatic activity. The lysozyme purified from goose egg white similarly elicited a sweet taste, although goose (g-type) lysozyme is quite different from hen egg lysozyme (c-type) on the basis of structural, immunological, and enzymatic properties. These findings indicate that a specific protein property of lysozyme is required for sweetness elicitation and that the enzymatic activity and carbohydrates produced by enzymatic reaction are not related to the sweet taste

Descriptors:Enzymology (Biochemistry and Molecular Biophysics); Foods. lysozyme: enzymatic activity, goose egg origin, hen egg origin, hydrolytic activity, protein properties, sweetness

Organism Descriptors:chicken (Galliformes): egg; goose (Anseriformes): egg

Supplemental Descriptors:Anseriformes: Aves, Vertebrata, Chordata, Animalia; Galliformes: Aves, Vertebrata, Chordata, Animalia. Animals; Birds; Chordates; Nonhuman Vertebrates; Vertebrates

Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Foods

ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

249. Title:beta-Lactoglobulin A with N-ethylmaleimide-modified sulfhydryl residue, polymerized through intermolecular disulfide bridge on heating in the presence of dithiothreitol

View Article: Journal of Agricultural and Food Chemistry. 49 (10). October, 2001. 4971-4976
CD Volume:369
Print Article: Pages: 4971-4976

Author(s):Wada Ritsuko Kitabatake Naofumi
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Language:English
Language of Summary:English (EN)

Abstract:Roles of sulfhydryl groups on thermal aggregation of beta-lactoglobulin A (betaLG A) at pH 7.5 were investigated. It is known that betaLG A modified at Cys121 with N-ethylmaleimide (NEM-betaLG A) does not form an aggregate by heating and that dithiothreitol (DTT) reduces cystine residues and induces the intermolecular sulfhydryl/disulfide interchange reaction and/or oxidation. NEM-betaLG A was heated in the presence of DTT. The molecules were linked together with an intermolecular disulfide bridge, and the polymer formed increased with increase in DTT concentration. The largest portion of polymer was formed when DTT was added at around the same molar concentration as that of NEM-betaLG A. Then, polymer formation decreased with further increase in DTT concentration. The results suggest that sulfhydryl/disulfide residues other than Cys121, generated from cysteine residues, can induce intermolecular sulfhydryl/disulfide interchange reactions to polymer and that thiol compounds, for example, added DTT, are capable of starting such reactions

Descriptors:molecular aggregation; sulfhydryl/disulfide interchange reaction. Biochemistry and Molecular Biophysics; Foods. N-ethylmaleimide-modified sulfhydryl residue: heating, intermolecular disulfide bridge, polymerization; beta- lactoglobulin; beta-lactoglobulin A; dithiothreitol

Subject Codes:Biochemistry and Molecular Biophysics; Foods

ISSN:0021-8561
Year:2001

Journal Title:Journal of Agricultural and Food Chemistry

250. Title:Acid hydrolysis of secoiridoid aglycons during storage of virgin olive oil
View Article: Journal of Agricultural and Food Chemistry. 49 (11). November, 2001. 5609-5614
CD Volume:369
Print Article: Pages: 5609-5614
Author(s):Brenes M Garcia A Garcia P Garrido A
Author Affiliation:Food Biotechnology Department, Instituto de la Grasa (CSIC), Avda. Padre Garcia Tejero 4, 41012, Sevilla; E-Mail: brenes@cica.es
Language:English
Abstract:The main change found in the phenolic composition of virgin olive oils of Arbequina, Hojiblanca, and Picual varieties during storage in darkness at 30degreeC was the hydrolysis of the secoiridoid aglycons. This reaction gave rise to an increase in the free phenolics hydroxytyrosol and tyrosol in the oil. Filtration of oil and acidity influenced the hydrolysis to a large extent. Thus, the addition of commercial oleic acid to Hojiblanca and Picual oils increased the hydrolysis rate of the secoiridoid aglycons. In contrast, the concentration of lignans 1-acetoxypinoresinol and pinoresinol remained constant during storage. It must also be stressed that the total molar concentration of the phenolic compounds analyzed in the oils changed slightly (<20% reduction) after one year of storage, which is important from a nutritional point of view. However, the transformation of the secoiridoid aglycons into free phenolics may have consequences on oil taste and antioxidant capacity
Descriptors:virgin olive oil: antioxidant activity, fats and oils, flavor, storage. Biochemistry and Molecular Biophysics; Foods. hydroxytyrosol: free phenolic; secoiridoid aglycons: acid hydrolysis; tyrosol: free phenolic
Organism Descriptors:olive (Oleaceae): cultivar-Arbequina, cultivar-Hojiblanca, cultivar- Picual
Supplemental Descriptors:Oleaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Biochemistry and Molecular Biophysics; Foods
ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

251. Title:Sotolone production by hairy root cultures of Trigonella foenum-graecum in airlift with mesh bioreactors
View Article: Journal of Agricultural and Food Chemistry. 49 (12). December, 2001. 6012-6019. http://pubs.acs.org/journals/jafcau
CD Volume:369
Print Article: Pages: 6012-6019
Author(s):Peraza Luna Fernando Rodriguez Mendiola Martha Arias Castro Carlos Bessiere Jean Marie Calva Calva Graciano
Author Affiliation:Centro de Investigacion y Graduados Agropecuarios/Instituto Tecnologico Agropecuario de Jalisco, Tlajomulco de Zuniga, JAL; E-Mail: carias56@prodigy.net.mx, gcalva@mail.cinvestav.mx
Language:English
Abstract:3-Hydroxy-4,5-dimethyl-2(5H)-furanone (sotolone) and 3-amino-4,5-dimethyl-2(5H)-furanone, the postulated precursor of sotolone, were detected in hairy root cultures of Trigonella foenum-graecum (fenugreek) by GC-MS. The hairy root cultures in both conical flasks and airlift with mesh bioreactors were achieved from hypocotyl of

seedling by infection with Agrobacterium rhizogenes. In flasks, the mathematical relationship between hairy root growth and conductivity was established and afterward used to evaluate the biomass evolution in bioreactor cultures due to the difficulty of obtaining direct biomass samples from the bioreactor. The GC-MS analyses of ethanolic extracts from hairy roots revealed the presence of two important compounds: sotolone (1.2% of the volatile fraction) and 3-amino-4,5-dimethyl-2(5H)-furanone (17% of the volatile fraction). These results point out that biotechnological production of sotolone in bioreactors is possible. Additionally, these hairy root cultures offer, for the first time, an excellent biological model to study the biosynthetic pathway of sotolone in fenugreek

Descriptors:biosynthetic pathways: analysis; biotechnology. Biochemistry and Molecular Biophysics; Bioprocess Engineering; Metabolism; Pharmacognosy (Pharmacology). sotolone: analysis, applications, production

Organism Descriptors:Trigonella foenum-graecum [fenugreek] (Leguminosae)

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

Subject Codes:Biochemistry and Molecular Biophysics; Bioprocess Engineering; Metabolism; Pharmacognosy (Pharmacology)

ISSN:0021-8561
Year:2001
Journal Title:Journal of Agricultural and Food Chemistry

252. Title:Intermuscular variation in tenderness: Association with the ubiquitous and muscle-specific calpains

View Article: Journal of Animal Science. 79 (1). January, 2001. 122-132
CD Volume:358
Print Article: Pages: 122-132

Author(s):Ilian M A Morton J D Kent M P Le Couteur C E Hickford J Cowley R Bickerstaffe R

Author Affiliation:Molecular Biotechnology Group, Animal and Food Sciences Division, Lincoln University, Canterbury: Alayanm@whio.Lincoln.ac.nz

Language:English

Language of Summary:English (EN)

Abstract:The biochemistry of intermuscular variation in tenderness is not fully understood. To investigate the role of the calpains in this process we performed two experiments using bovine and ovine species. In the bovine experiment, two distinct muscles, longissimus thoracis et lumborum (LT) and psoas major (PM), were used. In the ovine experiment, four muscles, LT, PM, semimembranosus (SM), and semitendinosus (ST), were used. Muscles were sampled at death for the determination of the steady-state mRNA level of calpains and calpastatin and the activities of calpain 1, 2, and calpastatin. Muscles were also sampled to determine the temporal changes in pH, tenderness, and the activity of the ubiquitous calpain system during postmortem aging. The results of the relative rate of tenderization in both species was found to be related to muscle type; LT had the highest value in both species. Within species, the mRNA steady-state levels of calpain 1 and calpastatin were similar in various bovine and ovine muscles. Bovine calpain 2 mRNA level was significantly lower in the LT than in the PM. Ovine calpain 2 mRNA level was lower, but not significantly different, in the LT compared to the other muscles. The mRNA level of bovine calpain 3 was significantly higher in the LT muscle than in the PM. In the ovine, the mRNA level of calpain 3 was highest in the LT, followed by SM, PM, and ST. Results on the activity

of the ubiquitous calpain system in various muscles at death were dependent on muscle type and species. Temporal changes in the activity of calpains and calpastatin during the first 24 h of postmortem aging were similar in the muscles studied: calpain 1 and calpastatin declined significantly and calpain 2 remained relatively unchanged. The temporal changes in muscle pH in both experiments indicated that the extent and rate of pH decline during aging was related to muscle type. Correlation analysis between the relative rate of tenderization and mRNA expression of calpains revealed a strong relationship with calpain 3 in both species

Descriptors:meat tenderness; pH. Foods; Muscular System (Movement and Support). calpain 1; calpain 2; calpain 3; calpastatin

Organism Descriptors:bovine (Bovidae); sheep (Bovidae). longissimus thoracis et lumborum: muscular system; psoas major: muscular system

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

Subject Codes:Foods; Muscular System (Movement and Support)

ISSN:0021-8812
Year:2001
Journal Title:Journal of Animal Science

253. Title:Inbreeding and effective population size of Japanese Black cattle

View Article: Journal of Animal Science. 2001. 79 (2). 366-370
CD Volume:358
Print Article: Pages: 366-370

Author(s):Nomura T Honda T Mukai F
Author Affiliation:Faculty of Engineering, Department of Biotechnology, Kyoto Sangyo University, Kyoto 603-8555, Japan

Language:English

Abstract:The objective of this research was to estimate the amount of inbreeding and effective population size of the Japanese Black breed using pedigree records from bulls and heifers registered between 1985 and 1997. Inbreeding was quantified by 3 F-statistics: actual inbreeding, inbreeding expected under random mating, and inbreeding due to population subdivision. During the period of 1985 to 1997, the inbreeding expected under random mating increased from 2.3% to 5.0%, whereas the increase of actual inbreeding was more gradual (from 4.7% to 5.4%). The inbreeding due to population subdivision decreased almost linearly and reached 0.5% in 1997, indicating that genetic subdivision of the Japanese Black cattle population has essentially disappeared. The effective size of the breed was estimated from the increasing rate of inbreeding expected under random mating. In the earlier half of this period (1986 to 1990), the breed maintained an effective size of approximately 30. However, after 1991 the effective size sharply decreased and the harmonic mean between 1993 and 1997 was only 17.2. The main cause of this reduction of the effective size was considered to be the intensive use of a few prominent sires. To increase the effective size, an upper limit in the use of AI semen per sire should be imposed

Descriptors:effective-population-size. generation-interval. inbreeding. Japanese-Black

Organism Descriptors:cattle

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

Subject Codes:LL240

Supplementary Info:34 ref

ISSN:0021-8812

Year:2001
Journal Title:Journal of Animal Science

254. Title:Cell release from alginate immobilized Lactococcus lactis ssp. lactis in chitosan and alginate coated beads
View Article: Journal of Dairy Science. 84 (5). May, 2001. 1118-1127
CD Volume:359
Print Article: Pages: 1118-1127
Author(s):Klinkenberg G Lystad K Q Levine D W Dyrset N
Author Affiliation:Department of Biotechnology, Norwegian University of Science and Technology, N-7491, Trondheim: geir.klinkenberg@chem.sintef.no
Language:English
Language of Summary:English (EN)
Abstract:The effects of chitosan and alginate coatings of alginate beads with entrapped Lactococcus lactis ssp. lactis were studied in batch and continuous fermentations. Chitosan coating reduced the final concentrations of free cells, the initial release of free cells and the rate of lactate production in milk fermented batch-wise to a final pH of 4.7 in five consecutive batch fermentations. An alternative experimental system based on continuous fermentation with controlled pH and a high dilution rate was developed to better study the phenomenon of cell release. To estimate the effects of different bead coatings on cell release, alginate beads were coated with chitosan or alginate, or sequentially with chitosan/alginate or chitosan/alginate/chitosan. Chitosan coating alone seemed to reduce the rate of cell release only in the early stages of the fermentation, while sequential coatings with chitosan and alginate showed significant reduction throughout the whole test period. To examine whether the observed effects of bead coating could be explained only by a decrease in cell activity, the ratios between the rate of cell release and the rate of lactate production were examined during the fermentations for the different beads. This ratio showed qualitatively the same behavior as direct results of volumetric cell release
Descriptors:alginated coated beads; cell release; fermentation; immobilized cell technology; pH. Foods. alginate; chitosan; lactate
Organism Descriptors:Lactococcus lactis lactis (Gram-Positive Cocci)
Supplemental Descriptors:Gram-Positive Cocci: Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Foods
ISSN:0022-0302
Year:2001
Journal Title:Journal of Dairy Science

255. Title:Soil, water and nutrient conservation in mountain farming systems: Case-study from the Sikkim Himalaya
View Article: Journal of Environmental Management. 61 (2). February, 2001. 123-135
CD Volume:380
Print Article: Pages: 123-135
Author(s):Sharma E Rai S C Sharma R
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Language:English
Language of Summary:English (EN)
Abstract:The Khanikhola watershed in Sikkim is agrarian with about 50% area under rain-fed agriculture representing the conditions of the middle mountains all over the Himalaya. The study was conducted to assess

overland flow, soil loss and subsequent nutrient losses from different land uses in the watershed, and identify biotechnological inputs for management of mountain farming systems. Overland flow, soil and nutrient losses were very high from open agricultural (cropped) fields compared to other land uses, and more than 72% of nutrient losses were attributable to agriculture land use. Forests and large cardamon agroforestry conserved more soil compared to other land uses. Interventions, like cultivation of broom grass upon terrace risers, N2-fixing Albizia trees for maintenance of soil fertility and plantation of horticulture trees, have reduced the soil loss (by 22%). Soil and water conservation values (>80%) of both large cardamom and broom grass were higher compared to other crops. Use of N2-fixing Albizia tree in large cardamom agroforestry and croplands contributed to soil fertility, and increased productivity and yield. Bio-composting of farm resources ensured increase in nutrient availability specially phosphorus in cropped areas. Agricultural practices in mountain areas should be strengthened with more agroforestry components, and cash crops like large cardamom and broom grass in agroforestry provide high economic return and are hydroecologically sustainable

Descriptors:agricultural land use; agroforestry; biotechnology; cash croplands; ecological sustainability; economic return; horticultural plantations; mounting farming systems; nutrient availability; nutrient loss; overland flow; soil conservation; soil erosion; soil fertility; water conservation; watershed management. Conservation; Forestry. nitrogen: fixation; phosphorus: nutrient

Geographic Locator:Sikkim (India, Asia, Oriental region)

Organism Descriptors:broom grass (Gramineae): crop; cardamom (Zingiberaceae): crop

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

Subject Codes:Conservation; Forestry

ISSN:0301-4797
Year:2001
Journal Title:Journal of Environmental Management

256. Title:Effects of gamma radiation on the allergenic and antigenic properties of milk proteins

View Article: Journal of Food Protection. 64 (2). February, 2001. 272-276
CD Volume:362
Print Article: Pages: 272-276

Author(s):Lee Ju Woon Kim Jae Hun Yook Hong Sun Kang Kun Ok Lee Soo Young Hwang Han Joon Byun Myung Woo

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Language:English
Language of Summary:English (EN)

Abstract:This study was carried out to evaluate the application of food irradiation technology as a method for reducing milk allergies. Bovine alpha-casein (ACA) and beta-lactoglobulin (BLG) were used as milk proteins. Using milk-hypersensitive patients' immunoglobulin E (IgE) and rabbit IgGs individually produced to ACA and BLG, the changes of allergenicity and antigenicity of irradiated proteins were observed by competitive indirect enzyme-linked immunosorbent assay. Allergenicity and antigenicity of the irradiated proteins were changed

with different slopes of the inhibition curves. The disappearance of the band on sodium dodecyl sulfate-polyacrylamide gel electrophoresis and increase of the turbidity showed that solubility of the proteins decreased by radiation, and this decrease might be caused by agglomeration of the proteins. These results indicated that epitopes on milk allergens were structurally altered by gamma irradiation
Descriptors:milk: dairy product. Immune System (Chemical Coordination and Homeostasis); Foods. milk allergy: immune system disease. alpha-casein: allergenic properties, antigenic properties, milk protein; beta-lactoglobulin: allergenic properties, antigenic properties, milk protein; immunoglobulin E; immunoglobulin G
Organism Descriptors:human (Hominidae); rabbit (Leporidae)
Supplemental Descriptors:Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia. Animals; Chordates; Humans; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Primates; Vertebrates
Subject Codes:Immune System (Chemical Coordination and Homeostasis); Foods
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

257. Title:Biogenic amines in packed table olives and pickles
View Article: Journal of Food Protection. 64 (3). March, 2001. 374-378
CD Volume:362
Print Article: Pages: 374-378
Author(s):Garcia Garcia P Brenes Balbuena M Romero Barranco C Garrido Fernandez A
Author Affiliation:Food Biotechnology Department, Instituto de la Grasa (C.S.I.C.), Avda Padre Garcia Tejero 4, 41012, Sevilla: pedrog@cica.es
Language:English
Language of Summary:English (EN)
Abstract:The content of biogenic amines in different commercial preparations of table olives and other pickled foods was determined. Concentration of amines in packed table olives, capers, caperberries, and cucumbers was less than 60 mg of total biogenic amines per kg of fruit, and, therefore, these products represent no risk to human health. The highest concentrations of putrescine (50 mg/kg) and histamine (38 mg/kg) were found in untreated natural black olives and caperberries, respectively. Canned ripe olives were completely free of biogenic amines. Putrescine was found in all the samples of green olives and cucumbers but at levels lower than 18 mg/kg
Descriptors:caperberries: fruit; capers: ethnic food; cucumbers: vegetable; human health; olive: black, ethnic food, green, packed; pickles: packed, vegetable. Foods. biogenic amines; histamine; putrescine
Subject Codes:Foods
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

258. Title:Incidence and characterization of Listeria spp. from foods available in Korea
View Article: Journal of Food Protection. 64 (4). April, 2001. 554-558
CD Volume:362
Print Article: Pages: 554-558
Author(s):Choi Young Chun Cho Sun Young Park Boo Kil Chung Duck Hwa Oh Deog Hwan

Author Affiliation:Division of Food and Biotechnology, Kangwon National University, Chunchon: deoghwa@cc.kangwon.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:A total of 410 domestic Korean food samples were analyzed for the presence of Listeria spp. by the conventional U.S. Department of Agriculture protocol, and presumptive strains were identified by morphological, cultural and biochemical tests according to Bergey's manual and confirmed by API-Listeria kit. Among the total 410 food samples, 46 samples (11.2%) were found to be contaminated with Listeria species. Among the 46 strains of Listeria spp. isolates, 8 strains (17.42%) for Listeria monocytogenes, 3 strains (6.5%) for Listeria seeligeri, 33 strains (71.7%) for Listeria innocua, and 2 strains (4.4%) for Listeria welshimeri were identified, respectively. Also, only beef, chicken, pork, frozen foods, and sausage were contaminated with L. monocytogenes, and the other products were free of L. monocytogenes. Of 46 Listeria spp. isolates, L. innocua (71.7%) was the most predominantly isolated in a variety of foods compared to other Listeria spp. An in vitro virulence assay for Listeria spp. using myeloma and hybridoma cells from murine and human sources was performed. The result showed that only L. monocytogenes killed approximately 95 to 100% hybridoma cells after 6 h and the other Listeria species, such as L. innocua, L. seeligeri, and L. welshimeri strains had about 0 to 10% lethal effect on hybridoma cells. Also, an antibiotic susceptibility test showed that Listeria spp. isolates were very susceptible to the antibiotics tested, except for nalidixic acid. Also, serotyping results showed 75% of L. monocytogenes isolates from beef, chicken, and frozen pizza belonged to serotype 1 and 25% from sauage were type 4
Descriptors:Korean food samples: food product, microbial analysis; bacterial food contamination: analysis, prevention; bacterial virulence; food protection; infection outbreaks; serotypes. Foods; Infection; Microbiology
Geographic Locator:Korea (Palearctic region)
Organism Descriptors:Listeria spp. (Regular Nonsporing Gram-Positive Rods): foodborne pathogen; human (Hominidae); mouse (Muridae)
Supplemental Descriptors:Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia; Regular Nonsporing Gram-Positive Rods: Eubacteria, Bacteria, Microorganisms. Animals; Bacteria; Chordates; Eubacteria; Humans; Mammals; Microorganisms; Nonhuman Mammals; Nonhuman Vertebrates; Primates; Rodents; Vertebrates
Subject Codes:Foods; Infection; Microbiology
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

259. Title:Evaluation of surface contamination and the presence of Listeria monocytogenes in fish processing factories
View Article: Journal of Food Protection. 64 (5). May, 2001. 635-639
CD Volume:362
Print Article: Pages: 635-639
Author(s):Miettinen Hanna Aarnisalo Kaarina Salo Satu Sjoberg Anna Maija
Author Affiliation:VTT Biotechnology, FIN-02044, VTT: hanna.miettinen@vtt.fi
Language:English
Language of Summary:English (EN)
Abstract:The main objective of this study was to determine the level of surface contamination in fish processing factories and the presence of

Listeria in the factory environment and products. Another objective was evaluation of the different hygiene-monitoring methods. Total aerobic heterotrophic and enterobacteria, yeast and mold samples were collected and ATP levels measured in 28 factories. The number of well or adequately washed and disinfected factories was small (2 of 28), in terms of total aerobic heterotrophic bacterial counts on the surfaces. Most surfaces contaminated with bacteria were heavily contaminated. Results of the ATP and the total bacteria contact agar slide methods were poorly correlated (r = 0.21) although 68% of the samples were categorized as good to moderate or unacceptable with both methods. The Listeria-positive surface samples usually contained increased numbers of total bacteria (70.9%). The contamination of products and raw fish together with Listeria spp. was 45% and with Listeria monocytogenes 12%. Cold smoked fish was the most contaminated, with 75% Listeria spp. and cold salted fish with 20% L. monocytogenes. Listeria innocua was found in the samples more than twice as often as L. monocytogenes

Descriptors:cold salted fish: fish; cold smoked fish: fish; fish processing factories; raw fish: fish. Foods. ATP

Organism Descriptors:Listeria innocua (Regular Nonsporing Gram-Positive Rods): food contaminant; Listeria monocytogenes (Regular Nonsporing Gram-Positive Rods): food contaminant, pathogen; Listeria spp. (Regular Nonsporing Gram-Positive Rods): food contaminant; enterobacteria (Enterobacteriaceae): food contaminant; heterotrophic bacteria (Bacteria): aerobic, food contaminant; mold (Fungi): food contaminant; yeast (Fungi): food contaminant

Supplemental Descriptors:Bacteria: Microorganisms; Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Fungi: Plantae; Regular Nonsporing Gram-Positive Rods: Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Fungi; Microorganisms; Nonvascular Plants; Plants

Subject Codes:Foods
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

260. Title:Bile salt hydrolase activity of enterococci isolated from food: Screening and quantitative determination

View Article: Journal of Food Protection. 64 (5). May, 2001. 725-729
CD Volume:362
Print Article: Pages: 725-729

Author(s):Franz Charles M A P Specht Ingrid Haberer Petra Holzapfel Wilhelm H
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Language:English
Language of Summary:English (EN)

Abstract:One hundred seventeen enterococcal strains isolated from food (47 Enterococcus faecium, 48 Enterococcus faecalis, 16 Enterococcus durans, 2 Enterococcus gallinarum, 3 Enterococcus casseliflavus, and 1 Enterococcus malodoratus) were screened for bile salt hydrolase (BSH) activity on de Man, Rogosa, and Sharpe agar medium containing taurocholic acid and calcium chloride. The highest incidence of BSH-active strains was observed for E. faecalis (81%) followed by E. faecium (50%) and E. durans (44%). Isolates were grouped into four putative activity groups (no, low, medium, and high activity) based on the size of precipitation zones observed in the screening experiment. Our results showed that assumptions on BSH activity based on the size

of bile precipitation zones in screening experiments did not correlate with actual activity as quantified by high-pressure liquid chromatography, but the screening assay is useful for assessing the presence or absence of BSH activity
Descriptors:Enzymology (Biochemistry and Molecular Biophysics); Foods; Methods and Techniques. bile salt hydrolase
Organism Descriptors:Enterococcus casseliflavus (Gram-Positive Cocci): food contaminant; Enterococcus durans (Gram-Positive Cocci): food contaminant; Enterococcus faecalis (Gram-Positive Cocci): food contaminant; Enterococcus faecium (Gram-Positive Cocci): food contaminant; Enterococcus gallinarum (Gram-Positive Cocci): food contaminant; Enterococcus malodoratus (Gram-Positive Cocci): food contaminant
Supplemental Descriptors:Gram-Positive Cocci: Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Foods; Methods and Techniques
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

261. Title:Presence of Escherichia coli O157:H7 in ground beef and ground baby beef meat
View Article: Journal of Food Protection. 64 (6). June, 2001. 862-864
CD Volume:362
Print Article: Pages: 862-864
Author(s):Uhitil S Jaksic S Petrak T Botka Petrak K
Author Affiliation:Department of Food Technology Engineering, Faculty of Food Technology and Biotechnology, University of Zagreb, 10 000, Zagreb: tpetrak@mapbf.pbf.hr
Language:English
Language of Summary:English (EN)
Abstract:A total of 114 beef and baby beef samples were examined. The samples included ground baby beef, mixed ground baby beef and pork, and chopped and shaped meat. The samples were analyzed from 30 different grocery stores in Zagreb, Croatia. The object of this study was to evaluate the prevalence of Escherichia coli O157:H7 in the samples that can enhance the potential risk of outbreaks of hemorrhagic colitis and hemolytic uremic syndrome. The results in all tested samples of E. coli O157:H7 were negative. A single sample was positive in a latex agglutination test using antiserum to O157:H7. It was identified as Proteus vulgaris at the Pasteur Institute, Paris, France. This result correlates positively with cross-contamination with Yersinia enterocolitica 09, Brucella abortus, Salmonella type N, and Pseudomonas maltophila
Descriptors:ground baby beef: meat product; mixed ground baby beef and pork: meat product. Foods. hemolytic uremic syndrome: bacterial disease, blood and lymphatic disease, urologic disease; hemorrhagic colitis: bacterial disease, digestive system disease
Organism Descriptors:Brucella abortus (Gram-Negative Aerobic Rods and Cocci): food contaminant; Escherichia coli (Enterobacteriaceae): O157:H7, food contaminant, pathogen; Proteus vulgaris (Enterobacteriaceae): food contaminant; Pseudomonas maltophila (Pseudomonadaceae): food contaminant; Salmonella (Enterobacteriaceae): food contaminant, type N; Yersinia enterocolitica (Enterobacteriaceae): food contaminant
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Gram-Negative Aerobic Rods and Cocci: Eubacteria, Bacteria, Microorganisms;

Pseudomonadaceae: Gram-Negative Aerobic Rods and Cocci, Eubacteria, Bacteria, Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Foods
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

262. Title:Shiga toxin - producing Escherichia coli in beef heifers grazing an irrigated pasture
View Article: Journal of Food Protection. 2001. 64 (10). 1613-1616
CD Volume:362
Print Article: Pages: 1613-1616
Author(s):Thran B H Hussein H S Hall M R Khaiboullina S F
Author Affiliation:School of Veterinary Medicine, College of Agriculture, Biotechnology and Natural Resources, University of Nevada-Reno, Reno, NV 89557, USA
Language:English
Abstract:Shiga toxin producing Escherichia coli (STEC) produce toxins that have been associated with several human illnesses. E. coli O157:H7 is the most well-studied STEC and was first associated with consumption of improperly cooked ground beef in 1982. E. coli O157:H7 is not the only foodborne STEC because other STEC serotypes are also associated with human illnesses. The objective of this study was to assess prevalence of STEC in 23 yearling beef (Angus) heifers grazing an irrigated grass pasture in spring (April), summer (July), fall (October), and winter (December) of 1999. A total of 86 faecal samples were rectally collected and were subjected to microbiological testing for the presence of STEC. Nine E. coli isolates from five heifers (one in spring and fall and three in winter) were toxic to Vero cells. Of these isolates, four were E. coli O157:H7, two belonged to the serogroup O6, one O39:NM, one O113:H-, and the final isolate was untypable. The STEC prevalence rate in our herd ranged from 4% (spring) to 15% (winter). Based on detecting both O157:H7 and non-O157:H7 STEC in our heifers, it is clear that screening faecal samples should not be limited to E. coli O157:H7. Identification of STEC-positive cattle prior to slaughter should help in reducing the risk of beef contamination with such foodborne pathogens if pre- and/or postharvest control measures are applied to such animals
Descriptors:beef. disease-prevalence. foodborne-diseases. grazing. heifers. irrigated-pastures. seasonal-variation
Identifiers:shiga toxin-producing Escherichia coli. shiga toxins
Organism Descriptors:cattle. Escherichia-coli
Supplemental Descriptors:Bos. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:VV210. QQ030. QQ200. QQ500. LL821
Supplementary Info:44 ref
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

263. Title:Inhibitory activity of Bifidobacterium longum HY8001 against vero cytotoxin of Escherichia coli O157:H7
View Article: Journal of Food Protection. 64 (11). November, 2001. 1667-1673
CD Volume:362
Print Article: Pages: 1667-1673

Author(s):Kim So Hyun Yang Soo Jin Koo Hye Cheong Bae Won Ki Kim Ji Yeon Park Jong Hwan Baek Young Jin Park Yong Ho
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Language:English
Abstract:Vero cytotoxin (VT)-producing Escherichia coli (VTEC), such as E. coli O157:H7, are emerging foodborne pathogens worldwide. VTs are associated with hemorrhagic colitis and hemolytic uremic syndrome in humans. Attachment of the B subunit of VTs to its receptor, globotriaosylceramide (Gb3), at gut epithelium is the primary step and, consequently, the A subunit of VTs inhibits protein synthesis in the target cell. Proinflammatory cytokines, such as tumor necrosis factor (TNF)-alpha and interleukin (IL)-1beta, up-regulate Gb3 expression, increase sensitivity to VTs, and enhance VT action in developing disease. Currently, there is a growing interest in probiotics, given the increasing occurrence of antibiotic-resistant bacteria. In particular, much work on bifidobacteria among probiotics, regarded as microorganisms targeted for technological and therapeutic applications, has been performed. In Korea, the neutralizing effect of the culture supernatant of Bifidobacterium longum HY8001, Korean isolate, against the VTs from E. coli O157:H7 was found. Therefore, this study focused on the raveling of the inhibitory effect of B. longum HY8001 against VTs, through the interference B subunit of VTs and Gb3 interaction. Mice were inoculated intragastrically with B. longum HY8001 culture supernatant before and after challenge with E. coli O157:H7. Control mice were inoculated intragastrically only with E. coli O157:H7. Cytokine, TNF-alpha, and IL-1beta levels in sera and expression of their mRNA were decreased, and expression of Gb3 in renal tubular epithelial cells was reduced in mice treated with B. longum HY8001 culture supernatant. In competitive enzyme-linked immunosorbent assays (ELISAs), the culture supernatant of B. longum HY8001 primarily binds VTs to interfere the VTs with Gb3 interaction. These results suggest that soluble substance(s) in B. longum HY8001 culture supernatant may have inhibitory activity on the expression of Gb3, VT-Gb3 interaction, or both. Further study should be done to elucidate the property of soluble substances in B. longum HY8001 culture supernatant
Descriptors:Infection; Toxicology. Escherichia coli infection: bacterial disease. globotriaosylceramide; interleukin-1-beta; mRNA; tumor necrosis factor-alpha; vero cytotoxin: interference B subunit
Organism Descriptors:Bifidobacterium longum (Irregular Nonsporing Gram-Positive Rods): antibacterial activity, probiotic, strain-HY8001; Escherichia coli (Enterobacteriaceae): O157:H7, food contaminant, pathogen; mouse (Muridae): animal model, host. renal tubular epithelial cells: excretory system; serum: blood and lymphatics
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Irregular Nonsporing Gram- Positive Rods: Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms; Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia. Animals; Bacteria; Chordates; Eubacteria; Mammals; Microorganisms; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
Subject Codes:Infection; Toxicology
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

264. Title:Evaluation of the Petrifilm plate method for the enumeration of aerobic microorganisms and coliforms in retailed meat samples
View Article: Journal of Food Protection. 64 (11). November, 2001. 1841-1843
CD Volume:362
Print Article: Pages: 1841-1843
Author(s):Park Yong Ho Seo Keun Seok Ahn Jong Sam Yoo Han Sang Kim Sang Pil
Author Affiliation:Department of Microbiology, College of Veterinary Medicine and School of Agricultural Biotechnology, Seoul National University, Seoul; E-Mail: yhp@plaza.snu.ac.kr
Language:English
Abstract:This study was designed to compare the effectiveness and applicability of the Petrifilm plate method with the Association of Official Analytical Chemists' (AOAC) standard aerobic count method and violet red bile agar method for meat products. The comparison was carried out using 303 meat samples collected from various retailers: 110 pork samples, 87 chicken samples, and 107 beef samples. In the comparison of the correlation coefficient (R) between the conventional method and the Petrifilm plate method by a linear regression analysis, the correlation coefficient in total microorganisms was 0.99, 0.95, and 0.94 in pork, beef, and chicken samples, respectively. The correlation coefficient in coliform count was 0.83, 0.96, and 0.81 in pork, beef, and chicken samples, respectively. Based on the high correlation in the total microorganism count, it might be possible to replace the conventional methods with the Petrifilm plate method. For coliform counts, the Petrifilm plate method also showed a generally high correlation coefficient, except for pork samples, which are more subject to contamination. The Petrifilm plate method was simpler and less time-consuming in sample preparation and, in procedures, faster than the conventional method. These results suggested that the 3M Petrifilm plate method could replace the conventional methods in the analysis of microorganism contamination measurement in meat products
Descriptors:beef: meat; chicken: poultry product; pork: meat. Foods; Methods and Techniques
Organism Descriptors:aerobic microorganism (Microorganisms): food contaminant; coliform (Enterobacteriaceae): food contaminant
Supplemental Descriptors:Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Microorganisms. Bacteria; Eubacteria; Microorganisms
Subject Codes:Foods; Methods and Techniques
ISSN:0362-028X
Year:2001
Journal Title:Journal of Food Protection

265. Title:Modulation in isozyme profiles in relation to Al toxicity tolerance in rice
View Article: Journal of Genetics & Breeding. 2001. 55 (2). 111-118
CD Volume:361
Print Article: Pages: 111-118
Author(s):Chowdhury B Sheeja T E Mandal A B
Author Affiliation:Biotechnology Laboratory, Central Agricultural Research Institute, P.B. No. 181, Port Blair, Andamans, India
Language:English
Abstract:Putative Al tolerant rice somaclones were evolved through in vitro screening of mature seed derived calluses of an indigenous variety C 14-8 in Andamans. The de novo synthesized variants were screened under hydroponics supplemented with 30, 60 and 90 ppm of Al stress that led to identification of true tolerant lines. They were profiled for a few important isozymes viz. glucose-6-phosphate isomerase

(G6PI), esterase (EST), peroxidase (PER), malate dehydrogenase (MDH), glucose-6-phosphate dehydrogenase (G6PDH), isocitrate dehydrogenase (ICDH), lactate dehydrogenase (LDH) and alcohol dehydrogenase (ADH) to underpin their involvement in governing Al toxicity tolerance. Prominent differences including changes in activity/band intensity, mobility shift and number of polymorphic loci with respect to Al toxicity were evident. Loci 1 (rf, 0.23) of G6PI, loci 3 (rf, 0.43) of PER, loci 1 (rf, 0.44) of G6PDH, loci 3 (rf, 0.43) and 4 (rf, 0.5) of ICDH showed reduced activity in response to Al stress. Loci 1 (rf, 0.27), 4 (rf, 0.79) and 5 (rf, 0.87) of EST; loci 2 (rf, 0.19), 3 (rf, 0.26) and 4 (rf, 0.38) of MDH; loci 1 (rf, 0.23) of ICDH and loci 1 (rf, 0.19) of ADH displayed an increase in activity with stress intensity. All those bands, which showed differential band intensities in response to stress, may be the stress injury markers. Novel bands appeared at loci 4 (rf, 0.49) in G6PI, loci 5 (rf, 0.80) and 6 (rf, 0.88) in PER, loci 2 (rf, 0.62) in G6PDH, loci 2 (rf, 0.4) in ICDH and 3 (rf, 0.71) in esterase and loci 1 (rf, 0.08) and 2 (rf, 0.17) in LDH. Disappearance of loci 2 (rf, 0.42) of ADH and loci 5 (rf, 0.53) of G6PI is indicative of their high susceptibility towards Al toxicity stress. The bands disappeared or newly appeared possibly due to activation or inactivation of diverse domains in the genome seemed to be involved in governing Al toxicity tolerance. They may be classified as stress markers generally since they show stringent specificity in defending Al toxicity. Some of the bands were found to be unaltered even at very high Al concentration viz. loci 2 (rf, 0.40), 3 (rf, 0.44) and 6 (rf, 0.57) of G6PI, loci 2 (rf, 0.59) of EST, loci 1 (rf, 0.12), 2 (rf, 0.22), 4 (rf, 0.62) and 7 (rf, 0.97) of PER, loci 1 (rf, 0.07), 5 (rf, 0.58) 6 (rf, 0.73) of MDH and loci 3 (rf, 0.21) and 4 (rf, 0.55) of LDH. Maximum stress induced alterations were observed with G6PDH and minimum with PER enzyme system

Descriptors:alcohol-dehydrogenase. aluminium. enzyme-activity. enzymes. esterases. glucose-6-phosphate-dehydrogenase. glucose-6-phosphate-isomerase. in-vitro-culture. isocitrate-dehydrogenase. isoenzymes. lactate-dehydrogenase. malate-dehydrogenase. peroxidase. rice. tolerance. toxicity

Organism Descriptors:Oryza. Oryza-sativa

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

Subject Codes:FF005. FF060. FF900

Supplementary Info:35 ref

ISSN:0394-9257

Year:2001

Journal Title:Journal of Genetics & Breeding

266. Title:Prediction of heterotic combinations using RAPD polymorphism in rice

View Article: Journal of Genetics & Breeding. 2001. 55 (2). 135-141

CD Volume:361

Print Article: Pages: 135-141

Author(s):Reddy O U K Siddiq E A Ali J Ramasamy P Hussain A J Nimmakayala P Arti P Viraktamath B C Sarma N P

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Language:English

Abstract:Performance of hybrids depends on the choice of parents with good combining ability. The present study uses randomly amplified polymorphic DNA in rice over a set of diverse parents. The aim was to investigate the use of RAPD derived molecular distances for prediction

of parental combinations which can produce superior heterotic F1s. A total of 73 polymorphic bands were used to estimate genetic distances. Sixty-five crosses were made using various indica and japonica types. The genetic distances estimated for various parental combinations were grouped into three overlapping classes namely class-I with narrowly distant combinations (0.0 to 0.3 plus or minus 0.05), class-II with moderately diverse combinations (0.3 plus or minus 0.05 to 5.0 plus or minus 0.05) and class-III with highly diverse combinations with 0.6 plus or minus 0.05 and above respectively. The per se performance of the 65 hybrids were assessed for seven metric traits by giving a final score which helped to grade the hybrids into seven categories. Eleven of indica/japonica (inter-specific) and eight indica/indica (intraspecific) hybrids were in the first two ranks. Nine inter-specific hybrids were incidentally from the class-II whose genetic distances were moderate. All the top ranking intra-specific hybrids are from class-III or class-II/III where genetic diversity between the parents involved was high. In the present study, the correlations between GD and per se overall appears to be insignificant in all the seven traits which clearly indicates that superior parental combinations can not be predicted. However, our study shows how a survey of diversity using molecular markers, can help to understand the further useable diversity range for indica/japonica and indica/indica programmes. Though significant relationship was not observed between GD and most of the traits, there is a clear trend that the most of inter-specific hybrids in class-II and intraspecific hybrids in class-III had top ranking superior hybrids

Descriptors:combining-ability. crosses. genetic-distance. genetic-diversity. hybrids. random-amplified-polymorphic-DNA. rice

Organism Descriptors:Oryza. Oryza-sativa

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

Subject Codes:FF005. FF020

Supplementary Info:24 ref

ISSN:0394-9257

Year:2001

Journal Title:Journal of Genetics & Breeding

267. Title:Genotype, explant and medium effects on adventitious shoot bud formation and plant regeneration in Capsicum annuum L

View Article: Journal of Genetics & Breeding. 2001. 55 (2). 143-149

CD Volume:361

Print Article: Pages: 143-149

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Author Affiliation:Plant Biotechnology Laboratory, Department of Botany, Kakatiya University, Warangal - 506 009, A.P., India

Language:English

Abstract:There is a tremendous variability among various genotypes, explants and plant growth regulators requirement for adventitious shoot bud formation in C. annuum. In vitro plant regeneration was achieved in C. annuum cultivars CA960, NP46-A, PC1, Pusajwala, Selection 1, Surya Mukhi Cluster and X-235. Adventitious shoot buds were induced from hypocotyl, cotyledon and leaf explants on MS medium supplemented with 1.0 mg-1 IAA + 3.0 mgl-1 BAP [benzyladenine] (medium A); 5.0 mgl-1 BAP (medium B); and 10.0 mgl-1 BAP (medium C). Of the seven genotypes tested, X-235 regenerated highest number of shoots and selection 1, the least with CA960, NP46-A, PC1, Pusajwala and Surya Mukhi Cluster as moderate. Leaf explants were more amenable for shoot regeneration than cotyledon and hypocotyl explants. Among three different media

examined medium A and B were superior to medium C in inducing maximum number of adventitious shoots. Of the all genotypes, explants and media evaluated, it was observed that leaf and hypocotyl explants regenerated maximally on medium B whereas cotyledon explants preferred medium A. Elongation of multiple shoots occurred when subcultured on medium supplemented with low concentration of BAP (0.05 mgl-1) in combination with IAA (0.05 mgl-1). Rooting of regenerated shoots were achieved on 1.0 mgl-1 IAA containing medium. Complete plantlets were normal diploids (2n=24) and devoid of any chromosomal aberrations, when transferred to soil 60-75% of these plantlets survived and grew well
Descriptors:adventitious-shoots. benzyladenine. cultivars. explants. genotypes. hypocotyls. IAA. in-vitro-culture. in-vitro-regeneration. organogenesis. plant-growth-regulators. tissue-culture
Organism Descriptors:Capsicum-annuum
Supplemental Descriptors:Capsicum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. FF170
Supplementary Info:29 ref
ISSN:0394-9257
Year:2001
Journal Title:Journal of Genetics & Breeding
Copyright:Copyright CAB International

268. Title:Purification and characterization of a natural agglutinin in the hemolymph of the prawn Penaeus indicus H. Milne Edwards
View Article: Journal of Invertebrate Pathology. 2001. 77 (4). 237-242
CD Volume:358
Print Article: Pages: 237-242
Author(s):Jayasree S
Author Affiliation:Biochemistry and Genetic Engineering Research Unit, Department of Biotechnology, Cochin University of Science and Technology, Cochin 682 022, India
Language:English
Abstract:Agglutinin from the serum of Penaeus indicus was isolated, purified and characterized according to its ability to react with bacteria and vertebrate red blood cells (RBCs). Prawn agglutinin was non-dialysable, but precipitable at 45% ammonium sulfate saturation; it was soluble only in 0.85% saline, indicating its macromolecular nature. The native molecular mass of the agglutinin of P. indicus was estimated to be 181 kDa, and its subunits have molecular mass of approximately 97 and 84 kDa. The proteinaceous nature of the agglutinin was suggested by its sensitivity to TCA, phenol and chloroform extraction; heat lability and sensitivity to extreme pH. Purified agglutinin strongly agglutinated Vibrio alginolyticus (v-5) strain and vertebrate RBCs, but demonstrated less activity towards Pseudomonas fluorescens MS-47 and MS-51 strains. The antibacterial nature of P. indicus agglutinin was observed in a bacterial lawn of V. alginolyticus (v-5), through the formation of a zone of clearance
Descriptors:agglutinins. antibacterial-properties. erythrocytes
Identifiers:Vibrio alginolyticus
Organism Descriptors:Penaeus-indicus. Pseudomonas-fluorescens. Vibrio
Supplemental Descriptors:Penaeus. Penaeidae. Decapoda. Malacostraca. Crustacea. arthropods. invertebrates. animals. aquatic-animals. aquatic-organisms. Pseudomonas. Pseudomonadaceae. Gracilicutes. bacteria. prokaryotes. Vibrionaceae. Vibrio
Subject Codes:LL650. LL821. MM120
Supplementary Info:33 ref
ISSN:0022-2011

Year:2001
Journal Title:Journal of Invertebrate Pathology
Copyright:Copyright CAB International

269. Title:Stability engineering of antibody single-chain Fv fragments
View Article: J Mol Biol 2001 Feb 2;305(5):989-1010
CD Volume:340
Print Article: Pages: 989-1010
Author(s):Worn A Pluckthun A
Author Affiliation:Biochemisches Institut, Universitat Zurich, Winterthurerstrasse 190, CH-8057, Switzerland
Abstract:The application of single-chain Fv fragments (scFv) in medicine and biotechnology places great demands on their stability. Only recently has attention been given to the production of highly stable scFvs, and in a number of examples it was found that such fragments indeed perform better during practical applications. The structural parameters influencing scFv stability are now beginning to be elucidated. This review summarizes progress in rational and evolutionary engineering methods, the structural implications of these results, as well as some examples where stability engineering has been successfully applied
Descriptors:Animal. Binding Sites. Complementarity Determining. Directed Molecular Evolution. Disulfides. Human. Immunoglobulin Variable Region. Mutation. Peptide Library. *Protein Engineering. Protein Structure, Tertiary. Support, Non-U.S. Gov't. Thermodynamics
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

270. Title:A 2.1 A resolution structure of an uncleaved alpha(1)-antitrypsin shows variability of the reactive center and other loops
View Article: J Mol Biol 2001 Feb 9;306(1):109-19
CD Volume:340
Print Article: Pages: 109-119
Author(s):Kim S Woo J Seo EJ Yu M Ryu S
Author Affiliation:Center for Cellular Switch Protein Structure, Korea Research Institute of Bioscience and Biotechnology, Yusong, Taejon, 305-600, Korea
Abstract:Serpin (serine protease inhibitor) proteins are involved in diverse physiological processes including inflammation, coagulation, matrix remodeling, and cell differentiation. Deficiency of normal serpin functions leads to various hereditary diseases. Besides their clinical importance, serpin proteins draw much attention due to the large conformational changes that occur upon interaction with proteases. We present here the crystal structure of an uncleaved alpha(1)-antitrypsin determined by the multiple isomorphous replacement method and refined to 2.1 A resolution. The structure, which is the first active serpin structure based on experimental phases, reveals novel conformations in the flexible loops, including the proximal hinge region of the reactive center loop and the surface cavity region in the central beta-sheet, sheet A. The determined loop conformation explains the results of recent mutagenesis studies and provides detailed insights into the protease inhibition mechanism. The high-resolution structure of active alpha(1)-antitrypsin also provides evidence for the existence of localized van-der-Waals strain in the central hydrophobic core

Descriptors:Amino Acid Sequence. Binding Sites. Crystallography, X-Ray. Models, Molecular. Molecular Sequence Data. Pliability. Protein Structure, Secondary. Sequence Alignment. Thermodynamics. alpha 1-Antitrypsin
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

271. Title:A repeated beta -turn structure in poly(Ala-Gly) as a model for silk I of Bombyx mori silk fibroin studied with two-dimensional spin-diffusion NMR under off magic angle spinning and rotational echo double resonance
View Article: Journal of Molecular Biology. 2001. 306 (2). 291-305
CD Volume:340
Print Article: Pages: 291-305
Author(s):Asakura T Ashida J Yamane T Kameda T Nakazawa Y Ohgo K Komatsu K
Author Affiliation:Department of Biotechnology, Tokyo University of Agriculture and Technology, Koganei, Tokyo, 184-8588, Japan
Language:English
Abstract:A detailed study was carried out of the structure of a crystalline form of Bombyx mori silk fibroin (silk I), with 13 2-dimensional spin-diffusion solid state nuclear magnetic resonance and rotation echo, double-resonance
Descriptors:biochemistry. silk. silkworms
Organism Descriptors:Bombyx-mori
Supplemental Descriptors:Bombyx. Bombycidae. Lepidoptera. insects. arthropods. invertebrates. animals
Subject Codes:YY400. LL020
Supplementary Info:47 ref
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

272. Title:The high-resolution X-ray crystallographic structure of the ferritin (EcFtnA) of Escherichia coli; comparison with human H ferritin (HuHF) and the structures of the Fe(3+) and Zn(2+) derivatives
View Article: J Mol Biol 2001 Mar 23;307(2):587-603
CD Volume:341
Print Article: Pages: 587-603
Author(s):Stillman TJ Hempstead PD Artymiuk PJ Andrews SC Hudson AJ Treffry A Guest JR Harrison PM
Author Affiliation:The Krebs Institute Department of Molecular Biology and Biotechnology, The University of Sheffield, Sheffield S10 2TN, UK
Abstract:The high-resolution structure of the non-haem ferritin from Escherichia coli (EcFtnA) is presented together with those of its Fe(3+) and Zn(2+) derivatives, this being the first high-resolution X-ray analysis of the iron centres in any ferritin.The binding of both metals is accompanied by small changes in the amino acid ligand positions. Mean Fe(A)(3+)-Fe(B)(3+) and Zn(A)(2+)-Zn(B)(2+) distances are 3.24 A and 3.43 A, respectively. In both derivatives, metal ions at sites A and B are bridged by a glutamate side-chain (Glu50) in a syn-syn conformation. The Fe(3+) derivative alone shows a third metal site (Fe(C)(3+)) joined to Fe(B)(3+) by a long anti-anti bidentate bridge through Glu130 (mean Fe(B)(3+)-Fe(C)(3+) distance 5.79 A). The third metal site is unique to the non-haem bacterial ferritins.The dinuclear site lies at the inner end of a hydrophobic channel connecting it to the outside surface of the protein shell, which may provide access for dioxygen and possibly for metal ions shielded by

water. Models representing the possible binding mode of dioxygen to the dinuclear Fe(3+) pair suggest that a gauche micro-1,2 mode may be preferred stereochemically.Like those of other ferritins, the 24 subunits of EcFtnA are folded as four-helix bundles that assemble into hollow shells and both metals bind at dinuclear centres in the middle of the bundles. The structural similarity of EcFtnA to the human H chain ferritin (HuHF) is remarkable (r.m.s. deviation of main-chain atoms 0.66 A) given the low amino acid sequence identity (22 %). Many of the conserved residues are clustered at the dinuclear centre but there is very little conservation of residues making inter-subunit interactions

Descriptors:Amino Acid Sequence. Binding Sites. Ceruloplasmin. Comparative Study. Computer Simulation. Conserved Sequence. Crystallography, X-Ray. Escherichia coli. Evolution, Molecular. Ferric Compounds. Ferritin. Human. Iron. Models, Molecular. Molecular Sequence Data. Oxygen. Protein Binding. Protein Structure, Quaternary. Protein Structure, Secondary. Protein Structure, Tertiary. Protein Subunits. Reproducibility of Results. Sequence Homology, Amino Acid. Species Specificity. Support, Non-U.S. Gov't. Zinc

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

273. Title:Phosphorylation-induced structural changes in the amyloid precursor protein cytoplasmic tail detected by NMR

View Article: J Mol Biol 2001 Mar 30;307(3):871-84
CD Volume:341
Print Article: Pages: 871-884

Author(s):Ramelot TA Nicholson LK
Author Affiliation:Department of Molecular Biology and Genetics, Cornell University, 239 Biotechnology Building, Ithaca, NY 14853, USA

Abstract:The cytoplasmic tail of the amyloid precursor protein (APPc) interacts with several cellular factors implicated in intracellular signaling or proteolytic production of amyloid beta peptide found in senile plaques of Alzheimer's disease patients. APPc contains two threonine residues (654 and 668 relative to APP695, or 6 and 20 relative to APPc) and a serine residue (655 or 7, respectively) that are known to be phosphorylated in vivo and may play regulatory roles in these events. We show by solution NMR spectroscopy of a 49 residue cytoplasmic tail peptide (APP-C) that in all three cases, phosphorylation induces changes in backbone dihedral angles that can be attributed to formation of local hydrogen bonds between the phosphate group and nearby amide protons. Phosphorylation of S7 also induces chemical shift changes in the hydrophobic cluster (residues I8-V13), indicating additional medium-range effects. The most pronounced changes occur upon phosphorylation of T20, a neuron-specific phosphorylation site, where the N-terminal helix capping box previously characterized for this region is altered. Characterization of torsion angles and transient hydrogen bonds indicates that prolyl isomerization of the pThr-Pro peptide bond results from both destabilization of the N-terminal helix capping box and stabilization of the cis isomer by transient hydrogen bonds. The significant population of the cis isomer (9 %) present after phosphorylation of T20 suggests a potential role of selective recognition of cis versus trans isomers in response to phosphorylation of APP. Together, these structural changes indicate that phosphorylation may act as a conformational switch in the cytoplasmic tail of APP to alter specificity and affinity of binding

to cytosolic partners, particularly in response to the abnormal phosphorylation events associated with Alzheimer's disease
Descriptors:Amino Acid Sequence. Amyloid beta-Protein Precursor. Ca(2+)-Calmodulin Dependent Protein Kinase. Human. Hydrogen Bonding. Hydrogen-Ion Concentration. Isomerism. Models, Molecular. Molecular Sequence Data. *Nuclear Magnetic Resonance, Biomolecular. Peptide Fragments. Phosphorylation. Phosphoserine. Phosphothreonine. Proline. Protein Conformation. Support, Non-U.S. Gov't. Support, U.S. Gov't, Non-P.H.S.. Support, U.S. Gov't, P.H.S.. Titrimetry
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

274. Title:Two divalent metal ions in the active site of a new crystal form of human apurinic/apyrimidinic endonuclease, Ape1: implications for the catalytic mechanism
View Article: J Mol Biol 2001 Apr 6;307(4):1023-34
CD Volume:341
Print Article: Pages: 1023-1034
Author(s):Beernink PT Segelke BW Hadi MZ Erzberger JP Wilson DM 3rd Rupp B
Author Affiliation:Molecular and Structural Biology Division, Biology and Biotechnology Research Program, Lawrence Livermore National Laboratory, Livermore, CA, 94550, USA
Abstract:The major human abasic endonuclease, Ape1, is an essential DNA repair enzyme that initiates the removal of apurinic/apyrimidinic sites from DNA, excises 3' replication-blocking moieties, and modulates the DNA binding activity of several transcriptional regulators. We have determined the X-ray structure of the full-length human Ape1 enzyme in two new crystal forms, one at neutral and one at acidic pH. The new structures are generally similar to the previously determined structure of a truncated Ape1 protein, but differ in the conformation of several loop regions and in spans of residues with weak electron density. While only one active-site metal ion is present in the structure determined at low pH, the structure determined from a crystal grown at the pH optimum of Ape1 nuclease activity, pH 7.5, has two metal ions bound 5 A apart in the active site. Enzyme kinetic data indicate that at least two metal-binding sites are functionally important, since Ca(2+) exhibits complex stimulatory and inhibitory effects on the Mg(2+)-dependent catalysis of Ape1, even though Ca(2+) itself does not serve as a cofactor. In conjunction, the structural and kinetic data suggest that Ape1 catalyzes hydrolysis of the DNA backbone through a two metal ion-mediated mechanism
Descriptors:Binding Sites. Calcium. Catalysis. Cations, Divalent. Coenzymes. Crystallization. Crystallography, X-Ray. DNA. DNA-Binding Proteins. Exodeoxyribonucleases. Human. Hydrogen-Ion Concentration. Hydrolysis. Kinetics. Magnesium. Metals. Models, Molecular. Motion. Oxidation-Reduction. Protein Binding. Protein Structure, Tertiary. Structure-Activity Relationship. Support, U.S. Gov't, Non-P.H.S.. Support, U.S. Gov't, P.H.S.
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

275. Title:Regulatory potential, phyletic distribution and evolution of ancient, intracellular small-molecule-binding domains
View Article: J Mol Biol 2001 Apr 13;307(5):1271-92
CD Volume:341

Print Article: Pages: 1271-1292
Author(s):Anantharaman V Koonin EV Aravind L
Author Affiliation:National Center for Biotechnology Information National Library of Medicine, National Institutes of Health, Bethesda, MD, 20894, USA
Abstract:Central cellular functions such as metabolism, solute transport and signal transduction are regulated, in part, via binding of small molecules by specialized domains. Using sensitive methods for sequence profile analysis and protein structure comparison, we exhaustively surveyed the protein sets from completely sequenced genomes for all occurrences of 21 intracellular small-molecule-binding domains (SMBDs) that are represented in at least two of the three major divisions of life (bacteria, archaea and eukaryotes). These included previously characterized domains such as PAS, GAF, ACT and ferredoxins, as well as three newly predicted SMBDs, namely the 4-vinyl reductase (4VR) domain, the NIFX domain and the 3-histidines (3H) domain. Although there are only a limited number of different superfamilies of these ancient SMBDs, they are present in numerous distinct proteins combined with various enzymatic, transport and signal-transducing domains. Most of the SMBDs show considerable evolutionary mobility and are involved in the generation of many lineage-specific domain architectures. Frequent re-invention of analogous architectures involving functionally related, but not homologous, domains was detected, such as, fusion of different SMBDs to several types of DNA-binding domains to form diverse transcription regulators in prokaryotes and eukaryotes. This is suggestive of similar selective forces affecting the diverse SMBDs and resulting in the formation of multidomain proteins that fit a limited number of functional stereotypes. Using the "guilt by association approach", the identification of SMBDs allowed prediction of functions and mode of regulation for a variety of previously uncharacterized proteins
Descriptors:Amino Acid Sequence. Animal. Archaeal Proteins. Bacterial Proteins. Carrier Proteins. Computational Biology. Enzymes. Eukaryotic Cells. *Evolution, Molecular. Genome. Membrane Proteins. Models, Molecular. Molecular Sequence Data. Molecular Weight. *Phylogeny. Protein Binding. *Protein Structure, Tertiary. Proteins. Sequence Alignment. Signal Transduction. Structure-Activity Relationship. Transcription Factors
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

276. Title:A novel method of protein secondary structure prediction with high segment overlap measure: support vector machine approach
View Article: J Mol Biol 2001 Apr 27;308(2):397-407
CD Volume:341
Print Article: Pages: 397-407
Author(s):Hua S Sun Z
Author Affiliation:Institute of Bioinformatics, State key Laboratory of Biemembrane and Membrane Biotechnology, Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing 100084, China
Abstract:We have introduced a new method of protein secondary structure prediction which is based on the theory of support vector machine (SVM). SVM represents a new approach to supervised pattern classification which has been successfully applied to a wide range of pattern recognition problems, including object recognition, speaker identification, gene function prediction with microarray expression profile, etc. In these cases, the performance of SVM either matches or

is significantly better than that of traditional machine learning approaches, including neural networks.The first use of the SVM approach to predict protein secondary structure is described here. Unlike the previous studies, we first constructed several binary classifiers, then assembled a tertiary classifier for three secondary structure states (helix, sheet and coil) based on these binary classifiers. The SVM method achieved a good performance of segment overlap accuracy SOV=76.2 % through sevenfold cross validation on a database of 513 non-homologous protein chains with multiple sequence alignments, which out-performs existing methods. Meanwhile three-state overall per-residue accuracy Q(3) achieved 73.5 %, which is at least comparable to existing single prediction methods. Furthermore a useful "reliability index" for the predictions was developed. In addition, SVM has many attractive features, including effective avoidance of overfitting, the ability to handle large feature spaces, information condensing of the given data set, etc. The SVM method is conveniently applied to many other pattern classification tasks in biology

Descriptors:*Computer Simulation. Databases. Models, Molecular. Pattern Recognition. Protein Structure, Secondary. Proteins. Reproducibility of Results. Sensitivity and Specificity. Sequence Alignment. Software. Support, Non-U.S. Gov't

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

277. Title:NMR structure of cysteinyl-phosphorylated enzyme IIB of the N,N'-diacetylchitobiose-specific phosphoenolpyruvate-dependent phosphotransferase system of Escherichia coli

View Article: J Mol Biol 2001 May 18;308(5):993-1009
CD Volume:341
Print Article: Pages: 993-1009

Author(s):Ab E Schuurman Wolters GK Nijlant D Dijkstra K Saier MH Robillard GT Scheek RM

Author Affiliation:The Groningen Biomolecular Science and Biotechnology Institute (GBB), University of Groningen, Nijenborgh 4, Groningen, 9747 AG, The Netherlands

Abstract:The determination by NMR of the solution structure of the phosphorylated enzyme IIB (P-IIB(Chb)) of the N,N'-diacetylchitobiose-specific phosphoenolpyruvate-dependent phosphotransferase system of Escherichia coli is presented. Most of the backbone and side-chain resonances were assigned using a variety of mostly heteronuclear NMR experiments. The remaining resonances were assigned with the help of the structure calculations.NOE-derived distance restraints were used in distance geometry calculations followed by molecular dynamics and simulated annealing protocols. In addition, combinations of ambiguous restraints were used to resolve ambiguities in the NOE assignments. By combining sets of ambiguous and unambiguous restraints into new ambiguous restraints, an error function was constructed that was less sensitive to information loss caused by assignment uncertainties. The final set of structures had a pairwise rmsd of 0.59 A and 1.16 A for the heavy atoms of the backbone and side-chains, respectively.Comparing the P-IIB(Chb) solution structure with the previously determined NMR and X-ray structures of the wild-type and the Cys10Ser mutant shows that significant differences between the structures are limited to the active-site region. The phosphoryl group at the active-site cysteine residue is surrounded by a loop formed by residues 10 through 16. NOE and chemical shift data suggest that the phosphoryl group makes hydrogen bonds with the backbone amide protons

of residues 12 and 15. The binding mode of the phosphoryl group is very similar to that of the protein tyrosine phosphatases. The differences observed are in accordance with the presumption that IIB(Chb) has to be more resistant to hydrolysis than the protein tyrosine phosphatases. We propose a proton relay network by which a transfer occurs between the cysteine SH proton and the solvent via the hydroxyl group of Thr16

Descriptors:Binding Sites. Crystallography, X-Ray. Cysteine. Disaccharides. Escherichia coli. Hydrogen Bonding. Models, Molecular. Mutation. *Nuclear Magnetic Resonance, Biomolecular. Phosphoenolpyruvate Sugar Phosphotransferase. Phosphorylation. Protein Structure, Secondary. Protons. Solvents. Substrate Specificity. Thermodynamics

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

278. Title:Covalent joining of the subunits of a homodimeric type II restriction endonuclease: single-chain PvuII endonuclease

View Article: J Mol Biol 2001 May 25;309(1):89-97
CD Volume:342
Print Article: Pages: 89-97

Author(s):Simoncsits A Tjornhammar ML Rasko T Kiss A Pongor S
Author Affiliation:International Centre for Genetic Engineering and Biotechnology, Trieste, Italy. simoncs@icgeb.trieste.it

Abstract:The PvuII restriction endonuclease has been converted from its natural homodimeric form into a single polypeptide chain by tandemly linking the two subunits through a short peptide linker. The arrangement of the single-chain PvuII (sc PvuII) is (2-157)-GlySerGlyGly-(2-157), where (2-157) represents the amino acid residues of the enzyme subunit and GlySerGlyGly is the peptide linker. By introducing the corresponding tandem gene into Escherichia coli, PvuII endonuclease activity could be detected in functional in vivo assays. The sc enzyme was expressed at high level as a soluble protein. The purified enzyme was shown to have the molecular mass expected for the designed sc protein. Based on the DNA cleavage patterns obtained with different substrates, the cleavage specificity of the sc PvuII is indistinguishable from that of the wild-type (wt) enzyme. The sc enzyme binds specifically to the cognate DNA site under non-catalytic conditions, in the presence of Ca2+, with the expected 1:1 stoichiometry. Under standard catalytic conditions, the sc enzyme cleaves simultaneously the two DNA strands in a concerted manner. Steady-state kinetic parameters of DNA cleavage by the sc and wt PvuII showed that the sc enzyme is a potent, but somewhat less efficient catalyst; the k(cat)/K(M) values are 1.11 x 10(9) and 3.50 x 10(9) min(-1) M(-1) for the sc and wt enzyme, respectively. The activity decrease is due to the lower turnover number and to the lower substrate affinity. The sc arrangement provides a facile route to obtain asymmetrically modified heterodimeric enzymes

Descriptors:Amino Acid Sequence. Base Sequence. Calcium. Catalysis. DNA. DNA-Binding Proteins. Deoxyribonucleases, Type II Site-Specific. Dimerization. Escherichia coli. Kinetics. Models, Molecular. Mutation. Protein Binding. *Protein Engineering. Protein Structure, Quaternary. Protein Subunits. Proteus vulgaris. Solubility. Substrate Specificity. Support, Non-U.S. Gov't. Thermodynamics

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

279. Title:The N-terminal domain of Homer/Vesl is a new class II EVH1 domain
View Article: J Mol Biol 2001 May 25;309(1):155-69
CD Volume:342
Print Article: Pages: 155-169
Author(s):Barzik M Carl UD Schubert WD Frank R Wehland J Heinz DW
Author Affiliation:Department of Structural Biology and German National Center of Biotechnology (GBF), Braunschweig
Abstract:Cellular activities controlled by signal transduction processes such as cell motility and cell growth depend on the tightly regulated assembly of multiprotein complexes. Adapter proteins that specifically interact with their target proteins are key components required for the formation of these assemblies. Ena/VASP-homology 1 (EVH1) domains are small constituents of large modular proteins involved in microfilament assembly that specifically recognize proline-rich regions. EVH1 domain-containing proteins are present in neuronal cells, like the Homer/Vesl protein family that is involved in memory-generating processes. Here, we describe the crystal structure of the murine EVH1 domain of Vesl 2 at 2.2 A resolution. The small globular protein consists of a seven-stranded antiparallel beta-barrel with a C-terminal alpha-helix packing alongside the barrel. A shallow groove running parallel with beta-strand VI forms an extended peptide-binding site. Using peptide library screenings, we present data that demonstrate the high affinity of the Vesl 2 EVH1 domain towards peptide sequences containing a proline-rich core sequence (PPSPF) that requires additional charged amino acid residues on either side for specific binding. Our functional data, substantiated by structural data, demonstrate that the ligand-binding of the Vesl EVH1 domain differs from the interaction characteristics of the previously examined EVH1 domains of the Evl/Mena proteins. Analogous to the Src homology 3 (SH3) domains that bind their cognate ligands in two distinct directions, we therefore propose the existence of two distinct classes of EVH1 domains
Descriptors:Amino Acid Sequence. Animal. Binding Sites. Binding, Competitive. Carrier Proteins. Cloning, Molecular. Crystallography, X-Ray. Ligands. Mice. Models, Molecular. Molecular Sequence Data. Neuropeptides. Peptide Library. Proline. Protein Structure, Secondary. Protein Structure, Tertiary. Structure-Activity Relationship. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

280. Title:A study of the structure-activity relationship for diazaborine inhibition of Escherichia coli enoyl-ACP reductase
View Article: J Mol Biol 2001 May 25;309(1):171-80
CD Volume:342
Print Article: Pages: 171-180
Author(s):Levy CW Baldock C Wallace AJ Sedelnikova S Viner RC Clough JM Stuitje AR Slabas AR Rice DW Rafferty JB
Author Affiliation:Krebs Institute for Research, Department of Molecular Biology and Biotechnology, University of Sheffield, UK
Abstract:Enoyl acyl carrier protein (ACP) reductase catalyses the last reductive step of fatty acid biosynthesis, reducing the enoyl group of a growing fatty acid chain attached to ACP to its acyl product using NAD(P)H as the cofactor. This enzyme is the target for the diazaborine class of antibacterial agents, the biocide triclosan, and one of the targets for the front-line anti-tuberculosis drug isoniazid. The structures of

complexes of Escherichia coli enoyl-ACP reductase (ENR) from crystals grown in the presence of NAD+ and a family of diazaborine compounds have been determined. Analysis of the structures has revealed that a mobile loop in the structure of the binary complex with NAD+ becomes ordered on binding diazaborine/NAD+ but displays a different conformation in the two subunits of the asymmetric unit. The work presented here reveals how, for one of the ordered conformations adopted by the mobile loop, the mode of diazaborine binding correlates well with the activity profiles of the diazaborine family. Additionally, diazaborine binding provides insights into the pocket on the enzyme surface occupied by the growing fatty acid chain

Descriptors:Binding Sites. Boron Compounds. Crystallography, X-Ray. Enzyme Inhibitors. Escherichia coli. Models, Molecular. NAD. Oxidoreductases. Protein Binding. Protein Conformation. Protein Subunits. Structure-Activity Relationship. Support, Non-U.S. Gov't. Triclosan

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

281. Title:The Lys103Asn mutation of HIV-1 RT: a novel mechanism of drug resistance

View Article: J Mol Biol 2001 Jun 1;309(2):437-45
CD Volume:342
Print Article: Pages: 437-445

Author(s):Hsiou Y Ding J Das K Clark AD Jr Boyer PL Lewi P Janssen PA Kleim JP Rosner M Hughes SH Arnold E

Author Affiliation:Center for Advanced Biotechnology and Medicine (CABM) and Rutgers University Chemistry Department, 679 Hoes Lane, Piscataway, NJ 08854-5638, USA

Abstract:Inhibitors of human immunodeficiency virus (HIV) reverse transcriptase (RT) are widely used in the treatment of HIV infection. Loviride (an alpha-APA derivative) and HBY 097 (a quinoxaline derivative) are two potent non-nucleoside RT inhibitors (NNRTIs) that have been used in human clinical trials. A major problem for existing anti-retroviral therapy is the emergence of drug-resistant mutants with reduced susceptibility to the inhibitors. Amino acid residue 103 in the p66 subunit of HIV-1 RT is located near a putative entrance to a hydrophobic pocket that binds NNRTIs. Substitution of asparagine for lysine at position 103 of HIV-1 RT is associated with the development of resistance to NNRTIs; this mutation contributes to clinical failure of treatments employing NNRTIs. We have determined the structures of the unliganded form of the Lys103Asn mutant HIV-1 RT and in complexes with loviride and HBY 097. The structures of wild-type and Lys103Asn mutant HIV-1 RT in complexes with NNRTIs are quite similar overall as well as in the vicinity of the bound NNRTIs. Comparison of unliganded wild-type and Lys103Asn mutant HIV-1 RT structures reveals a network of hydrogen bonds in the Lys103Asn mutant that is not present in the wild-type enzyme. Hydrogen bonds in the unliganded Lys103Asn mutant but not in wild-type HIV-1 RT are observed between (1) the side-chains of Asn103 and Tyr188 and (2) well-ordered water molecules in the pocket and nearby pocket residues. The structural differences between unliganded wild-type and Lys103Asn mutant HIV-1 RT may correspond to stabilization of the closed-pocket form of the enzyme, which could interfere with the ability of inhibitors to bind to the enzyme. These results are consistent with kinetic data indicating that NNRTIs bind more slowly to Lys103Asn mutant than to wild-type HIV-1 RT. This novel drug-resistance mechanism explains the broad cross-resistance of

Lys103Asn mutant HIV-1 RT to different classes of NNRTIs. Design of NNRTIs that make favorable interactions with the Asn103 side-chain should be relatively effective against the Lys103Asn drug-resistant mutant
Descriptors:Acetamides. Acetophenones. Amino Acid Substitution. Antiviral Agents. Binding Sites. Crystallography, X-Ray. Drug Design. Drug Resistance, Microbial. Enzyme Stability. HIV-1. HIV-1 Reverse Transcriptase. Hydrogen Bonding. Ligands. Models, Molecular. Mutation, Missense. Protein Conformation. Protein Subunits. Reverse Transcriptase Inhibitors. Support, Non-U.S. Gov't. Support, U.S. Gov't, P.H.S.. Thermodynamics
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

282. Title:Interpreting trends in the binding of cyclic ureas to HIV-1 protease
View Article: J Mol Biol 2001 Jun 1;309(2):507-17
CD Volume:342
Print Article: Pages: 507-517
Author(s):Mardis KL Luo R Gilson MK
Author Affiliation:Center for Advanced Research in Biotechnology, 9600 Gudelsky Drive, Rockville, MD 20850, USA
Abstract:The design of new HIV protease inhibitors requires an improved understanding of the physical basis of inhibitor/protein binding. Here, the binding affinities of seven aliphatic cyclic ureas to HIV-1 protease are calculated using a predominant states method and an implicit solvent model based upon finite difference solutions of the Poisson-Boltzmann equation. The calculations are able to reproduce the observed U-shaped trend of binding free energy as a function of aliphatic chain length. Interestingly, the decrease in affinity for the longest chains is attributable primarily to the energy cost of partly desolvating charged aspartic and arginine groups at the mouths of the active site. Even aliphatic chains too short to contact these charged groups directly are subject to considerable desolvation penalties. We are not aware of other systems where binding affinity trends have been attributed to long-ranged electrostatic desolvation of ionized groups. A generalized Born/surface area solvation model yields a much smaller change in desolvation energy with chain length and, therefore, does not reproduce the experimental binding affinity trends. This result suggests that the generalized Born model should be used with caution for complex, partly desolvated systems like protein binding sites. We also find that changing the assumed protonation state of the active site aspartyl dyad significantly affects the computed binding affinity trends. The protonation state of the aspartyl dyad in the presence of cyclic ureas is discussed in light of the observation that the monoprotonated state reproduces the experimental results best
Descriptors:Arginine. Aspartic Acid. Binding Sites. Cyclization. Drug Design. Electrostatics. HIV Protease. HIV Protease Inhibitors. HIV-1. Ions. Models, Molecular. Molecular Conformation. Poisson Distribution. Protein Binding. Solvents. Support, Non-U.S. Gov't. Support, U.S. Gov't, P.H.S.. Thermodynamics. Urea
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

283. Title:Sfl1 functions via the co-repressor Ssn6-Tup1 and the cAMP-dependent protein kinase Tpk2
View Article: J Mol Biol 2001 Jun 22;309(5):1007-15
CD Volume:342
Print Article: Pages: 1007-1015
Author(s):Conlan RS Tzamarias D
Author Affiliation:Institute of Molecular Biology & Biotechnology-Foundation of Research & Technology, Vassilika Vouton, Heraklion, Crete, GR-711 10, Greece. r.s.conlan@swan.ac.uk
Abstract:Ssn6 (Cyc8) is a component of the yeast general corepressor Ssn6-Tup1 that inhibits the transcription of many diversely regulated genes. The corepressor does not interact directly with DNA but is recruited to different promoters through interactions with distinct pathway-specific, DNA-binding repressor proteins. Using yeast two-hybrid and GST chromatography interaction experiments, we have determined that Sfl1, a novel repressor protein, interacts directly with Ssn6, and in vivo repression data suggest that Sfl1 inhibits transcription by recruiting Ssn6-Tup1 via a specific domain in the Sfl1 protein. Sin4 and Srb10, components of specific RNA polymerase II sub-complexes that are required for Ssn6-Tup1 repression activity, are found to be required for Sfl1 repression function. These results indicate a possible mechanism for Sfl1-mediated repression via Ssn6-Tup1 and specific subunits of the RNA polymerase II holoenzyme. Electrophoretic mobility shift and chromatin immuno-precipitation assays demonstrate that Sfl1 is present at the promoters of three Ssn6-Tup1-repressible genes; namely, FLO11, HSP26, and SUC2. Sfl1 is known to interact with Tpk2, a cAMP-dependent protein kinase that negatively regulates Sfl1 function. Consistently, we show that phosphorylation by protein kinase A inhibits Sfl1 DNA binding in vitro, and that a tpk2Delta mutation increases the levels of Sfl1 protein associated with specific promoter elements in vivo. These data indicate a possible mechanism for regulating Sfl1-mediated repression through modulation of DNA binding by cAMP-dependent protein kinase-dependent phosphorylation. Taken together with previous data, these new observations suggest a link between cAMP signaling and Ssn6-Tup1-mediated transcriptional repression
Descriptors:Bacterial Proteins. Chromatin. Cyclic AMP. Cyclic AMP-Dependent Protein Kinases. Cyclin-Dependent Kinases. DNA, Fungal. Fungal Proteins. Gene Expression Regulation, Fungal. Holoenzymes. Membrane Proteins. Mutation. Phosphorylation. Precipitin Tests. Promoter Regions (Genetics). Protein Binding. Protein Kinases. RNA Polymerase II. Repressor Proteins. Saccharomyces cerevisiae. Serine Endopeptidases. Signal Transduction. Support, Non-U.S. Gov't. Transcription, Genetic. Two-Hybrid System Techniques
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

284. Title:Very high resolution structure of a trematode hemoglobin displaying a TyrB10-TyrE7 heme distal residue pair and high oxygen affinity
View Article: Journal of Molecular Biology. 2001. 309 (5). 1153-1164
CD Volume:342
Print Article: Pages: 1153-1164
Author(s):Pesce A Dewilde S Kiger L Milani M Ascenzi P Marden M C Hauwaert M L van Vanfleteren J Moens L Bolognesi M
Author Variant:van-Hauwaert-M-L
Author Affiliation:Department of Physics, INFM Advanced Biotechnology Centre, University of Genova, Largo Rosanna Benzi, 10 I-16132, Genova, Italy

Language:English
Abstract:A study was conducted to determine the oxygenation and carbonylation parameters of wild-type Paramphistomum epiclitum haemoglobin (Hb), as well as that of single- and double-site mutants, with residue substitutions at positions B10, E7 and E11, in the light of the protein atomic resolution crystal structure. Monomeric haemoglobin from the trematode P. epiclitum displayed very high oxygen affinity (P50<0.001 mmHg) and an unusual haeme distal site containing tyrosyl residues at the B10 and E7 positions. The crystal structure of aquo-met P. epiclitum haemoglobin, solved at 1.17 amstrong units resolution via multiwavelength anomalous dispersion techniques (R-factor=0.121), showed that the haeme distal site pocket residue TyrB10 was engaged in hydrogen bonding to the iron-bound ligand. By contrast, residue TyrE7 was unexpectedly locked next to the CD globin region, in a conformation unsuitable for haeme-bound ligand stabilization. This structural organization of the E7 distal residue differed strikingly from that observed in the nematode Ascaris suum haemoglobin (bearing TyrB10 and GlnE7 residues), which also displayed a very high oxygen affinity
Descriptors:carbonyl-compounds. haemoglobin. human-diseases. hydrogen-bonding. ligands. molecular-conformation. oxygen. trematode-infections
Organism Descriptors:man. Paramphistomum-epiclitum
Supplemental Descriptors:Homo. Hominidae. Primates. mammals. vertebrates. Chordata. animals. Paramphistomum. Paramphistomidae. Digenea. Trematoda. Platyhelminthes. invertebrates
Subject Codes:VV220. YY400
Supplementary Info:58 ref
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

285. Title:The crystal structure of Escherichia coli MoeA, a protein from the molybdopterin synthesis pathway
View Article: J Mol Biol 2001 Jul 6;310(2):419-31
CD Volume:342
Print Article: Pages: 419-431
Author(s):Schrag JD Huang W Sivaraman J Smith C Plamondon J Larocque R Matte A Cygler M
Author Affiliation:Biotechnology Research Institute, National Research Council of Canada, 6100 Royalmount Avenue, Montreal, PQ, Canada. joe@bri.nrc.ca
Abstract:MoeA is involved in synthesis of the molybdopterin cofactor, although its function is not yet clearly defined. The three-dimensional structure of the Escherichia coli protein was solved at 2.2 A resolution. The locations of highly conserved residues among the prokaryotic and eukaryotic MoeA homologs identifies a cleft in the dimer interface as the likely functional site. Of the four domains of MoeA, domain 2 displays a novel fold and domains 1 and 4 each have only one known structural homolog. Domain 3, in contrast, is structurally similar to many other proteins. The protein that resembles domain 3 most closely is MogA, another protein required for molybdopterin cofactor synthesis. The overall similarity between MoeA and MogA, and the similarities in a constellation of residues that are strongly conserved in MoeA, suggests that these proteins bind similar ligands or substrates and may have similar functions
Descriptors:Amino Acid Sequence. Bacterial Proteins. Binding Sites. Coenzymes. Conserved Sequence. Crystallography, X-Ray. Dimerization. Escherichia coli. Light. Metalloproteins. Models, Molecular. Molecular Sequence

Data. Protein Structure, Quaternary. Protein Structure, Secondary. Protein Structure, Tertiary. Pteridines. Scattering, Radiation. Sequence Alignment. Sulfurtransferases
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

286. Title:Crystal structure of alkaline cellulase K: insight into the alkaline adaptation of an industrial enzyme
View Article: J Mol Biol 2001 Jul 27;310(5):1079-87
CD Volume:342
Print Article: Pages: 1079-1087
Author(s):Shirai T Ishida H Noda J Yamane T Ozaki K Hakamada Y Ito S
Author Affiliation:Department of Biotechnology and Biomaterial Chemistry, Graduate School of Engineering, Nagoya University, Japan. i45282a@nucc.cc.nagoya-u.ac.jp
Abstract:The crystal structure of the catalytic domain of alkaline cellulase K was determined at 1.9 A resolution. Because of the most alkaliphilic nature and it's highest activity at pH 9.5, it is used commercially in laundry detergents. An analysis of the structural bases of the alkaliphilic character of the enzyme suggested a mechanism similar to that previously proposed for alkaline proteases, that is, an increase in the number of Arg, His, and Gln residues, and a decrease in Asp and Lys residues. Some ion pairs were formed by the gained Arg residues, which is similar to what has been found in the alkaline proteases. Lys-Asp ion pairs are disfavored and partly replaced with Arg-Asp ion pairs. The alkaline adaptation appeared to be a remodeling of ion pairs so that the charge balance is kept in the high pH range
Descriptors:*Adaptation, Physiological. Amino Acid Sequence. Amino Acids. Bacillus. Binding Sites. *Biotechnology. Cellobiose. Cellulase. Crystallography, X-Ray. *Detergents. Evolution, Molecular. Hydrogen-Ion Concentration. Models, Molecular. Molecular Sequence Data. Phylogeny. Protein Binding. Protein Conformation. Sequence Alignment. Support, Non-U.S. Gov't
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

287. Title:Correlated sequence-signatures as markers of protein-protein interaction
View Article: J Mol Biol 2001 Aug 24;311(4):681-92
CD Volume:343
Print Article: Pages: 681-692
Author(s):Sprinzak E Margalit H
Author Affiliation:Department of Molecular Genetics and Biotechnology, The Hebrew University--Hadassah Medical School, Jerusalem, 91120, Israel
Abstract:As protein-protein interaction is intrinsic to most cellular processes, the ability to predict which proteins in the cell interact can aid significantly in identifying the function of newly discovered proteins, and in understanding the molecular networks they participate in. Here we demonstrate that characteristic pairs of sequence-signatures can be learned from a database of experimentally determined interacting proteins, where one protein contains the one sequence-signature and its interacting partner contains the other sequence-signature. The sequence-signatures that recur in concert in various pairs of interacting proteins are termed correlated sequence-signatures, and it is proposed that they can be used for predicting

putative pairs of interacting partners in the cell. We demonstrate the potential of this approach on a comprehensive database of experimentally determined pairs of interacting proteins in the yeast Saccharomyces cerevisiae. The proteins in this database have been characterized by their sequence-signatures, as defined by the InterPro classification. A statistical analysis performed on all possible combinations of sequence-signature pairs has identified those pairs that are over-represented in the database of yeast interacting proteins. It is demonstrated how the use of the correlated sequence-signatures as identifiers of interacting proteins can reduce significantly the search space, and enable directed experimental interaction screens

Descriptors:Computational Biology. Computer Simulation. Databases. Protein Binding. Protein Structure, Tertiary. Proteins. Support, Non-U.S. Gov't

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

288. Title:Crystal structure of histidinol phosphate aminotransferase (HisC) from Escherichia coli, and its covalent complex with pyridoxal-5'-phosphate and l-histidinol phosphate

View Article: J Mol Biol 2001 Aug 24;311(4):761-76
CD Volume:343
Print Article: Pages: 761-776

Author(s):Sivaraman J Li Y Larocque R Schrag JD Cygler M Matte A
Author Affiliation:Biotechnology Research Institute, 6100 Royalmount Ave., Montreal, H4P 2R2 and, Canada

Abstract:The biosynthesis of histidine is a central metabolic process in organisms ranging from bacteria to yeast and plants. The seventh step in the synthesis of histidine within eubacteria is carried out by a pyridoxal-5'-phosphate (PLP)-dependent l-histidinol phosphate aminotransferase (HisC, EC 2.6.1.9). Here, we report the crystal structure of l-histidinol phosphate aminotransferase from Escherichia coli, as a complex with pyridoxamine-5'-phosphate (PMP) at 1.5 A resolution, as the internal aldimine with PLP, and in a covalent, tetrahedral complex consisting of PLP and l-histidinol phosphate attached to Lys214, both at 2.2 A resolution. This covalent complex resembles, in structural terms, the gem-diamine intermediate that is formed transiently during conversion of the internal to external aldimine.HisC is a dimeric enzyme with a mass of approximately 80 kDa. Like most PLP-dependent enzymes, each HisC monomer consists of two domains, a larger PLP-binding domain having an alpha/beta/alpha topology, and a smaller domain. An N-terminal arm contributes to the dimerization of the two monomers. The PLP-binding domain of HisC shows weak sequence similarity, but significant structural similarity with the PLP-binding domains of a number of PLP-dependent enzymes. Residues that interact with the PLP cofactor, including Tyr55, Asn157, Asp184, Tyr187, Ser213, Lys214 and Arg222, are conserved in the family of aspartate, tyrosine and histidinol phosphate aminotransferases. The imidazole ring of l-histidinol phosphate is bound, in part, through a hydrogen bond with Tyr110, a residue that is substituted by Phe in the broad substrate specific HisC enzymes from Zymomonas mobilis and Bacillus subtilis.Comparison of the structures of the HisC internal aldimine, the PMP complex and the HisC l-histidinol phosphate complex reveal minimal changes in protein or ligand structure. Proton transfer, required for conversion of the gem-diamine to the external aldimine, does not appear to be limited by the distance between

substrate and lysine amino groups. We propose that the tetrahedral complex has resulted from non-productive binding of l-histidinol phosphate soaked into the HisC crystals, resulting in its inability to be converted to the external aldimine at the HisC active site
Descriptors:Amino Acid Sequence. Binding Sites. Crystallography, X-Ray. Dimerization. Escherichia coli. Histidinol. Models, Molecular. Molecular Sequence Data. Phosphates. Protein Binding. Protein Structure, Quaternary. Protein Structure, Secondary. Pyridoxal Phosphate. Sequence Alignment. Spectrum Analysis. Transaminases
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

289. Title:Escherichia coli maltose-binding protein as a molecular chaperone for recombinant intracellular cytoplasmic single-chain antibodies
View Article: J Mol Biol 2001 Sep 7;312(1):79-93
CD Volume:343
Print Article: Pages: 79-93
Author(s):Bach H Mazor Y Shaky S Shoham Lev A Berdichevsky Y Gutnick DL Benhar I
Author Affiliation:Department of Molecular Microbiology and Biotechnology, The George S. Wise Faculty of Life Sciences, Tel-Aviv University, Green Building, Room 202, Ramat Aviv 69978, Israel
Abstract:Recombinant single-chain antibodies (scFvs) that are expressed in the cytoplasm of cells are of considerable biotechnological and therapeutic potential. However, the reducing environment of the cytoplasm inhibits the formation of the intradomain disulfide bonds that are essential for correct folding and functionality of these antibody fragments. Thus, scFvs expressed in the cytoplasm are mostly insoluble and inactive.Here, we describe a general approach for stabilizing scFvs for efficient functional expression in the cell cytoplasm in a soluble, active form. The scFvs are expressed as C-terminal fusions with the Escherichia coli maltose-binding protein (MBP). We tested a large panel of scFvs that were derived from hybridomas and from murine and human scFv phage display and expression libraries by comparing their stability and functionality as un-fused versus MBP fused proteins. We found that MBP fused scFvs are expressed at high levels in the cytoplasm of E. coli as soluble and active proteins regardless of the redox state of the bacterial cytoplasm. In contrast, most un-fused scFvs can be produced (to much lower levels) in a functional form only when expressed in trxB(-) but not in trxB(+) E. coli cells. We show that MBP-scFv fusions are more stable than the corresponding un-fused scFvs, and that they perform more efficiently in vivo as cytoplasmic intrabodies in E. coli. Thus, MBP seems to function as a molecular chaperone that promotes the solubility and stability of scFvs that are fused to it
Descriptors:Antibodies. Carrier Proteins. Cytoplasm. Enzyme Activation. Escherichia coli. Fluorescein. Immunoglobulin Variable Region. Molecular Chaperones. Protein Engineering. Recombinant Fusion Proteins. Support, Non-U.S. Gov't. beta-Galactosidase
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

290. Title:The crystal structure of Thermotoga maritima maltosyltransferase and its implications for the molecular basis of the novel transfer specificity

View Article: J Mol Biol 2001 Sep 7;312(1):119-31
CD Volume:343
Print Article: Pages: 119-131
Author(s):Roujeinikova A Raasch C Burke J Baker PJ Liebl W Rice DW
Author Affiliation:Krebs Institute for Biomolecular Research, Department of Molecular Biology and Biotechnology, The University of Sheffield, S10 2TN, England
Abstract:Maltosyltransferase (MTase) from the hyperthermophile Thermotoga maritima represents a novel maltodextrin glycosyltransferase acting on starch and malto-oligosaccharides. It catalyzes the transfer of maltosyl units from alpha-1,4-linked glucans or malto-oligosaccharides to other alpha-1,4-linked glucans, malto-oligosaccharides or glucose. It belongs to the glycoside hydrolase family 13, which represents a large group of (beta/alpha)(8) barrel proteins sharing a similar active site structure. The crystal structures of MTase and its complex with maltose have been determined at 2.4 A and 2.1 A resolution, respectively. MTase is a homodimer, each subunit of which consists of four domains, two of which are structurally homologous to those of other family 13 enzymes. The catalytic core domain has the (beta/alpha)(8) barrel fold with the active-site cleft formed at the C-terminal end of the barrel. Substrate binding experiments have led to the location of two distinct maltose-binding sites; one lies in the active-site cleft, covering subsites -2 and -1; the other is located in a pocket adjacent to the active-site cleft. The structure of MTase, together with the conservation of active-site residues among family 13 glycoside hydrolases, are consistent with a common double-displacement catalytic mechanism for this enzyme. Analysis of maltose binding in the active site reveals that the transfer of dextrinyl residues longer than a maltosyl unit is prevented by termination of the active-site cleft after the -2 subsite by the side-chain of Lys151 and the stretch of residues 314-317, providing an explanation for the strict transfer specificity of MTase
Descriptors:Binding Sites. Biological Transport. Comparative Study. Crystallography, X-Ray. Dimerization. Glucans. Glucosyltransferases. Glycogen Debranching Enzyme System. Maltose. Models, Molecular. Protein Conformation. Protein Folding. Substrate Specificity. Support, Non-U.S. Gov't. Thermotoga maritima
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

291. Title:Transgenic plastids in basic research and plant biotechnology
View Article: Journal of Molecular Biology. 2001. 312 (3). 425-438
CD Volume:343
Print Article: Pages: 425-438
Author(s):Bock R
Author Affiliation:Westfalische Wilhelms-Universitat Munster, Institut fur Biochemie und Biotechnologie der Pflanzen, Hindenburgplatz 55, D-48143 Munster, Germany
Language:English
Abstract:This paper reviews current knowledge of plastid transformation systems, describes the molecular biology of transformation processes, highlights in vivo systems for studying plastid gene expression and chloroplast functional genomics by reverse genetics, and discusses the use of transgenic chloroplasts in biotechnology
Descriptors:biotechnology. chloroplast-genetics. chloroplasts. gene-expression. genes. genetic-transformation. genome-analysis. plastids. reviews. transgenic-plants

Organism Descriptors:plants
Subject Codes:FF020. WW000
Supplementary Info:108 ref
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology
Copyright:Copyright CAB International

292. Title:Internalins from the human pathogen Listeria monocytogenes combine three distinct folds into a contiguous internalin domain
View Article: Journal of Molecular Biology. 2001. 312 (4). 783-794
CD Volume:343
Print Article: Pages: 783-794
Author(s):Schubert W D Gobel G Diepholz M Darji A Kloer D Hain T Chakraborty T Wehland J Domann E Heinz D W
Author Affiliation:Department of Structural Biology, German Research Center for Biotechnology (GBF), Mascheroder Weg 1, D-38124 Braunschweig, Germany
Language:English
Abstract:High-resolution crystal structures of the cap, leucine-rich repeats (LRR) and inter-repeat (IR) regions of the N-terminal domains of internalins A (InlA) and B (InlB) - members of a family of listerial cell surface proteins - are described. Structure analysis showed that the IR-region is a minimal immunoglobulin (Ig)-like fold, contiguously fused to the LRR section. The cap, together with the Ig-like domain contain a continuous hydrophobic core and an extended beta -sheet structure, ideally suited for interactions with host cell partners. It is also demonstrated that the lack of inlH gene in Listeria monocytogenes mutants cancels the ability of these bacteria to persist and multiply in spleens and livers of infected mice. Results indicate an important role of molecules harboring the internalin domain in the pathogenesis of Listeria
Descriptors:amino-acid-sequences. crystal-proteins. surface-proteins
Identifiers:internalins
Organism Descriptors:Listeria-monocytogenes. mice
Supplemental Descriptors:Listeria. Lactobacillaceae. Firmicutes. bacteria. prokaryotes. Muridae. rodents. mammals. vertebrates. Chordata. animals. small-mammals
Subject Codes:VV210. ZZ394
Supplementary Info:57 ref
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology
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293. Title:The 1.2 A structure of a novel quorum-sensing protein, Bacillus subtilis LuxS
View Article: J Mol Biol 2001 Oct 12;313(1):111-22
CD Volume:344
Print Article: Pages: 111-122
Author(s):Ruzheinikov SN Das SK Sedelnikova SE Hartley A Foster SJ Horsburgh MJ Cox AG McCleod CW Mekhalfia A Blackburn GM Rice DW Baker PJ
Author Affiliation:Krebs Institute for Biomolecular Research, Department of Molecular Biology and Biotechnology, University of Sheffield, Firth Court, Western Bank, Sheffield S10 2TN, UK
Abstract:In bacteria, the regulation of gene expression in response to changes in cell density is called quorum sensing. The autoinducer-2 production protein LuxS, is involved in a novel quorum-sensing system and is thought to catalyse the degradation of S-ribosylhomocysteine to homocysteine and the autoinducer molecule 4,5-dihydroxy-2,3-

pentadione. The crystal structure of Bacillus subtilis LuxS has been determined at 1.2 A resolution, together with the binary complexes of LuxS with S-ribosylhomocysteine and homocysteine to 2.2 and 2.3 A resolution, respectively. These structures show that LuxS is a homodimer with an apparently novel fold based on an eight-stranded beta-barrel, flanked by six alpha-helices. Each active site contains a zinc ion coordinated by the conserved residues His54, His58 and Cys126, and includes residues from both subunits. S-ribosylhomocysteine binds in a deep pocket with the ribose moiety adjacent to the enzyme-bound zinc ion. Access to the active site appears to be restricted and possibly requires conformational changes in the protein involving the movement of residues 125-129 and those at the N terminus. The structure contains an oxidised cysteine residue in the active site whose role in the biological process of LuxS has not been determined. The autoinducer-2 signalling pathway has been linked to aspects of bacterial virulence and pathogenicity. The structural data on LuxS will provide opportunities for targeting this enzyme for the rational design of new antibiotics

Descriptors:Amino Acid Sequence. Bacillus subtilis. Bacterial Proteins. Binding Sites. Crystallography, X-Ray. Homocysteine. Models, Molecular. Molecular Sequence Data. Protein Binding. Protein Structure, Quaternary. Protein Structure, Secondary. Selenomethionine. Sequence Alignment. Support, Non-U.S. Gov't. Zinc

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

294. Title:A minor capsid protein P30 is essential for bacteriophage PRD1 capsid assembly

View Article: J Mol Biol 2001 Nov 2;313(4):785-95
CD Volume:344
Print Article: Pages: 785-795

Author(s):Rydman PS Bamford JK Bamford DH
Author Affiliation:Department of Biosciences and Institute of Biotechnology Viikki Biocenter, University of Helsinki, 00014, Finland

Abstract:Bacteriophage PRD1 is a double-stranded DNA virus infecting Gram-negative hosts. It has a membrane component located in the interior of the isometric capsid. In addition to the major capsid protein P3, the capsid contains a 9 kDa protein P30. Protein P30 is proposed to be located between the adjacent facets of the icosahedral capsid and is required for stable capsid assembly. In its absence, an empty phage-specific membrane vesicle is formed. The major protein component of this vesicle is a phage-encoded assembly factor, protein P10, that is not present in the final structure

Descriptors:Bacteriophage PRD1. Capsid. Centrifugation, Density Gradient. Escherichia coli. Genetic Complementation Test. Microscopy, Electron. Mutation. Salmonella enterica. Support, Non-U.S. Gov't. Virion. *Virus Assembly

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

295. Title:Characterization of AloI, a restriction-modification system of a new type

View Article: J Mol Biol 2001 Nov 23;314(2):205-16
CD Volume:344
Print Article: Pages: 205-216

Author(s):Cesnaviciene E Petrusyte M Kazlauskiene R Maneliene Z Timinskas A Lubys A Janulaitis A
Author Affiliation:Institute of Biotechnology, Graiciuno 8, 2028 Vilnius, Lithuania
Abstract:We report the properties of the new AloI restriction and modification enzyme from Acinetobacter lwoffi Ks 4-8 that recognizes the DNA target 5' GGA(N)6GTTC3' (complementary strand 5' GAAC(N)6TCC3'), and the nucleotide sequence of the gene encoding this enzyme. AloI is a bifunctional large polypeptide (deduced M(r) 143 kDa) revealing both DNA endonuclease and methyltransferase activities. Depending on reaction cofactors, AloI cleaves double-stranded DNA on both strands, seven bases on the 5' side, and 12-13 bases on the 3' side of its recognition sequence, and modifies adenine residues in both DNA strands in the target sequence yielding N6-methyladenine. For cleavage activity AloI maintains an absolute requirement for Mg(2+) and does not depend on or is stimulated by either ATP or S-adenosyl-L-methionine. Modification function requires the presence of S-adenosyl-L-methionine and is stimulated by metal ions (Ca(2+)). The C-terminal and central parts of the protein were found to be homologous to certain specificity (HsdS) and modification (HsdM) subunits of type I R-M systems, respectively. The N-terminal part of the protein possesses the putative endonucleolytic motif DXnEXK of restriction endonucleases. The deduced amino acid sequence of AloI shares significant homology with polypeptides encoding HaeIV and CjeI restriction-modification proteins at the N-terminal and central, but not at the C-terminal domains. The organization of AloI implies that its evolution involved fusion of an endonuclease and the two subunits, HsdM and HsdS, of type I restriction enzymes. According to the structure and function properties AloI may be regarded as one more representative of a newly emerging group of HaeIV-like restriction endonucleases. Discovery of these enzymes opens new opportunities for constructing restriction endonucleases with a new specificity
Descriptors:Acinetobacter. Adenosine Triphosphate. Amino Acid Sequence. Base Sequence. Calcium. Cations, Divalent. Chromatography, Gel. Cloning, Molecular. Coenzymes. *DNA Methylation. DNA Modification Methylases. DNA Restriction Enzymes. Hydrogen-Ion Concentration. Magnesium. Molecular Sequence Data. Molecular Weight. Multienzyme Complexes. Osmolar Concentration. Protein Structure, Tertiary. S-Adenosylmethionine. Sequence Alignment. Substrate Specificity. Support, Non-U.S. Gov't
Geographic Locator:England
ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

296. Title:Structure of the major membrane protein complex from urinary bladder epithelial cells by cryo-electron crystallography
View Article: J Mol Biol 2001 Nov 23;314(2):245-52
CD Volume:344
Print Article: Pages: 245-252
Author(s):Oostergetel GT Keegstra W Brisson A
Author Affiliation:Biophysical Chemistry, Groningen Biomolecular Sciences and Biotechnology Institute, University of Groningen, Nijenborgh 4, AG Groningen, NL-9747, The Netherlands. oostergetel@chem.rug.nl
Abstract:Numerous protein plaques cover the apical surface of mammalian urinary bladder epithelial cells. These plaques contain four integral membrane proteins, called uroplakins, which form a well-ordered array of hexameric complexes. The 3D structure of these naturally occurring 2D crystals was studied by cryo-electron-crystallographic methods using a

slow-scan charged-coupled device (CCD) camera to record the electron micrographs. A 1.2 nm projection map calculated from untilted crystals shows that each hexamer comprises a ring of six inner and six outer domains at a radius of 5.7 nm and 9.2 nm respectively. The 3D structure shows that the mass is distributed strongly asymmetrically with respect to the membrane, with most of the mass protruding from the luminal face. Both domains in the asymmetric unit traverse the membrane and protrude from the membrane on the cytoplasmic side. On the luminal side, the two domains are bridged forming a stretched arc. The total thickness of the complex is about 13.2 nm. A model of the urothelial plaque reveals that contacts between the hexamers are much less extended than within the hexamers

Descriptors:Amyloidosis. Animal. Bladder. *Cryoelectron Microscopy. Crystallization. Epithelial Cells. Fourier Analysis. Freezing. Macromolecular Systems. Membrane Glycoproteins. Membrane Proteins. Mice. Models, Molecular. Molecular Weight. Protein Structure, Quaternary

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

297. Title:Importance of two ATP-binding sites for oligomerization, ATPase activity and chaperone function of mitochondrial Hsp78 protein

View Article: J Mol Biol 2001 Dec 7;314(4):901-10
CD Volume:344
Print Article: Pages: 901-910

Author(s):Krzewska J Konopa G Liberek K
Author Affiliation:Department of Molecular and Cellular Biology, Faculty of Biotechnology, University of Gdansk, Kladki 24, Gdansk, 80-822, Poland

Abstract:The yeast mitochondrial chaperone Hsp78, a homologue of yeast cytosolic Hsp104 and bacterial ClpB, is required for maintenance of mitochondrial functions under heat stress. Here, Hsp78 was purified to homogeneity and shown to form a homo-hexameric complex, with an apparent molecular mass of approximately 440 kDa, in an ATP-dependent manner. Analysis of its ATPase activity reveals that the observed positive cooperativity effect depends both on Hsp78 and ATP concentration. Site-directed mutagenesis of the two putative Hsp78 nucleotide-binding domains suggest that the first nucleotide-binding domain is responsible for ATP hydrolysis and the second one for protein oligomerization. Studies on the chaperone activity of Hsp78 show that its cooperation with the mitochondrial Hsp70 system, consisting of Ssc1p, Mdj1p and Mge1p, is needed for the efficient reactivation of substrate proteins. These studies also suggest that the oligomerization but not the Hsp78 ATPase activity is essential for its chaperone activity

Descriptors:Adenosine Triphosphate. Adenosinetriphosphatase. Allosteric Site. Chromatography, Gel. Cross-Linking Reagents. Fungal Proteins. Glutaral. Heat-Shock Proteins. Luciferase. Microscopy, Electron. Models, Molecular. Molecular Chaperones. Molecular Weight. Mutation. Protein Denaturation. Protein Renaturation. Protein Structure, Quaternary. Protein Structure, Tertiary. Saccharomyces cerevisiae. Support, Non-U.S. Gov't. Urea

Geographic Locator:England

ISSN:0022-2836
Year:2001
Journal Title:Journal of Molecular Biology

298. Title:Impact of environmental factors on fungal respiration and dry matter losses in wheat straw
View Article: Journal of Stored Products Research. 2001. 37 (1). 35-45
CD Volume:368
Print Article: Pages: 35-45
Author(s):Willcock J Naresh Magan
Author Variant:Magan-N
Author Affiliation:Applied Mycology Group, Cranfield Biotechnology Centre, Cranfield University, Cranfield, Bedford MK43 0AL, UK
Language:English
Abstract:An automatic electrolytic respirometer enabled replicated determinations of the respiration rates of individual fungi on sterile straw, and the mixed mycoflora of naturally contaminated wheat straw at different steady-state temperatures (10-30 deg C) and water activities (aw, 0.75-0.98) over periods of 8-14 days. Generally, the respiratory activity of individual spoilage fungi (Alternaria alternata, Cladosporium cladosporioides, Eurotium amstelodami, Fusarium culmorum and Penicillium aurantiogriseum) on sterile wheat straw increased linearly with increasing aw at 25 deg C. The calculated maximum dry matter loss of wheat straw due to colonisation by individual species was about 10%, regardless of aw. On naturally contaminated wheat straw fungal activity was also related to temperature and aw, with maximum respiration at 30 deg C and 0.98 aw. At the lowest temperature examined, 10 deg C, there was a slight lag prior to respiratory activity occurring. The respiratory activity was also significantly reduced (by half) when available water was reduced to 0.95-0.90 aw. In contrast to the colonisation of sterile straw by individual species, the maximum dry matter loss caused by fungal deterioration of naturally contaminated wheat straw was 3.4% at 0.98 aw and 30 deg C. The dominant fungal genera and species varied with aw and temperature. These results are discussed in relation to the storage of cereal straw without spoilage
Descriptors:environmental-factors. plant-pathogenic-fungi. plant-pathogens. postharvest-losses. respiration. storage-decay. storage-disorders. storage-losses. temperature. wheat-straw
Identifiers:Eurotium amstelodami. Hyphomycetes
Organism Descriptors:Alternaria-alternata. Cladosporium-cladosporioides. Fusarium-culmorum. Penicillium-aurantiogriseum
Supplemental Descriptors:Alternaria. Deuteromycotina. Eumycota. fungi. Cladosporium. Eurotium. Eurotiales. Ascomycotina. Fusarium. Penicillium
Subject Codes:SS200. FF610. SS230. FF005. PP500
Supplementary Info:28 ref
ISSN:0022-474X
Year:2001
Journal Title:Journal of Stored Products Research

299. Title:Effect of a copper, cobalt and selenium soluble glass bolus given to grazing sheep
View Article: Livestock Production Science. 2001. 68 (1). 31-39
CD Volume:375
Print Article: Pages: 31-39
Author(s):Kendall N R Mackenzie A M Telfer S B
Author Affiliation:Centre for Animal Sciences, Leeds Institute of Biotechnology and Agriculture, University of Leeds, Leeds LS2 9JT, UK
Language:English
Abstract:Three field trials were carried out during the summer grazing period to evaluate the performance of a sintered soluble glass copper, cobalt

and selenium bolus for maintaining adequate levels of the three trace elements. Thirty-four and 36 growing lowland lambs were used for trials 1 and 2, respectively, whilst trial 3 used 50 year-old nonproductive female upland sheep. In each trial, a bolus was administered to half the population of sheep (bolused) and half remained as control. Blood samples were taken immediately prior to bolus administration and then at regular intervals throughout each trial. The samples were analysed for copper status (serum caeruloplasmin activity and plasma copper concentration), cobalt status (serum vitamin B12 concentration) and selenium status (erythrocyte glutathione peroxidase activity). For trial 1, the bolused sheep at all post-treatment samplings (days 20, 42, and 63) were significantly increased in both cobalt and selenium status ($P<0.001$) compared to the controls; however, there were no significant differences in any other blood parameter. For trial 1, liver copper concentrations were analysed on slaughter samples and were significantly increased for the bolused lambs ($P<0.001$). In trial 2, the bolused sheep had significantly increased selenium and cobalt status ($P<0.001$) for all samples (days 28, 51, 69, 91). In trial 3, the selenium status of the bolused sheep was significantly increased at all three samplings (day 21, $P<0.05$, and days 51 and 105, $P<0.001$), whilst the cobalt status was also significantly increased on all sample days (day 21, $P<0.05$; day 51, $P<0.01$ and day 105 P0.001). The sintered soluble glass copper, cobalt and selenium bolus was able to prevent or correct deficient and/or marginal cobalt and selenium status of sheep throughout these trials. The bolus had little measured effect on the already adequate blood parameters of copper status, although the liver copper concentrations of the bolused sheep were higher in the trial for which they were analysed

Descriptors:boluses. ceruloplasmin. cobalt. copper. ewes. glutathione-peroxidase. grazing. lambs. liver. mineral-deficiencies. selenium. trace-elements. vitamin-B12

Geographic Locator:UK

Organism Descriptors:sheep

Supplemental Descriptors:Ovis. Bovidae. ruminants. Artiodactyla. mammals. vertebrates. Chordata. animals. ungulates. British-Isles. Western-Europe. Europe. Developed-Countries. Commonwealth-of-Nations. European-Union-Countries. OECD-Countries

Subject Codes:LL120. LL500. LL510

Supplementary Info:18 ref

ISSN:0301-6226

Year:2001

Journal Title:Livestock Production Science

300. Title:Electrical stimulation: When more is less

View Article: Meat Science. 57 (2). February, 2001. 145-151

CD Volume:377

Print Article: Pages: 145-151

Author(s):Geesink G H Mareko M H D Morton J D Bickerstaffe R

Author Affiliation:Molecular Biotechnology Group, Animal and Food Sciences Division, Lincoln University, Canterbury: geesinkg@lincoln.ac.nz

Language:English

Language of Summary:English (EN)

Abstract:This study was conducted to determine whether electrical stimulation per se can be omitted when other electrical inputs to beef carcasses (stunning and immobilisation) are used. In addition, we investigated which sample preparation method at 1 day post mortem (p.m.), cooked fresh, frozen, or after thawing, had the best predictive value for

shear force after ageing of the muscle. Beef carcasses were electrically immobilized (75 V, 15 Hz) before and during exsanguination for 20 or 80 s and meat quality characteristics of the longissimus were determined at 1 and 7 days post mortem. Muscles from carcasses receiving the higher electrical input were similar in tenderness at 1 day p.m., but tougher at 7 days p.m. This result could be explained by the effect of muscle shortening and post mortem proteolysis on tenderness. These results indicate that even low electrical input during immobilization can adequately stimulate carcasses and avoid cold shortening. Freezing samples resulted in a considerable improvement in tenderness and cooking samples from the frozen state had the highest predictive value for tenderness after ageing. In a second experiment it was determined that freezing and thawing did not result in appreciable differences in cooking loss or proteolysis. The tenderising effect of freezing may be explained by tissue damage due to ice formation

Descriptors:beef: meat; meat quality; post mortem proteolysis; sheer force; tenderness. Foods; Methods and Techniques

Organism Descriptors:cattle (Bovidae): breed-Angus, steer. muscle: muscular system, shortening

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

Subject Codes:Foods; Methods and Techniques

ISSN:0309-1740
Year:2001
Journal Title:Meat Science

301. Title:Effects of stress and high voltage electrical stimulation on tenderness of lamb m. longissimus

View Article: Meat Science. 57 (3). March, 2001. 265-271
CD Volume:377
Print Article: Pages: 265-271

Author(s):Geesink G H Mareko M H D Morton J D Bickerstaffe R
Author Affiliation:Molecular Biotechnology Group, Animal and Food Sciences Division, Lincoln University, Canterbury: geesinkg@lincoln.ac.nz

Language:English
Language of Summary:English (EN)

Abstract:This study was conducted to investigate the reported effect of pre-slaughter stress on meat tenderness independent from its effect on ultimate pH, and its interaction with electrical stimulation. From a group of 80 Coopworth lamb, 40 were stressed by subjecting the animals to a swim wash 3 h before slaughter and the use of dogs to assemble the animals to the access ramp of the abbatoir. Half of the carcasses of each group was electrically stimulated within 30 min post mortem. Temperature and pH decline of the longissimus was monitored and shear force of the cooked muscle was determined at 2 days post mortem and after 6 weeks vacuum storage at 1degreeC. To investigate an effect of stress independent of ultimate pH, 10 muscles with an ultimate pH below 5.8 were selected from each group for detailed analysis. This analysis consisted of determination of calpastatin activity and sarcomere length, and immunoblotting of mu- calpain and calpain substrates. The stress treatment led to an increase in the number of muscles with an ultimate pH above 5.8 (32.5 vs 15%), and muscles with an ultimate pH above 5.8 were significantly tougher than muscles with an ultimate pH below 5.8 at 2 days post mortem. Electrical stimulation improved tenderness at two days post mortem. This effect could be attributed to an effect on muscle contraction, but not on post mortem

proteolysis of calpain substrates. A large variation in tenderness at 2 days post mortem was observed and this was not reduced by electrical stimulation. Six weeks of vacuum storage resulted in a 6 kgF drop in mean shear force and a uniformly tender product. Despite the fact that the stress treatment was similar to those in earlier studies, we failed to observe an effect of stress independent of ultimate pH on tenderness. The reason for this is unclear, but differences in the response to stress between breeds may be responsible. The results of the present study underscore the importance of minimizing pre-slaughter stress and adequate post mortem storage for meat quality
Descriptors:lamb musculus longissimus: meat, pH, temperature, tenderness; pre-slaughter stress effect; sarcomere length. Foods. calpain substrates; calpastatin; mu-calpain
Organism Descriptors:sheep (Bovidae): breed-Coopworth, lamb
Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Foods
ISSN:0309-1740
Year:2001
Journal Title:Meat Science

302. Title:Metmyoglobin reducing activity and colour stability of ovine longissimus muscle
View Article: Meat Science. 57 (4). April, 2001. 427-435
CD Volume:377
Print Article: Pages: 427-435
Author(s):Bekhit A E D Geesink G H Morton J D Bickerstaffe R
Author Affiliation:Molecular Biotechnology Group, Animal and Food Sciences Division, Lincoln University, Canterbury: bickerst@lincoln.ac.nz
Language:English
Language of Summary:English (EN)
Abstract:Characteristics of metmyoglobin reducing activity in ovine longissimus were determined, and its effect on colour and colour stability of muscle was investigated in two experiments. In the first experiment vacuum packed ovine longissimus samples were incubated at 5-35degreeC during the first 16 h post mortem (n = 8 per treatment). Metmyoglobin reducing activity was negatively affected by incubation temperatures above 30degreeC, but colour and colour stability were little affected at 24 h post mortem and after 2 weeks of vacuum storage at 2degreeC. In the second experiment the effects of pre-slaughter stress and electrical stimulation on metmyoglobin reducing activity, colour and colour stability of ovine longissimus (n = 40) with an ultimate pH below 5.8 were investigated. Neither of the treatments had an effect on metmyoglobin reducing activity or colour parameters. The relatively large variation in metmyoglobin activity and colour parameters allowed correlation analysis. Metmyoglobin reducing activity was not correlated to colour or the colour stability parameters. The results of the present study indicate that metmyoglobin reducing activity is not the primary determinant of colour or colour stability of ovine longissimus muscle
Descriptors:food chemistry; lamb: chemical analysis, meat, preparation, storage; meat color; meat science; rigor; stress. Foods. metmyoglobin: reducing activity analysis
Organism Descriptors:ovine (Bovidae). longissimus muscle: chemistry, color stability, muscular system

Supplemental Descriptors:Bovidae: Artiodactyla, Mammalia, Vertebrata, Chordata, Animalia. Animals; Artiodactyls; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates
Subject Codes:Foods
ISSN:0309-1740
Year:2001
Journal Title:Meat Science

303. Title:Volatile compounds released during ripening in Italian dried sausage
View Article: Meat Science. 58 (1). May, 2001. 93-97
CD Volume:377
Print Article: Pages: 93-97
Author(s):Sunesen L O Dorigoni V Zanardi E Stahnke L
Author Affiliation:Department of Biotechnology, Technical University of Denmark, Building 221, DK-2800, Lyngby: los@ibt.dtu.dk
Language:English
Language of Summary:English (EN)
Abstract:A commercial production was analysed at six stages during ripening. Water content, pH and bacterial counts were followed, and volatile compounds from sausages were extracted by dynamic headspace sampling and analysed by gas chromatography/mass spectrometry. Total concentrations of all classes increased during ripening. Pepper compound concentrations peaked in the middle of the ripening period. Lipid oxidation products increased especially towards the end of ripening, in particular, the compounds 2-heptanol, 1-octen-3- ol, 2-heptanone and 2-nonanone. Surface moulds probably caused 4- heptanone to appear late in the processing. Benzeneacetaldehyde was absent in fresh mince, but increased to become one of the most abundant volatiles. Compounds from carbohydrate catabolism disappeared during the processing
Descriptors:Italian dried sausage; bacterial count; carbohydrate catabolism; pH; sausage ripening; water content. Foods. 1-octen-3-ol; 2-heptanol; 2-heptanone; 2-nonanone; benzeneacetaldehyde; lipid oxidation products; pepper compounds; volatile compounds
Organism Descriptors:mold (Fungi)
Supplemental Descriptors:Fungi: Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Foods
ISSN:0309-1740
Year:2001
Journal Title:Meat Science

304. Title:Lipolytic and proteolytic properties of dry-cured boneless hams ripened in modified atmospheres
View Article: Meat Science. 59 (1). September, 2001. 15-22
CD Volume:377
Print Article: Pages: 15-22
Author(s):Wang Feng Sheng
Author Affiliation:Laboratory of Meat Science and Biotechnology, Lee-Tah Farm Industries (Inc), Kaohsiung: wangfs@ms33.hinet.net
Language:English
Language of Summary:English (EN)
Abstract:We studied proteolytic and lipolytic properties of dry-cured boneless ham (porcine quadriceps femoris) made with chilled (10degreeC, 48 h) or frozen/thawed meat (frozen at -20degreeC frozen for 90 days and followed by thawing at 10degreeC for 48 h) were determined. Dry-cured meats were stored in modified atmosphere packages (100% N2 and a

mixture of 75% N2+25% CO2) at 15degreeC with the intention of reducing ripening space. Results showed that dry-cured hams made with frozen/thawed raw meat had more salt, volatile fatty acids and free fatty acid content after salting and smoking. Whereas, samples prepared with chilled meats contained more nitrogenous compounds (water-soluble nitrogen, non-protein nitrogen, and free amino acids). Volatile and free fatty acid contents in all samples significantly increased with storage. Acetic acid was the predominant volatile fatty acid. To confirm lipolytic activity in dry-cured ham stored in modified atmospheres, we calculated the lipolytic coefficient. The lipolytic coefficients of all samples were positive values and significantly (P<0.05) increased with storage indicating lipolysis in samples were still active. Furthermore, nitrogenous compounds in dry-cured ham significantly (P<0.05) increased with storage indicating proteolysis in samples were not affected by modified atmosphere storage. Aerobic, anaerobic and lactic acid bacteria counts in dry-cured meats were stable to modified atmospheres storage for 20 weeks at 15degreeC. Flavor, texture and color score in sensory evaluation for dry-cured ham made with chilled meat were significantly higher than that made with forzen/thawed meat. All samples had high overall acceptance scores in sensory evaluation. Results in this study suggested that dry-cured boneless ham stored in modified atmospheres for 20 weeks at 15degreeC was another feasibility to ripen the meat without affecting lipolysis, proteolysis, microbiology and sensory quality

Descriptors:dry-cured boneless ham: lipolytic properties, meat product, microbiology, proteolytic properties, sensory quality. Foods. acetic acid; free fatty acids; non-protein nitrogen; salt; volatile fatty acids; water-soluble nitrogen

Organism Descriptors:aerobic bacteria (Bacteria); anaerobic bacteria (Bacteria); lactic acid bacteria (Bacteria)

Supplemental Descriptors:Bacteria: Microorganisms. Bacteria; Eubacteria; Microorganisms

Subject Codes:Foods

ISSN:0309-1740
Year:2001
Journal Title:Meat Science

305. Title:Quality properties of sausage made with gamma-irradiated natural pork and lamb casing

View Article: Meat Science. 59 (3). November, 2001. 223-228
CD Volume:377
Print Article: Pages: 223-228

Author(s):Byun M W Lee J W Jo C Yook H S
Author Affiliation:Team for Radiation Food Science and Biotechnology, Korea Atomic Energy Research Institute, Yusong, Taejon, 305-600

Language:English
Language of Summary:English (EN)

Abstract:Quality properties in emulsion-type sausage stuffed into irradiated natural casing were studied. Fresh salted and semidried natural pork and lamb casing was washed and irradiated at 0, 3, and 5 kGy by gamma-ray and emulsion-type pork sausage (Brattella Weiss Wurst) was manufactured. The sausage was stored in a 4degreeC refrigerator. The numbers of total aerobic bacteria, Enterococcus and coliform bacteria in the irradiated natural casing or sausage prepared from irradiated casing were significantly decreased or eliminated compared to those of the nonirradiated control. The D10 values of total aerobic bacteria of the pork and lamb casing were 0.87 and 0.92 kGy, respectively. The

vacuum-packaged sausages made with irradiated casings had a higher 2-thiobarbituric acid reactive substances value than that of the nonirradiated controls only at 5- day with pork casing and at 10-day with lamb casing. The total working force for shear of the sausages was decreased in both irradiated casings but the sensory evaluation showed no difference. Therefore, the gamma irradiation was a useful technique to sanitize the natural pork and lamb casings and to extend shelf-life, primarily microbial quality, of the sausage made with natural casings

Descriptors:natural lamb casing; natural pork casing; pork sausage: meat product, microbial quality, shelf-life. Foods. 2-thiobarbituric acid reactive substances

Organism Descriptors:Enterococcus (Gram-Positive Cocci); aerobic bacteria (Bacteria); coliform (Enterobacteriaceae)

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

Subject Codes:Foods

ISSN:0309-1740
Year:2001
Journal Title:Meat Science

306. Title:Impact of introducing specifications on the tenderness of retail meat

View Article: Meat Science. 59 (3). November, 2001. 303-315
CD Volume:377
Print Article: Pages: 303-315

Author(s):Bickerstaffe R Bekhit A E D Robertson L J Roberts N Geesink G H
Author Affiliation:Molecular Biotechnology Group, Animal and Food Sciences Division, Lincoln University, Canterbury: bickerst@lincoln.ac.nz

Language:English
Language of Summary:English (EN)

Abstract:Over a 3-year period (1997-1999), the shear force of 4371 retail beef, lamb and pork midloin samples collected from 363 retail outlets were tested using a MIRINZ tenderometer. Information about aging time, processor and retail chain was recorded. Consumers (n = 2313) were also surveyed on their perception of the tenderness of beef and lamb midloin samples with known shear force. The results validated that shear force, as measured by the MIRINZ tenderometer, could be used to create instrumental tenderness categories which reflected consumer perceptions of tenderness. Over the 3-year sampling period, the shear force of beef and lamb decreased by 21.9 and 17.2%, respectively, and there was a consistent decrease in the number of 'tough' samples. The improvement in tenderness coincided with the introduction of a Quality Mark program in 1997 for beef and lamb and 3 years of implementation by auditing. The Quality Mark program sets specifications for the quality of retail meat in New Zealand and guidelines to achieve these specifications. In comparison to retail beef and lamb, the shear force of retail pork decreased marginally by 7.9%. Furthermore, the decrease in the number of 'tough' pork samples was not consistent over the testing period. Analysis of these data showed that for all three meats a considerable improvement in tenderness can be achieved by adopting a minimum post-slaughter aging time and optimizing the processing conditions

Descriptors:Quality Mark program; food processor chain; food retail chain; retail beef midloin: meat, tenderness; retail lamb midloin: meat, tenderness; retail pork midloin: meat, tenderness. Foods

Subject Codes:Foods

ISSN:0309-1740
Year:2001
Journal Title:Meat Science

307. Title:Quality properties of pork sausage prepared with water-soluble chitosan oligomer
View Article: Meat Science. 59 (4). December, 2001. 369-375
CD Volume:377
Print Article: Pages: 369-375
Author(s):Jo C Lee J W Lee K H Byun M W
Author Affiliation:Team for Radiation Food Science and Biotechnology, Korea Atomic Energy Research Institute, Yusong, Taejon, 305-600: mwbyun@kaeri.re.kr
Language:English
Language of Summary:English (EN)
Abstract:Emulsion type sausage was prepared with the addition of a chitosan oligomer (molecular weight 5000, 0.2%) and compared to a control. Sausages were aerobic- or vacuum-packaged and stored in a 4degreeC refrigerator for 3 weeks. Difference of microbial growth between the sample with added chitosan oligomer or control was not observed (P>0.05). Lipid oxidation was lower in the sausage with chitosan oligomer at 3 weeks in aerobic packaging (P<0.05) than in the control sausage. The surface color of the sausage with chitosan oligomer had higher Hunter color L*- and b*-value. Hunter color a*- values were lower in the chitosan oligomer-added sausage and the a*- value increased during storage regardless of packaging (P<0.05). Sensory panels did not detect any difference in color, flavor, texture, and overall acceptance, and mechanical texture analysis also showed no difference. Therefore, the quality of the sausage with added chitosan oligomer (0.2%) was acceptable
Descriptors:microbial growth; pork sausage: acceptance, color, flavor, meat, quality properties, surface color, texture. Foods. chitosan oligomer: water-soluble; lipid: oxidation
Subject Codes:Foods
ISSN:0309-1740
Year:2001
Journal Title:Meat Science
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308. Title:Comparative absorption, translocation, and metabolism of foliar-applied oxyfluorfen in wheat and barley
View Article: Pesticide Biochemistry and Physiology. 70 (2). June, 2001. 118-125
CD Volume:372
Print Article: Pages: 118-125
Author(s):Chun Jae Chul Lee Hee Jae Lim Sung Jin Kim Sung Eun Guh Ja Ock
Author Affiliation:Faculty of Biotechnology, Chonbuk National University, Chonju, 561-756: jcchun@moak.chonbuk.ac.kr
Language:English
Language of Summary:English (EN)
Abstract:Wheat is known to be relatively tolerant to diphenyl ether herbicides. The absorption, translocation, and metabolism of foliar- applied oxyfluorfen in wheat were examined in comparison with those of oxyfluorfen-susceptible barley. Epicuticular wax contents in the first fully expanded leaves were similar in wheat and barley, but the wheat leaves had a 1.74-fold higher cuticle content than the barely leaves. Absorption of (14C)oxyfluorfen, as estimated by the amount of (14C)oxyfluorfen penetrating the cuticle, appeared to be similar in the leaves of both species, although most of the radioactivity

remained in the epicuticular wax. Little translocation of the herbicide out of the treated leaf was observed in either species, but slightly more translocation of (14C)oxyfluorfen to shoots other than the treated leaf or to roots was found in barley than in wheat leaves. Autoradiographs of the (14C)oxyfluorfen-treated leaves of both species also showed that the radioactivity was distributed mainly in the treated site. Thin- layer chromatographic analysis of leaf extracts revealed that oxyfluorfen metabolism did not occur in intact leaves of either species. The binding constants for the herbicide were estimated as 44.2 and 191 nM, respectively, for wheat and barley etioplasts, showing that the herbicide had higher affinity to barley than to wheat etioplasts. These results indicate that the differential susceptibilities of wheat and barley to oxyfluorfen are not due to the differential absorption, translocation, and metabolism of the herbicide, but to the differential affinity of the herbicide

Descriptors:Biochemistry and Molecular Biophysics; Pesticides. [carbon-14 labeled] oxyfluorfen; diphenyl ether herbicide: herbicide; epicuticuar wax; oxyfluorfen

Organism Descriptors:barley (Gramineae); wheat (Gramineae). leaf; root

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

Subject Codes:Biochemistry and Molecular Biophysics; Pesticides

ISSN:0048-3575
Year:2001
Journal Title:Pesticide Biochemistry and Physiology

309. Title:Relationship between transmembrane ion movements, production of reactive oxygen species and the hypersensitive response during the challenge of tobacco suspension cells by zoospores of Phytophthora nicotianae

View Article: Physiological and Molecular Plant Pathology. 2001. 58 (5). 189-198
CD Volume:378
Print Article: Pages: 189-198

Author(s):Able A J Guest D I Sutherland M W
Author Affiliation:Centre for Rural and Environmental Biotechnology, Department of Biological and Physical Sciences, Faculty of Sciences, University of Southern Queensland, Toowoomba, Qld. 4350, Australia

Language:English

Abstract:The defence responses of tobacco (Nicotiana tabacum) cells challenged with zoospores of the tobacco black shank pathogen Phytophthora nicotianae were studied. To examine the role of Ca2+, calcium chloride and/or a range of widely used Ca2+ modulators, which included a chelator (EGTA), and ionophore (A23187) and a Ca2+ channel blocker (LaCl3) were added to the tobacco/Phytophthora system. The results suggest that both reactive oxygen species (ROS) production and the hypersensitive response (HR) in resistant cell cultures are dependent on early transmembrane movements of endogenous extracellular Ca2+ reserves. K+ efflux is a late event that is independent of H+ movements, dependent on the release of ROS and coincident with the onset of the HR. The exterior cell medium became more acidic in all treatments, arguing against the activation of alkaline peroxidases as a major source of the ROS burst

Descriptors:calcium-ions. cell-cultures. defence-mechanisms. efflux. hydrogen-ions. plant-pathogenic-fungi. plant-pathogens. potassium. tobacco. zoospores

Organism Descriptors:Nicotiana. Nicotiana-tabacum

Supplemental Descriptors:Nicotiana. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF060. FF610. HH600
Supplementary Info:57 ref
ISSN:0885-5765
Year:2001
Journal Title:Physiological and Molecular Plant Pathology
Copyright:Copyright CAB International

310. Title:In this issue "phytoalexins into the 21st century"
View Article: Physiological and Molecular Plant Pathology. 2001. 59 (2). 59-61
CD Volume:378
Print Article: Pages: 59-61
Author(s):Hammerschmidt R Kagan I A
Language:English
Abstract:The role of phytoalexins in plant defence against pathogens are reviewed. Techniques for isolating, characterizing and describing these substances and their functions are presented. Some of these techniques include the use of biotechnology and molecular biology in studying and quantifying phytoalexins
Descriptors:analytical-methods. biotechnology. characterization. chemical-composition. defence-mechanisms. molecular-biology. plant-pathogens. phytoalexins. plant-composition. quantitative-techniques. disease-resistance
Subject Codes:FF020. FF040. FF610. WW000. ZZ900. HH600
Supplementary Info:26 ref
ISSN:0885-5765
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Journal Title:Physiological and Molecular Plant Pathology
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311. Title:Ellagic acid rhamnosides from the stem bark of Eucalyptus globulus
View Article: Phytochemistry (Oxford). 57 (4). June, 2001. 587-591
CD Volume:371
Print Article: Pages: 587-591
Author(s):Kim Jong Pyung Lee In Kyoung Yun Bong Sik Chung Sung Hyun Shim Gyu Seop Koshino Hiroyuki Yoo Ick Dong
Author Affiliation:Korea Research Institute of Bioscience and Biotechnology, Yusong, Taejon, 305-600: idyoo@mail.kribb.re.kr
Language:English
Language of Summary:English (EN)
Abstract:Four ellagic acid rhamnosides were isolated from the stem bark of Eucalyptus globulus. Their structures have been established on the basis of the analysis of their 1H NMR, 13C NMR, HMBC, IR and MS spectral data. The HMBC data of these compounds were most useful for their structure determinations, with these bring determined to be 3-O-methylellagic acid 3'-O-alpha-rhamnopyranoside, 3-O- methylellagic acid 3'-O-alpha-3''-O-acetylrhamnopyranoside, 3-O- methylellagic acid 3'-O-alpha-2''-O-acetylrhamnopyranoside, 3-O- methylellagic acid 3'-O-a-4''-O-acetylrhamnopyranoside, respectively. Their antioxidant activities were evaluated by measuring the inhibition of lipid peroxidation using rat liver microsomes, with IC50 values of 10.0-14.0 mug/ml
Descriptors:antioxidant activity. Biochemistry and Molecular Biophysics. ellagic acid rhamnosides
Organism Descriptors:Eucalyptus globulus (Myrtaceae); rat (Muridae). liver: digestive system; stem bark
Supplemental Descriptors:Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia; Myrtaceae: Dicotyledones, Angiospermae, Spermatophyta,

Plantae. Angiosperms; Animals; Chordates; Dicots; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Plants; Rodents; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Biochemistry and Molecular Biophysics
ISSN:0031-9422
Year:2001
Journal Title:Phytochemistry

312. Title:Glycosides and xanthine oxidase inhibitors from Conyza bonariensis
View Article: Phytochemistry. 2001. 58 (4). 645-651
CD Volume:371
Print Article: Pages: 645-651
Author(s):Kong L D Abliz Z Zhou C X Li L J Cheng C H K Tan R X
Author Affiliation:Institute of Functional Biomolecule, State Key Laboratory of Pharmaceutical Biotechnology, School of Life Science, Nanjing University, Nanjing 210093, China
Language:English
Abstract:Fractionation of the xanthine oxidase (the enzyme related to hyperuricemia and gout) inhibitory methanol extract of C. bonariensis (collected from Xuanwu Lake Park, China on 19 June 1996) afforded three glycosides, in addition to nine known compounds including amyrin, beta -sitosterol daucosterol [beta -phytosterol daucosterol], syringic acid 3-hydroxy-5-methoxybenzoic acid, eugenol 4-O-glucopyranoside, and luteolin, apigenin and takakin 8-O-glucuronide. The structures of the glycosides were established by a combination of spectroscopic methods (IR,MS, 1H, 13C NMR, DEPT, COSY, HMQC and HMBC) as 4-hydroxypyridin-3-carboxylic acid 4-O-glucopyranoside, 8-hydroxy-6,7-dihydrolinalool 8-O-glucopyranoside and bonaroside [viz. 1, 3, 4, 12-tetrahydroxy-2-(9-hexadecenoylamino)octadecane 1-O-glucopyranoside]. The in vitro enzyme assay showed that syringic acid and takakin 8-O-glucuronide displayed weak inhibitory activity against xanthine oxidase with IC50 values of 500 plus or minus 41 micro M and 170 plus or minus 12 micro M, respectively
Descriptors:chemical-composition. chemical-structure. enzyme-inhibitors. enzymes. glycosides. medicinal-plants. medicinal-properties. phytosterols. plant-composition. plant-extracts. xanthine-oxidase
Geographic Locator:China
Organism Descriptors:Conyza-bonariensis
Supplemental Descriptors:East-Asia. Asia. Developing-Countries. Conyza. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF040. SS200. SS230. VV730
Supplementary Info:32 ref
ISSN:0031-9422
Year:2001
Journal Title:Phytochemistry

313. Title:A serine endopeptidase from cucumber leaves is inhibited by L-arginine, guanidino compounds and divalent cations
View Article: Phytochemistry (Oxford). 58 (5). November, 2001. 677-682
CD Volume:371
Print Article: Pages: 677-682
Author(s):Yamauchi Yasuo Sugimoto Toshio Sueyoshi Kuni Oji Yoshikiyo Tanaka Kiyoshi
Author Affiliation:Laboratory of Plant Biotechnology, Faculty of Agriculture, Tottori University, Koyama, Tottori, 680-8553: yamauchi@muses.tottori-u.ac.jp

Language:English
Language of Summary:English (EN)
Abstract:An endopeptidase was purified and characterized from green leaves of cucumber (Cucumis sativus L. suyo). The purified enzyme, a basic amino acid-specific endopeptidase with a pI of 5.0, was a monomeric protein of 80 kDa whose pH optimum was 9.5. Inhibitor analysis suggested that it was a serine endopeptidase and contained sulfhydryl groups essential for catalytic activity. Analysis of internal amino acid sequences of the endopeptidase showed no significant similarity to other proteins. Its activity was inhibited by L-Arg and quanidino compounds having high hydrophobicity, as well as divalent cations such as Mg2+ and Ca2+. The Ki values of L-Arg and Mg2+, which are also likely in vivo inhibitors, were 3.5 and 10 mM, respectively. Inhibition by L-Arg and Mg2+ was additive, and more than 70% of the activity was reversibly inhibited under their physiologically significant concentrations. These results suggest that the enzyme is possibly regulated by L-Arg and/or guanidino compounds, and by divalent cations in vivo
Descriptors:photochemistry. Enzymology (Biochemistry and Molecular Biophysics). L-arginine: enzyme inhibitor; arginine; calcium ion: enzyme inhibitor; divalent cations: enzyme inhibitor; guanidino compounds: enzyme inhibitor; magnesium ion: enzyme inhibitor; serine endopeptidase
Organism Descriptors:Cucumis sativus (Cucurbitaceae). leaf
Supplemental Descriptors:Cucurbitaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae. Angiosperms; Dicots; Plants; Spermatophytes; Vascular Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics)
ISSN:0031-9422
Year:2001
Journal Title:Phytochemistry

314. Title:Physiological function of bromoperoxidase in the red marine alga, Corallina pilulifera: Production of bromoform as an allelochemical and the simultaneous elimination of hydrogen peroxide
View Article: Phytochemistry (Oxford). 58 (5). November, 2001. 683-692
CD Volume:371
Print Article: Pages: 683-692
Author(s):Ohsawa Noboru Ogata Yasuhiro Okada Noriyuki Itoh Nobuya
Author Affiliation:Biotechnology Research Center, Toyama Prefectural University, Kurokawa 5180, Kosugi, Toyama, 939-0398: itoh@pu-toyama.ac.jp
Language:English
Language of Summary:English (EN)
Abstract:The physiological function of vanadium-bromoperoxidase (BPO) in the marine red alga, Corallina pilulifera, has been characterized from the viewpoint of allelochemical formation. The algae emit bromoform (CHBr3) depending on the enzyme activity level in vivo (Itoh, N., Shinya, M., 1994. Seasonal evolution of bromomethanes from coralline algae and its effect on atmospheric ozone. Marine Chemistry 45, 95-103). We demonstrated that bromoform produced by C. pilulifera played an important role in eliminating epiphytic organisms, especially microalgae on the surface. Such data suggest a strong relationship between the coralline algae and the coralline flat (deforested area in the marine environment: called isoyake in Japanese). Lithophyllum yessoense, the main inhabitant of coralline flats in Japan, produced a lower level of CHBr3 than C. pilulifera, and showed BPO activity. On the other hand, the seasonal change of BPO activity in C. pilulifera in vivo was in proportion to superoxide dismutase (SOD) activity and in inverse proportion to catalase activity. The phenomenon implies

that BPO could be a potential substitute for catalase, because the enzyme catalyzes and efficient Br--dependent catalase reaction
Descriptors:photochemistry. Enzymology (Biochemistry and Molecular Biophysics); Physiology. bromoform: allelochemical, production; bromoperoxidase: physiological function; hydrogen peroxide: simultaneous elimination; vanadium-bromoperoxidase
Organism Descriptors:Corallina pilulifera (Rhodophyta): marine species
Supplemental Descriptors:Rhodophyta: Algae, Plantae. Algae; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Enzymology (Biochemistry and Molecular Biophysics); Physiology
ISSN:0031-9422
Year:2001
Journal Title:Phytochemistry

315. Title:Induction of phenylalanine ammonia-lyase activity by tryptophan in Ustilago maydis
View Article: Phytochemistry (Oxford). 58 (6). November, 2001. 849-857
CD Volume:371
Print Article: Pages: 849-857
Author(s):Kim Seong Hwan Kronstad James W Ellis Brian E
Author Affiliation:Biotechnology Laboratory, Faculty of Agricultural Sciences, University of British Columbia, 2424 Main Mall, Vancouver, BC, V6T 1Z4; E-Mail: bee@interchg.ubc.ca
Language:English
Abstract:To understand the regulation of phenylalanine ammonia-lyase (PAL) activity in the corn smut fungus, Ustilago maydis, we examined the effects of different media, metabolic effectors (including aromatic amino acids), and environmental factors on induction and repression of PAL activity. PAL was detected only in cell extracts and not in the culture medium. U. maydis PAL is constitutively produced at a low level in all media tested but its regulation can be influenced by aromatic amino acids. L-Tryptophan (0.3 mM) induces PAL activity 3- to 5-fold but tryptophan analogs and tryptophan-related metabolites do not. The enzyme is most readily induced during the early stationary phase of growth and the induced activity remains relatively constant during stationary stage. No induction or inhibition of PAL activity was observed as a function of culture temperature, pH or light. PAL induction was repressed by glucose but not by its reaction product, t-cinnamic acid. Induction did not require de novo protein synthesis, suggesting that some form of post-translational protein modification or a metabolic effect may be involved. This study shows that the regulation of U. maydis PAL is very different from the patterns known for plants and other fungi
Descriptors:Biochemistry and Molecular Biophysics; Enzymology (Biochemistry and Molecular Biophysics); Infection. corn smut: fungal disease. phenylalanine ammonia-lyase: activity induction, regulation; tryptophan: enzyme inducer
Organism Descriptors:Ustilago maydis (Basidiomycetes): pathogen
Supplemental Descriptors:Basidiomycetes: Fungi, Plantae. Fungi; Microorganisms; Nonvascular Plants; Plants
Subject Codes:Biochemistry and Molecular Biophysics; Enzymology (Biochemistry and Molecular Biophysics); Infection
ISSN:0031-9422
Year:2001
Journal Title:Phytochemistry

316. Title:High molecular compounds (polysaccharides and proanthocyanidins) from Hamamelis virginiana bark: Influence on human skin keratinocyte proliferation and differentiation and influence on irritated skin
View Article: Phytochemistry (Oxford). 58 (6). November, 2001. 949-958
CD Volume:371
Print Article: Pages: 949-958
Author(s):Deters Alexandra Dauer Andreas Schnetz Esther Fartasch Manige Hensel Andreas
Author Affiliation:Pharmaceutical Biotechnology, Glycopharmacy Research Group, Hochschule Wadenswil, University of Applied Sciences, Gruental, CH-8820, Wadenswil; E-Mail: a.hensel@hswzfh.ch
Language:English
Abstract:Although extracts from Hamamelis bark have long been used in therapy of skin diseases and in cosmetic formulas there are only few pharmacological investigations verifying the activity of distinct Hamamelis bark constituents. Therefore two major classes of constituents, namely polymeric proanthocyanidins and polysaccharides were isolated from Hamamelis bark and tested concerning their influence on proliferation and differentiation of cultured human keratinocytes. While the polysaccharide fraction, consisting mainly of arabans and arabinogalactans, did not effect human keratinozytes, the proanthocyanidins strongly increased the proliferation of the cells, while the differentiation was not influenced significantly. Within a preliminary cumulative in vivo study on SLS-irritated skin, proanthocyanidins (ProcyanoPlus) were proven to reduce transepidermal water loss and erythema formation. Furthermore, a clinical scoring indicated that procyanidins can influence irritative processes significantly
Descriptors:Biochemistry and Molecular Biophysics; Dermatology (Human Medicine, Medical Sciences); Pharmacognosy (Pharmacology). ProcyanoPlus: dermatological-drug; polysaccharides; proanthocyanidins
Organism Descriptors:Hamamelis virginiana (Hamamelidaceae): medicinal plant; human (Hominidae). skin: integumentary system, keratinocyte proliferation
Supplemental Descriptors:Hamamelidaceae: Dicotyledones, Angiospermae, Spermatophyta, Plantae; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia. Angiosperms; Animals; Chordates; Dicots; Humans; Mammals; Plants; Primates; Spermatophytes; Vascular Plants; Vertebrates
Subject Codes:Biochemistry and Molecular Biophysics; Dermatology (Human Medicine, Medical Sciences); Pharmacognosy (Pharmacology)
ISSN:0031-9422
Year:2001
Journal Title:Phytochemistry

317. Title:Taxines from the needles of Taxus wallichiana
View Article: Phytochemistry (Oxford). 58 (8). December, 2001. 1167-1170
CD Volume:371
Print Article: Pages: 1167-1170
Author(s):Prasain Jeevan Kumar Stefanowicz Piotr Kiyota Taira Habeichi Farida Konishi Yasuo
Author Affiliation:Biotechnology Research Institute, National Research Council Canada, 6100 Royalmount Avenue, Montreal, Quebec, H4P 2R2; E-Mail: yasuo.konishi@nrc.ca
Language:English
Abstract:A taxine, 5alphaO-(3'-dimethylamino-3'-phenylpropionyl) taxinine M (1) together with two known compounds 7-O-acetyltaxine A (2) and 2alpha-acetoxy-2'beta-deacetylaustrospicatine (3) were isolated from the

needles of the Himalayan yew, Taxus wallichiana Zucc. Their structures were elucidated on the basis of the NMR spectral data, ESI-MS/MS analysis and chemical methods. Compounds 1 and 3 showed moderate cytotoxic activity against the lung cancer cell line A549 in vitro

Descriptors:Biochemistry and Molecular Biophysics; Pharmacognosy (Pharmacology). 2 alpha-acetoxy-2'beta-deacetylaustrospicatine; 5 alpha O-(3'-dimethylamino-3'-phenylpropionyl) taxinine: cytotoxicity, taxine; 7-O-acetyltaxine

Organism Descriptors:A549 cell line (Hominidae); Taxus wallichiana [Himalayan yew] (Taxopsida): medicinal plant. needle

Supplemental Descriptors:Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Taxopsida: Gymnospermae, Spermatophyta, Plantae. Animals; Chordates; Gymnosperms; Humans; Mammals; Plants; Primates; Spermatophytes; Vascular Plants; Vertebrates

Subject Codes:Biochemistry and Molecular Biophysics; Pharmacognosy (Pharmacology)

ISSN:0031-9422
Year:2001
Journal Title:Phytochemistry

318. Title:Corn uptake and microbial immobilization of 15N-labeled urea-N in soil as affected by composted pig manure

View Article: Plant and Soil. 2001. 235 (1). 1-9
CD Volume:372
Print Article: Pages: 1-9

Author(s):Choi WooJung Jin SeongAhi Lee SangMo Ro HeeMyong Yoo SunHo
Author Variant:Choi-W-J. Jin-S-A. Lee-S-M. Ro-H-M. Yoo-S-H
Author Affiliation:School of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Suwon 441-744, Korea Republic

Language:English

Abstract:A pot experiment using sandy loam soils was conducted to study the effect of combined application of composted pig manure and urea on the availability of urea for maize (Zea mays). Maize was cultivated for 30 and 60 days. 15N-Labelled urea (6.17 15N atom %) was added to soil at 0, 37.5, 75 and 150 kg N ha-1, and unlabelled compost (0.37 15N atom %) was added at 0 and 150 kg N ha-1. After 30 days growth, the uptake efficiencies of applied N by maize were 51.6 and 55.8%, for the treatments of 75 kg urea and 150 kg compost-N ha-1, respectively. However, the efficiencies decreased to 32.5% for urea-N and 31.6% for compost-N under the mixed treatment of both N inputs at the rate of 75 kg urea and 150 kg compost-N ha-1, due to the competition of N for maize uptake. After 60 days growth, the urea-N efficiencies were 38.7, 46,8 and 49.6% for the treatments receiving urea at 37.5, 75 and 150 kg N ha-1, they then decreased to 32.9, 39.3 and 39.7%, respectively, by the combined application of 150 kg compost-N ha-1. However, the efficiency of compost-N was approx equal to 60% irrespective of urea-N addition. The urea-N uptake efficiency, measured using non-isotopic regression technique, was slightly higher by approx equal to 10% than the isotopic technique, an indication of pool substitution. However, a large increase in maize uptake of soil-N or compost-N was not observed. After a 60-day growth period, the percentages of applied urea-N which was immobilized in the soil in 2 M KCl non-extractable form were 13.6 to 21.7% for treatments without compost and 32.8 to 41.2% with compost. These results suggest that the high immobilization of urea-N in soils through the combined application of compost compared to treatments without compost was responsible for the lower uptake efficiency of urea-N by maize

Descriptors:application-rates. composts. immobilization. maize. microbial-activities. nitrogen. nitrogen-fertilizers. nutrient-availability. nutrient-uptake. pig-manure. plant-nutrition. pot-experimentation. sandy-loam-soils. soil-types. urea
Organism Descriptors:Zea-mays
Supplemental Descriptors:Zea. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF061. JJ100. JJ700. XX100
Supplementary Info:37 ref
ISSN:0032-079X
Year:2001
Journal Title:Plant and Soil
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319. Title:Isolation, partial characterization, and the effect of plant growth-promoting bacteria (PGPB) on micro-propagated sugarcane in vitro
View Article: Plant and Soil. 2001. 237 (1). 47-54
CD Volume:372
Print Article: Pages: 47-54
Author(s):Mirza M S Waseem Ahmad Latif F Haurat J Bally R Normand P Malik K A
Author Affiliation:Biofertilizer Division, National Institute for Biotechnology and Genetic Engineering (NIBGE), P.O.Box 577, Jhang Road, Faisalabad, Pakistan
Language:English
Abstract:We report the isolation of nitrogen fixing, phytohormone producing bacteria from sugarcane and their beneficial effects on the growth of micropropagated sugarcane plantlets. Detection of the nitrogen fixing bacteria by ARA-based MPN (acetylene reduction assay-based most probable number) method indicated the presence of up to 106 bacteria per gram dry weight of stem and 107 bacteria per gram dry weight of root of field-grown sugarcane. Two nitrogen fixing bacterial isolates were obtained from stem (SC11, SC20) and two from the roots (SR12, SR13) of field-grown plants. These isolates were identified as Enterobacter spp. strains on the basis of their morphological characteristics and biochemical tests. The isolate SC20 was further characterized by 16S rRNA sequence analysis, which showed high sequence similarity to the sequence of Enterobacter cloacae and Klebsiella oxytoca. All the isolates produced the phytohormone indoleacetic acid (IAA) in pure culture and this IAA production was enhanced in growth medium containing tryptophan. The bacterial isolates were used to inoculate micro-propagated sugarcane in vitro where maximum increase in the root and shoot weight over control was observed in the plantlets inoculated with strain SC20. By using the 15N isotope dilution technique, maximum nitrogen fixation contribution (28% of total plant nitrogen) was detected in plantlets inoculated with isolate SC20
Descriptors:growth. IAA. in-vitro-culture. micropropagation. nitrogen-fixation. nitrogen-fixing-bacteria. nucleotide-sequences. plant-growth-regulators. roots. stems. sugarcane. tryptophan
Organism Descriptors:Enterobacter-cloacae. Klebsiella-oxytoca. Saccharum. Saccharum-officinarum
Supplemental Descriptors:Enterobacter. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. Klebsiella. Saccharum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF007. FF060. FF170. JJ100
Supplementary Info:many ref
ISSN:0032-079X
Year:2001
Journal Title:Plant and Soil

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320. Title:Variation in sensitivity of Western Australian isolates of Phytophthora cinnamomi to phosphite in vitro
View Article: Plant Pathology. 2001. 50 (1). 83-89
CD Volume:372
Print Article: Pages: 83-89
Author(s):Wilkinson C J Shearer B L Jackson T J Hardy G E St J
Author Affiliation:School of Biological Sciences and Biotechnology, Murdoch University, South Street, Perth, Western Australia 6150, Australia
Language:English
Abstract:Seventy-one Australian isolates of Phytophthora cinnamomi (68 from Western Australia) were tested for sensitivity to phosphite on Ribeiro's modified medium. Isolates formed a continuum in their response to phosphite, but could be divided into sensitive (9% of isolates), intermediate (82%) and tolerant (9%) groups. Sensitivity varied between isolates, with EC50 values ranging from 4 to 148 micro g phosphite mL-1. Phytophthora cinnamomi A1 mating-type isolates were at the upper end of the range of tolerance shown by the A2 mating-type isolates
Descriptors:fungicide-tolerance. fungicides. plant-pathogenic-fungi. plant-pathogens
Geographic Locator:Australia. Western-Australia
Identifiers:isolates. phosphite
Organism Descriptors:Phytophthora-cinnamomi
Supplemental Descriptors:Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Phytophthora. Peronosporales. Mastigomycotina. Eumycota. fungi. Australia
Subject Codes:FF610. HH410
Supplementary Info:20 ref
ISSN:0032-0862
Year:2001
Journal Title:Plant Pathology
Copyright:Copyright CAB International

321. Title:Population structure and possible origin of Amylostereum areolatum in South Africa
View Article: Plant Pathology. 2001. 50 (2). 206-210
CD Volume:372
Print Article: Pages: 206-210
Author(s):Slippers B Wingfield M J Coutinho T A Wingfield B D
Author Affiliation:Faculty of Agricultural and Biological Sciences, Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa
Language:English
Abstract:The woodwasp, Sirex noctilio, and its symbiotic fungus, Amylostereum areolatum, cause extensive damage to pine plantations in the Southern Hemisphere. S. noctilio was first reported from South Africa in 1994. In this study, the population diversity of A. areolatum isolates from South Africa, South America, Australasia and Europe was determined by vegetative incompatibility testing. All 108 South African and 26 South American isolates belonged to the same vegetative compatibility group (VCG). This VCG showed a weak incompatibility reaction with the single Tasmanian and single New Zealand isolates tested. This VCG differed from VCGs from Europe. It also differed from isolates associated with the biocontrol nematode, Deladenus siricidicola, which is produced in Australia. It is concluded that the South African and South American populations of A. areolatum share a common origin

Descriptors:biological-control-agents. forest-pests. incompatibility. insect-pests. plant-pests. population-structure
Geographic Locator:Europe. New-Zealand. South-Africa. South-America. Tasmania
Identifiers:Deladenus siricidicola. Tylenchida
Organism Descriptors:Amylostereum-areolatum. Deladenus. insects. Sirex-noctilio
Supplemental Descriptors:Amylostereum. Aphyllophorales. Basidiomycotina. Eumycota. fungi. Neotylenchidae. Nematoda. invertebrates. animals. Deladenus. Allantonematidae. Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Sirex. Siricidae. Hymenoptera. insects. arthropods. Southern-Africa. Africa-South-of-Sahara. Africa. Developing-Countries. Threshold-Countries. Anglophone-Africa. America. Australia
Subject Codes:FF620. YY700. ZZ380. ZZ395
Supplementary Info:31 ref
ISSN:0032-0862
Year:2001
Journal Title:Plant Pathology

322. Title:Molecular characterization of Endothia gyrosa isolates from Eucalyptus in South Africa and Australia
View Article: Plant Pathology. 2001. 50 (2). 211-217
CD Volume:372
Print Article: Pages: 211-217
Author(s):Venter M Wingfield M J Coutinho T A Wingfield B D
Author Affiliation:Tree Pathology Co-operative Programme (TPCP), Faculty of Agricultural and Biological Sciences, Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), Pretoria 0002, South Africa
Language:English
Abstract:Endothia gyrosa is a canker pathogen best known as the causal agent of pin oak blight in North America, and causes cankers on other woody hosts such as Castanea spp. and Liquidambar spp. In South Africa, Australia and Tasmania, a fungus identified as E. gyrosa has been recorded on Eucalyptus spp. Some morphological differences exist between the North American fungus and the isolates from Eucalyptus. Phylogenetic relationships between E. gyrosa from North America and E. gyrosa from South Africa and Australia, as well as that of the related fungi Cryphonectria parasitica and C. cubensis, were studied using PCR-based restriction fragment length polymorphism (RFLP) and sequences of the internal transcribed spacer (ITS) region of the rRNA (ribosomal RNA) operon. Endothia gyrosa isolates from South Africa produced the same RFLP banding patterns as those from Australia, which differed markedly from North American isolates of E. gyrosa. In a phylogram-based on the DNA sequences, the Australian and South African isolates of E. gyrosa resided in a single, well resolved clade, distinct from North American isolates. Isolates of Cryphonectria parasitica grouped in the same clade as the South African and Australian isolates of E. gyrosa, but C. cubensis was distantly related to them. The molecular data suggest that the E. gyrosa isolates from South Africa and Australia represent a distinct taxon, and probably belong to the genus Cryphonectria
Descriptors:fungal-diseases. fungal-morphology. molecular-taxonomy. nucleotide-sequences. phylogenetics. phylogeny. plant-diseases. plant-pathogenic-fungi. plant-pathogens. ribosomal-RNA. taxa. taxonomy
Geographic Locator:Australia. North-America. South-Africa. Tasmania
Identifiers:Endothia gyrosa. Valsaceae
Organism Descriptors:Cryphonectria-cubensis. Cryphonectria-gyrosa. Cryphonectria-parasitica. Endothia. Eucalyptus

Supplemental Descriptors:Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Cryphonectria. Diaporthales. Ascomycotina. Eumycota. fungi. Endothia. Myrtaceae. Myrtales. dicotyledons. angiosperms. Spermatophyta. plants. America. Southern-Africa. Africa-South-of-Sahara. Africa. Developing-Countries. Threshold-Countries. Anglophone-Africa. Australia
Subject Codes:FF610. KK100. WW000. ZZ380. ZZ395
Supplementary Info:39 ref
ISSN:0032-0862
Year:2001
Journal Title:Plant Pathology
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323. Title:First report of Phytophthora nicotianae associated with Eucalyptus die-back in South Africa
View Article: Plant Pathology. 2001. 50 (3). 413
CD Volume:372
Print Article: Pages: 413
Author(s):Maseko B Burgess T Coutinho T Wingfield M
Author Affiliation:Forestry and Agricultural Biotechnology Institute (FABI), Tree Pathology Co-operative Programme (TPCP), Department of Microbiology and Plant Pathology, University of Pretoria, Pretoria, 0002, South Africa
Language:English
Abstract:Since 1999, Phytophthora nicotianae var. parasitica has been recovered from dead and dying Eucalyptus trees such as E. macarthurii and E. smithii in South Africa. Symptoms include leaf chlorosis and gum exudation through cankers on the tree collar. As the disease progresses, the trees usually wilt and die due to girdling. This is the first report on the occurrence of P. nicotianae in Eucalyptus spp. in South Africa
Descriptors:fungal-diseases. geographical-distribution. new-geographic-records. plant-diseases. plant-pathogenic-fungi. plant-pathogens
Geographic Locator:South-Africa
Organism Descriptors:Eucalyptus-macarthurii. Eucalyptus-smithii. Phytophthora-nicotianae-var.-parasitica
Supplemental Descriptors:Eucalyptus. Myrtaceae. Myrtales. dicotyledons. angiosperms. Spermatophyta. plants. Phytophthora-nicotianae. Phytophthora. Peronosporales. Mastigomycotina. Eumycota. fungi. Southern-Africa. Africa-South-of-Sahara. Africa. Developing-Countries. Threshold-Countries. Anglophone-Africa. Commonwealth-of-Nations
Subject Codes:FF610. KK100
Supplementary Info:5 ref
ISSN:0032-0862
Year:2001
Journal Title:Plant Pathology
Copyright:Copyright CAB International

324. Title:Effect of phosphite on in planta zoospore production of Phytophthora cinnamomi
View Article: Plant Pathology. 2001. 50 (5). 587-593
CD Volume:372
Print Article: Pages: 587-593
Author(s):Wilkinson C J Holmes J M Dell B Tynan K M McComb J A Shearer B L Colquhoun I J Hardy G E S J
Author Affiliation:School of Biological Sciences and Biotechnology, Murdoch University, South Street, Perth, Western Australia 6150, Australia
Language:English

Abstract:The efficacy of phosphite to control the production of zoospores of Phytophthora cinnamomi on infected trees grown in a glasshouse and in a revegetated mined area [Western Australia, Australia; 1999] was examined. Banksia grandis and Eucalyptus marginata seedlings in a glasshouse and E. marginata seedlings in the minepit were sprayed with 0, 5 and 10 g phosphite/litre. In both trials, zoospores were produced from infected tissue of plants treated with all concentrations of phosphite. In the glasshouse, spray application of 5 and 10 g phosphite/litre significantly reduced the production of zoospores from both B. grandis and E. marginata seedlings. In the mined area, there was a similar, though nonsignificant, reduction in the number of zoospores produced from phosphite-treated and nontreated E. marginata seedlings. However, the average number of zoospores produced was greater in plants nor treated with phosphite (1.75 zoospores/ml) than from plants treated with 5 or 10 g phosphite/litre (0.04 and 0.09 zoospores/ml, respectively). Pimelea ferruginea leaves were used to bait the water surrounding the plants in the mined area to determine if zoospores produced from phosphite-treated plants were able to infect plant material. Significantly more baits were infected by zoospores from plants not treated with phosphite compared with plants treated with 5 or 10 g phosphite/litre. These results suggest that phosphite reduces, but does not prevent, the production of viable zoospores on infected trees. Thus, phosphite application may not remove the risk of P. cinnamomi spreading from infested, sprayed areas
Descriptors:chemical-control. fungicides. leaves. plant-disease-control. plant-pathogenic-fungi. plant-pathogens. seedlings. zoospores
Geographic Locator:Australia. Western-Australia
Identifiers:phosphite. Pimelea ferruginea. Thymelaeales
Organism Descriptors:Banksia-grandis. Eucalyptus-marginata. Phytophthora-cinnamomi. Pimelea
Supplemental Descriptors:Australasia. Oceania. Developed-Countries. Commonwealth-of-Nations. OECD-Countries. Banksia. Proteaceae. Proteales. dicotyledons. angiosperms. Spermatophyta. plants. Eucalyptus. Myrtaceae. Myrtales. Phytophthora. Peronosporales. Mastigomycotina. Eumycota. fungi. Thymelaeaceae. Pimelea. Australia
Subject Codes:FF610. HH405. KK100. ZZ396
Supplementary Info:24 ref
ISSN:0032-0862
Year:2001
Journal Title:Plant Pathology

325. Title:Pepper races 7, 8 and 10 of Xanthomonas axonopodis pv. vesicatoria isolated from diseased pepper plants in Turkey
View Article: Plant Pathology. 2001. 50 (6). 809
CD Volume:372
Print Article: Pages: 809
Author(s):Sahin F
Author Affiliation:Department of Plant Protection, Faculty of Agriculture, Biotechnology Application and Research Center, Ataturk University, 25240 Erzurum, Turkey
Language:English
Abstract:In the summer of 1999 and 2000, twenty-one strains of Xanthomonas axonopodis pv. vesicatoria [X. vesicatoria] (Xav) isolated from infected pepper plants grown in greenhouses and fields in the Mediterranean and eastern Anatolia regions of Turkey, were characterized based on physiological tests, analysis of whole-cell fatty acids (FAME), indirect enzyme-linked immunosorbent assay, and pathogenicity and hypersensitivity tests. All strains had similar

fatty acid profiles and matched the strain to Xav with similarity indices ranging from 0.43 to 0.79. All strains reacted with a set of Xav-specific monoclonal antibodies (MABs) Xv1, 5, 6 and 10, but not with MABs Xv8, 15 and 30 known to react positively with X. vesicatoria and/or X. gardneri (the other taxa besides Xav into which X. campestris pv. vesicatoria has been reclassified). All strains were pathogenic to pepper cv. Marengo plants. Hypersensitivity tests on pepper differential lines including Capsicum pubescens PI 235047, C. annuum cv. Early Calwonder (ECW) and its nearest isogenic lines (designated ECW-10R, ECW-20R and ECW-30R) showed that 8, 2 and 11 of the strains belong to Xav pepper races 7, 8 and 10, respectively. This is the first report of the observation of Xav pepper races 7, 8 and 10 causing bacterial spot disease on pepper in Turkey
Descriptors:plant-pathogenic-bacteria. plant-pathogens. races. strains
Geographic Locator:Turkey
Identifiers:Capsicum pubescens
Organism Descriptors:Capsicum-annuum. Xanthomonas-vesicatoria
Supplemental Descriptors:Capsicum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants. West-Asia. Asia. Mediterranean-Region. Developing-Countries. OECD-Countries. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF003. FF610
Supplementary Info:4 ref
ISSN:0032-0862
Year:2001
Journal Title:Plant Pathology
Copyright:Copyright CAB International

326. Title:Amorpha-4,11-diene synthase: cloning and functional expression of a key enzyme in the biosynthetic pathway of the novel antimalarial drug artemisinin
View Article: Planta. 2001. 212 (3). 460-465
CD Volume:355
Print Article: Pages: 460-465
Author(s):Wallaart T E Bouwmeester H J Hille J Poppinga L Maijers N C A
Author Affiliation:GenoClipp biotechnology B. V., Meditech Center, L. J. Zielstraweg 1, 9713 GX Groningen, Netherlands
Language:English
Abstract:The sesquiterpenoid artemisinin, isolated from the plant Artemisia annua and its semi-synthetic derivatives are a new and very effective group of antimalarial drugs. A branch point in the biosynthesis of this compound is the cyclization of the ubiquitous precursor farnesyl diphosphate into the first specific precursor of artemisinin, namely amorpha-4,11-diene. Here we describe the isolation of a cDNA clone encoding amorpha-4,11-diene synthase. The deduced amino acid sequence exhibits the highest identity (50%) with a putative sesquiterpene cyclase [trichodiene synthase] of A. annua. When expressed in Escherichia coli, the recombinant enzyme catalyses the formation of amorpha-4,11-diene from farnesyl diphosphate. Introduction of the gene into tobacco (Nicotiana tabacum cv. Petite Havana) resulted in the expression of an active enzyme and the accumulation of amorpha-4,11-diene ranging from 0.2 to 1.7 ng per g fresh weight
Descriptors:amino-acid-sequences. antimalarial-properties. antimalarials. artemisinin. chemical-composition. clones. complementary-DNA. enzyme-activity. enzymes. gene-expression. genes. medicinal-plants. plant-composition. sesquiterpenoid-lactones. tobacco
Identifiers:trichodiene synthase
Organism Descriptors:Artemisia-annua. Escherichia-coli. Nicotiana-tabacum

Supplemental Descriptors:Artemisia. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants. Escherichia. Enterobacteriaceae. Gracilicutes. bacteria. prokaryotes. Nicotiana. Solanaceae. Solanales
Subject Codes:FF003. FF020. FF040. FF060. WW000
Supplementary Info:30 ref
ISSN:0032-0935
Year:2001
Journal Title:Planta
Copyright:Copyright CAB International

327. Title:Plasma-membrane H+-ATPases are expressed in pitchers of the carnivorous plant Nepenthes alata Blanco
View Article: Planta. 2001. 212 (4). 547-555
CD Volume:355
Print Article: Pages: 547-555
Author(s):An ChungIl Fukusaki E I Kobayashi A
Author Variant:An-C-I
Author Affiliation:Department of Biotechnology, Graduate School of Engineering, Osaka University, 2-1 Yamadaoka, Suita, Osaka 565-0871, Japan
Language:English
Abstract:Nepenthes is a unique genus of carnivorous plants that can capture insects in trapping organs called pitchers and digest them in pitcher fluid. The pitcher fluid includes digestive enzymes and is strongly acidic. We found that the fluid pH decreased when prey accumulates in the pitcher fluid of N. alata. The pH decrease may be important for prey digestion and the absorption of prey-derived nutrients. To identify the proton pump involved in the acidification of pitcher fluid, plant proton-pump homologs were cloned and their expressions were examined. In the lower part of pitchers with natural prey, expression of one putative plasma-membrane (PM) H+-ATPase gene, NaPHA3, was considerably higher than that of the putative vacuolar H+-ATPase (subunit A) gene, NaVHA1, or the putative vacuolar H+-pyrophosphatase gene, NaVHP1. Expression of one PM H+-ATPase gene, NaPHA1, was detected in the head cells of digestive glands in the lower part of pitchers, where proton extrusion may occur. Involvement of the PM H+-ATPase in the acidification of pitcher fluid was also supported by experiments with proton-pump modulators; vanadate inhibited proton extrusion from the inner surface of pitchers, whereas bafilomycin A1 did not, and fusicoccin induced proton extrusion. These results strongly suggest that the PM H+-ATPase is responsible for acidification of the pitcher fluid of Nepenthes
Descriptors:absorption. acidification. adenosinetriphosphatase. carnivorous-plants. digestion. enzymes. gene-expression. genes. pH. plasma-membranes. proton-pump
Identifiers:Nepenthes alata
Organism Descriptors:Nepenthes. plants
Supplemental Descriptors:Nepenthaceae. Nepenthales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. FF060
Supplementary Info:39 ref
ISSN:0032-0935
Year:2001
Journal Title:Planta
Copyright:Copyright CAB International

328. Title:Acclimation of Arabidopsis thaliana to the light environment: the existence of separate low light and high light responses
View Article: Planta. 2001. 213 (5). 794-801

CD Volume:355
Print Article: Pages: 794-801
Author(s):Bailey S Walters R G Jansson S Horton P
Author Affiliation:Robert Hill Institute, Department of Molecular Biology and Biotechnology, University of Sheffield, Western Bank, Sheffield, S10 2TN, UK
Language:English
Abstract:The capacity for photosynthetic acclimatization in A. thaliana cv. Landsberg erecta was assessed during growth over a broad range of irradiance. The discontinuity in the response to growth irradiance was revealed for the light- and CO2-saturated rate of photosynthesis (Pmax) and the ratio of chlorophyll a to chlorophyll b (Chl a/b). Three separate phases in the response of Pmax and Chl a/b to growth light were evident, with increases at low and high irradiance ranges and a plateaux at intermediate irradiance. By measuring all chlorophyll-containing components of the thylakoid membrane that contribute to Chl a/b, we reveal that distinct strategies for growth at low and high irradiance underlie the discontinuous response. These strategies include, in addition to changes in the major light-harvesting complexes of photosystem II (LHCII), large shifts in the amounts of both reaction centres as well as significant changes in the levels of minor LHCII and LHCI components
Descriptors:acclimatization. chlorophyll. growth. light-harvesting-complexes. light-intensity. photosynthesis. photosystem-II. thylakoids
Organism Descriptors:Arabidopsis-thaliana
Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF060. FF500
Supplementary Info:39 ref
ISSN:0032-0935
Year:2001
Journal Title:Planta
Copyright:Copyright CAB International

329. Title:Regeneration of transgenic loblolly pine (Pinus taeda L.) from zygotic embryos transformed with Agrobacterium tumefaciens
View Article: Planta. 2001. 213 (6). 981-989
CD Volume:355
Print Article: Pages: 981-989
Author(s):Tang W Sederoff R Whetten R
Author Affiliation:Forest Biotechnology Group, Department of Forestry, North Carolina State University, Raleigh, NC 27695-7247, USA
Language:English
Abstract:Embryos of 24 open-pollinated families of loblolly pine (P. taeda) were used as explants to conduct in vitro regeneration. Then, A. tumefaciens strain GV3101 harbouring the plasmid pPCV6NFHygGUSINT was used to transform mature zygotic embryos of seven families of loblolly pine. The frequency of transformation varied among families infected with A. tumefaciens. The highest frequency (100%) of transient beta -glucuronidase (GUS)-expressing embryos was obtained from family 11-1029 with over 300 blue spots per embryo. Expression of the GUS reporter gene was observed in cotyledons, hypocotyls, and radicles of co-cultivated mature zygotic embryos, as well as in callus and shoots derived from co-cultivated mature zygotic embryos. Ninety transgenic plants were regenerated from hygromycin-resistant callus derived from families WO3, 8-1082 and 11-1029, and 19 transgenic plantlets were established in soil. The presence of the GUS gene in the plant genome was confirmed by polymerase chain reaction, Southern blot, and plant DNA/T-DNA junction analysis. These results suggest that an efficient

A. tumefaciens-mediated transformation protocol for stable integration of foreign genes into loblolly pine has been developed and that this transformation system could be useful for future studies on transferring economically important genes to loblolly pine
Descriptors:beta-glucuronidase. callus. cell-culture. cotyledons. DNA. explants. gene-expression. genes. genetic-transformation. genotypes. hygromycin-B. hypocotyls. in-vitro-culture. in-vitro-regeneration. micropropagation. plant-embryos. plasmids. radicles. reporter-genes. shoots. T-DNA. tissue-culture. transgenic-plants
Organism Descriptors:Agrobacterium-tumefaciens. Pinus-taeda. plants
Supplemental Descriptors:Agrobacterium. Rhizobiaceae. Gracilicutes. bacteria. prokaryotes. Pinus. Pinaceae. Pinopsida. gymnosperms. Spermatophyta. plants
Subject Codes:FF020. KK100. WW000
Supplementary Info:34 ref
ISSN:0032-0935
Year:2001
Journal Title:Planta
Copyright:Copyright CAB International

330. Title:Developmental consequences of embryo and cell manipulation in mice and farm animals
View Article: Reproduction 2001 Oct;122(4):507-18
CD Volume:379
Print Article: Pages: 507-518
Author(s):McEvoy TG Robinson JJ Sinclair KD
Author Affiliation:Scottish Agricultural College, Animal Biology Division, Craibstone Estate, Bucksburn, Aberdeen AB21 9YA, UK
Abstract:Advances in biotechnology in recent decades have revolutionized our understanding of early mammalian development and promise to provide ever more finely tuned and precisely targeted techniques for genetic enhancement of domestic animal species. In demonstrating what is both technically and biologically possible, not only in mice but also in larger animal species, research has provided hope that previously intractable diseases and genetic defects can be successfully combated. Crucial to this research is the ability to culture oocytes, embryos and somatic cells in vitro and to sustain their development without inducing adverse short- or long-term consequences. There is a need to refine current culture strategies in farm animal species to avoid jeopardizing their dependent technologies. A key to resolving current limitations of culture strategies is to identify, acknowledge and then address those features of in vitro culture that compromise early regulation of mammalian development. The aim of this review is to appraise critically in vitro embryo and somatic cell production strategies in the context of their impact on developmental competence and normality at embryonic, fetal and later stages. In addition, effects of physically manipulating embryos and cells, most notably via nuclear and gene transfer technologies, are considered with a view to identifying how detrimental consequences can be avoided
Geographic Locator:England
ISSN:1470-1626
Year:2001
Journal Title:Reproduction

331. Title:Changes in the relative abundance of mRNA transcripts for insulin-like growth factor (IGF-I and IGF-II) ligands and their receptors (IGF-IR/IGF-IIR) in preimplantation bovine embryos derived from different in vitrosystems
View Article: Reproduction 2001 Oct;122(4):601-10

CD Volume:379
Print Article: Pages: 601-610
Author(s):Yaseen MA Wrenzycki C Herrmann D Carnwath JW Niemann H
Author Affiliation:Department of Biotechnology, Institut fur Tierzucht und Tierverhalten, Mariensee, 31535 Neustadt, Germany
Abstract:The aim of this study was to determine the relative abundance of mRNAs for the insulin-like growth factor I (IGF-I) and IGF-II ligands, and for the IGF receptors (IGF-IR and IGF-IIR) in in vitro preimplantation bovine embryos from the oocyte to the hatched blastocyst stage using two different culture systems: TCM-199 supplemented with oestrous cow serum, or synthetic oviduct fluid supplemented with polyvinyl alcohol. Development to the two- to four-cell stage and blastocyst stage was significantly higher (P </= 0.05) in embryos cultured in TCM supplemented with oestrous cow serum than in those cultured in synthetic oviduct fluid supplemented with polyvinyl alcohol (61 and 25% versus 55 and 17%, respectively). A semi-quantitative RT-PCR assay did not detect IGF-I transcripts at any stage of preimplantation bovine development, including the hatched blastocyst stage. In both culture systems, IGF-IR, IGF-II and IGF-IIR were expressed throughout preimplantation development up to the hatched blastocyst stage in a varying pattern. The expression patterns of IGF-IR, IGF-II and IGF-IIR in embryos generated in the two culture systems were not significantly different, except at the expanded blastocyst stage, at which significantly higher amounts of IGF-IIR were observed in the TCM system than in the synthetic oviduct fluid system. These results indicate that transcripts of IGF-IR and IGF-IIR follow the standard pattern in which maternal stores of mRNA in the oocyte are slowly depleted up to the 16-cell stage and then re-established at the onset of embryonic expression of these genes. The lack of detectable IGF-I transcripts in the bovine embryo indicates a predominantly paracrine mode of action. The bovine embryo is capable of producing IGF-II, IGF-IIR and IGF-IR in large amounts, particularly after hatching, which may be important for the formation of the filamentous conceptus. Results indicate an autocrine mechanism for IGF-II and modulation of IGF family expression by culture conditions
Geographic Locator:England
ISSN:1470-1626
Year:2001
Journal Title:Reproduction

332. Title:Protein and lipopolysaccharide profiles of a salt-sensitive Rhizobium sp. and its exopolysaccharide-deficient mutant
View Article: Soil Biology & Biochemistry. 2001. 33 (1). 111-115
CD Volume:373
Print Article: Pages: 111-115
Author(s):Unni S Rao K K
Author Affiliation:Department of Microbiology and Biotechnology Centre, Faculty of Science, M.S. University of Baroda, Baroda 390 002, Gujarat, India
Language:English
Abstract:A fast-growing, salt-sensitive rhizobium (Rhizobium sp. ST1) with a narrow host range of infectivity was isolated from the root nodules of locally grown pigeonpea (Cajanus cajan). One of the Tn5 mutants of Rhizobium sp. ST1 was exopolysaccharide (EPS) deficient (exo-) and showed a 50% growth inhibition (GI50) at 350 mM NaCl, compared to the GI50 value of the wild type strain at 250 mM NaCl. Whole cell protein profiles of the wild type in the presence of NaCl showed an overall increase in the levels of several proteins (22, 38, 68, >97 kDa), whereas in its exo- mutant, certain low molecular weight outer membrane proteins (38 and 22 kDa) decreased. Other outer membrane

proteins (22, 38, 40, 42, 62 and 68 kDa) also markedly decreased in both the wild type and the exo- mutant in the presence of salt. Similarly, both the wild type and the exo- mutant showed decreased levels of both the lipopolysaccharide (LPS) components (LPS I and LPS II) in the presence of NaCl. These observations suggest the possible involvement of the outer membrane components, along with other factors, during growth under salt stress, in both salt-sensitive and relatively salt-tolerant strains of rhizobia
Descriptors:lipopolysaccharides. mutants. polysaccharides. protein. salinity
Organism Descriptors:Rhizobium
Supplemental Descriptors:Rhizobiaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:JJ100. ZZ395
Supplementary Info:29 ref
ISSN:0038-0717
Year:2001
Journal Title:Soil Biology & Biochemistry

333. Title:Dynamics of 14C-labelled glucose in alkaline saline soil
View Article: Soil Biology & Biochemistry. 2001. 33 (6). 707-719
CD Volume:373
Print Article: Pages: 707-719
Author(s):Luna Guido M L Beltran Hernandez R I Dendooven L
Author Affiliation:Laboratory of Soil Ecology, Department of Biotechnology and Bioengineering, CINVESTAV-IPN, Apartado Postal 14740, CP 07000 Mexico DF, Mexico
Language:English
Abstract:The application of glucose C or sewage sludge C to undrained alkaline saline soil of the former lake of Texcoco in Mexico and soils drained for 1, 5 and 8 years significantly increased CO2 production only for the 8-year site. The added organic material could have been immobilized in the microbial biomass or sequestered. To discover the mechanisms involved, we investigated the fate of 14C-labelled glucose when added to soil, under laboratory conditions. Soil was sampled on 27 March 1998 from an undrained plot and from plots drained for 1, 5 and 8 years, amended with 1000 mg 14C-labelled glucose C kg-1 dry soil (DS) and 200 mg NH4+-N kg-1 DS, and incubated aerobically for 97 days at 22 plus or minus 1 deg C. 14CO2 and CO2 production, inorganic-N dynamics (NH4+, NO2-, NO3-), microbial biomass, 14C, C and ninhydrin N, glucose and NH3 volatilization were monitored. The 14CO2 production was fastest in the soil drained for 8 years with electrolytic conductivity of 2.6 dS m-1 and lowest in the soil drained for 1 year with conductivity of 79.9 dS m-1. There was a lag between uptake of glucose and production of 14CO2, which increased with increased conductivity. A priming effect of 250, 674 and 221 mg CO2-C kg-1 DS was observed in the undrained soil and soils drained for 1 and 5 years, but it was absent in the soil drained for 8 years. The priming effect was explained by a replacement of the microbial biomass by newly formed biomass in the undrained soil and soil drained for 5 years but partly by increased decomposition of soil organic matter in the soil drained for 1 year. Nitrification, as indicated by increases in NO3- concentrations, occurred even in the soil drained for 1 year, but oxidizers of NO2- were inhibited as indicated by temporal increases in concentrations of NO2-. Calculated efficiencies for 14C were affected by soil characteristics. We found that sequestration of added organic C as found in previous experiments was not confirmed but soil characteristics changed by drainage affected decomposition of added organic material. Care should be taken when salts are applied to

soil to study possible effects of conductivity on C and N dynamics as microorganisms adapt to these specific conditions
Descriptors:alkaline-soils. ammonia. carbon. carbon-dioxide. carbon-sequestration. decomposition. drainage. glucose. nitrification. nitrite. nitrogen. organic-carbon. saline-soils. sewage-sludge. soil-amendments. soil-organic-matter
Geographic Locator:Mexico
Identifiers:inorganic nitrogen. microbial biomass
Supplemental Descriptors:North-America. America. Developing-Countries. Threshold-Countries. Latin-America. OECD-Countries
Subject Codes:JJ100. JJ200. JJ700. JJ600. JJ800
Supplementary Info:42 ref
ISSN:0038-0717
Year:2001
Journal Title:Soil Biology & Biochemistry

334. Title:Soil microbial community responses to dairy manure or ammonium nitrate applications
View Article: Soil Biology & Biochemistry. 2001. 33 (7/8). 1011-1019
CD Volume:373
Print Article: Pages: 1011-1019
Author(s):Peacock A D Mullen M D Ringelberg D B Tyler D D Hedrick D B Gale P M White D C
Author Affiliation:Center for Environmental Biotechnology, 10515 Research Drive, Suite 300, University of Tennessee, Knoxville, TN 37932, USA
Language:English
Abstract:Soil management practices that result in increased soil C also impact soil microbial biomass and community structure. In this study, the effects of dairy manure applications and inorganic N fertilizer on microbial biomass and microbial community composition were determined. Treatments examined were: (1) control with no nutrient additions (CT); (2) ammonium nitrate at 218 kg N ha-1 (AN); and (3) manure N rates of 252 kg manure-N ha-1 (LM) and 504 kg manure-N ha-1 (HM). All plots (established in May 1991 at the Martin Agricultural Experiment Station in northwest Tennessee, USA) were no-till cropped to silage maize (Zea mays) followed by a crimson clover (Trifolium incarnatum)/annual ryegrass (Lolium multiflorum) winter cover crop. Treatments were applied yearly, with two-thirds of the N applied in late April or early May, and the remainder applied in September. Soil samples (0-5, 5-10, and 10-15 cm) were taken in the plots in March 1996, prior to the spring nutrient application. Polar lipid fatty acid (PLFA) analysis was used to assess changes in microbial biomass and community structure. Significantly greater soil C, N and microbial biomass in the 0-5 cm depth were observed under both manure treatments than in the CT and AN treatments. There was also a definable shift in the microbial community composition of the surface soils (0-5cm). Typical Gram negative bacteria PLFA biomarkers were 15 and 27% higher in the LM and HM treatments than in the control. The AN treatment resulted in a 15% decrease in these PLFA compared with the control. Factor analysis of the polar lipid fatty acid profiles from all treatments revealed that the two manure amendments were correlated and could be described by a single factor comprised of typical Gram negative bacterial biomarkers. The AN treatments from all three depths were also correlated and were described by a second factor comprised of typical Gram positive bacterial biomarkers. These results demonstrate that soil management practices, such as manuring, that result in accumulations of organic carbon will result in increased microbial biomass and changes in community structure

Descriptors:application-rates. maize. nitrogen-fertilizers. organic-carbon. soil-amendments. soil-biology. soil-chemical-properties. soil-management
Identifiers:cattle manuresoil bacteria. microbial biomass. microbial communities
Organism Descriptors:Lolium-perenne. Trifolium-incarnatum. Zea-mays
Supplemental Descriptors:Lolium. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Trifolium. Papilionoideae. Fabaceae. Fabales. dicotyledons. Zea
Subject Codes:FF005. JJ100. JJ200. JJ700
Supplementary Info:35 ref
ISSN:0038-0717
Year:2001
Journal Title:Soil Biology & Biochemistry

335. Title:Vertical transport of a field-released genetically engineered microorganism through soil
View Article: Soil Biology & Biochemistry. 2001. 33 (12/13). 1873-1877
CD Volume:373
Print Article: Pages: 1873-1877
Author(s):Ripp S Nivens D E Werner C Sayler G S
Author Affiliation:Center for Environmental Biotechnology, University of Tennessee, 676 Dabney Hall, Knoxville, TN 37996-1605, USA
Language:English
Abstract:The vertical movement of a genetically-engineered bacterium released into a sub-surface soil contained within a lysimeter was investigated. The strain used was Pseudomonas fluorescens HK44, a lux-based microbe capable of bioremediating specific polyaromatic hydrocarbons (PAHs). Strain HK44 was inoculated into a 4 m deep by 2.5 m diameter soil lysimeter outfitted with a hydraulic assembly to control groundwater levels. After 230 days, the lysimeter was subjected to a water table manipulation that resulted in significant transport of HK44 cells to depths 60 cm below the original inoculation zone within 20 days. A lysimeter not exposed to water level fluctuations exhibited no significant vertical transport. These results demonstrate the potential distribution of genetically engineered microorganisms in subsurface soil due to groundwater effects
Descriptors:genetically-engineered-microorganisms. microbial-activities. soil-bacteria. strains. transport-processes
Organism Descriptors:Pseudomonas-fluorescens
Supplemental Descriptors:Pseudomonas. Pseudomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:JJ100. JJ200. WW000. ZZ395
Supplementary Info:24 ref
ISSN:0038-0717
Year:2001
Journal Title:Soil Biology & Biochemistry

336. Title:Estimation of nitrate leaching in an entisol under optimum citrus production
View Article: Soil Science Society of America Journal. 2001. 65 (3). 914-921
CD Volume:377
Print Article: Pages: 914-921
Author(s):Paramasivam S Alva A K Fares A Sajwan K S
Author Affiliation:Center for Marine, Environmental Sciences and Biotechnology Research, Drew Griffith Hall, Savannah State Univ., Savannah, GA 31404, USA
Language:English

Abstract:Leaching of fertilizer nutrients and widespread NO3-N contamination of drinking water wells in proximity to citrus growing regions of central Florida, USA, are a serious concern. We evaluated NO3-N distribution in soil solution at various depths in the vadose zone, and N leaching below the root zone for two cropping seasons under the canopy of 21-year-old Hamlim orange (Citrus sinensis) trees on Cleopatra mandarin (Citrus reticulata) rootstock, on an Entisol of central Florida. The treatments included 112, 168, 224, and 280 kg N ha-1 year-1 as either dry granular fertilizer (DGF; broadcast, in 4 equal doses) or fertigation (FRT; 15 applications year-1), and 56, 112, and 168 N kg ha-1 year-1 as controlled-release fertilizer (CRF; single application year-1). Irrigation was scheduled using recommended tensiometer set points as guidelines, with a target wetting depth of 90 cm. The NO3-N was measured in soil solutions bi-weekly at 60-, 120-, and 240-cm depths using suction lysimeters installed under the tree canopy. The 240-cm depth sample represented soil solution below the rooting depth of the trees, and the NO3-N at this depth could contaminate groundwater. At the 60- or 120-cm depths, the NO3-N concentrations occasionally peaked at 12 to 100 mg litre-1, but at 240 cm NO3-N concentration mostly remained below 10 mg litre-1. The careful irrigation management, split fertilizer application, and timing of application contributed to the low leaching of NO3-N below the root zone. Calculated NO3-N leaching losses below the rooting depth increased with increasing rate of N application and the amount of water drained, and accounted for 1 to 16% of applied fertilizer N
Descriptors:application-rates. Entisols. fertigation. irrigation. irrigation-scheduling. leaching. losses-from-soil. mandarins. nitrate. nitrate-nitrogen. nitrogen. nitrogen-fertilizers. oranges. pollution-control. rhizosphere. slow-release-fertilizers. soil-fertility. soil-properties. water-pollution
Geographic Locator:Florida. USA
Organism Descriptors:Citrus. Citrus-reticulata. Citrus-sinensis
Supplemental Descriptors:Citrus. Rutaceae. Sapindales. dicotyledons. angiosperms. Spermatophyta. plants. South-Atlantic-States-of-USA. Southern-States-of-USA. USA. North-America. America. Developed-Countries. OECD-Countries. Gulf-States-of-USA. Southeastern-States-of-USA
Subject Codes:FF003. FF060. JJ200. JJ600. JJ700. JJ800. PP600
Supplementary Info:27 ref
ISSN:0361-5995
Year:2001
Journal Title:Soil Science Society of America Journal

337. Title:Simple sequence repeat (SSR) markers survey of the cassava (Manihot esculenta Crantz) genome: towards an SSR-based molecular genetic map of cassava
View Article: Theoretical and Applied Genetics. 2001. 102 (1). 21-31
CD Volume:373
Print Article: Pages: 21-31
Author(s):Mba R E C Stephenson P Edwards K Melzer S Nkumbira J Gullberg U Apel K Gale M Tohme J Fregene M
Author Affiliation:Biotechnology Research Unit, International Center for Tropical Agriculture (CIAT), AA6713 Cali, Colombia
Language:English
Abstract:The development of PCR-based, easily automated molecular genetic markers, such as SSR markers, are required for realistic cost-effective marker-assisted selection schemes. This paper describes the development and characterization of 172 new SSR markers for the

cassava genome. The placement of 36 of these markers on the existing RFLP framework map of cassava is also reported. Two similar enrichment methods were employed. The first method yielded 35 SSR loci, for which primers could be designed, out of 148 putative DNA clones. A total of 137 primer pairs could be designed from 544 putative clones sequenced for the second enrichment. Most of the SSRs (95%) were di-nucleotide repeats, and 21% were compound repeats. A major drawback of these methods of SSR discovery is the redundancy - 20% duplication; in addition, primers could not be designed for many SSR loci that were too close to the cloning site - 45% of the total. All 172 SSRs amplified the corresponding loci in the parents of the mapping progeny, with 66% of them revealing a unique allele in at least one of the parents, and 26% having unique alleles in both of the parents. Of the 36 SSRs that have been mapped, at least 1 was placed on 16 out of the 18 linkage groups of the framework map, indicating a broad coverage of the cassava genome. This preliminary mapping of the 36 markers has led to the joining of a few small groups and the creation of one new group. The abundance of allelic bridges as shown by these markers will lead to the development of a consensus map of the male- and female-derived linkage groups. In addition, the relatively higher number of these allelic bridges, 30% as against 10% for RFLPs in cassava, underscores SSR as the marker of choice for cassava. The 100% primer amplification obtained for this set of primers also confirms the appropriateness of SSR markers for use in cassava genome analysis and the transferability of the technology as a low-cost approach to increasing the efficiency of cassava breeding. Current efforts are geared towards the generation of more SSR markers to attain a goal of 200 SSR markers, or 1 SSR marker every 10 cM

Descriptors:cassava. genetic-markers. polymerase-chain-reaction. repetitive-DNA. restriction-fragment-length-polymorphism

Organism Descriptors:Manihot-esculenta

Supplemental Descriptors:Manihot. Euphorbiaceae. Euphorbiales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. FF005. WW000

Supplementary Info:25 ref

ISSN:0040-5752

Year:2001

Journal Title:Theoretical and Applied Genetics

338. Title:Flow cytometric evidence for endopolyploidy in seedlings of some Brassica species

View Article: Theoretical and Applied Genetics. 2001. 102 (1). 104-110

CD Volume:373

Print Article: Pages: 104-110

Author(s):Kudo N Kimura Y

Author Affiliation:Division of Plant Biotechnology, Gunma Horticultural Experiment Station, 493 Nishi-Obokata, Sawa-Azuma, Gunma 379-2224, Japan

Language:English

Abstract:Flow cytometric analysis of the nuclear DNA contents of somatic tissues from seedlings of Brassica rapa [B. campestris] and B. oleracea revealed extensive endoreduplication, resulting in tissues that contain cells with multiple ploidy levels (also called endopolyploidy). Multiples of the haploid nuclear genome complement (1C) corresponding to 2C, 4C, 8C, 16C, 32C and 64C were observed in Brassica rapa, while B. oleracea exhibited a mixture of cells with five ploidy levels, 2C, 4C, 8C, 16C and 32C. The distribution of cells with the different ploidy levels was tissue-specific and

characteristic of the stage of development. Multiploidy was not found in the embryos of dry seeds. Rapid endoreduplication occurred during seedling development. It is most probable that multiploidy is, if not a general feature, at least very common in Brassica species. The physiological and genetic implications of this original feature are discussed
Descriptors:flow-cytometry. ploidy. polyploidy
Organism Descriptors:Brassica-campestris. Brassica-oleracea
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF005. FF030
Supplementary Info:36 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

339. Title:Isolation, characterization and chromosomal location of a novel zinc-finger protein gene that is down-regulated by salt stress
View Article: Theoretical and Applied Genetics. 2001. 102 (2/3). 363-368
CD Volume:373
Print Article: Pages: 363-368
Author(s):Li Z Y Chen S Y
Author Affiliation:Laboratory of Plant Biotechnology, Institute of Genetics, Chinese Academy of Sciences, Beijing, 100101, China
Language:English
Abstract:mRNA transcripts from salt-stressed and unstressed rice cv. ZYQ8 seedlings were detected by differential display to show alterations in abundance. One transcript, designated OsZFP1, was found to be significantly down-regulated by salt stress. OsZFP1 encodes a protein of 145 amino acids with three putative Cys2/Cys2-type zinc-finger domains. A homology search of GenBank databases showed that OsZFP1 is homologous to the rat and human ZIS (zinc-finger, splicing) proteins and the human nucleopore complex protein Nup358 in the zinc-finger domains. Genomic Southern analysis indicated that the OsZFP1 gene was present as a single-copy sequence in the rice genome. Restriction fragment length polymorphism mapping assigned the OsZFP1 gene to the distal position of chromosome 6. RT-PCR assay showed that the OsZFP1 transcripts were more abundant in rice shoots than in the roots. Decreases in the level of OsZFP1 transcripts were detected in the shoots and roots after 6 and 3 h, respectively, of salt stress. In addition, the expression of OsZFP1 in rice shoots was significantly repressed by exogenous application of abscisic acid. The results suggest that OsZFP1 represents a novel type of zinc-finger protein gene in plants and that it is implicated in the responses of rice plants to salt stress
Descriptors:abscisic-acid. amino-acid-sequences. chromosomes. cysteine. DNA-binding-proteins. gene-location. genes. genetic-mapping. growth-inhibitors. messenger-RNA. plant-growth-regulators. rice. roots. salinity. seedlings. shoots. stress-response
Organism Descriptors:Oryza-sativa. Oryza
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. FF900
Supplementary Info:23 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

340. Title:Development and characterisation of simple sequence repeat (SSR) markers for perennial ryegrass (Lolium perenne L.)
View Article: Theoretical and Applied Genetics. 2001. 102 (2/3). 405-415
CD Volume:373
Print Article: Pages: 405-415
Author(s):Jones E S Dupal M P Kolliker R Drayton M C Forster J W
Author Affiliation:Plant Biotechnology Centre, Agriculture Victoria, La Trobe University, Bundoora, Victoria 3083, Australia
Language:English
Abstract:Enrichment methods were optimized to isolate large numbers of simple sequence repeat (SSR) markers for perennial ryegrass (Lolium perenne), with the aim of developing a comprehensive set of loci for trait mapping and cultivar identification. Two libraries were constructed showing greater than 50% enrichment for a variety of SSR-motif types. Sequence characterization of 1853 clones identified 859 SSR-containing clones, of which 718 were unique. Truncation of flanking sequences limited potential primer design to 366 clones. One hundred selected SSR primer pairs were evaluated for amplification and genetic polymorphism across a panel of diverse genotypes. The efficiency of amplification was 81%. A relatively high level of SSR polymorphism was detected (67%), ranging from 2-7 alleles per locus. Mendelian segregation of alleles detected by selected SSR-locus primer pairs was demonstrated in the F1 progeny of a pair cross. Cross-species amplification was detected in a number of related pasture and turfgrass species, with high levels of transfer to other Lolium species and members of the related genus Festuca. The identity of putative SSR ortholoci in these related species was confirmed by DNA sequence analysis. These loci constitute a valuable resource of ideal markers for the molecular breeding of ryegrasses and fescues
Descriptors:alleles. clones. genetic-markers. genetic-polymorphism. genotypes. loci. polymerase-chain-reaction. segregation
Organism Descriptors:Lolium-perenne
Supplemental Descriptors:Lolium. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF007. FF020. WW000
Supplementary Info:60 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

341. Title:Development and characterisation of simple sequence repeat (SSR) markers for white clover (Trifolium repens L.)
View Article: Theoretical and Applied Genetics. 2001. 102 (2/3). 416-424
CD Volume:373
Print Article: Pages: 416-424
Author(s):Kolliker R Jones E S Drayton M C Dupal M P Forster J W
Author Affiliation:Plant Biotechnology Centre, Agriculture Victoria, La Trobe University, Bundoora, Victoria 3083, Australia
Language:English
Abstract:The aim of this study was to develop and characterize a comprehensive set of SSR markers for white clover (Trifolium repens), which can be used to tag genes and quantitative trait loci controlling traits of agronomic interest. Sequence analysis of 1123 clones from genomic libraries enriched for (CA)n repeats yielded 793 clones containing SSR loci. The majority of SSRs consisted of perfect dinucleotide repeats, only 7% being trinucleotide repeats. After exclusion of redundant sequences and SSR loci with less than 25 bp of flanking sequence, 397

potentially useful SSRs remained. Primer pairs were designed for 117 SSR loci and PCR products in the expected size range were amplified from 101 loci. These markers were highly polymorphic, 88% detecting polymorphism across 7 white clover genotypes with an average allele number of 4.8. Four primer pairs were tested in an F2 population revealing Mendelian segregation. Successful cross-species amplification was achieved in at least one out of 8 legume species for 46 of 54 primer pairs. The rate of successful amplification was significantly higher for Trifolium species when compared to species of other genera. The markers developed in this study not only provide valuable tools for molecular breeding of white clover but may also have applications in related taxa
Descriptors:alleles. clones. gene-tagging. genetic-markers. genetic-polymorphism. genotypes. quantitative-trait-loci. segregation
Organism Descriptors:Trifolium-repens
Supplemental Descriptors:Trifolium. Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF007. FF020. WW000
Supplementary Info:46 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

342. Title:QTL analysis of field resistance to Xanthomonas axonopodis pv. manihotis in cassava
View Article: Theoretical and Applied Genetics. 2001. 102 (4). 564-571
CD Volume:373
Print Article: Pages: 564-571
Author(s):Jorge V Fregene M Velez C M Duque M C Tohme J Verdier V
Author Affiliation:Biotechnology Research Unit, Centro International de Agricultura Tropical (CIAT), Institut de Recherche pour le Developpement (IRD), A.A. 6713, Cali, Colombia
Language:English
Abstract:We evaluated cassava bacterial blight (CBB) infection in an pair-cross population of 150 individuals derived from an intra-specific cross between two non-inbred cassava (Manihot esculenta) lines (TMS 30572 and CM 2177-2). The replicated trials were carried out in the field [place not given] and under high disease pressure over two consecutive crop cycles. Evaluations were conducted in 1997 and 1998 after 4 and 7 months of planting for the two cycles. Simple regression analysis and the nonparametric Kruskal-Wallis rank-sum test revealed that eight quantitative trait loci (QTLs) were involved in resistance. We detected changes in QTLs from crop cycle to crop cycle. The pathogen population (X. axonopodis pv. manihotis) was also monitored over the period, using a restriction fragment length polymorphism probe and pathogenic tests. Changes in QTL detection over the 2 years could be correlated with changes in pathogen population structure. One QTL, located in linkage group D, was conserved over the two crop cycles, and in field to greenhouse evaluations. This study thus identified molecular markers useful for marker assisted-selection, a technique that can accelerate the long, multiple-season process of breeding for CBB resistance
Descriptors:cassava. disease-resistance. genetic-markers. linkage. plant-diseases. plant-pathogenic-bacteria. plant-pathogens. population-structure. quantitative-trait-loci. restriction-fragment-length-polymorphism
Organism Descriptors:Manihot-esculenta. Xanthomonas-axonopodis-pv.-manihotis

Supplemental Descriptors:Manihot. Euphorbiaceae. Euphorbiales. dicotyledons. angiosperms. Spermatophyta. plants. Xanthomonas-axonopodis. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF005. FF020. FF610. WW000
Supplementary Info:29 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

343. Title:Designing of an artificial expression cassette for the high-level expression of transgenes in plants
View Article: Theoretical and Applied Genetics. 2001. 102 (4). 635-644
CD Volume:373
Print Article: Pages: 635-644
Author(s):Sawant S Singh P K Madanala R Tuli R
Author Affiliation:National Botanical Research Institute, Rana Pratap Marg, Lucknow - 226001, India
Language:English
Abstract:A dataset of highly expressed plant genes was developed from the nucleic acids sequence database. The characteristic features of the nucleotide sequences in TATA-box, transcription initiation, untranslated leader and translation initiation regions in the highly expressible genes in plants and the conserved sequences present 500 bp upstream of transcription initiation site were identified. These features were employed to theoretically design a 'minimal expression cassette' and a promoter-upstream 'activation module.' The 'minimal expression cassette' was sufficient to express the gusA reporter gene in transient transformation of tobacco leaf. The context on the 3' side of the initiator codon, conserved in a majority of the highly expressible genes, gave approximately a ninefold increase in the expression of beta -glucuronidase. The artificially designed, upstream 'activation module' enhanced gusA expression further by about 30-fold in transiently transformed tobacco leaves. A 450-bp-long complete expression cassette, containing both the 'minimal expression cassette' and the 'activation module' expressed gusA at a high level in cotton leaves, potato tubers and cabbage stem also. In stably transformed tobacco plants, the 'complete expression cassette' expressed gusA at levels higher than the native CaMV 35S promoter. Histological studies established that the 'complete expression cassette' was expressed at a high level in different cell types in the roots, leaves, vascular tissues and flower parts of the transgenic tobacco plants. The results substantiate the functional validity of the features identified by us and demonstrate the potential of computational biology in designing artificial expression cassettes for applications in biotechnology
Descriptors:beta-glucuronidase. cabbages. cotton. gene-expression. genes. leaves. potatoes. roots. tata-box. tobacco. transcription. translation. vascular-system
Organism Descriptors:Brassica-oleracea-var.-capitata. Gossypium. Nicotiana. Nicotiana-tabacum. Solanum-tuberosum
Supplemental Descriptors:Brassica-oleracea. Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Solanum. Solanaceae. Solanales. Malvaceae. Malvales. Nicotiana
Subject Codes:FF003. FF005. FF020. WW000
Supplementary Info:43 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

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344. Title:Flow cytometric sorting of maize chromosome 9 from an oat-maize chromosome addition line
View Article: Theoretical and Applied Genetics. 2001. 102 (5). 658-663
CD Volume:373
Print Article: Pages: 658-663
Author(s):Li L J Arumuganathan K Rines H W Phillips R L Riera Lizarazu O Sandhu D Zhou Y Gill K S
Author Affiliation:Center for Biotechnology, University of Nebraska, Lincoln, NE 68588-0665, USA
Language:English
Abstract:Large numbers of maize chromosome 9 can be collected with high purity by flow cytometric sorting of chromosomes isolated from a disomic maize chromosome addition line of oat. Metaphase chromosome suspensions were prepared from highly synchronized seedling root tips of an oat-maize chromosome 9 addition line (OM9) and its parental oat and maize lines. Chromosomes were stained with propidium iodide for flow cytometric analysis and sorting. Flow karyotypes of the oat-maize addition line showed an extra peak not present in the parental oat line. This peak was due to the presence of a maize chromosome 9 pair within the genome of OM9. Separation of maize chromosome 9 by flow cytometric sorting of a chromosome preparation from a normal maize line was not possible because of its size similarity (DNA content) to maize chromosomes 6, 7 and 8. However, it is possible to separate maize chromosome 9 from oat chromosomes and chromatids. An average of about 6x103 chromosomes of maize chromosome 9 can be collected by flow-sorting from chromosomes isolated from 30 root tips (ten seedlings) of the oat-maize addition line. Purity of the maize chromosome 9, sorted from the oat-maize chromosome addition line, was estimated to be more than 90% based on genomic in situ hybridization analysis. Sorting of individual chromosomes provides valuable genomic tools for physical mapping, library construction and gene isolation
Descriptors:addition-lines. chromosome-addition. chromosomes. flow-cytometry. maize. metaphase. oats. root-tips. transgenic-plants
Organism Descriptors:Avena-sativa. plants. Zea-mays
Supplemental Descriptors:Avena. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Zea
Subject Codes:FF005. FF020. WW000
Supplementary Info:20 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

345. Title:A two-component gene (NTHK1) encoding a putative ethylene-receptor homolog is both developmentally and stress regulated in tobacco
View Article: Theoretical and Applied Genetics. 2001. 102 (6/7). 815-824
CD Volume:373
Print Article: Pages: 815-824
Author(s):Zhang J S Xie C Shen Y G Chen S Y
Author Affiliation:Plant Biotechnology Laboratory, Institute of Genetics, Chinese Academy of Sciences, Beijing 100101, China
Language:English
Abstract:The full-length of a two-component gene NTHK1 (Nicotiana tabacum histidine kinase-1) was isolated from tobacco (N. tabacum cv. Xanthi) using a previously obtained NTHK1 cDNA fragment as a probe. Sequence analysis revealed that NTHK1 shared high homology with LeETR4 from tomato and encoded an ethylene receptor homologue. The predicted NTHK1

protein had a putative signal peptide, three transmembrane domains, a histidine kinase domain and a receiver domain. The putative autophosphorylation site at His378 and the phosphate receiver site at Asp689 were also identified. By using the in situ hybridization technique, NTHK1 mRNA was detected during flower organ development. It was also highly expressed in the processes of pollen formation and embryo development. The expression of NTHK1 in response to wounding and other stresses was investigated using competitive RT-PCR. The results demonstrated that NTHK1 was inducible upon wounding (cutting). Floating of the cut leaf pieces in 0.5x MS, with shaking, led to a relatively rapid and strong expression. This phenomenon was confirmed by the in situ hybridization results. In addition to the upregulation by wounding, NTHK1 expression was also induced following NaCl and PEG treatment, indicating a possible role for NTHK1 in multiple stress responses

Descriptors:complementary-DNA. cutting. embryonic-development. flowers. gene-expression. genes. genetic-regulation. histidine. hybridization. kinases. messenger-RNA. phosphorylation. pollen. proteins. salinity. signal-peptide. stress. tobacco

Organism Descriptors:Nicotiana. Nicotiana-tabacum

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

Subject Codes:FF005. FF020. FF060. WW000

Supplementary Info:48 ref

ISSN:0040-5752

Year:2001

Journal Title:Theoretical and Applied Genetics

346. Title:Detection of in vitro culture-induced instability through inter-simple sequence repeat analysis

View Article: Theoretical and Applied Genetics. 2001. 102 (6/7). 885-891

CD Volume:373

Print Article: Pages: 885-891

Author(s):Leroy X J Leon K Hily J M Chaumeil P Branchard M

Author Affiliation:Biotechnology and Plant Physiology Laboratory, Isamor - Brittany University, Technopole Brest-Iroise, 29280 Plouzane, France

Language:English

Abstract:This paper reports on investigations focused on trinucleotide and tetranucleotide repeats in cauliflower calluses (Brassica oleracea var. botrytis cultivars Meurz, Jakez, H524 and double haploid lines 2, 3, 5 and 6), carried out to determine their utility in the detection of genetic variations induced by tissue culture. Out of 224 calluses 6, exhibited original patterns; in one of these, PCR patterns differed at four polymorphic loci. The observed tetranucleotide-repeat classes were polymorphic, whereas fingerprinting patterns were stable with (CAG)5. The most frequent polymorphic and useful primer for detecting genetic variation appeared to be (CAA)5. We also characterized an inter-simple sequence repeat (ISSR) marker homologous to a gene involved in cellular proliferation, and modifications of this gene on callogenesis and/or differentiation are examined

Descriptors:cauliflowers. cell-culture. chromosome-polymorphism. genes. genetic-variation. in-vitro-culture. loci. repetitive-DNA. somaclonal-variation. somatic-embryogenesis. tissue-culture

Identifiers:cell proliferation

Organism Descriptors:Brassica-oleracea-var.-botrytis

Supplemental Descriptors:Brassica-oleracea. Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF005. FF020. FF170. WW000

Supplementary Info:28 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

347. Title:Molecular mapping of genes conferring aluminum tolerance in rice (Oryza sativa L.)
View Article: Theoretical and Applied Genetics. 2001. 102 (6/7). 1002-1010
CD Volume:373
Print Article: Pages: 1002-1010
Author(s):Nguyen V T Burow M D Nguyen H T Le B T Le T D Paterson A H
Author Affiliation:Institute of Biotechnology, Hanoi, Vietnam
Language:English
Abstract:Crop productivity on acid soil is restricted by multiple abiotic stress factors. Aluminium (Al) tolerance seems to be a key to productivity on soil with a pH below 5.0, but other factors such as Mn toxicity and the deficiency of P, Ca and Mg also play a role. The development of Al tolerant genotypes of rice is an urgent necessity for improving crop productivity in developing countries. Inhibition of root growth is a primary and early symptom of Al toxicity. The present study was conducted to identify genetic factors controlling the aluminium tolerance of rice. Several parameters related to Al tolerance, most importantly the relative root growth under Al stress versus non-stress conditions, were scored in 188 F3 selfed families from a cross between an Al tolerant Vietnamese local cultivar, Chiembau, and an Al susceptible improved cultivar, Omon269-65. The two cultivars are both Oryza sativa subsp. indica, but showed a relatively high level of DNA polymorphism, permitting the assembly of an RFLP map consisting of 164 loci spanning 1 715.8 cM, and covering most of the rice genome. A total of nine different genomic regions on eight chromosomes have been implicated in the genetic control of root and shoot growth under aluminium stress. By far, the greatest effects on aluminium tolerance were associated with the region near WG110 on chromosome 1. This region does not seem to correspond to most of the genes that have been mapped for aluminium tolerance in other species, nor do they correspond closely to one another. Most results, both from physiological studies and from molecular mapping studies, tend to suggest that aluminium tolerance is a complex multigenic trait. The identification of DNA markers (such as WG110) that are diagnostic for aluminium tolerance in particular gene pools provides an important starting point for transferring and pyramiding genes that may contribute to the sustainable improvement of crop productivity in aluminum-rich soils. The isolation of genes responsible for aluminium tolerance is likely to be necessary to gain a comprehensive understanding of this complex trait
Descriptors:aluminium. chromosomes. cultivars. DNA. gene-mapping. genes. genetic-factors. genetic-markers. genetic-polymorphism. genetic-regulation. genomes. growth. loci. metal-tolerance. rice. roots. stress
Geographic Locator:Vietnam
Organism Descriptors:Oryza. Oryza-sativa
Supplemental Descriptors:Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Indochina. South-East-Asia. Asia. Developing-Countries. ASEAN-Countries
Subject Codes:FF005. FF020. FF900. PP600. WW000
Supplementary Info:61 ref
ISSN:0040-5752
Year:2001

Journal Title:Theoretical and Applied Genetics
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348. Title:Pyramiding three bacterial blight resistance genes (xa5, xa13 and Xa21) using marker-assisted selection into indica rice cultivar PR106
View Article: Theoretical and Applied Genetics. 2001. 102 (6/7). 1011-1015
CD Volume:373
Print Article: Pages: 1011-1015
Author(s):Singh S Sidhu J S Huang N Vikal Y Li Z Brar D S Dhaliwal H S Khush G S
Author Affiliation:Biotechnology Center, Punjab Agricultural University, Ludhiana, Punjab, India
Language:English
Abstract:Bacterial blight (BB) of rice caused by Xanthomonas oryzae pv. oryzae (Xoo) is a major disease of rice in several countries. Three BB resistance genes, xa5, xa13 and Xa21, were pyramided into cv. PR106, which is widely grown in Punjab, India, using marker-assisted selection. Lines of PR106 with pyramided genes were evaluated after inoculation with 17 isolates of the pathogen from Punjab and six races of Xoo from the Philippines. Genes in combinations were found to provide high levels of resistance to the predominant Xoo isolates from the Punjab and six races from the Philippines. Lines of PR106 with two and three BB resistance genes were also evaluated under natural conditions at 31 sites (including Ludhiana, Jallandhar, Ferozepur and Sangrur) in commercial fields during 1999. The combination of genes provided a wider spectrum of resistance to the pathogen population prevalent in the region; Xa21 was the most effective, followed by xa5. Resistance gene xa13 was the least effective against Xoo. Only 1 of the BB isolates, PX04, was virulent on the line carrying Xa21 but avirulent on the lines having xa5 and xa13 genes in combination with Xa21
Descriptors:cultivars. disease-resistance. genetic-markers. geographical-races. lines. plant-diseases. plant-pathogenic-bacteria. plant-pathogens. rice. selection. virulence
Geographic Locator:India. Indian-Punjab. Philippines
Identifiers:isolates
Organism Descriptors:Oryza. Oryza-sativa. Xanthomonas-oryzae-pv.-oryzae
Supplemental Descriptors:South-Asia. Asia. Developing-Countries. Commonwealth-of-Nations. India. Oryza. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. South-East-Asia. ASEAN-Countries. Xanthomonas-oryzae. Xanthomonas. Xanthomonadaceae. Gracilicutes. bacteria. prokaryotes
Subject Codes:FF005. FF020. HH600. WW000
Supplementary Info:12 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics
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349. Title:Genetic diversity among Texas bluegrass genotypes (Poa arachnifera Torr.) revealed by AFLP and RAPD markers
View Article: Theoretical and Applied Genetics. 2001. 102 (6/7). 1037-1045
CD Volume:373
Print Article: Pages: 1037-1045
Author(s):Renganayaki K Read J C Fritz A K
Author Affiliation:Crop Biotechnology Center, Texas A&M University, College Station, TX-77843, USA
Language:English
Abstract:Texas (USA) bluegrass, Poa arachnifera, is a vigorous sod-forming perennial, dioecious grass tolerant to heat. It is native to the

Southern Great Plains. Genetic relationships existing among 28 Texas bluegrass genotypes from Foard, Wilbarger, Archer, Jack, Shackelford, Collin, Dallas, Mills and Bee, were investigated using amplified fragment length polymorphism (AFLP) and randomly amplified polymorphic DNA (RAPD). A total of 3756 AFLP markers were generated from the 28 genotypes of Texas bluegrass. A wide range of polymorphism (23.08-85.33%) was observed among primer combinations with a mean of 64.11%. Among 441 RAPDs assayed, 335 were polymorphic with a mean polymorphic rate of 73.71%. The unweighted pair-group method using an arithmetic average cluster analysis utilizing AFLP and RAPD data separated the 28 Texas bluegrass accessions into two broad groups. With a few exceptions, the females clustered with females and males with males. These results indicate that it may be possible to discriminate between males and females using molecular markers. Principal coordinate analysis of AFLP and RAPD data also indicated two distinct groups and revealed genetic variability among and within the groups. Based on their genetic similarity indices, high correlation was observed between AFLP and RAPD markers

Descriptors:genetic-diversity. genetic-markers. genetic-polymorphism. plant-genetic-resources. random-amplified-polymorphic-DNA

Geographic Locator:Texas. USA

Identifiers:amplified fragment length polymorphism. Poa arachnifera

Organism Descriptors:Poa

Supplemental Descriptors:Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Poa. Southern-Plains-States-of-USA. West-South-Central-States-of-USA. Southern-States-of-USA. USA. North-America. America. Developed-Countries. OECD-Countries. Great-Plains-States-of-USA. Gulf-States-of-USA

Subject Codes:FF007. FF020. PP720. WW000

Supplementary Info:47 ref

ISSN:0040-5752

Year:2001

Journal Title:Theoretical and Applied Genetics

350. Title:Molecular markers associated with leptinine production are located on chromosome 1 in Solanum chacoense

View Article: Theoretical and Applied Genetics. 2001. 102 (6/7). 1065-1071

CD Volume:373

Print Article: Pages: 1065-1071

Author(s):Hutvagner G Banfalvi Z Milankovics I Silhavy D Polgar Z Horvath S Wolters P Nap J P

Author Affiliation:Agricultural Biotechnology Center, P.O. Box 411, H-2101 Godollo, Hungary

Language:English

Abstract:Leptines of Solanum chacoense are effective natural deterrents against the Colorado potato beetle (Leptinotarsa decemlineata). Leptines are the acetylated forms of the glycoalkaloids solanine and chaconine and are supposed to be synthesized via hydroxylated derivatives, called leptinines. Inheritance of leptinine production was studied in crosses of closely related S. chacoense genotypes. The segregation data supported a single-gene model for the inheritance of leptinine production. In the segregating F1 population of an S. chacoense cross, AFLP, RFLP and RAPD markers segregating with the leptinine production have been identified. The locus involved in leptinine synthesis was localized to the short arm of chromosome 1 of the potato where a major quantitative trait locus for solanidine production, and markers with tight linkage to leptine production, have been mapped before. Our data further support the previous finding that the short arm of chromosome

1 is involved in steroid alkaloid synthesis in potato, and suggest that the genes involved in leptinine and leptine production are tightly linked in S. chacoense
Descriptors:antifeedants. chemical-composition. chromosomes. crosses. genetic-markers. genetic-models. genotypes. glycoalkaloids. inheritance. insect-pests. linkage. pest-resistance. plant-composition. plant-pests. quantitative-trait-loci. segregation. solanidine. solanine. steroid-alkaloids. wild-relatives
Organism Descriptors:insects. Leptinotarsa-decemlineata. Solanum-chacoense
Supplemental Descriptors:Leptinotarsa. Chrysomelidae. Coleoptera. insects. arthropods. invertebrates. animals. Solanum. Solanaceae. Solanales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. FF040. HH600. PP720. WW000
Supplementary Info:29 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

351. Title:Inheritance of downy mildew resistance, beta -1,3-glucanases and peroxidases in pearl millet [Pennisetum glaucum (L.) R. Br.] crosses
View Article: Theoretical and Applied Genetics. 2001. 102 (8). 1221-1226
CD Volume:373
Print Article: Pages: 1221-1226
Author(s):Shetty H S Vasanthi N S Sarosh B R Kini K R
Author Affiliation:Downy Mildew Research Laboratory, Department of Studies in Applied Botany and Biotechnology, University of Mysore, Manasagangotri, Mysore - 570 006, India
Language:English
Abstract:The inheritance of resistance to downy mildew disease and the defence-related enzymes beta -1,3-glucanase and peroxidase was studied in crosses of pearl millet using a generation-mean analysis. The study material comprised six generations (susceptible and resistant parents, F1, F2, BC1 and BC2) in three crosses. Seedlings from these generations were inoculated with the downy mildew pathogen, Sclerospora graminicola and disease incidence was recorded. Analysis of constitutive levels of beta -1,3-glucanase and peroxidase in the seedlings of different generations indicated that the resistant populations showed higher enzyme activities, while lower activities of the enzymes were recorded in the susceptible populations. In the generation-mean analysis, the significance of scaling tests revealed the existence of non-allelic interactions in the inheritance of resistance to downy mildew as well as with the enzymes. Among the gene effects, both additive and dominant effects were significant. All the non-allelic interaction effects were significant in the crosses. Studies on the isoenzyme patterns of the enzymes substantiated the results of the disease-incidence experiments in most of the generations. The results indicated that the inheritance of downy mildew disease resistance and the expression of beta -1,3-glucanase and peroxidase in pearl millet is not only under the control of additive and dominant genes but are also governed by complex non-allelic interactions
Descriptors:crosses. disease-resistance. enzyme-activity. enzymes. fungal-diseases. genetic-effects. inheritance. interactions. isoenzymes. pearl-millet. peroxidase. plant-diseases. plant-pathogenic-fungi. plant-pathogens
Identifiers:beta-1,3-glucanase
Organism Descriptors:Pennisetum-glaucum. Sclerospora-graminicola

Supplemental Descriptors:Pennisetum. Poaceae. Cyperales. monocotyledons. angiosperms. Spermatophyta. plants. Sclerospora. Peronosporales. Mastigomycotina. Eumycota. fungi
Subject Codes:FF005. FF020. FF060. FF610. HH600
Supplementary Info:34 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

352. Title:Cytogenetic analysis of interspecific sunflower hybrids and molecular evaluation of their progeny
View Article: Theoretical and Applied Genetics. 2001. 102 (8). 1280-1285
CD Volume:373
Print Article: Pages: 1280-1285
Author(s):Binsfeld P C Wingender R Schnabl H
Author Affiliation:Department of Physiology and Biotechnology of Plants, Institute of Agricultural Botany, University of Bonn, Karlrobert-Kreiten-Strasse 13, D-53115 - Bonn, Germany
Language:English
Abstract:Meiotic cells of transgenic asymmetric somatic hybrid (ASH) plants obtained by fusion of microprotoplasts of the donor species Helianthus giganteus or Helianthus maximiliani and recipient protoplasts of Helianthus annuus were investigated. Over 85% of the ASH meiocytes showed regular bivalent chromosome pairing. However, several anomalies like anaphase bridges, laggard chromosomes, univalent and multivalent pairing were also observed. Pollen viability of the ASH plants ranged from 79.2 to 95% with a strong negative correlation to chromosome number which varied between 34 and 42. Molecular investigation of ASH progeny using random amplified polymorphic DNA markers revealed the presence of donor genotype markers in 68% of the offspring. These results suggest that asymmetric somatic hybridization offers an efficient alternative method to overcome sexual barriers for gene flow and the genetic improvement of H. annuus by introgression of economical important traits from wild Helianthus species
Descriptors:anaphase. bivalents. cells. chromosome-number. chromosome-pairing. chromosomes. cytogenetics. genetic-analysis. genetic-markers. interspecific-hybridization. meiosis. pollen. protoplasts. random-amplified-polymorphic-DNA. somatic-hybridization. sunflowers. transgenic-plants. viability
Identifiers:Helianthus giganteus. Helianthus maximiliani
Organism Descriptors:Helianthus-annuus. plants
Supplemental Descriptors:Helianthus. Asteraceae. Asterales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. WW000
Supplementary Info:27 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics
Copyright:Copyright CAB International

353. Title:Intra- and inter-specific variations in the mitochondrial gene orf138 of Ogura-type male-sterile cytoplasm from Raphanus sativus and Raphanus raphanistrum
View Article: Theoretical and Applied Genetics. 2001. 103 (5). 725-732
CD Volume:373
Print Article: Pages: 725-732
Author(s):Yamagishi H Terachi T

Author Affiliation:Department of Biotechnology, Faculty of Engineering, Kyoto Sangyo University, Motoyama, Kamigamo, Kita-ku, Kyoto 603-8555, Japan
Language:English
Abstract:In order to gain a better understanding of the evolution of Ogura male-sterile cytoplasm in radish, a large-scale sequence analysis of mitochondrial orf138 was conducted using 107 Japanese wild radishes, 29 cultivated radishes and seven Raphanus raphanisturum. A single approximately 0.8-kb fragment containing the orf138 locus was amplified from each plant by PCR, and the nucleotide sequence of an entire coding region of orf138 was determined by direct-sequencing procedures. An identical sequence to the published orf138 (Type A) was identified in Japanese wild radish, including a single plant in a population near Kagoshima prefecture, Japan where Ogura (1968) first found 'Ogura male-sterile radish'. Thus, it was confirmed that the 'Ogura male-sterile cytoplasm' was derived from Japanese wild radish, with a Type A orf138 sequence, growing in this area. A total of six nucleotide changes and a single insertion/deletion (indel) were found in orf138 from both wild and cultivated radishes. By a combination of mutations, the orf138 sequences of the 143 radish plants were classified into nine types. Based on the pattern of mutations and the distribution of orf138 variants, it was concluded that the orf138 variants are derived from Type B or C, after Ogura-type cytoplasm was introduced from R. raphanistrum into Japanese wild radish
Descriptors:cytoplasmic-male-sterility. DNA-sequencing. mitochondrial-DNA. radishes. wild-relatives
Organism Descriptors:Raphanus-raphanistrum. Raphanus-sativus
Supplemental Descriptors:Raphanus. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF003. FF020. PP720
Supplementary Info:32 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

354. Title:Seed quality QTLs identified in a molecular map of early maturing soybean
View Article: Theoretical and Applied Genetics. 2001. 103 (6/7). 912-919
CD Volume:373
Print Article: Pages: 912-919
Author(s):Csanadi G Vollmann J Stift G Lelley T
Author Affiliation:Department of Plant Biotechnology, Institute for Agrobiotechnology, Konrad Lorenz Strasse 20, A-3430 Tulln, Austria
Language:English
Abstract:This study identified quantitative trait loci (QTLs) influencing seed quality characters in a cross of two early maturing soyabean (Glycine max) cultivars (Ma.Belle and Proto) adapted to the short growing seasons of Central Europe in field experiments conducted in eastern Austria (Raasdorf and Vienna in 1997 and Raasdorf, Vienna, and Pama in 1998). A molecular linkage map was constructed by using 113 simple sequence repeats, 6 random amplified polymorphic DNA and 1 restricted fragment length polymorphism marker/s segregating in 82 individuals of an F2 population. The map consists of 23 linkage groups and corresponds well to previously published soyabean maps. Using phenotypic data of the F2-derived lines grown in five environments, four markers for protein content, three for oil content and eight for seed weight were identified. Four from fifteen seed quality QTL-regions identified in the present study were also found by other authors. Markers associated with seed weight QTLs were consistent

across all environments and proved to have effects large enough to be useful in a marker-assisted breeding programme, whereas protein and oil QTLs showed environmental interactions
Descriptors:chemical-composition. chromosome-maps. plant-composition. protein-content. quantitative-trait-loci. repetitive-DNA. seed-quality. seed-weight. soyabean-oil. soyabeans
Geographic Locator:Austria
Organism Descriptors:Glycine-(Fabaceae). Glycine-max
Supplemental Descriptors:Central-Europe. Europe. Developed-Countries. European-Union-Countries. OECD-Countries. Glycine-(Fabaceae). Papilionoideae. Fabaceae. Fabales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF005. FF020. FF040. SS230. WW000
Supplementary Info:34 ref
ISSN:0040-5752
Year:2001
Journal Title:Theoretical and Applied Genetics

355. Title:Problem-solving approaches and philosophies in biological engineering: challenges from technical, social, and ethical arenas
View Article: Transactions of the ASAE. 2001. 44 (4). 1037-1041
CD Volume:370
Print Article: Pages: 1037-1041
Author(s):Hall S G Lima M
Author Affiliation:Department of Biological and Agricultural Engineering, Room 149, E. B. Doran Building, LSU Agricultural Center, Baton Rouge, LA 70803-4505, USA
Language:English
Abstract:Biological Engineering (BE) is a relatively new and evolving discipline that is fundamental in nature and uses principles of life science at its core. Considerable literature has been devoted to the emergence of BE as a profession during the past 30 years. Compared to traditional systems, biological systems present special challenges, which require new tools and approaches that are just now being developed. Traditional engineering approaches result in limited success because biological systems are characterized by non-linearities in system properties and dynamics, temporal and spatial variation, and emergent properties. We discuss these properties and the resulting need for novel approaches to problem solving in biological engineering. We assert that to truly serve society, the biology of the system, as well as cultural, social, and ethical issues, must be central to the design process in biological engineering. These issues are addressed through case study and literature review
Descriptors:biotechnology. ethics. philosophy
Identifiers:biological engineering
Subject Codes:NN000. WW000
Supplementary Info:36 ref
ISSN:0001-2351
Year:2001
Journal Title:Transactions of the ASAE

356. Title:From foraging to cropping: the transition to plantation forestry, and implications for wood supply and demand
View Article: Unasylva 2001. 52 (204). 24-32
CD Volume:380
Print Article: Pages: 24-32
Author(s):Sedjo R A Libby W J

Author Affiliation:Forest Economics and Policy Program, Resources for the Future, Washington, District of Columbia, USA
Language:English
Abstract:In the main paper by Sedjo, the transition to plantation forestry, begun during the latter part of the 20th century and ongoing, is discussed in relation to industrial wood demand and supply in particular, and conservation, the environment and the future of forestry in general. Alternatives to wood, the effects of new technology on costs, tree improvement and biotechnology, and confounding effects of global warming are also examined. An article by Libby is included: Some thoughts on plantations and global cooling (28-29, 6 ref.)
Descriptors:biotechnology. costs. demand. forest-plantations. supply. technology. timber-supply. timber-trade. tree-breeding. wood
Subject Codes:EE130. KK110. KK500. EE112. FF020. PP500
Supplementary Info:9 ref
ISSN:0041-6436
Year:2001
Journal Title:Unasylva
Copyright:Copyright CAB International

357. Title:The role and implications of biotechnological tools in forestry
View Article: Unasylva (FAO). 2001. 52 (204). 53-62
CD Volume:380
Print Article: Pages: 53-62
Author(s):Yanchuk A
Author Affiliation:British Columbia Forest Service, Victoria, Canada
Language:English
Abstract:The current direction of research, and issues to be considered in future decision-making regarding the use of biotechnology in forestry
ISSN:0041-6436
Year:2001
Journal Title:Unasylva

358. Title:The role and implications of biotechnological tools in forestry
View Article: Unasylva 2001. 52 (204). 53-61
CD Volume:380
Print Article: Pages: 53-61
Author(s):Yanchuk A D Henn G Thies C
Author Affiliation:Research Branch of the British Columbia Forest Service, Victoria, Canada
Language:English
Abstract:The main article by Yanchuk summarizes the biotechnologies currently used in forestry, including vegetative propagation (micropropagation, cryopreservation and in vitro selection), molecular genetic markers, genetic transformation, protoplast fusion, haploidization and embryo rescuing. The main issues and controversies related to their use, are discussed, stressing the importance of evaluating these scientifically and within socially accepted decision-making processes. An short article by Henne and Thies discusses the continued destruction of ancient forests and consequent effects on biodiversity and the environment
Descriptors:biotechnology. embryo-culture. forest-trees. forestry. genetic-markers. genetic-transformation. micropropagation. protoplast-fusion. techniques. trees. vegetative-propagation
Subject Codes:FF020. KK100. WW000
Supplementary Info:24 ref
ISSN:0041-6436
Year:2001

Journal Title:Unasylva
Copyright:Copyright CAB International

359. Title:Suitability of moist olive pomace as soil amendment
View Article: Water Air and Soil Pollution. 128 (1-2). May, 2001. 13-22
CD Volume:374
Print Article: Pages: 13-22
Author(s):Saviozzi A Levi Minzi R Cardelli R Biasci A Riffaldi R
Author Affiliation:Department of Agricultural Chemistry and Biotechnology, University of Pisa, Pisa: alesavio@agr.unipi.it
Language:English
Language of Summary:English (EN)
Abstract:A laboratory experiment was performed to evaluate the suitability of moist olive pomace (MOP) as soil amendment. Moist olive pomace was obtained from a new olive-oil industrial process called the 'two-phases method'. Soil samples were mixed with MOP to approximate a field application of 40 t ha-1 and incubated under aerobic conditions at 20 degreeC and 60% of soil water holding capacity. To estimate the effect of different loading rates and N supply on mineralization, 40, 80, 120 and 160 t ha-1 of MOP and 200 ppm of N as (NH4)2SO4 were used. Cumulative CO2-C evolution, total microbial activity and biomass-C were monitored during a 60-day period. Results indicate that the CO2-C evolution from MOP depends on soil type and is temporarily inhibited in acidic soils. Evolution of CO2-C increases with incremental addition of MOP, but the percentages of the added C that were mineralized decreased with increasing application rates. Mineral N supplements result in more efficiency of the mineralization process. Among the kinetic models tested to describe the mineralization dynamics, a first-order exponential model including a constant term provides the best fit to the experimental data. Both amount and activity of soil microbial biomass are enhanced by MOP added at the 40 t ha-1 rate, at least in the first period of incubation. At higher rates of MOP addition, a constant increase of biomass C during incubation is observed, while the biological activity decreases at the end of incubation. Following application of mineral N, both amount and activity of microbial biomass is enhanced
Descriptors:Mineral N supplements; biomass-C; mineralization dynamics; moist olive pomace: soil amendment; olive-oil industrial processes. Soil Science
Subject Codes:Soil Science
ISSN:0049-6979
Year:2001
Journal Title:Water, Air, and Soil Pollution

360. Title:High throughput synthesis and screening: the partner of genomics for discovery of new chemicals for agriculture
View Article: Weed Science. 2001. 49 (2). 249-256
CD Volume:374
Print Article: Pages: 249-256
Author(s):Hess F D Anderson R J Reagan J D
Author Affiliation:AffyAgro Unit of Affymax Research Institute, 3410 Central Expressway, Santa Clara, CA 95051, USA
Conference Title:Proceedings of the Weed Science Society of America Meeting - Impact of Biotechnology and Genomics on Weed Science, held at Toronto, Canada, 2000
Language:English
Abstract:As new targets for herbicide action are identified from genomics research, large and diverse chemical collections and high-throughput

assays will be required to maximize the probability of identifying compounds with activity at these targets. The new technology of combinatorial synthesis and high-throughput, miniaturized, in vitro screening, which has become an integral part of pharmaceutical discovery, is now being applied to discover new herbicides, insecticides, and fungicides. Depending on the synthesis design, the products of a combinatorial synthesis, referred to as a library, may be either unbiased or biased toward an intended target. Unbiased libraries are generally prepared to maximize chemical diversity around a central core structure or scaffold. Often containing 10 000 to 30 000 compounds each, these libraries are encoded and prepared by a combinatorial methodology known as mix-and-split, which produces compounds as mixtures. The preparation of these large libraries requires robust synthetic methodology that will accommodate reactants (building blocks) with diverse structures. Biased libraries tend to be smaller in size, ranging from 100 to 2500 compounds. They are prepared using synthetic methodology that produces collections of discrete compounds (parallel synthesis) or pools of five to 10 compounds per pool (mix-and-split synthesis). Compounds in biased libraries are rationally designed to contain structural motifs or pharmacophores that are presumed to be beneficial for activity on the intended target. Screening is conducted in microtiter assay plates containing from 96 to 864 wells per plate. For in vitro assays, high-density formats (864 wells per plate) are preferred. The higher density format allows for testing higher concentrations and fewer compounds per well, which leads to a more rapid identification of the active molecules. For in vivo assays, 96-well formats are preferred. Regardless of the microtiter plate format, multiple beads are distributed into plates by robotic pipetting, and single beads are distributed via robot-controlled suction pipets. Test compounds are cleaved from the beads and transferred in solvent to assay plates. Required reagents are added to the plate to initiate the assay. A wide range of in vitro and in vivo herbicide, insecticide, and fungicide assays can be conducted in microtiter plates
Descriptors:agricultural-chemicals. fungicides. genome-analysis. genomes. herbicides. insecticides. methodology. techniques
Subject Codes:HH400. WW000. ZZ900
Supplementary Info:16 ref
ISSN:0043-1745
Year:2001
Journal Title:Weed Science

361. Title:Plant diversity: new insights from molecular biology and genomics technologies
View Article: Weed Science. 2001. 49 (2). 257-265
CD Volume:374
Print Article: Pages: 257-265
Author(s):Jasieniuk M Maxwell B D
Author Affiliation:Department of Land Resources and Environmental Sciences, Montana State University, Bozeman, MT 59717, USA
Conference Title:Proceedings of the Weed Science Society of America Meeting - Impact of Biotechnology and Genomics on Weed Science, held at Toronto, Canada, 2000
Language:English
Abstract:Technological advances in molecular biology have contributed substantially to our understanding of plant genetic diversity. Early studies of alloenzyme variation employing protein electrophoresis revealed that plant populations have high levels of genetic diversity,

most of the variation at polymorphic loci is found within populations, and geographic range and breeding system explain the largest proportion of variation in genetic diversity. With the discovery of restriction endonucleases, the first DNA-based markers allowed the detection of variation in DNA sequences in plant population studies. More recently, techniques that utilize the polymerase chain reaction have allowed a more representative assessment of genetic variation in plants by screening multiple loci distributed throughout the genome. The analyses reveal sufficient polymorphism for the examination of fine-scale genetic differences among individuals. Information on plant genetic diversity is also emerging from studies of plant genome structure. Comparative genetic mapping studies of members of the Brassicaceae, Poaceae, and Solanaceae show that gene content is highly conserved between closely related species, although gene order on a chromosomal segment may differ between species. Comparative sequencing studies reveal higher degrees of diversity at the microstructural (less than 1 million base pairs) level than predicted at the genetic map level and suggest that genes are densely packed in gene-rich regions, rather than randomly distributed along chromosomes in species with large genomes. Sequencing of the entire genomes of rice and Arabidopsis thaliana will help identify genes controlling agronomically important traits, improve our understanding of genetic variation for fitness-related traits in wild plant populations including weed species, resolve evolutionary relationships among plant taxa, and potentially revolutionize current ideas on plant diversity and evolution

Descriptors:DNA. DNA-sequencing. enzymes. genes. genetic-diversity. genetic-mapping. genetic-markers. genetic-polymorphism. genetic-variation. genomes. loci. nucleotide-sequences. restriction-endonucleases. rice. techniques. weeds

Organism Descriptors:Arabidopsis-thaliana. Brassicaceae. Oryza. Oryza-sativa. Poaceae. Solanaceae

Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants. Oryza. Poaceae. Cyperales. monocotyledons. Solanales

Subject Codes:FF020. WW000

Supplementary Info:120 ref

ISSN:0043-1745

Year:2001

Journal Title:Weed Science

362. Title:From inhibitors to target site genes and beyond - herbicidal inhibitors as powerful tools for functional genomics

View Article: Weed Science. 2001. 49 (2). 266-272

CD Volume:374

Print Article: Pages: 266-272

Author(s):Zhen RuiGuang Singh B K

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Author Affiliation:BASF Plant Science, BASF Corporation, P.O. Box 400, Princeton, NJ 08543-0400, USA

Conference Title:Proceedings of the Weed Science Society of America Meeting - Impact of Biotechnology and Genomics on Weed Science, held at Toronto, Canada, 2000

Language:English

Abstract:With rapid progress being made in deciphering plant genomic sequences, determining the function of these genes is one of the main challenges that plant molecular biologists face today. Herbicidal inhibitors have been very useful for understanding gene function in at least two

examples, represented by herbicidal inhibitors of hydroxyphenylpyruvate dioxygenase (HPPD) and deoxyxylulosephosphate reductoisomerase (DXR). In the first, an albino mutant of Arabidopsis thaliana isolated during the study of carotenoid biosynthesis was found to have an intact carotenoid biosynthetic pathway. A number of "bleaching herbicides" in development at about the same time (e.g., sulcotrione) produced similar symptoms by strongly inhibiting HPPD, a key enzyme in plastoquinone biosynthesis. Examination of the A. thaliana mutant revealed that the HPPD gene had been inactivated in the albino plants. Inhibition of the HPPD pathway also led to reduced levels of tocopherol (vitamin E), an end product of the pathway. Further studies and manipulation of the pathway produced plants with significantly higher levels of vitamin E. This result is a clear demonstration of how an herbicidal inhibitor was able to lead to the identification of a gene that was responsible for a particular phenotype. As a second example, identification of fosmidomycin as a specific inhibitor of DXR in the recently elucidated nonmevalonate pathway of isopentenyl pyrophosphate (IPP) biosynthesis was instrumental in furthering the understanding of an important route to synthesis of many important terpenoid products

Descriptors:biochemical-pathways. biosynthesis. carotenoids. enzymes. genes. genomes. herbicides. inhibitors. mutants. mutations. terpenoids. vitamin-E

Identifiers:dioxygenase. reductoisomerase

Organism Descriptors:Arabidopsis-thaliana

Supplemental Descriptors:Arabidopsis. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants

Subject Codes:FF020. FF060. FF500. WW000

Supplementary Info:41 ref

ISSN:0043-1745

Year:2001

Journal Title:Weed Science

363. Title:A perspective on molecular-based research: integration and utility in weed science

View Article: Weed Science. 2001. 49 (2). 273-275

CD Volume:374

Print Article: Pages: 273-275

Author(s):Marshall G

Author Affiliation:Division of Plant and Crop Science, Scottish Agricultural College, Auchincruive, Ayr KA6 5HW, Great Britain, UK

Conference Title:Proceedings of the Weed Science Society of America Meeting - Impact of Biotechnology and Genomics on Weed Science, held at Toronto, Canada, 2000

Language:English

Abstract:A framework is presented to consider the value and utility of molecular-based research in weed science. Four themes are used to illustrate why adopting molecular approaches might be helpful. First, the rationale for academic institutions adopting molecular approaches is outlined, including strengths, weaknesses, opportunities, and threats (SWOT) analysis. Second, research strategy and synergies developed into other functions, such as education, consultancy, and business, is considered. Third, project management as a vehicle for integrating technical and personnel skills is examined. Finally, specific examples of outputs such as the application of functional genomics for herbicide discovery are described. The adoption of molecular-based methods can have far-reaching benefits in agriculture and biotechnology. Communicating these benefits within the scientific

community and beyond, particularly to end users, is of fundamental importance
Descriptors:agricultural-research. agriculture. biotechnology. herbicides. methodology. molecular-genetics. weeds
Subject Codes:AA500. HH400. WW000. ZZ900
ISSN:0043-1745
Year:2001
Journal Title:Weed Science

364. Title:Understanding auxinic herbicide resistance in wild mustard: physiological, biochemical, and molecular genetic approaches
View Article: Weed Science. 2001. 49 (2). 276-281
CD Volume:374
Print Article: Pages: 276-281
Author(s):Zheng HongGang Hall J C
Author Variant:Zheng-H-G
Author Affiliation:Department of Environmental Biology, University of Guelph, Guelph, Ontario N1G 2W1, Canada
Conference Title:Proceedings of the Weed Science Society of America Meeting - Impact of Biotechnology and Genomics on Weed Science, held at Toronto, Canada, 2000
Language:English
Abstract:The incidence of auxinic herbicide resistance in plants has increased worldwide. Auxinic herbicides were the first selective organic herbicides developed and have been used in agriculture for over 50 years, primarily for the selective control of broadleaf weeds in cereal crops. However, the mode of action of auxinic herbicides and the molecular basis of auxinic herbicide resistance remain unknown, although an auxin-binding protein (ABP) is proposed to be the primary target site. Using auxinic herbicide-resistant (R) and -susceptible (S) biotypes of wild mustard (Brassica kaber) as a model system, we have extensively studied the mode of action of auxinic herbicides and the resistance mechanisms at the physiological, biochemical, and molecular genetic levels. There are no differences in uptake, transport, and metabolism of auxinic herbicides between the R and S biotypes. Based on these results, as well as the studies on the role of auxin-enhanced ethylene biosynthesis and calcium in mediating the auxinic herbicide resistance, we hypothesize that resistance of the R biotype to auxinic herbicides is due to an altered target site, possibly an auxin receptor. We have identified and characterized a small ABP gene family as well as their cDNAs from both R and S of wild mustard. Amino acid changes were found in the ABP of the R biotype. Functional and mutational analyses of these genes are underway to determine the role of ABP in mediating auxinic herbicide resistance. In this review, we focus on the mode of action of auxinic herbicides and the molecular basis of auxinic herbicide resistance in wild mustard
Descriptors:auxins. biochemistry. complementary-DNA. DNA-sequencing. genes. herbicide-resistance. herbicides. mode-of-action. models. molecular-genetics. mutational-analysis. nucleotide-sequences. plant-physiology. reviews. weeds
Organism Descriptors:Brassica-kaber
Supplemental Descriptors:Brassica. Brassicaceae. Capparidales. dicotyledons. angiosperms. Spermatophyta. plants
Subject Codes:FF020. FF500. HH410. WW000. ZZ900
Supplementary Info:57 ref
ISSN:0043-1745
Year:2001

Journal Title:Weed Science
Copyright:Copyright CAB International

365. Title:The effect of genomics on weed management in the 21st century
View Article: Weed Science. 2001. 49 (2). 282-289
CD Volume:374
Print Article: Pages: 282-289
Author(s):Weller S C Bressan R A Goldsbrough P B Fredenburg T B Hasegawa P M
Author Affiliation:Department of Horticulture and Landscape Architecture, Purdue University, West Lafayette, IN 47907-1165, USA
Conference Title:Proceedings of the Weed Science Society of America Meeting - Impact of Biotechnology and Genomics on Weed Science, held at Toronto, Canada, 2000
Language:English
Abstract:This review provides a summary of the various plant genomic research methods being used. Information is provided concerning the current state of molecular research in various areas of weed science and specific genomic research currently being conducted at Purdue University using transfer DNA (T-DNA) activation tagging to generate large populations of mutated plants that can be screened for genes of importance to weed science
Descriptors:DNA. genes. genomes. methodology. molecular-genetics. mutants. mutations. reviews. T-DNA. transgenic-plants. weeds
Organism Descriptors:plants
Subject Codes:FF020. FF500. WW000
Supplementary Info:37 ref
ISSN:0043-1745
Year:2001
Journal Title:Weed Science
Copyright:Copyright CAB International

366. Title:Genetic Engineering and Trade: Panacea or Dilemma for Developing Countries
View Article: World Development. 29 (8) 2001. 1307-24
CD Volume:376
Print Article: Pages: 1307-1324
Author(s):Nielsen C P Robinson S Thierfelder K
Author Affiliation:Danish Institute of Agricultural & Fisheries Econ and U Copenhagen. IFPRI. US Naval Academy
Language:English
Abstract:Advocates of the use of genetic engineering techniques in agriculture contend that this new biotechnology promises increased productivity, better use of natural resources and more nutritious foods. Opponents are concerned about potentially adverse implications for the environment and food safety. In response to consumer reactions against genetically modified (GM) foods, in some countries crop production is being segregated into GM and non-GM varieties. This analysis finds that world markets for maize and soybeans adjust well to these changes and also that developing countries will divert their trade patterns in response to preference changes in important trading partner countries
Descriptors:Agricultural R&D; Agricultural Technology; Agricultural Extension Services. Agriculture in International Trade. International Linkages to Development; Role of International Organizations. Economic Development: Agriculture; Natural Resources; Environment; Other Primary Products. Food; Beverages; Cosmetics; Tobacco
Geographic Locator:LDCs
Subject Codes:EE110. EE450. EE520
ISSN:0305-750X
Year:2001