Summary

Adjuvant for breast cancer radiotherapy
Integr Cancer Ther. 2002 Mar;1(1):38-4; discussion 42-3

Phytoestrogenic
J Agric Food Chem. 2003 Apr 9;51(8):2193-9.
Barroga, C.F., A.C. Laurena, and E.M. T. Mendoza. 1985. Polyphenols in mung bean (Vigna radiata (L.) Wilczek): determinatoin and removal. J. Agric. Food Chem. 33: 1006.

Mung beans do not cause flatulence
Crit Rev Food Sci Nutr. 1986;25(1):73-105.

Abstracts for all papers related to Vigna radiata

Crit Rev Food Sci Nutr. 1986;25(1):73-105. Related Articles, Links

Chemistry and technology of green gram (Vigna radiata [L.] Wilczek).

Adsule RN, Kadam SS, Salunkhe DK.

Green gram or mung bean (Vigna radiata [L.] Wilczek) is an important food legume grown under tropical and subtropical conditions. It is an excellent source of protein and is almost free from flatulence-causing factors. Because of this, green gram seeds are preferred for feeding babies and those convalescing. The seeds contain a higher proportion of lysine than any other legume seeds. The seeds are processed and consumed as cooked whole beans or splits (dhals), sprouts, immature seeds, and flour and are used in various recipes. The proposed work will incorporate available information on nutritional composition, processing, and utilization of green gram. The results reported in the literature on the above aspects of green gram will be analyzed critically, and future research needs will be defined to improve the utilization of green gram as human food.

Publication Types:
Review

J Agric Food Chem. 2005 Feb 23;53(4):982-8. Related Articles, Links

Cloning and characterization of a plant defensin VaD1 from azuki bean.

Chen GH, Hsu MP, Tan CH, Sung HY, Kuo CG, Fan MJ, Chen HM, Chen S, Chen CS.

Institute of Microbiology and Biochemistry and Department of Agricultural Chemistry, National Taiwan University, Taipei 106, Taiwan.

A recombinant mungbean defensin VrD1 was previously shown to exhibit antifungal and bruchid-resistant activity. To study the function and regulation of VrD1, genomic DNAs of plant defensins were isolated from Vigna radiata VC6089A and azuki bean Vigna angularis Kao Hsiung No. 6. The azuki bean defensin genomic DNA VaD1 was sequenced and converted to VaD1 cDNA. VaD1 defensin was purified from Vigna angularis Kao Hsiung No. 6 to apparent homogeneity. The complete amino acid sequence of the purified VaD1 was determined and was found to be exactly the same as the sequence deduced from VaD1 cDNA. VaD1 is a basic protein containing

46 amino acids with four conserved disulfide bonds and shares high sequence homology (78.3%) with VrD1. VaD1 inhibited the growth of Fusarium oxysporum, Fusarium oxysporum f. sp. pisi, Staphylococcus epidermidis, and Salmonella typhimurium. VaD1 also inhibited in vitro protein synthesis and bruchid larval development, but was less active than the recombinant VrD1.

PMID: 15713009 [PubMed - in process]

2: Planta. 2004 Dec 15; [Epub ahead of print] Related Articles, Links

Chilling stress suppresses chloroplast development and nuclear gene expression in leaves of mung bean seedlings.

Yang MT, Chen SL, Lin CY, Chen YM.

Institute of Plant Biology, National Taiwan University, No. 1, Sec. 4, Roosevelt Rd, Taipei, 106, Taiwan (ROC), ymt100@ms2.food.gov.tw.

Etiolated leaves of 28 degrees C-dark-grown mung bean (Vigna radiata L. cv. 2937) seedlings fail to turn green after being shifted to a light and cold environment. At the visible phenotypic level, incapability of leaf greening is the only failure event for the de-etiolation of mung bean seedlings at low temperature. Ultrastructural studies revealed that chloroplast development was completely suppressed by chilling treatment. A cDNA library originating from 28 degrees C-light-grown seedling leaves was constructed for screening cold-suppressed (cos) genes. Thirteen full-length cDNA clones were obtained, with 12 clones encoding chloroplast proteins, which, according to their known physiological functions, were important for chloroplast development and photosynthesis. Another cos cDNA encodes CYP90A2, which is a cytochrome P450 protein involved in the biosynthesis of brassinosteroid hormones. All cos genes are light-regulated at normal temperature. The influence of chilling stress on cos expression was examined in 10 degrees C-light- and 10 degrees C-dark-grown etiolated seedlings, and in 10 degrees C-light-grown green plants. The data show that cos expression in these three treatments is severely suppressed. This suppression is controlled at the transcriptional level, as demonstrated by nuclear runoff experiments, and is reversible because cos mRNAs accumulate again after the cold-treated plants have been transferred to 28 degrees C.

PMID: 15599759 [PubMed - as supplied by publisher]

3: Theor Appl Genet. 2004 Dec;110(1):151-6. Epub 2004 Oct 15. Related Articles, Links

Construction of bacterial artificial chromosome libraries and their application in developing PCR-based markers closely linked to a major locus conditioning bruchid resistance in mungbean (Vigna radiata L. Wilczek).

Miyagi M, Humphry M, Ma ZY, Lambrides CJ, Bateson M, Liu CJ.

CSIRO Plant Industry, Queensland Bioscience Precinct, 306 Carmody Road, Brisbane, QLD 4067, Australia.

Bacterial artificial chromosome (BAC) libraries have been widely used in different aspects of genome research. In this paper we report the construction of the first mungbean (Vigna radiata L. Wilczek) BAC libraries. These BAC clones were obtained from two ligations and represent an estimated 3.5 genome equivalents. This correlated well with the screening of nine random single-copy restriction fragment length polymorphism probes, which detected on average three BACs each. These mungbean clones were successfully used in the development of two PCR-based markers linked closely with a major locus conditioning bruchid (Callosobruchus chinesis) resistance. These markers will be invaluable in facilitating the introgression of bruchid resistance into breeding programmes as well as the further characterisation of the resistance locus.

PMID: 15490104 [PubMed - in process]

4: Zhi Wu Sheng Li Yu Fen Zi Sheng Wu Xue Xue Bao. 2004 Dec;30(6):665-70. Related Articles, Links

[Effects of methyl jasmonate treatment on the hydrolytic activity and phosphorylation level of plasma membrane H+-ATPase in mung bean (Vigna radiata L.) hypocotyls.]

[Article in Chinese]

Wen B, Bin JH, Wang XJ.

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Employing both protein kinase inhibitors and phosphatase inhibitors to investigate the effect of MeJA (methyl jasmonate) on the H+-ATPase hydrolytic activity of plasma membrane, and the regulations involved with phosphorylation and dephosphorylation of plasma membrane H+-ATPase after treatments with MeJA. 3 d-old etiolated mung bean (Vigna radiata L.) seedlings were harvested and the hypocotyls (1-2 cm in length) under the hook were used to prepare the plasma membrane vesicles by means of aqueous two-phase partition. Hydrolytic activities of plasma membrane H+-ATPase were determined in responding to the treatment with MeJA. H(+)-ATPase activity stimulated by MeJA and FC was up to 30%, and the combination of MeJA and FC did not show significant additive effect. The phosphatase inhibitors, okadaic acid and cantharidin, enhanced MeJA-induced increase of the enzyme activity to 60% and 50%, respectively. Staurosporine and cheleythrine, two inhibitors of protein kinase, abolished completely the stimulative effect of MeJA on PM H+-ATPase activity (Fig. 2). The results from gamma-(32)P tracer experiments showed that treatment with MeJA and FC increased the level of isotope labeling on PM H+-ATPase. Okadaic acid and cantharidin could enhance the labeling of gamma-(32)P on PM H+-ATPase induced by MeJA and FC. Both MeJA- and FC-induced increase in gamma-(32)P level were inhibited when cheleythrine was applied (Fig. 3). Ca2+ strongly stimulated the PM H+-ATPase and the increase of the enzyme activity was two times higher than that of the control. But Ca2+ had no enhancement of the enzyme activity induced by FC and MeJA. In the presence of Ca2+, Okadaic acid could increase the MeJA stimulation slightly, but cantharidin had not any significant effect on the enzyme activity. Staurosporine and cheleythrine showed no effect on MeJA-induced increase in PM H+-ATPase, and which activity was similar to the control after treatment with either inhibitor (Figs. 5, 6). The changes in hydrolytic activity of H+-ATPase stimulating by MeJA is probably related to reversible phosphorylation, and the protein kinase is Ca2+-independent, phosphatase is Ca2+-dependent.

PMID: 15643087 [PubMed - in process]

5: J Hered. 2004 Nov-Dec;95(6):532-5. Related Articles, Links

Segregation distortion for seed testa color in Mungbean (Vigna radiata L. Wilcek).

Lambrides CJ, Godwin ID, Lawn RJ, Imrie BC.

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Genetic segregation experiments with plant species are commonly used for understanding the inheritance of traits. A basic assumption in these experiments is that each gamete developed from megasporogenesis has an equal chance of fusing with a gamete developed from microsporogenesis, and every zygote formed has an equal chance of survival. If gametic and/or zygotic selection occurs whereby certain gametes or zygotic combinations have a reduced chance of survival, progeny distributions are skewed and are said to exhibit segregation distortion. In this study, inheritance data are presented for the trait seed testa color segregating in large populations (more than 200 individuals) derived from closely related mungbean (Vigna radiata L. Wilcek) taxa. Segregation ratios suggested complex inheritance, including dominant and recessive epistasis. However, this genetic model was rejected in favor of a single-gene model based on evidence of segregation distortion provided by molecular marker data. The segregation distortion occurred after each generation of self-pollination from F1 thru F7 resulting in F7 phenotypic frequencies of 151:56 instead of the expected 103.5:103.5. This study highlights the value of molecular markers for understanding the inheritance of a simply inherited trait influenced by segregation distortion.

PMID: 15475401 [PubMed - indexed for MEDLINE]

1: Theor Appl Genet. 2004 Oct 15 [Epub ahead of print]

Construction of bacterial artificial chromosome libraries and their application in developing PCR-based markers closely linked to a major locus conditioning bruchid resistance in mungbean (Vigna radiata L. Wilczek).

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CSIRO Plant Industry, Queensland Bioscience Precinct, 306 Carmody Road, 4067, Brisbane, QLD, Australia.

Bacterial artificial chromosome (BAC) libraries have been widely used in different aspects of genome research. In this paper we report the construction of the first mungbean (Vigna radiata L. Wilczek) BAC libraries. These BAC clones were obtained from two ligations and represent an estimated 3.5 genome equivalents. This correlated well with the screening of nine random single-copy restriction fragment length polymorphism probes, which detected on average three BACs each. These mungbean clones were successfully used in the development of two PCR-based markers linked closely with a major locus conditioning bruchid (Callosobruchus chinesis) resistance. These markers will be invaluable in facilitating the introgression of bruchid resistance into breeding programmes as well as the further characterisation of the resistance locus.

PMID: 15490104 [PubMed - as supplied by publisher]

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Segregation Distortion for Seed Testa Color in Mungbean (Vigna radiata L. Wilcek).

Lambrides CJ, Godwin ID, Lawn RJ, Imrie BC.

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Genetic segregation experiments with plant species are commonly used for understanding the inheritance of traits. A basic assumption in these experiments is that each gamete developed from megasporogenesis has an equal chance of fusing with a gamete developed from microsporogenesis, and every zygote formed has an equal chance of survival. If gametic and/or zygotic selection occurs whereby certain gametes or zygotic combinations have a reduced chance of survival, progeny distributions are skewed and are said to exhibit segregation distortion. In this study, inheritance data are presented for the trait seed testa color segregating in large populations (more than 200 individuals) derived from closely related mungbean (Vigna radiata L. Wilcek) taxa. Segregation ratios suggested complex inheritance, including dominant and recessive epistasis. However, this genetic model was rejected in favor of a single-gene model based on evidence of segregation distortion provided by molecular marker data. The segregation distortion occurred after each generation of self-pollination from F(1) thru F(7) resulting in F(7) phenotypic frequencies of 151:56 instead of the expected 103.5:103.5. This study highlights the value of molecular markers for understanding the inheritance of a simply inherited trait influenced by segregation distortion.

PMID: 15475401 [PubMed - in process]

3: J Biosci. 2004 Sep;29(3):297-308.

Infectivity analysis of two variable DNA B components of Mungbean yellow mosaic virus-Vigna in Vigna mungo and Vigna radiata.

Balaji V, Vanitharani R, Karthikeyan AS, Anbalagan S, Veluthambi K.

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Mungbean yellow mosaic virus-Vigna (MYMV-Vig), a Begomovirus that causes yellow mosaic disease, was cloned from field-infected blackgram (Vigna mungo). One DNA A clone (KA30) and five different DNA B clones (KA21, KA22, KA27, KA28 and KA34) were obtained. The sequence identity in the 150-nt common region (CR) between DNA A and DNA B was highest (95%) for KA22 DNA B and lowest (85.6%) for KA27 DNA B. The Rep-binding domain had three complete 11-nt (5'-TGTATCGGTGT-3') iterons in KA22 DNA B (and KA21, KA28 and KA34), while the first iteron in KA27 DNA B (5'-ATCGGTGT-3') had a 3-nt deletion. KA27 DNA B, which exhibited 93.9% CR sequence identity to the mungbean-infecting MYMV, also shared the 3-nt deletion in the first iteron besides having an 18-nt insertion between the third iteron and the conserved nonanucleotide. MYMV was found to be closely related to KA27

DNA B in amino acid sequence identity of BV1 (94.1%) and BC1 (97.6%) proteins and in the organization of nuclear localization signal (NLS), nuclear export signal (NES) and phosphorylation sites. Agroinoculation of blackgram (V. mungo) and mungbean (V. radiata) with partial dimers of KA27 and KA22 DNA Bs along with DNA A caused distinctly different symptoms. KA22 DNA B caused more intense yellow mosaic symptoms with high viral DNA titre in blackgram. In contrast, KA27 DNA B caused more intense yellow mosaic symptoms with high viral DNA titre in mungbean. Thus, DNA B of MYMVVig is an important determinant of host-range between V. mungo and V. radiata.

PMID: 15381851 [PubMed - in process]

4: Arch Gerontol Geriatr. 1992 Jul-Aug;15(1):71-8.

Life prolonging effect of butylated hydroxy anisole in Callosobruchus maculatus F. (Coleoptera: Bruchidae).

Mahajan S, Garg SK.

Department of Molecular Biology and Biochemistry, Guru Nanak Dev University, Amritsar 143005, India.

The present study deals with the effect of butylated hydroxy anisole (BHA), an antioxidant, on longevity and fecundity of insects infesting BHA soaked seeds of Vigna radiata. Median (LT(50)) and maximum (LT(100)) life spans as well as post-reproductive period of the insect reared on optimal concentration (1 mM) of antioxidant soaked seeds were higher than the control. However, the reproductive period of the females and the number of eggs laid/female declined. The results are indicative of the increased life span of the insects on BHA feeding at the cost of the reproductive period.

PMID: 15374382 [PubMed - in process]

5: Plant Physiol Biochem. 2004 Jul-Aug;42(7-8):617-22.

Characterization of DNA end-binding activities in higher plants.

Yan KH, Liu PF, Tzeng HT, Chang WC, Chou WG, Pan RL.

Department of Life Sciences and Institute of Bioinformatics and Structural Biology, College of Life Sciences, National Tsing Hua University, Hsin Chu, Taiwan 30043, Republic of China.

DNA double-strand-breaks (DSB) are the most severe lesion in cells exposing to ionizing radiation and many other stress environments. Repair of DNA DSB is therefore critical to cellular survival. In this work, we observed the double-stranded DNA end-binding (DEB) like activities in rice (Oryza sativa L. cv. TN5) suspension cells and hypocotyls from etiolated mung bean (Vigna radiata L. TN5) seedlings. Higher plant DEB-like protein binds primarily to linearized double-stranded DNA ends. Competition of unlabeled probe was examined in double-stranded DEB assay of cell extracts from rice and mung bean. DEB-like activities of higher plants did not depend on sequence and types of

double-stranded DNA ends. Distinct electrophoretic mobility shift patterns and binding features further indicate that DEB-like factors from various sources might not share identical structure and function, and probably belong to different types of DEB proteins from higher plants. Our evidence suggests that DEB proteins are certainly ubiquitous in all organisms probably for repairing and processing double-stranded DNA breaks from formidable lethal lesion.

PMID: 15331090 [PubMed - in process]

6: J Environ Biol. 2003 Jul;24(3):289-94.

Effect of kinetin on leaf protein content and its profile in mung bean under salt stress.

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chakrabartinandini@hotmail.com

Application of NaCl resulted in about 67% reduction in amino acid content and 24% reduction in buffer soluble protein content in mung bean [Vigna radiata (L.) Wilczek.] leaf as compared with the control. Gel electrophoretic profile of buffer soluble protein content in leaf of mung bean showed an extra band in between 29 kD and 45 kD in stress protein profile as compared with control. It was noted that the foliar spray of kinetin (6-furfuryl aminopurine) used in the present study was able to overcome up to certain extent the adverse effects of stress caused by NaCl.

PMID: 15259605 [PubMed - indexed for MEDLINE]

7: Planta. 2004 Jun 5 [Epub ahead of print]

Electron-microscopic structure of the V-ATPase from mung bean.

Li Z, Zhang X.

National Laboratory of Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences, 100101, Beijing, China.

The vacuolar H(+)-ATPase from mung bean (Vigna radiata L. cv. Wilczek) was purified to homogeneity. The purified complex contained all the reported subunits from mung bean, but also included a 40-kDa subunit, corresponding to the membrane-associated subunit d, which has not previously been observed. The structure of the V-ATPase from mung bean was studied by electron microscopy of negatively stained samples. An analysis of over 6,000 single-particle images obtained by electron microscopy of the purified complex revealed that the complex, similar to other V-ATPases, is organized into two major domains V(1) and V(o) with overall dimensions of 25 nmx13.7 nm and a stalk region connecting the V(1) and V(o) domains. Several individual areas of protein density were observed in the stalk region, indicating its complexity. The projections clearly

showed that the complex contained one central stalk and at least two peripheral stalks. Subcomplexes containing subunits A, B and E, dissociated from the tonoplast membrane by KI, were purified. The structure of the subcomplex was also studied by electron microscopy followed by single-molecule analysis of 13,000 projections. Our preliminary results reveal an area of high protein density at the bottom of the subcomplex immediately below the cavity formed by the A and B subunits, indicating the position of subunit E.

PMID: 15185079 [PubMed - as supplied by publisher]

8: Biochim Biophys Acta. 2004 Jun 7;1656(2-3):88-95.

Thermoinactivation analysis of vacuolar H(+)-pyrophosphatase.

Yang SJ, Jiang SS, Hsiao YY, Van RC, Pan YJ, Pan RL.

Department of Radiological Technology, Chungtai Institute of Health Sciences and Technology, Taichung 40605, Taiwan, ROC.

Vacuolar H(+)-translocating pyrophosphatase (H(+)-PPase; EC 3.6.1.1) catalyzes both the hydrolysis of PP(i) and the electrogenic translocation of proton from the cytosol to the lumen of the vacuole. Vacuolar H(+)-PPase, purified from etiolated hypocotyls of mung bean (Vigna radiata L.), is a homodimer with a molecular mass of 145 kDa. To investigate the relationship between structure and function of this H(+)-translocating enzyme, thermoinactivation analysis was employed. Thermoinactivation studies suggested that vacuolar H(+)-PPase consists of two distinct states upon heat treatment and exhibited different transition temperatures in the presence and absence of ligands (substrate and inhibitors). Substrate protection of H(+)-PPase stabilizes enzyme structure by increasing activation energy from 54.9 to 70.2 kJ/mol. We believe that the conformation of this enzyme was altered in the presence of substrate to protect against the thermoinactivation. In contrast, the modification of H(+)-PPase by inhibitor (fluorescein 5'-isothiocyanate; FITC) augmented the inactivation by heat treatment. The native, substrate-bound, and FITC-labeled vacuolar H(+)-PPases possess probably distinct conformation and show different modes of susceptibility to thermoinactivation. Our results also indicate that the structure of one subunit of this homodimer exerts long distance effect on the other, suggesting a specific subunit-subunit interaction in vacuolar H(+)-PPase. A working model was proposed to interpret the relationship of the structure and function of vacuolar H(+)-PPase.

PMID: 15178470 [PubMed - indexed for MEDLINE]

9: J Agric Food Chem. 2004 May 5;52(9):2552-60.

8S globulin of mungbean [Vigna radiata (L.) Wilczek]: cloning and characterization of its cDNA isoforms, expression in Escherichia coli, purification, and crystallization of the major recombinant 8S isoform.

Bernardo AE, Garcia RN, Adachi M, Angeles JG, Kaga A, Ishimoto M, Utsumi S, Tecson-Mendoza EM.

Institute of Plant Breeding, College of Agriculture, University of the Philippines Los Banos, College, Laguna Philippines 4031.

Three isoforms of the cDNA of the major 8S globulin of mungbean, 8Salpha, 8Salpha', and 8Sbeta, were isolated, cloned, and characterized. The cDNA sequences of 8Salpha, 8Salpha', and 8Sbeta had open reading frames of 1362, 1359 or 1362, and 1359 bp, respectively, which code for 454, 453 or 454, and 453 amino acids corresponding to molecular weights of 51 973, 51 627 or 51 758, and 51 779, respectively. Homology in terms of cDNA and amino acid sequences was 91-92% between 8Salpha and 8Salpha', 87% between 8Salpha and 8Sbeta, and 86-88% between 8Salpha' and 8Sbeta. The signal peptide was found to be 1-25, 1-24 or 25, and 1-23 for 8Salpha, 8Salpha', and 8Sbeta, respectively, using the signalP website (Nielsen, H.; Engelbrecht, J.; Brunak, S.; von Heijne, G. Protein Eng. 1997, 10, 1-6). The propeptide was determined to be IVHREN. A single site for glycosylation (N-X-S/T) was observed about 90 amino acids from the C terminus. Homology between mungbean 8S isoforms and other 7-8S proteins ranged from 45 to 68% within members of the legume family and 29 to 34% for crops of different species. The major isoform 8Salpha was expressed in Escherichia coli and purified by successive ammonium sulfate fractionation, hydrophobic interaction, and Mono Q column chromatography. The recombinant 8Salpha, but not the native form, was successfully crystallized producing rhombohedral crystals.

PMID: 15113156 [PubMed - indexed for MEDLINE]

10: Environ Pollut. 1997;95(3):289-91.

Increased UV-B radiation reduces N(2)-fixation in tropical leguminous crops.

Singh A.

Department of Botany, Banaras Hindu University, Varanasi-221 005, India.

Net photosynthesis, leaf area, biomass, and number, size and activity of nodules were examined in three leguminous plants subjected under field conditions to supplemental UV-B radiation equivalent to a 15% ozone depletion at 25 degrees N latitude. Enhanced UV-B radiation adversely affected the net photosynthetic rate, growth characteristics and nodule activity in all three species. Maximum reduction in net photosynthesis occurred in Phaseolus mungo cv. Pant U-30, whereas the greatest reduction in nitrogenase activity occurred in Vigna radiata.

PMID: 15093442 [PubMed - in process]

11: Environ Pollut. 1989;61(2):157-70.

Effects of DDT on the growth of crop plants.

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The effects of DDT on the germination and growth of plants were studied using many crop species. Of the species tested, oil-rich seeds of plants, such as peanut (Arachis hypogaea) and mustard (Brassica juncea), were more prone to DDT induced inhibition of germination and subsequent plant growth than cereals, pulses and fibre crops, like rice (Oryza sativa), barley (Hordeum vulgare), mung bean Vigna radiata), pigeon pea (Cajanus cajan) and cotton (Gossypium hirsutum). Studies with (14)C labelled DDT showed that insecticide uptake by seeds was directly proportional to seed size. However, there was no direct relationship between DDT uptake by the seeds and its subsequent translocation to the growing regions or the degree of growth inhibition. Data suggest that oil content of the seeds per se has a bearing on the susceptibility or tolerance of a plant to DDT. It is suggested that lipids of the plant cell solubilize and disperse DDT in the cytoplasm, which, in turn, affects normal metabolism within the cell.

PMID: 15092369 [PubMed]

12: Aquat Toxicol. 2004 Feb 10;66(2):141-7.

Hydrophytes lack potential to exhibit cadmium stress induced enhancement in lipid peroxidation and accumulation of proline.

Dhir B, Sharmila P, Saradhi PP.

Department of Environmental Biology, University of Delhi, Delhi 110007, India.

Investigations were carried out to evaluate if hydrophytes (viz. Ceratophyllum, Wolffia, and Hydrilla) can be used as markers to assess the level of heavy metal pollution in aquatic bodies. The potential of these hydrophytes for lipid peroxidation and accumulation of proline in response to cadmium (Cd2+) pollution was studied. Hydrophytes were raised in artificial pond water (APW) supplemented with various levels of Cd2+. Interestingly, unlike mesophytes none of the hydrophytes showed ability to accumulate proline. Infact, in response to Cd2+ pollution hydrophytes exhibited a decline in proline levels in comparison to controls but mesophytes (viz. Brassica juncea, Vigna radiata and Triticum aestivum) showed progressive increase in the level of proline with increase in the extent of Cd2+ pollution. Mesophytes showed six to nine-fold increase in the level of proline in response to 1 mM Cd2+. The potential of the above hydrophytes for lipid peroxidation was also low under Cd2+ stress. In contrast, as expected a significant enhancement in the lipid peroxidation was observed in all three mesophytes in response to their exposure to Cd2+. About two-fold increase in production of malondialdehyde (a cytotoxic product of lipid peroxidation) was recorded in mesophytes exposed to 1 mM Cd2+. However, a decline in chlorophyll (Chl a and Chl b) levels was recorded in response to Cd2+pollution both in hydrophytes as well as mesophytes. In summary, hydrophytes neither have potential to accumulate proline nor have ability to accelerate lipid peroxidation under heavy metal stress. This suggests that the adaptive mechanism(s) existing in hydrophytes to tackle heavy metal stress is distinct from that in mesophytes.

PMID: 15036869 [PubMed - indexed for MEDLINE]

13: DNA Seq. 2003 Dec;14(6):420-6.

Cloning and characterization of two novel lipid transfer protein I genes in Vigna radiata.

Liu KH, Lin TY.

Department of Life Science, National Tsing Hua University, Hsinchu, Taiwan 30013, Republic of China.

Two full-length lipid transfer protein (LTP) cDNAs were isolated from mungbean (Vigna radiata) and designated Vrltp1 and Vrltp2. The deduced amino acid sequences contain the two highly conserved pentapeptides characteristic of plant LTPIs suggesting these Vrltps belong to the LTPI gene family. Vrltp1 mRNA was detected in developing seeds, but Vrltp2 mRNA was not. Within the vegetative tissues, the Vrltp1 and Vrltp2 mRNAs were present only in leaves and stems, but not root tips. Salt and dehydration stresses and exogenous abscisic acid (ABA) treatments resulted in increased mRNA levels of both Vrltps in leaves. We suggest that these unique Vrltps are specific to growing shoot tissues, and may play an important role in plant acclimation to water stress.

PMID: 15018351 [PubMed - indexed for MEDLINE]

14: Plant Physiol. 2004 Mar;134(3):1146-52. Epub 2004 Feb 26.

Evidence that sucrose loaded into the phloem of a poplar leaf is used directly by sucrose synthase associated with various beta-glucan synthases in the stem.

Konishi T, Ohmiya Y, Hayashi T.

Wood Research Institute, Kyoto University, Uji, Kyoto 611-0011, Japan.

Sucrose (Suc) synthase (SuSy) is believed to function in channeling UDP-Glc from Suc to various beta-glucan synthases. We produced transgenic poplars (Populus alba) overexpressing a mutant form (S11E) of mung bean (Vigna radiata) SuSy, which appeared in part in the microsomal membranes of the stems. Expression of SuSy in these membranes enhanced the incorporation of radioactive Suc into cellulose, together with the metabolic recycling of fructose (Fru), when dual-labeled Suc was fed directly into the phloem of the leaf. This overexpression also enhanced the direct incorporation of the glucosyl moiety of Suc into the glucan backbone of xyloglucan and increased recycling of Fru, although the Fru recycling system for cellulose synthesis at the plasma membrane might differ from that for xyloglucan synthesis in the Golgi network. These findings suggest that some of the Suc loaded into the phloem of a poplar leaf is used directly by SuSys associated with xyloglucan and cellulose synthases in the stem. This may be a key function of SuSy because the high-energy bond between the Glc and Fru moieties of Suc is conserved and used for polysaccharide syntheses in this sink tissue.

PMID: 14988476 [PubMed - indexed for MEDLINE]

15: Planta. 2004 Jun;219(2):310-8. Epub 2004 Feb 21.

Identification of elongating beta-1,4-galactosyltransferase activity in mung bean (Vigna radiata) hypocotyls using 2-aminobenzaminated 1,4-linked beta-D-galactooligosaccharides as acceptor substrates.

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Galactosyltransferase (GalT) activity that results in the transfer of galactose (Gal) from UDP-Gal to exogenous (1-->4)-beta-galactooligosaccharides labeled with 2-aminobenzamide (2AB) at their reducing ends was identified in a particulate preparation obtained from 2-day-old mung bean (Vigna radiata L. Wilezek) hypocotyls. The enzymes responsible were shown, by high-performance anion-exchange chromatography and normal-phase liquid chromatography-electrospray ionization mass spectrometry, to transfer up to eight Gals to the non-reducing end of 2AB-labeled galactooligosaccharide. Using 1H nuclear magnetic resonance spectroscopy, and beta-galactosidase and endo-beta-(1-->4)-galactanase treatments of the enzymatically formed 2AB-labeled galactooligosaccharides, the newly incorporated Gal residues were shown to be beta-(1-->4) linked. Time-course studies indicated that at least two different types of GalT isoform are involved in the elongation of the acceptor substrates. 2AB-labeled galactoheptaose was the most effective acceptor substrate analyzed, although galactooligosaccharides with a degree of polymerization between 4 and 6 were also acceptor substrates. 2AB-labeled penta- and heptasaccharides (RG5 and RG7) generated from rhamnogalacturonan I (RG-I) were not acceptor substrates, suggesting that the GalTs were not capable of adding Gal residues directly to the RG-I backbone. Maximum GalT activity was obtained at pH 6.5 and 20 degrees C in the presence of 25 mM Mn2+ and 0.75% (w/v) Triton X-100. The enzyme had an apparent Km of 20 microM for 2AB-labeled galactoheptaose and 32 microM for UDP-Gal. The characteristics of the enzyme in mung bean microsomal membranes and the usefulness of fluorogenic 2AB-labeled galactooligosaccharides for the assay of GalT are discussed. Copyright 2004 Springer-Verlag

PMID: 14986144 [PubMed - indexed for MEDLINE]

16: J Exp Bot. 2004 Mar;55(397):571-83. Epub 2004 Feb 13.

Solid-state 13C-NMR spectroscopy shows that the xyloglucans in the primary cell walls of mung bean (Vigna radiata L.) occur in different domains: a new model for xyloglucan-cellulose interactions in the cell wall.

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Xyloglucans (XG) with different mobilities were identified in the primary cell walls of mung beans (Vigna radiata L.) by solid-state 13C-NMR spectroscopy. To improve the signal:noise ratios compared with unlabelled controls, Glc labelled at either C-1 or C-4 with 13C-isotope was incorporated into the cell-wall polysaccharides of mung bean hypocotyls. Using cell walls from seedlings labelled with d-[1-13C]glucose and, by exploiting the differences in rotating-frame and spin-spin proton relaxation, a small signal was detected

which was assigned to Xyl of XGs with rigid glucan backbones. After labelling seedlings with d-[4-13C]glucose and using a novel combination of spin-echo spectroscopy with proton spin relaxation-editing, signals were detected that had 13C-spin relaxations and chemical shifts which were assigned to partly-rigid XGs surrounded by mobile non-cellulosic polysaccharides. Although quantification of these two mobility types of XG was difficult, the results indicated that the partly-rigid XGs were predominant in the cell walls. The results lend support to the postulated new cell-wall models in which only a small proportion of the total surface area of the cellulose microfibrils has XG adsorbed on to it. In these new models, the partly-rigid XGs form cross-links between adjacent cellulose microfibrils and/or between cellulose microfibrils and other non-cellulosic polysaccharides, such as pectic polysaccharides.

PMID: 14966211 [PubMed - indexed for MEDLINE]

17: Tree Physiol. 1996 Oct;16(10):841-5.

Molecular cloning of two classes of Em-like proteins from the seeds of the leguminous tree Robinia pseudoacacia.

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To check for the presence of Em-like proteins in seeds of the leguminous tree Robinia pseudoacacia L. (black locust), a cDNA library constructed from mRNA isolated from developing seeds was screened using radiolabeled cDNA encoding the Em protein from Vigna radiata as a probe. Sequence analysis of the identified cDNA clones revealed two classes of Em proteins in Robinia. The nucleotide sequence data for each class have been submitted to Genbank/EMBL Data library and are available under the accession numbers U40820 and U40821. Northern blot analysis demonstrated that the Robinia Em proteins are translated from mRNAs of approximately 800 nucleotides, which are abundant in the seed but are not expressed in the bark. Southern blot analysis indicated that the Em proteins in Robinia are encoded by at least two genes. The Robinia Em proteins have a high degree of sequence homology with previously characterized Em-like proteins from both monocots and dicots.

PMID: 14871674 [PubMed - as supplied by publisher]

18: Planta. 2004 Apr;218(6):976-88. Epub 2004 Jan 16.

Light differentially regulates the expression of two members of the auxin-induced 1-aminocyclopropane-1-carboxylate synthase gene family in mung bean (Vigna radiata L.) seedlings.

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Auxin induces the expression of the two ethylene-biosynthetic genes VR-ACS6 and VR-ACS7 in etiolated mung bean hypocotyls. However, while it also enhances VR-ACS6 expression in light-grown tissues, it does not up-regulate VR-ACS7 expression in these tissues. Here we show that transfer of 3-day-old etiolated seedlings into light quickly reduced the auxin-induced expression of both genes. However, while auxin-induced VR-ACS6 expression recovered after 24 h of light, VR-ACS7 transcription continued to reduce and was almost completely absent at 36 h. Thus, light differentially modulates the expression of the auxin-inducible VR-ACS genes. In hormone-treated etiolated seedlings, VR-ACS7 was primarily induced in the rapidly elongating zones of hypocotyl and epicotyl tissues, while auxin-induced VR-ACS6 mRNA was evenly distributed throughout the whole seedling. VR-ACS7 promoter-driven beta-glucuronidase (GUS) activity in auxin-treated etiolated transgenic Arabidopsis seedlings was observed in the highly elongating zones of the hypocotyl. During de-etiolation, the GUS activity gradually declined to become confined to the uppermost region of hypocotyls. In situ mRNA localization studies showed that in etiolated mung bean hypocotyls, the auxin-dependent VR-ACS7 transcript was predominantly present in the epidermis, which is the driving site for auxin-mediated elongation. Thus, it appears that the modulation by light of auxin-induced VR-ACS7 expression may correlate closely with the elongation growth response in early seedling development.

PMID: 14727113 [PubMed - indexed for MEDLINE]

19: FEBS Lett. 2004 Jan 2;556(1-3):127-36.

The Vr-PLC3 gene encodes a putative plasma membrane-localized phosphoinositide-specific phospholipase C whose expression is induced by abiotic stress in mung bean (Vigna radiata L.).

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Phosphoinositide-specific phospholipase C (PI-PLC) catalyzes the hydrolysis of phosphatidylinositol 4,5-bisphosphate to generate inositol 1,4,5-trisphosphate and diacylglycerol, both of which act as secondary messengers in animal cells. In this report, we identified in Vigna radiata L. (mung bean) three distinct partial cDNAs (pVr-PLC1, pVr-PLC2, and pVr-PLC3), which encode forms of putative PI-PLC. All three Vr-PLC genes were transcriptionally active and displayed unique patterns of expression. The Vr-PLC1 and Vr-PLC2 transcripts were constitutively expressed to varying degrees in every tissue of mung bean plants examined. In contrast, the Vr-PLC3 mRNA level was very low under normal growth conditions and was rapidly induced in an abscisic acid-independent manner under environmental stress conditions (drought and high salinity). An isolated genomic clone, about 8.2 kb in length, showed that Vr-PLC1 and Vr-PLC3 are in tandem array in the mung bean genome. The predicted primary sequence of Vr-PLC3 (M(r)=67.4 kDa) is reminiscent of the delta-isoform of animal enzymes which contain core sequences found in typical PI-PLCs, such as the catalytic domain comprising X and Y motifs, a lipid-binding C2 domain, and the less conserved EF-hand domain. Results of in vivo targeting experiment using a green fluorescent protein (GFP) showed that the GFP-Vr-PLC3 fusion protein was localized primarily to the plasma membrane of the Arabidopsis protoplast. The C2 domain was essential for Vr-PLC3 to be targeted to the plasma membrane. The

possible biological functions of stress-responsive Vr-PLC3 in mung bean plants are discussed.

PMID: 14706839 [PubMed - indexed for MEDLINE]

20: Integr Cancer Ther. 2002 Mar;1(1):38-4; discussion 42-3.

Radioprotective effects of vitexina for breast cancer patients undergoing radiotherapy with cobalt-60.

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Vitexina, a product containing the flavonoid vitexin as the main component, is derived from a plant, Vigna radiata (L.), that has been traditionally used in Vietnam for detoxification. This remedy is also used to treat the symptoms of conditions classified as "hot" in traditional medicine. The present study is a randomized, placebo-controlled comparative clinical trial for investigating the radioprotective effects of Vitexina for breast cancer patients undergoing radiotherapy with cobalt-60. No relevant weight loss, (even weight gain), occurred in 70% of patients in the Vitexina group, whereas 73% of the placebo group lost 1 to 2 kg of weight after 6 weeks of radiation therapy. The administration of Vitexina produced a significantly protective effect in peripheral blood cells in amount and in lymphocyte blast-transformation function. Condition of hot was observed in almost all cancer patients in this study by tongue examination. Hot condition did not change in the Vitexina group, but the incidence of hot and extreme hot cases were significantly increased in the placebo group after 6 weeks of radiation therapy. The results suggest that application of medicinal plants of the "clearing heat and detoxification" classification as an adjuvant would be a potential solution in integrative cancer therapy.

Publication Types:
Clinical Trial
Randomized Controlled Trial

PMID: 14664747 [PubMed - indexed for MEDLINE]

21: Genome. 2003 Oct;46(5):738-44.

Identification of a major locus conferring resistance to powdery mildew (Erysiphe polygoni DC) in mungbean (Vigna radiata L. Wilczek) by QTL analysis.

Humphry ME, Magner T, McIntyre CL, Aitken EA, Liu CJ.

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A major locus conferring resistance to the causal organism of powdery mildew, Erysiphe polygoni DC, in mungbean (Vigna radiata L. Wilczek) was identified using QTL analysis with a population of 147 recombinant inbred individuals. The

population was derived from a cross between 'Berken', a highly susceptible variety, and ATF 3640, a highly resistant line. To test for response to powdery mildew, F7 and F8 lines were inoculated by dispersing decaying mungbean leaves with residual conidia of E. polygoni amongst the young plants to create an artificial epidemic and assayed in a glasshouse facility. To generate a linkage map, 322 RFLP clones were tested against the two parents and 51 of these were selected to screen the mapping population. The 51 probes generated 52 mapped loci, which were used to construct a linkage map spanning 350 cM of the mungbean genome over 10 linkage groups. Using these markers, a single locus was identified that explained up to a maximum of 86% of the total variation in the resistance response to the pathogen.

PMID: 14608390 [PubMed - indexed for MEDLINE]

22: Acta Microbiol Pol. 2003;52(2):195-9.

Increased synthesis of dihydroxybenzoic acid in the presence of aluminum by Rhizobium MO1.

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Rhizobizum sp. MO1, a mung bean (Vigna radiata) symbiont, produces a catecholate type of siderophore, 2,3-dihydroxy benzoic acid (DHBA), in iron depleted medium. Addition of aluminum to the medium decreased the growth but increased the production of the siderophore.

PMID: 14594407 [PubMed - indexed for MEDLINE]

23: Environ Pollut. 2003;126(3):323-9.

Effect of air pollution on peri-urban agriculture: a case study.

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Peri-urban agriculture is vital for the urban populations of many developing countries. Increases in both industrialization and urbanization, and associated air pollution threaten urban food production and its quality. Six hour mean concentrations were monitored for SO(2), NO(2) and O(3) and plant responses were measured in terms of physiological characteristics, pigment, biomass and yield. Parameter reductions in mung bean (Vigna radiata), palak (Beta vulgaris), wheat (Triticum aestivum) and mustard (Brassica compestris) grown within the urban fringes of Varanasi, India correlated directly with the gaseous pollutants levels. The magnitude of response involved all three gaseous pollutants at peri-urban sites; O(3) had more influence at a rural site. The study concluded that air pollution in Varanasi could negatively influence crop yield.

PMID: 12963293 [PubMed - indexed for MEDLINE]

24: Appl Environ Microbiol. 2003 Sep;69(9):5238-42.

Enhanced production of alpha-galactosyl epitopes by metabolically engineered Pichia pastoris.

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A metabolically engineered Pichia pastoris strain was constructed that harbored three heterologous enzymes: an S11E mutated sucrose synthase from Vigna radiata, a truncated UDP-glucose C4 epimerase from Saccharomyces cerevisiae, and a truncated bovine alpha-1,3-galactosyltransferase. Each gene has its own methanol-inducible alcohol oxidase 1 promoter and transcription terminator on the chromosomal DNA of P. pastoris strain GS115. The proteins were coexpressed intracellularly under the induction of methanol. After permeabilization, the whole P. pastoris cells were used to synthesize alpha-galactosyl (alpha-Gal) trisaccharide (Galalpha1,3Galbeta1,4Glc) with in situ regeneration of UDP-galactose. Up to 28 mM alpha-Gal was accumulated in a 200-ml reaction. The Pichia system described here is simple and flexible. This work demonstrates that recombinant P. pastoris is an excellent alternative to Escherichia coli transformants in large-scale synthesis of oligosaccharides.

PMID: 12957908 [PubMed - indexed for MEDLINE]

25: Plant Physiol. 2003 Jul;132(3):1475-88.

Molecular and biochemical characterization of VR-EILs encoding mung bean ETHYLENE INSENSITIVE3-LIKE proteins.

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ETHYLENE INSENSITIVE3 (EIN3) is a transcription factor involved in the ethylene signal transduction pathway in Arabidopsis. Two full-length cDNA clones, pVR-EIL1 and pVR-EIL2, encoding EIN3-LIKE proteins were isolated by reverse transcriptase-polymerase chain reaction and by screening the cDNA library of mung bean (Vigna radiata) hypocotyls. VR-EIL1 and VR-EIL2 share 70% identity and display varying degrees of sequence conservation (39%-65%) with previously isolated EIN3 homologs from Arabidopsis, tobacco (Nicotiana tabacum) and tomato (Lycopersicon esculentum) plants. Gel retardation assay revealed that both VR-EILs were able to interact specifically with optimal binding sequence-1, the recently identified optimal binding sequence for tobacco TEIL, with the binding of VR-EIL2 being more efficient than that of VR-EIL1. Transient expression analysis using a VR-EIL::smGFP fusion gene in onion (Allium cepa) epidermal cells indicated that the VR-EIL proteins were effectively targeted to the nucleus. The fusion protein of VR-EIL2 with GAL4 DNA-binding domain strongly activated transcription of a reporter gene in yeast cells, and an essential

domain for transcription-stimulating activity was localized to the amino-terminal acidic region that consists of 50 amino acid residues. In contrast with what has been previously found in EIN3- and TEIL-overexpressing Arabidopsis plants, transgenic tobacco seedlings expressing the VR-EIL genes under the control of cauliflower mosaic virus 35S promoter did not exhibit a constitutive triple response. Instead, they displayed a markedly enhanced proliferation of root hairs, one of the typical ethylene response phenotypes, and increased sensitivity to exogenous ethylene. In addition, the pathogenesis-related (PR) genes encoding beta-1,3-glucanase, osmotin, and PR1 were constitutively expressed in 35S::VR-EIL lines without added ethylene, and were hyperinduced in response to ethylene treatment. These results indicate that VR-EILs are functional in tobacco cells, thereby effectively transactivating the GCC-box-containing PR genes and enhancing sensitivity to ethylene. The possible physiological role of VR-EILs is discussed in the light of the suggestion that they are active components of the ethylene-signaling pathway and their heterologous expressions constitutively turn on a subset of ethylene responses in tobacco plants.

PMID: 12857828 [PubMed - indexed for MEDLINE]

26: Chemosphere. 2003 Aug;52(7):1245-50.

Effect of lead on growth and nitrate assimilation of Vigna radiata (L.) Wilczek seedlings in a salt affected environment.

Singh RP, Tripathi RD, Dabas S, Rizvi SM, Ali MB, Sinha SK, Gupta DK, Mishra S, Rai UN.

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The inhibition of seedling growth and nitrate reductase activity in 5 d old Vigna radiata (L.) Wilczek cv. Pusa Baisakhi in the presence of 1.0 mM lead acetate increased drastically, if NaCl (6 and 12 EC) was also present in the nutrient media along with the metal salt. Correspondingly higher endogenous Na+ levels were accumulated in the roots and leaves of seedlings in presence of the two stresses. On the other hand, the levels of endogenous lead get reduced in presence of NaCl in both the roots and leaves. Roots accumulated more Pb2+ and Na+ than the leaves. The two stresses affect more drastically in the additive or even synergistic manner during the early growth phase of the seedlings.

PMID: 12821005 [PubMed - indexed for MEDLINE]

27: Plant Physiol. 2003 May;132(1):331-42.

Solubilization of an arabinan arabinosyltransferase activity from mung bean hypocotyls.

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The biosynthesis of polysaccharides destined for the plant cell wall and the subsequent assembly of the cell wall are poorly understood processes that are currently the focus of much research. Arabinan, a component of the pectic polysaccharide rhamnogalacturonan I, is composed of arabinosyl residues connected via various glycosidic linkages, and therefore, the biosynthesis of arabinan is likely to involve more than one arabinosyltransferase. We have studied the transfer of [(14)C]arabinose (Ara) from UDP-L-arabinopyranose onto polysaccharides using microsomal membranes isolated from mung bean (Vigna radiata) hypocotyls. [(14)C]arabinosyl and [(14)C]xylosyl residues were incorporated into endogenous products due to the presence of UDP-Xyl-4-epimerase activity. Enzymatic digestion of endogenous products with endo-arabinanase released very little radiolabeled sugars, whereas digestion with arabinofuranosidase released some [(14)C]Ara. Microsomal membranes solubilized with the detergent octyl glucoside were able to add a single [(14)C]Ara residue onto (1-->5)-linked alpha-L-arabino-oligosaccharide acceptors. The reaction had a pH optimum of 6.5 and a requirement for manganese ions. However, enzymatic digestion of the radiolabeled oligosaccharides with endo-arabinanase and arabinofuranosidases could not fully release the radiolabeled Ara residue, indicating that the [(14)C]Ara residue was not a (1-->2)-, (1-->3)-, or (1-->5)-linked alpha-L-arabinofuranosyl residue. Rather, mild acid treatment of the product suggested that the radiolabeled Ara residue was in a pyranose conformation, and this result was confirmed by thin-layer chromatography of radiolabeled partially methylated sugars. Using microsomal membranes separated on a discontinuous sucrose gradient, the arabinosyltransferase activity appears to be mainly localized to Golgi membranes.

PMID: 12746538 [PubMed - indexed for MEDLINE]

28: Folia Microbiol (Praha). 2003;48(1):83-9.

Competition among Bradyrhizobium strains for nodulation of green gram (Vigna radiata): use of dark-nodule strain.

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The competitiveness of dual-strain inoculum of Bradyrhizobium strains S24 and GR4 was demonstrated for nodulation of green gram (Vigna radiata). Strain S24 formed pink nodules, GR4 produced visually distinguishable dark-brown nodules. When a mixture of these Bradyrhizobium strains was applied as inoculum, nodules of both pink and dark-brown types were formed on the same root. The strain GR4, which was less competitive than strain S24, was mutagenized with N-methyl-N'-nitro-N-nitrosoguanidine to obtain pigment-diverse mutants and six selected mutants were screened for symbiotic parameters. One mutant produced pink nodules and appreciably increased plant dry mass. The competitive ability of this mutant lacking brown pigment was compared with that of strain S24 by using antibiotic resistance markers; it showed increased nodulation competitiveness than its parent strain GR4. The dark-brown nodule-phenotype could be useful in evaluating nodulation competitiveness of "cowpea miscellany" bradyrhizobia in soil where dark-brown nodule-forming strains are not indigenous.

PMID: 12744082 [PubMed - indexed for MEDLINE]

29: J Environ Biol. 2002 Oct;23(4):433-5.

Individual and combined effect of mercury and manganese on phenol and proline content in leaf and stem of mungbean seedlings.

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Mungbean (Vigna radiata L. Wilczelk cv. Pusa Baisakhi seedlings were raised in individual (0, 1, 10, 100 and 1000 ppm) and combined solutions (1 : 1, 10: 1, 1: 0 ppm Hg : Mn) of mercury and manganese for 6 days. Phenol and proline were found to accumulate in leaves in response to treatment with heavy metals. The magnitude of accumulation correlated with concentration of metals. However, a reverse trend was noticed in stem for phenol. Accumulation of phenol in response to heavy metal treatment was organ specific and occurred at higher rate in plant parts, which faced the stress mostly. However, accumulation of proline helped the plant to survive stress situation. In combined solutions, amelioration of mercurial toxicity by manganese was recorded.

PMID: 12674387 [PubMed - indexed for MEDLINE]

30: J Environ Biol. 2002 Oct;23(4):411-6.

Studies on phytotoxic effect of aluminium on growth and some morphological parameters of Vigna radiata L. Wilczek.

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Aluminium toxicity is a major deterrent for plant growth in acid soils below pH 5.0. This study deals with effect of aluminium toxicity on growth of mungbean (Vigna radiata L. Wilczek) seedlings. Seed germination (in %) declined with increased content of Al2(SO4)3, while promotive effect was observed at very low dosage. Different concentrations of aluminum sulphate salt were applied to mungbean seeds. Measurement of aluminium content in mungbean leaves was done through atomic absorption spectrophotometer. Root length (root and hypocotyl length) and shoot length (shoot and epicotyl length) was measured at seven days old seedling stage. Different concentrations of Al2(SO4)3 were found to have significant effect both on shoot and root length. Leaf area, fresh and dry weight was significantly reduced. Increased stomatal frequency and trichome density with an increase in concentrations of Al2(S04)3 was observed through scanning electron microscope.

PMID: 12674383 [PubMed - indexed for MEDLINE]

31: Can J Microbiol. 2003 Jan;49(1):45-50.

Scanning electron microscopy of native biofilms on mung bean sprouts.

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Native biofilms present on the adaxial surface of cotyledons of mung bean sprouts (Vigna radiata) were studied by use of scanning electron microscopy. Biofilms were abundant on the cotyledon surfaces and were comprised of rod-shaped bacteria, cocci-shaped bacteria, or yeasts, often with one type of microbe predominant. In contrast to our earlier study of biofilms on green sprouts (alfalfa, clover, broccoli, and sunflower), yeast and cocci were abundant on mung bean. Filamentous fungi were not observed. Sheet-like or fibrillar material (presumably composed of secreted microbial polysaccharides, proteins, lipids, and nucleic acids) fully or partially covered the biofilms. Biofilms up to 5 mm in length were observed, and some biofilms were comprised of more than just a monolayer of microbial cells. Native biofilms on sprout surfaces undoubtedly play an important role in the ecology of plant epiphytic microbes and may also afford protected sites for plant and human bacterial pathogens.

PMID: 12674347 [PubMed - indexed for MEDLINE]

32: J Agric Food Chem. 2003 Apr 9;51(8):2193-9.

Evaluation of the estrogenic effects of legume extracts containing phytoestrogens.

Boue SM, Wiese TE, Nehls S, Burow ME, Elliott S, Carter-Wientjes CH, Shih BY, McLachlan JA, Cleveland TE.

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Seven legume extracts containing phytoestrogens were analyzed for estrogenic activity. Methanol extracts were prepared from soybean (Glycine max L.), green bean (Phaseolus vulgaris L.), alfalfa sprout (Medicago sativa L.), mung bean sprout (Vigna radiata L.), kudzu root (Pueraria lobata L.), and red clover blossom and red clover sprout (Trifolium pratense L.). Extracts of kudzu root and red clover blossom showed significant competitive binding to estrogen receptor beta (ERbeta). Estrogenic activity was determined using an estrogen-dependent MCF-7 breast cancer cell proliferation assay. Kudzu root, red clover blossom and sprout, mung bean sprout, and alfalfa sprout extracts displayed increased cell proliferation above levels observed with estradiol. The pure estrogen antagonist, ICI 182,780, suppressed cell proliferation induced by the extracts, suggesting an ER-related signaling pathway was involved. The ER subtype-selective activities of legume extracts were examined using transiently transfected human embryonic kidney (HEK 293) cells. All seven of the extracts

exhibited preferential agonist activity toward ERbeta. Using HPLC to collect fractions and MCF-7 cell proliferation, the active components in kudzu root extract were determined to be the isoflavones puerarin, daidzin, genistin, daidzein, and genistein. These results show that several legumes are a source of phytoestrogens with high levels of estrogenic activity.

PMID: 12670155 [PubMed - indexed for MEDLINE]

33: Microbiol Res. 2003;158(1):77-81.

Combat of iron-deprivation through a plant growth promoting fluorescent Pseudomonas strain GRP3A in mung bean (Vigna radiata L. Wilzeck).

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Microorganisms and plants sustain themselves under iron-deprived conditions by releasing siderophores. Among others, fluorescent pseudomonads are known to exert extensive biocontrol action against soil and root borne phytopathogens through release of antimicrobials and siderophores. In this study, production and regulation of siderophores by fluorescent Pseudomonas strain GRP3A was studied. Among various media tested, standard succinate medium (SSM) promoted maximum siderophore production of 56.59 mg l(-1). There were low levels of siderophore in complex media like King's B medium, trypticase soya medium and nutrient medium (41.27, 29.86 and 27.63 mg l(-1)), respectively. In defferrated SSM, siderophore level was quantified to be 68.74 mg l(-1). Supplementation with iron (FeCl3) resulted in decreased siderophore levels depending on concentration. Siderophore production was promoted by Zn2+ (78.94 mg l(-1)), Cu2+ (68.80 mg l(-1)) whereas Co2+ (57.33 mg l(-1)) and Fe3+ reduced siderophore production (37.44 mg l(-1) as compared to control (55.97 mg l(-1)). Strain GRP3A showed plant growth promotion under iron limited conditions.

PMID: 12608583 [PubMed - indexed for MEDLINE]

34: J Exp Bot. 2003 Mar;54(384):1057-67.

Mechanisms of seed ageing under different storage conditions for Vigna radiata (L.) Wilczek: lipid peroxidation, sugar hydrolysis, Maillard reactions and their relationship to glass state transition.

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Two primary biochemical reactions in seed ageing (lipid peroxidation and non-enzymatic protein glycosylation with reducing sugars) have been studied under different seed water contents and storage temperatures, and the role of the glassy state in retarding biochemical deterioration examined. The viability loss of Vigna radiata seeds during storage is associated with Maillard

reactions; however, the contribution of primary biochemical reactions varies under different storage conditions. Biochemical deterioration and viability loss are greatly retarded in seeds stored below a high critical temperature (approximately 40 degrees C above glass transition temperature). This high critical temperature corresponds to the cross-over temperature (T(c)) of glass transition where molecular dynamics changes from a solid-like system to a normal liquid system. The data show that seed ageing slows down significantly, even before seed tissue enters into the glassy state.

PMID: 12598575 [PubMed - indexed for MEDLINE]

35: J Environ Biol. 2002 Jul;23(3):321-3.

Amelioration of mercurial toxicity by manganese. I. A case study in mung bean seedling.

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Mercury, a non essential element renders inhibitory effect on many physiological activities of plants even at a low concentration. Plants absorb "Hg" from soil through root system. Manganese, an essential element has been found to counter the inhibitory effect of mercury mostly by preventing it's uptake from soil. Mung bean (Vigna radiata L. Wilczek) cv. Pusa Baisakhi grown in individual (1, 10, 100 and 1000 ppm) solution of Hg and Mn showed varied uptake of these heavy metals. However, in combined solutions (1 : 1, 10 : 1 and 1 : 10 ppm Hg : Mn), mercury uptake was mostly prevented in presence of 10 ppm Mn, indicating it's ameliorating effect.

PMID: 12597577 [PubMed - indexed for MEDLINE]

36: J Environ Biol. 2002 Jul;23(3):295-300.

Effect of phytohormone pretreatment on metabolic changes in Vigna radiata under salt stress.

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Efficiency of pretreatment as foliar spray of indole-3-acetic acid, gibberellic acid and kinetin (6-furfuryl aminopurine) each ranging from 10(-7) to 10(-5) M in restoring the metabolic alterations imposed by NaCl salinity (E.C. value 4.0 m mhos/cm) was investigated in Vigna radiata (L.) Wilczek. Application of NaCl resulted in about 7% and 9% decrease in phenol content in mung bean leaf and root respectively. In leaf, NaCl caused 40% increase in polyphenol oxidase enzyme activity over the control set. This effect was accentuated in root, where salinity caused 200% increase in the enzyme activity. In leaf and root of mung-bean plant, ascorbic acid content decreased about 29% and 31% respectively

under salinity stress as compared with control. Ascorbic acid oxidase enzyme activity increased under stress by about 55% and 23% respectively in leaf and root. It was noted that all the three growth regulators used in the present study were able to overcome to variable extents the adverse effects of stress imposed by NaCl solution.

PMID: 12597575 [PubMed - indexed for MEDLINE]

37: J Environ Biol. 2002 Jul;23(3):253-7.

Effect of manganese toxicity on pigment content, Hill activity and photosynthetic rate of Vigna radiata L. Wilczek seedlings.

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Effect of different concentrations, viz. 10(-4) M, 5 x 10(-4) M, 10(-3) M and 5 x 10(-3) M of manganese sulphate (MnSO4, 7H2O) on chlorophyll, carotenoid pigment content and photosynthesis of mungbean seedlings was examined Progressive increase in manganese sulphate concentration upto 5 x 10(-3) M brought about a progressive decrease in total chlorophyll and chl a content. Chl b content changed very little by excess manganese treatment. Total carotenoid pigment content decreased considerably in comparison to control with every concentration of manganese sulphate tried here. Hill activity of chloroplasts isolated from leaves of mungbean seedling and rate of photosynthesis in terms of CO2 uptake showed progressive reduction along with the increase in concentration of the manganese.

PMID: 12597567 [PubMed - indexed for MEDLINE]

38: Theor Appl Genet. 2002 Jul;105(1):160-166. Epub 2002 May 23.

Development of a mungbean (Vigna radiata) RFLP linkage map and its comparison with lablab (Lablab purpureus) reveals a high level of colinearity between the two genomes.

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A genetic linkage map of mungbean (Vigna radiata, 2n = 2 x = 22) consisting of 255 RFLP loci was developed using a recombinant inbred population of 80 individuals. The population was derived from an inter-subspecific cross between the cultivated mungbean variety 'Berken' and a wild mungbean genotype 'ACC 41' (V. radiata subsp. sublobata). The total length of the map, which comprised 13 linkage groups, spanned 737.9 cM with an average distance between markers of 3.0 cM and a maximum distance between linked markers of 15.4 cM. The mungbean map was compared to a previously published map of lablab (Lablab purpureus, 2n = 2 x = 24) using a common set of 65 RFLP probes. In contrast to some other comparative mapping studies among members of the Fabaceae, where a high level of

chromosomal rearrangement has been observed, marker order between mungbean and lablab was found to be highly conserved. However, the two genomes have apparently accumulated a large number of duplications/deletions after they diverged.

PMID: 12582573 [PubMed - as supplied by publisher]

39: Hereditas. 2002;137(1):52-6.

Genetic basis of plant height and its degree of indetermination in mungbean (Vigna radiata (L.) Wilczek).

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The genetic basis of plant height at various growth stages and the degree of indetermination of plant height in six mungbean genotypes (NM 92, 6601, NM 89, VC 1560D and VC 3902A) were assessed through half diallel cross. Cultivars, 6601 and NM 92, were the best general combiner for pre-flowering dry matter accumulation and minimum increase in plant height from first flower to 90% pods maturity, respectively. For these traits, the combination NM 92 x NM 89 was the best specific combiner of all the crosses. Both additive and dominant gene effects controlled the inheritance of plant height at first pod and to 90% pods maturity, degree of indetermination of plant height (DDh) from first flower to first pod maturity (DDh1), DDh from first flower to 90% pods maturity (DDh2) and DDh from first pod maturity to 90% pods maturity (DDh3). Plant height at first flower was additively inherited. The additive gene action was predominant as compared to dominant gene action for all the traits examined. High narrow and broad sense heritability estimates for DDh2 showed that better response to selection is possible for the development of mungbean genotypes with minimum increase in plant height during post-flowering development.

PMID: 12564632 [PubMed - indexed for MEDLINE]

40: Indian J Exp Biol. 2001 Jun;39(6):572-7.

Growth, CO2 exchange rate and dry matter partitioning in mungbean (Vigna radiata L.) grown under elevated CO2.

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This study was conducted to determine the effects of anticipated future level of CO2 on growth and dry matter partitioning of mungbean (Vigna radiata). Plants were grown from seedlings to maturity inside the open top chamber under amhient CO2 (350 +/- 25 microL L(-1)) and elevated CO2 (600 +/- 50 microL L(-1)) at Indian Agricultural Research Institute, New Delhi (India). Plants were harvested at 20, 35 and 50 days after germination. Mungbean plants grown under elevated

CO2 concentration resulted in greater photosynthetic rate on a leaflet area basis and no acclimation in photosynthesis was recorded due to high CO2. Plants grown under CO, enrichmcnt were taller and attained greater leaf area along with more dry matter than ambient CO2 grown plants at all growth stages. Response to high CO, depends upon the growth stage of the plant and it was more at early growth stages compared to maturity stages. The high CO2 grown mungbean plants also exhibited increased root growth along with stem and leaves. There was a substantial increase in pod number and seed number/plant under elevated CO2 conditions. The increase in dry matter and growth of root, stem and leaves proved that CO2 enrichment of the atmosphere can stimulate photosynthetic rate which can ultimately lead to an increase in dry matter and growth.

PMID: 12562021 [PubMed - indexed for MEDLINE]

41: J Environ Qual. 2002 Nov-Dec;31(6):1893-900.

Lead phytoextraction from contaminated soil with high-biomass plant species.

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In this study, cabbage [Brassica rapa L. subsp. chinensis (L.) Hanelt cv. Xinza No 1], mung bean [Vigna radiata (L.) R. Wilczek var. radiata cv. VC-3762], and wheat (Triticum aestivum L. cv. Altas 66) were grown in Pb-contaminated soils. Application of ethylenediaminetetraacetic acid (EDTA) (3.0 mmol of EDTA/kg soil) to the soil significantly increased the concentrations of Pb in the shoots and roots of all the plants. Lead concentrations in the cabbage shoots reached 5010 and 4620 mg/kg dry matter on Days 7 and 14 after EDTA application, respectively. EDTA was the best in solubilizing soil-bound Pb and enhancing Pb accumulation in the cabbage shoots among various chelates (EDTA, diethylenetriaminepentaacetic acid [DTPA], hydroxyethylenediaminetriacetic acid [HEDTA], nitrilotriacetic acid [NTA], and citric acid). Results of the sequential chemical extraction of soil samples showed that the Pb concentrations in the carbonate-specifically adsorbed and Fe-Mn oxide phases were significantly decreased after EDTA treatment. The results indicated that EDTA solubilized Pb mainly from these two phases in the soil. The relative efficiency of EDTA enhancing Pb accumulation in shoots (defined as the ratio of shoot Pb concentration to EDTA concentration applied) was highest when 1.5 or 3.0 mmol EDTA/kg soil was used. Application of EDTA in three separate doses was most effective in enhancing the accumulation of Pb in cabbage shoots and decreased mobility of Pb in soil compared with one- and two-dose application methods. This approach could help to minimize the amount of chelate applied in the field and to reduce the potential risk of soluble Pb movement into ground water.

PMID: 12469839 [PubMed - indexed for MEDLINE]

42: J Appl Microbiol. 2002;93(5):835-9.

Construction of green fluorescent protein (GFP)-marked strains of Bradyrhizobium for ecological studies.

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AIM: To introduce the gfp gene encoding green fluorescent protein (GFP) into bradyrhizobia for their identification in nodules, soil and carrier-based inoculants. METHODS AND RESULTS: Bradyrhizobium sp. strains M29 and GN7, which nodulate mungbean (Vigna radiata), were conjugated with Escherichia coli S17-1 carrying plasmid EDS 15 (a suicide plasmid carrying a promoterless gfp gene fused with Tn5). The GFP-marked strain expressed the gfp gene from a Bradyrhizobium promoter and gave green fluorescence when observed under an epifluorescent microscope or u.v. transilluminater. All the GFP-marked strains were able to nodulate mungbean and fix nitrogen. The GFP-marked bradyrhizobia were recovered at a frequency of 90-100% and 16-63% from nodules formed under sterilized and unsterilized conditions, respectively. The GFP-marked bradyrhizobia were identified from soil and from charcoal-based inoculants on the basis of green fluorescence. CONCLUSIONS: The GFP-marked Bradyrhizobium was successfully identified on the basis of green fluorescence to study its competition and survival in the soil and in charcoal-based inoculants. SIGNIFICANCE AND IMPACT OF THE STUDY: Introduction of the gfp gene into Bradyrhizobium provides a simple, specific and cost-effective method of strain identification for ecological studies.

PMID: 12392530 [PubMed - indexed for MEDLINE]

43: Plant Physiol. 2002 Oct;130(2):1054-62.

Distinct N-terminal regulatory domains of Ca(2+)/H(+) antiporters.

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The regulation of intracellular Ca(2+) levels is achieved in part by high-capacity vacuolar Ca(2+)/H(+) antiporters. An N-terminal regulatory region (NRR) on the Arabidopsis Ca(2+)/H(+) antiporter CAX1 (cation exchanger 1) has been shown previously to regulate Ca(2+) transport by a mechanism of N-terminal auto-inhibition. Here, we examine the regulation of other CAX transporters, both within Arabidopsis and from another plant, mung bean (Vigna radiata), to ascertain if this mechanism is commonly used among Ca(2+)/H(+) antiporters. Biochemical analysis of mung bean VCAX1 expressed in yeast (Saccharomyces cerevisiae) showed that N-terminal truncated VCAX1 had approximately 70% greater antiport activity compared with full-length VCAX1. A synthetic peptide corresponding to the NRR of CAX1, which can strongly inhibit Ca(2+) transport by CAX1, could not dramatically inhibit Ca(2+) transport by truncated VCAX1. The N terminus of Arabidopsis CAX3 was also shown to contain an NRR. Additions of either the CAX3 or VCAX1 regulatory regions to the N terminus of an N-terminal truncated CAX1 failed to inhibit CAX1 activity. When fused to N-terminal truncated CAX1, both the CAX3 and VCAX1 regulatory regions could only auto-inhibit CAX1 after mutagenesis of specific amino acids within this NRR region. These findings demonstrate that N-terminal regulation is present in other plant CAX transporters, and suggest distinct regulatory features among

these transporters.

PMID: 12376668 [PubMed - indexed for MEDLINE]

44: J Biol Chem. 2002 Dec 6;277(49):47756-64. Epub 2002 Oct 03.

In vitro fusion of plant Golgi membranes can be influenced by divalent cations.

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The fusogenic activity of plant Golgi membranes was studied in a cell-free system by assaying lipid mixing and content leakages of fluorescence probes. Golgi membranes from mung bean (Vigna radiata L.) hypocotyl cells fused to liposomes in the absence of any cytosolic proteins and nucleotides. It was demonstrated that the fusion was mediated by integral membrane protein(s), and was influenced by divalent cations (mm). Mg(2+), Ca(2+), and Mn(2+) ions enhanced the lipid mixing by reducing repulsive forces between membranes. In the content leakage assay, Mg(2+) ions also showed a stimulative effect. However, other divalent cations were inhibitory. It is suggested that the fusion system of Golgi membranes comprises at least two components: one that mediates the formation of fusion intermediates prior to pore opening, and one that mediates the subsequent processes. The latter must be sensitive to divalent cations at millimolar concentrations. The fusion of Golgi and biological membranes was induced by divalent cations. We speculated about the biological role of the fusion system studied here.

PMID: 12368278 [PubMed - indexed for MEDLINE]

45: Planta. 2002 Sep;215(5):770-8. Epub 2002 Jun 18.

Roles of the plasma membrane and the cell wall in the responses of plant cells to freezing.

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In an effort to clarify the responses of a wide range of plant cells to freezing, we examined the responses to freezing of the cells of chilling-sensitive and chilling-resistant tropical and subtropical plants. Among the cells of the plants that we examined, those of African violet (Saintpaulia grotei Engl.) leaves were most chilling-sensitive, those of hypocotyls in mungbean [Vigna radiata (L.) R. Wilcz.] seedlings were moderately chilling-sensitive, and those of orchid [Paphiopedilum insigne (Wallich ex Lindl.) Pfitz.] leaves were chilling-resistant, when all were chilled at -2 degrees C. By contrast, all these plant cells were freezing-sensitive and suffered extensive damage when they were frozen at -2 degrees C. Cryo-scanning electron microscopy (Cryo-SEM) confirmed that, upon chilling at -2 degrees C,

both chilling-sensitive and chilling-resistant plant cells were supercooled. Upon freezing at -2 degrees C, by contrast, intracellular freezing occurred in Saintpaulia leaf cells, frost plasmolysis followed by intracellular freezing occurred in mungbean seedling cells, and extracellular freezing (cytorrhysis) occurred in orchid leaf cells. We postulate that chilling-related destabilization of membranes might result in the loss of the ability of the plasma membrane to act as a barrier against the propagation of extracellular ice in chilling-sensitive plant cells. We also examined the role of cell walls in the response to freezing using cells in which the plasma membrane had been disrupted by repeated freezing and thawing. In chilling-sensitive Saintpaulia and mungbean cells, the cells with a disrupted plasma membrane responded to freezing at -2 degrees C by intracellular freezing. By contrast, in chilling-resistant orchid cells, as well as in other cells of chilling-resistant and freezing-resistant plant tissues, including leaves of orchard grass (Dactylis glomerata L.), leaves of Arabidopsis thaliana (L.) Heynh. and cortical tissues of mulberry (Morus bombycis Koids.), cells with a disrupted plasma membrane responded to freezing by extracellular freezing. Our results indicate that, in the chilling-sensitive plants cells that we examined, not only the plasma membrane but also the cell wall lacked the ability to serve as a barrier against the propagation of extracellular ice, whereas in the chilling-resistant plant cells that we examined, not only the plasma membrane but also the cell wall acted as a barrier against the propagation of extracellular ice. It appears, therefore, that not only the plasma membrane but also the cell wall greatly influences the freezing behavior of plant cells.

PMID: 12244442 [PubMed - indexed for MEDLINE]

46: Plant Physiol. 1994 Dec;106(4):1527-1532.

Biosynthesis of Cardiolipin in Plant Mitochondria.

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The properties of cardiolipin synthase were investigated in mitochondria and submitochondrial fractions from etiolated mung bean (Vigna radiata L.) seedlings. Direct evidence is presented that the enzyme utilizes CDP-diacylglycerol in addition to phosphatidylglycerol for the synthesis of cardiolipin. Cardiolipin synthase had an alkaline pH optimum of about 9 and required divalent cations for activity. Maximal activity was obtained in the presence of 16 mM MnCl2. The apparent Km values for CDP-diacylglycerol and phosphatidylglycerol were 0.8 and 50 [mu]M, respectively. Cardiolipin synthase was localized predominantly in the inner membrane of mung bean mitochondria and displayed a substrate species specificity. Highest activities were measured with the dioleoyl species of both CDP-diacylglycerol and phosphatidylglycerol, and somewhat lower activities were measured with mixed species of the two substrates containing a palmitoyl and an oleoyl group. On the other hand, the cardiolipin synthase hardly used the dipalmitoyl species and strongly discriminated against CDP-dipalmitoylglycerol from a mixture with CDP-dioleoylglycerol.

PMID: 12232427 [PubMed - as supplied by publisher]

47: Plant Physiol. 1994 Nov;106(3):1151-1156.

Immobilized and Free Apoplastic Pectinmethylesterases in Mung Bean Hypocotyl.

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The nature and the action pattern of apoplastic pectinmethylesterase (PME) isoforms were investigated in mung bean [Vigna radiata (L.) Wilzeck] hypocotyls. Successive extractions of neutral and alkaline PME isoforms present in hypocotyl native cell walls (referred to as PE1, PE2, PE3, PE4, with increasingly basic isoelectric points) revealed that solubilization of PE1, PE2, and PE4 did not induce any significant decrease in the cell-wall-bound PME activity. The in vitro de-esterification occurring when isolated cell walls were incubated with pectin resulted, then, from the activity of PE3. In addition, pH control of PME activity was shown to be much stronger for enzymes bound to cell walls, in their native state or reintroduced after solubilization, than for enzymes in solution. Mature cell walls showed much more activity than young cell walls, and were relatively enriched in two acidic PME isoforms missing in young cell walls. One acidic PME was also detected in the extracellular fluid. The acidic and neutral isoforms that could be easily transferred from their binding sites to their substrate might be those involved in the demethylation process developing along the mung bean hypocotyl.

PMID: 12232398 [PubMed - as supplied by publisher]

48: Plant Physiol. 1994 Nov;106(3):1095-1102.

Characterization and Localization of a Phenoloxidase in Mung Bean Hypocotyl Cell Walls.

Chabanet A, Goldberg R, Catesson AM, Quinet-Szely M, Delaunay AM, Faye L.

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The occurrence of proteins able to oxidize polyphenols even in the absence of H_2O_2 was recently reported in mung bean (Vigna radiata L.) hypocotyl cell wall extracts (R. Goldberg, A. Chabanet, A.M. Catesson [1993] In K.G. Welinder, S.K. Rasmussen, C. Penel, H. Greppin, eds, Plant Peroxidases: Biochemistry and Physiology, pp. 296-300). Therefore, the possible presence of a laccase in the extracts was investigated using immunocytological and biochemical approaches. An enzyme catalyzing phenol oxidation in the presence of molecular O_2 was extracted and purified from the cell walls. This 38-kD cationic protein, like o-diphenoloxidases, was unable to oxidize p-diphenols or p-diamines. However, it crossreacted with an anti-laccase antiserum and, like laccases, its activity was inhibited by N-cetyl-N,N,N-trimethylammonium bromide but not by ferulic acid salts. Immunolabeling data showed that the 38-kD oxidase was absent from all cellulosic cell walls. It was localized only in lignifying and lignified cell walls. This restricted localization suggests that this laccase-like

phenoloxidase could participate in the lignification process but not in the primary wall stiffening, which develops in the epidermal and cortical tissues along the mung bean hypocotyl.

PMID: 12232390 [PubMed - as supplied by publisher]

49: Plant Physiol. 1994 Aug;105(4):1269-1274.

Biosynthesis of Phosphatidylglycerol in Isolated Mitochondria of Etiolated Mung Bean (Vigna radiata L.) Seedlings.

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Phosphatidylglycerophosphate synthase (sn-glycerol-3-phosphate:CDP-diacylglycerol phosphatidyltransferase) and phosphatidylglycerophosphate phosphatase were characterized in mung bean (Vigna radiata L.) mitochondria. The synthase has a rather broad pH optimum between 7 and 9, whereas the phosphatase has one of about 7. Both enzymic activities are stimulated by Triton X-100 and require divalent cations but differ in their cation specificities. The synthase shows apparent Km values of 9 and 3 [mu]M for sn-glycerol-3-phosphate and CDP-diacylglycerol, respectively. Phosphatidylglycerophosphate, in contrast to lysophosphatidic and phosphatidic acid, is effectively dephosphorylated by the phosphatase, which exhibits an apparent Km value of 12 [mu]M for its substrate. Each enzyme shows higher activities with the dipalmitoyl species of its substrate than with the dioleoyl species. These substrate specificities of both enzymes are predominantly based on differences in apparent Vmax values.

PMID: 12232283 [PubMed - as supplied by publisher]

50: Plant Physiol. 1994 Apr;104(4):1131-1138.

Low Temperature-Induced Cytoplasmic Acidosis in Cultured Mung Bean (Vigna radiata [L.] Wilczek) Cells.

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Cold-induced changes in vivo in the cytoplasmic pH of suspension-cultured cells of mung bean (Vigna radiata [L.] Wilczek) were investigated by fluorescence-ratio imaging cryomicroscopy with special reference to the variations in the chilling sensitivity of cells during the growth cycle. Because of the preferential localization of the fluorophore in the cytoplasm under specified conditions and the ideal response of fluorescence to pH, fluorescein diacetate allows measurements to be made of temporal changes in cytoplasmic pH at low temperature. A remarkable difference was demonstrated in the cold-induced changes in cytoplasmic pH between cells at the early and late stages of

exponential growth. The cells at the early stage of exponential growth were most sensitive to chilling, and the cytoplasmic pH decreased dramatically within a short period of incubation at 0[deg]C, decreasing from 7.4 to 6.8 after 4 h and to 6.3 after 18 h. The cells at the late stage of exponential growth were chilling tolerant, and no significant decrease in the cytoplasmic pH was observed during the incubation at 0[deg]C for 24 h or even longer. From the results presented here, it appears that cold-induced cytoplasmic acidosis is characteristic of chilling-sensitive mung bean suspension-cultured cells.

PMID: 12232153 [PubMed - as supplied by publisher]

51: Plant Physiol. 1994 Feb;104(2):691-697.

Modulation of Fusicoccin-Binding Protein Activity in Mung Bean (Vigna radiata L.) Hypocotyls by Tissue Maturation and by Fusicoccin.

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The phytotoxin fusicoccin (FC), after binding to a plasma membrane-localized receptor, causes higher plant cells to excrete protons. Ligand-binding analysis has been used to show that the plasma membrane of mung bean (Vigna radiata L.) hypocotyls contains both high-affinity (HA) and low-affinity (LA) binding sites for FC. The effect of tissue maturation on these sites was determined on isolated membrane vesicles from the meristematic region (hook) and the elongation zone and from mature hypocotyl tissues. In the meristematic region the HA:LA ratio was 1:20. As hypocotyl tissues matured, the site density of HA increased and there was no change in LA density, so that the HA:LA ratio increased to 1:2 in maturet issues. FC-induced proton excretion correlates with the HA density, not the LA density. When sections isolated from each region were incubated with FC prior to isolation of membranes, there was an apparent conversion of LA to HA sites during the first 90 min in all regions. During the next 1 to 3 h there was a further 2.5- to 3- fold increase in binding sites in all regions, accompanied by a slight decline in dissociation constant. The increase in binding sites, but not the apparent conversion of LA to HA, was partly blocked by cycloheximide. These data suggest that FC alters FC-binding protein activity in two ways: first, by causing an increase in affinity for FC of preexisting LA receptors, and second by inducing the synthesis of additional FC receptors. This apparent up-regulation of a phytotoxin receptor by its ligand in plants has not previously been reported.

PMID: 12232120 [PubMed - as supplied by publisher]

52: Plant Physiol. 1994 Jan;104(1):153-159.

Aminomethylenediphosphonate: A Potent Type-Specific Inhibitor of Both Plant and Phototrophic Bacterial H+-Pyrophosphatases.

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The suitability of different pyrophosphate (PPi) analogs as inhibitors of the vacuolar H+-translocating inorganic pyrophosphatase (V-PPase; EC 3.6.1.1) of tonoplast vesicles isolated from etiolated hypocotyls of Vigna radiata was investigated. Five 1,1-diphosphonates and imidodiphosphate were tested for their effects on substrate hydrolysis by the V-PPase at a substrate concentration corresponding to the Km of the enzyme. The order of inhibitory potency (apparent inhibition constants, Kiapp values, [mu]M, in parentheses) of the compounds examined was aminomethylenediphosphonate (1.8) > hydroxymethylenediphosphonate (5.7) [almost equal to] ethane-1-hydroxy-1,1-diphosphonate (6.5) > imidodiphosphate (12) > methylenediphosphonate (68) >> dichloromethylenediphosphonate (>500). The specificity of three of these compounds, aminomethylenediphosphonate, imidodiphosphate, and methylenediphosphonate, was determined by comparing their effects on the V-PPase and vacuolar H+-ATPase from Vigna, plasma membrane H+-ATPase from Beta vulgaris, H+-PPi synthase of chromatophores prepared from Rhodospirillum rubrum, soluble PPase from Saccharomyces cerevisiae, alkaline phosphatase from bovine intestinal mucosa, and nonspecific monophosphoesterase from Vigna at a PPi concentration equivalent to 10 times the Km of the V-PPase. Although all three PPi analogs inhibited the plant V-PPase and bacterial H+-PPi synthase with qualitatively similar kinetics, whether substrate hydrolysis or PPi-dependent H+-translocation was measured, neither the vacuolar H+-ATPase nor plasma membrane H+-ATPase nor any of the non-V-PPase-related PPi hydrolases were markedly inhibited under these conditions. It is concluded that 1, 1-diphosphonates, in general, and aminomethylenediphosphonate, in particular, are potent type-specific inhibitors of the V-PPase and its putative bacterial homolog, the H+-PPi synthase of Rhodospirillum.

PMID: 12232069 [PubMed - as supplied by publisher]

53: Plant Physiol. 1993 Nov;103(3):845-854.

Covalent and Noncovalent Dimers of the Cyanide-Resistant Alternative Oxidase Protein in Higher Plant Mitochondria and Their Relationship to Enzyme Activity.

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Evidence for a mixed population of covalently and noncovalently associated dimers of the cyanide-resistant alternative oxidase protein in plant mitochondria is presented. High molecular mass (oxidized) species of the alternative oxidase protein, having masses predicted for homodimers, appeared on immunoblots when the sulfhydryl reductant, dithiothreitol (DTT), was omitted from sodium dodecyl sulfate-polyacrylamide gel sample buffer. These oxidized species were observed in mitochondria from soybean (Glycine max [L.] Merr. cv Ransom), Sauromatum guttatum Schott, and mung bean (Vigna radiata [L.] R. Wilcz). Reduced species of the alternative oxidase were also present in the same mitochondrial samples. The reduced and oxidized species in isolated soybean cotyledon mitochondria could be interconverted by incubation with the sulfhydryl reagents DTT and azodicarboxylic acid bis(dimethylamide) (diamide). Treatment with chemical cross-linkers resulted in cross-linking of the reduced species, indicating a noncovalent dimeric association among the reduced alternative

oxidase molecules. Alternative pathway activity of soybean mitochondria increased following reduction of the alternative oxidase protein with DTT and decreased following oxidation with diamide, indicating that electron flow through the alternative pathway is sensitive to the sulfhydryl/disulfide redox poise. In mitochondria from S. guttatum floral appendix tissue, the proportion of the reduced species increased as development progressed through thermogenesis.

PMID: 12231983 [PubMed - as supplied by publisher]

54: Plant Physiol. 1995 Oct;109(2):659-665.

Chill-Induced Changes in the Activity and Abundance of the Vacuolar Proton-Pumping Pyrophosphatase from Mung Bean Hypocotyls.

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Changes in the properties of extractable vacuolar H+-pumping pyrophosphatase (V-PPase) and vacuolar ATPase activities in chilling-sensitive seedlings of mung bean (Vigna radiata) were investigated. Following chilling at 4[deg]C for 48 h, both hydrolytic and proton-pumping activities of the V-PPase increased 1.5- to 2-fold over controls and remained elevated even after 72 h at low temperatures. Vacuolar ATPase levels did not change significantly throughout the chilling regime. However a large increase in alcohol dehydrogenase activity during chilling suggests a shift toward fermentative metabolism, which can be expected to decrease ATPase activity in situ. Western blotting of vacuolar membrane-enriched fractions from control and treated plants has confirmed that the changes in V-PPase activity are mirrored by increases in the amount of pump protein. Results suggest a specific role for the V-PPase in protecting chill-sensitive plants from the injurious effects of low temperatures via the maintenance of the proton gradient across the vacuolar membrane.

PMID: 12228620 [PubMed - as supplied by publisher]

55: Plant Physiol. 1995 Sep;109(1):177-185.

1-Chloro-2,4-Dinitrobenzene-Elicited Increase in Vacuolar Glutathione-S-Conjugate Transport Activity.

Li ZS, Zhen RG, Rea PA.

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Unlike most other characterized organic solute transport in plants, uptake of the model compound S-(2,4-dinitrophenyl)glutathione (DNP-GS) and related glutathione-S-conjugated by vacuolar membranes is directly energized by MgATP. Here we show that exogenous application of the DNP-GS precursor 1-chloro-2,4-dinitrobenzene (CDNB) to seedlings of Vigna radiata (mung bean)

increases the capacity of vacuolar membrane vesicles isolated from hypocotyls for MgATP-dependent DNP-GS transport in vitro. Our findings are 4-fold: (a) Pretreatment of seedlings with CDNB causes a progressive increase in MgATP-dependent DNP-GS uptake by vacuolar membrane vesicles, whereas the same range of CDNB concentrations causes only marginal stimulation when the compound benoxacor [4-(dichloroacetyl)-3,4-dihydro-3-methyl-2H-1,4-benzoxazine] is included in the pretreatment solution. (b) Increased DNP-GS uptake is accompanied by a proportionate and selective increase in Vmax(DNP-GS) but not in Km(DNP-GS) or Km(MgATP). (c) CDNB-enhanced DNP-GS uptake is not accompanied by a change in the density profile or sidedness of the vacuolar membrane fraction. (d) Basal and CDNB-enhanced DNP-GS uptake are indistinguishable in terms of their inhibitor profiles. On the basis of these findings, it is inferred that pretreatment with CDNB increases the amount or recruitment of functional transporter into the vacuolar membrane and that agents such as benoxacor antagonize the effects otherwise seen with CDNB in this sytem.

PMID: 12228588 [PubMed - as supplied by publisher]

56: Plant Physiol. 1995 Jun;108(2):693-701.

Characterization and Physiological Function of Class I Low-Molecular-Mass, Heat-Shock Protein Complex in Soybean.

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Examination of an ammonium sulfate-enriched fraction (70-100% saturation) of heat-shock proteins (HSPs) by nondenaturing polyacrylamide gel electrophoresis revealed the presence of a high molecular mass complex (280 kD) in soybean (Glycine max) seedlings. This complex cross-reacted with antibodies raised against soybean class I low-molecular-mass (LMW) HSPs. Dissociation of the complex by denaturing polyacrylamide gel electrophoresis showed the complex to contain at least 15 polypeptides of the 15-to 18-kD class I LMW HSPs that could be detected by staining, radiolabeling, and western blotting. A similar LMW-HSP complex was observed in mung bean (Vigna radiata L.; 295 kD), in pea (Pisum sativum L.; 270 kD), and in rice (Oryza sativa L.; 310 kD). The complex was stable under high salt conditions (250 mM KCI), and the integrity was not affected by 1% Nonidet P-40 and 3 [mu]g/ML RNase treatment. The size of the isolated HSP complex in vitro was conserved to 55[deg]C; however, starting at 37.5[deg]C, it changed to higher molecular forms in the presence of soluble proteins. The isolated HSP complex was able to protect up to 75% of the soluble proteins from heat denaturation in vitro.

PMID: 12228501 [PubMed - as supplied by publisher]

57: Plant Physiol. 1996 May;111(1):195-202.

The Role of Magnesium, Pyrophosphate, and Their Complexes as Substrates and Activators of the Vacuolar H+-Pumping Inorganic Pyrophosphatase (Studies Using Ligand Protection from Covalent Inhibitors).

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Inhibitors preferentially and covalently reactive with cysteine, arginine, histidine, and carboxyl-containing residues were inhibitory to the plant vacuolar H+-transporting inorganic pyrophosphatase (H+-PPase) from Vigna radiata (mung bean) and Beta vulgaris (red beet), but hydrophobic compounds and those reactive with tyrosine and lysine were less effective. Inhibition by 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide, phenylglyoxal, and N-ethylmaleimide was decreased in the presence of Mg2+ or mixtures of Mg2+ and inorganic pyrophosphate (PPi) but not by PPi alone. None of these ligands affected inhibition by reagents reactive with histidine. The Mg2+ dependence of protection from 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide inhibition followed first-order kinetics and yielded a Km for free Mg2+ of 20 to 23 [mu]M. Protection from inhibition by N-ethylmaleimide and phenylglyoxal varied as a function of Mg2PPi concentration, suggesting that this is the substrate for the H+-PPase. Protection by Mg2PPi followed Michaelis-Menten kinetics with a Km of approximately 2 [mu]M. These results are consistent with the predictions of a kinetic model for the H+-PPase (R.A. Leigh, A.J. Pope, I.R. Jennings, D. Sanders [1992] Plant Physiol 100: 1698-1750), which identified free Mg2+ as an allosteric activator (Km = 25 [mu]M) and Mg2PPi as the substrate (Km = 2.5-5 [mu]M).

PMID: 12226285 [PubMed - as supplied by publisher]

58: Plant Physiol. 1997 Oct;115(2):727-736.

L-myo-lnositol 1-Phosphate Synthase from Plant Sources (Characteristics of the Chloroplastic and Cytosolic Enzymes).

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L-myo-inositol 1-phosphate synthase (EC 5.5.1.4) from cyanobacterial (Spirulina platensis), algal (Euglena gracilis), and higher plant (Oryza sativa, Vigna radiata) sources was purified to electrophoretic homogeneity, biochemically characterized, and compared. Both chloroplastic and cytosolic forms of the enzyme were detected in E. gracilis, O. sativa, and V. radiata, whereas only the cytosolic form was detected in streptomycin-bleached or chloroplastic mutants of E. gracilis and in S. platensis. Both the chloroplastic and cytosolic forms from different sources could be purified following the same three-step chromatographic protocol. L-myo-inositol 1-phosphate synthases purified from these different sources do not differ significantly with respect to biochemical and kinetic parameters except for the molecular mass of the chloroplastic and cytosolic native holoenzymes, which appear to be homotetrameric and homotrimeric associations of their constituent subunits, respectively. Monovalent and divalent cations, sugar alcohols, and sugar phosphates are inhibitory to the enzyme activity. N-ethylmaleimide inhibition of synthase activity could be protected by the combined presence of the substrate glucose-6-phosphate and cofactor NAD+. Antibody raised against the cytosolic enzyme from E. gracilis

immunoprecipitates and cross-reacts with both chloroplastic and cytosolic forms from the other sources studied.

PMID: 12223840 [PubMed - as supplied by publisher]

59: Plant Physiol. 1997 Jul;114(3):901-905.

Tris Is a Competitive Inhibitor of K+ Activation of the Vacuolar H+-Pumping Pyrophosphatase.

Gordon-Weeks R, Koren'kov VD, Steele SH, Leigh RA.

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The effects of a range of commonly used pH buffers on the hydrolytic activity of the plant vacuolar H+-transporting inorganic pyrophosphatase (V-PPase) from mung bean (Vigna radiata L.) hypocotyls were tested. All of the buffers inhibited K+ stimulation of the V-PPase, and the degree of inhibition was dependent on the concentrations of both the buffer and K+. The effects were dependent on the organic cation used in the buffers, and those tested inhibited in the order: Tris > Bis-Tris-propane > Bicine = Tricine > imidazole. Detailed studies revealed that a model in which Tris affects both the Km and Vmax for K+ stimulation provided an accurate description of the observed kinetics. The ability of different cations to stimulate the V-PPase was measured with a noncompeting buffer (5 mM imidazole-HCl) and the order of effectiveness was K+ = Rb+ > NH4+ >> Cs+ > Na+ > Li+, with the Km for K+ stimulation being about 1 to 2 mM. Published experiments performed in the presence of Tris were re-evaluated and all could be fitted to mixed inhibition kinetics, with kinetic parameters similar to those measured for the mung bean V-PPase. It is concluded that the variations in the published Km for K+ stimulation of the V-PPase are probably due to the effects of pH buffer cations and that the real value for this parameter is in the low millimolar range. The implications of this for regulation of the V-PPase by K+ in vivo and for the role of the enzyme in K+ transport into the vacuole are discussed.

PMID: 12223751 [PubMed - as supplied by publisher]

60: Chemosphere. 2002 Jun;47(10):1065-72.

Biochemical responses of Cr-tolerant and Cr-sensitive mung bean cultivars grown on varying levels of chromium.

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Biochemical investigations were carried out in Cr-tolerant and Cr-sensitive cultivars of mung bean (Vigna radiata L.) with different concentrations of hexavalent chromium (as K2Cr2O7) in hydroponics culture. Seeds were germinated and grown in the presence or absence of chromium under controlled environmental

conditions. Protein, pigment and enzyme analysis were conducted in both Cr-tolerant and Cr-sensitive cultivars of mung bean after 72 h of treatments. Chlorophyll and protein contents were reduced in Cr-sensitive cultivars more than those of the tolerant ones. The enzyme activity varied among the Cr-tolerant and Cr-sensitive ones. Activities of catalase, peroxidase, glucose-6-phosphate dehydrogenase and superoxide dismutase were greater in Cr-sensitive than tolerant cultivars.

PMID: 12137039 [PubMed - indexed for MEDLINE]

61: Physiol Plant. 2002 Jun;115(2):213-220.

Non-enzymatic protein modification by the Maillard reaction reduces the activities of scavenging enzymes in Vigna radiata.

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The non-enzymatic modification of proteins through the Maillard reaction plays an important role in the loss of seed viability during seed storage. In the present study we examined whether the Maillard reaction reduces the activities of scavenging enzymes in Vigna radiata (mung bean) seeds during storage. Seeds were stored under various conditions for different duration. Maillard products were monitored by measuring protein fluorescence, and the activities of glutathione reductase (GR), superoxide dismutase (SOD), ascorbate peroxidase (APX), catalase (CAT) and peroxidase (POX) were determined. The accumulation of Maillard products in seed axes increased during storage with increasing moisture content and temperature, and was correlated with the decline in seed vigour. The activities of GR, CAT and APX decreased in proportion to the increase in Maillard products at all the moisture contents and temperatures tested. These enzymatic changes were also correlated with seed vigour. However, the activities of SOD and POX remained unchanged and appeared to be less sensitive to the Maillard reaction.

PMID: 12060238 [PubMed - as supplied by publisher]

62: Indian J Exp Biol. 2001 Aug;39(8):821-3.

Symbiotic effectiveness of bacteriocin producing and non-producing strains of Rhizobium in green gram (Vigna radiata).

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Rhizobium strains nodulating green gram [Vigna radiata (L.) Wilczek] were found to produce bacteriocin on modified Bergersen's medium and inhibited the growth of homologous Rhizobium strains. Four bacteriocin producing and four bacteriocin non-producing strains were compared for their effect on nodulation, in planta nitrogenase activity and plant dry weight of green gram. The bacteriocin

producers formed more nodules in comparison to non-bacteriocin producers. However, the symbiotic effectiveness of bacteriocin producers was less in terms of plant dry weight in comparison to non-bacteriocin producers.

PMID: 12018589 [PubMed - indexed for MEDLINE]

63: Mol Phylogenet Evol. 2002 Jan;22(1):1-19.

Molecular evolution and phylogenetic implications of internal transcribed spacer sequences of nuclear ribosomal DNA in the Phaseolus-Vigna complex.

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Molecular phylogeny based on internal transcribed spacer (ITS) sequences was studied to resolve the taxonomic contradiction in Vigna and its relation to Phaseolus. The ITS region of the 18S-26S nuclear ribosomal DNA repeat was sequenced for 29 Vigna species, selected from five of the nine subgenera, and 9 species of Phaseolus. The length of ITS-1 ranged from 187 to 243 bp and 217 to 290 bp, and that of ITS-2 from 187 to 219 bp and 225 to 243 bp, within Vigna and Phaseolus species, respectively. Phylogenies derived from ITS sequences based on maximum-parsimony and neighbor-joining methods gave trees essentially of similar topology. The ITS phylogeny was generally congruent with recent classifications based largely on morphological, biochemical, cytogenetical, and palynological features, except that subgenus Plectotropis of Neotropical origin was revealed to be closely related to subgenus Vigna instead of forming a link between African (subgenus Vigna) and Asiatic (subgenus Ceratotropis) vignas, and subgenus Sigmoidotropis, featuring morphological characters of both Vigna and Phaseolus, was placed as the sister group to the Phaseolus taxa. The ITS sequences were shown to be useful for identifying wild progenitors of V. mungo, V. radiata, V. umbellata, and V. unguiculata and for clarifying taxonomy-related problems in many previously controversial cases. This study also affirms that V. umbellata and V. angularis are the diploid progenitors of the only tetraploid species (V. glabrescens) known in the genus.

PMID: 11796025 [PubMed - indexed for MEDLINE]

64: Hereditas. 2001;134(3):211-7.

Genetic basis of variation of yield, and yield components in mungbean (Vigna radiata (L.) Wilczek).

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Additive, dominance, and epistasis genetic basis of seed yield per plant, number of pods per plant, number of seeds per pod, and 1000 seed weight in mungbean (Vigna radiata (L.) Wilczek) have been examined, using Triple Test Cross (TTC)

analysis. The material for TTC test was evaluated in two seasons i.e., kharif (July-October) and spring/summer (March-June), at the research station of the Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan. Epistasis was present significantly for number of pods per plant and number of seeds per pod when grown in the spring/summer season (March to June). Partition of epistasis showed that additive x additive ('i' type) interaction was an important component of number of pods per plant, and number of seeds per pod was found to be of both types 'i' type, and additive x dominance, and dominance x dominance ('j' and 'l' type) interactions. This indicated that epistasis might be a non-trivial factor in the inheritance of pods per plant, and seeds per pod in mungbean. The expression of epistasis was influenced differentially by particular genotypes, indicating that a limited number of genotypes may not be sufficient to detect non-allelic interactions for a trait in mungbean. Additive and dominance genetic components were significant for all four traits in kharif season (July to October) but only for seed yield and 1000 seed weight in spring/summer season. This suggests that the genes controlling seed yield per plant, and 1000 seed weight are equally sensitive to the environment. The predominance additive gene action in those traits is not significantly influenced by epistasis, suggesting that improvement of the traits can be achieved through standard selection procedures.

PMID: 11833283 [PubMed - indexed for MEDLINE]

65: Plant Mol Biol. 2001 Dec;47(6):761-70.

Cloning and characterization of a DEAD box RNA helicase from the viable seedlings of aged mung bean.

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Seeds stored under adverse conditions will reduce the viability of germination as a result of induced aging. We have established a procedure to induce accelerated aging for studying the process of aging in mung bean (Vigna radiata) seeds at the molecular level. A full-length cDNA was isolated from acceleratedly aged mung bean seedlings. The cDNA, VrRH1 (Vigna radiata RNA helicase 1), contains an open reading frame of 2139 bp encoding a protein of 713 amino acids. VrRHI has seven highly conserved motifs including the DEAD box as in the case of other plant RNA helicases. VrRHI was sub-cloned into an expression vector pET-28b (+), over-expressed in Escherichia coli BL 21 and purified by a Ni2+-agarose column. The expressed protein showed double-stranded RNA unwinding and ATPase activities. Either ATP or dATP is required for the unwinding activity, indicating that VrRHI is an ATP/dATP-dependent RNA helicase. Northern blot analysis showed the presence of mRNAs hybridized with a full-length cDNA fragment of VrRHI (VrRH transcripts) in mung bean seeds that were imbibed for 16 to 32 h after accelerated aging treatment. The amount of these mRNAs reached a maximum in 24 h imbibed seeds after the treatment. The accumulation of VrRH transcripts was shown to lead to the appearance of 25S and 18S rRNAs in the imbibed aging mung bean seeds. The results suggest that VrRHI may play a role in the viability of mung bean seeds.

PMID: 11785937 [PubMed - indexed for MEDLINE]

66: Microbiol Res. 2001;156(4):353-8.

Chitinolytic and cellulolytic Pseudomonas sp. antagonistic to fungal pathogens enhances nodulation by Mesorhizobium sp. Cicer in chickpea.

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Pseudomonas strains isolated from the rhizosphere of chickpea (Cicer arietinum L.) and green gram (Vigna radiata L.) were screened for the production of chitinases and cellulases. Five Pseudomonas strains were found to produce appreciable amounts of both enzymes in culture-free supernatants and showed growth inhibition of the two fungi Pythium aphanidermatum (Oomycete) and Rhizoctonia solani (Basidiomycete) in plates on potato dextrose agar medium. The fungal growth inhibition was not correlated with cell wall-degrading enzyme activity, which suggested that other antifungal compounds produced by these rhizobacteria were also involved in antagonism. Coinoculation of the Pseudomonas strains with the Mesorhizobium sp. Cicer strain Ca 181 resulted in a significant increase in nodule biomass when grown under sterilized chillum jar conditions. The results suggest that hydrolytic enzymes produced by Pseudomonas sp. contribute to suppression of plant diseases by inhibiting growth of phytopathogenic fungi and also promote nodulation of legumes by rhizobia.

PMID: 11770853 [PubMed - indexed for MEDLINE]

67: Biochim Biophys Acta. 2002 Jan 2;1558(1):14-25.

Transmembrane topography of plasma membrane constituents in mung bean (Vigna radiata L.) hypocotyl cells. II. The large scale asymmetry of surface peptides.

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The large scale asymmetry in surface (poly)peptides of the plasma membrane (PM) of mung bean (Vigna radiata L.) hypocotyl cells was investigated by protease and 1 M KCl treatments of PM vesicles obtained by an aqueous two-phase partition technique. Proteases only slightly reduced the protein content of right-side-out PM vesicles and the treatment with 1 M KCl resulted in the dissociation of only a few peripheral proteins from the outer surface of right-side-out PM vesicles, indicating that few surface peptides including peripheral proteins existed on the outer surface. From experiments of the re-partitioning of endomembrane vesicles removed from surface peptides, it was found that the surface peptide content is a factor determining the partitioning, and the hypothesis that sterols are asymmetrically distributed across higher plant PM was proposed. We speculate that asymmetrical properties between the outer and the inner surfaces of plant PM, especially in partitioning in the two-phase system, derive from the asymmetry of the bulk of surface peptides and PM sterols. The comparatively low

hydrophilicity of the outer surface of the PM would be important for the partitioning of right-side-out PM vesicles in the upper phase of the two-phase system.

PMID: 11750260 [PubMed - indexed for MEDLINE]

68: Planta. 2001 Oct;213(6):881-7.

Visualizing rhizosphere chemistry of legumes with mid-infrared synchrotron radiation.

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A bright synchrotron light source operated by the Lawrence Berkeley National Laboratory served as an external source for infrared (IR) microscopy of plant root microcosms. Mid-IR light from synchrotrons is 2-3 orders of magnitude brighter than conventional sources, providing contrast based on the chemical information in the reflected signal at a spatial resolution near the diffraction-limit of 3-10 microm. In an experiment using plant root microcosms fitted with zinc selenide IR-transmissive windows (50 mm x 20 mm x 1 mm), we describe chemical differences and similarities within the root zone of mung bean (Vigna radiata L.), grown with or without phosphorus, and revealed by reflectance spectromicroscopy. Comparative root and root-exudate profiles are described in sand/silt culture over the wavelength range of 2.5 to 16 pm (4.000 to 650 cm(-1)) in the mid-IR. the spectral region most useful for the analytical identification of small organic molecules. Root epidermal tissue of plants grown with low phosphorus showed a greater lipid contribution and less lignin than nutrient-sufficient plants. In the zone 200 microm from the root axis, control plants were enriched with simple sugars and monomeric lignin precursors. In low-phosphorus plants, the rhizosphere possessed IR signatures from protein and sugars. Individual soil minerals could be easily discriminated from biological material. Synchrotron IR spectromicroscopy, therefore, complements existing root imaging techniques.

PMID: 11722124 [PubMed - indexed for MEDLINE]

69: Planta. 2001 Sep;213(5):788-93.

Effect of membrane surface charge on nickel uptake by purified mung bean root protoplasts.

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The influence of membrane surface charge on cation uptake was investigated in protoplasts prepared from roots of mung bean (Vigna radiata L.). Confocal laser scanning microscopy showed that a fluorescent trivalent cation accumulated to very high concentrations at the surface of the protoplasts when they were

incubated in medium containing low concentrations of Ca or other cations, but that this accumulation could be completely reversed by suppression of membrane surface negativity by high cation concentrations. Influx of 63Ni was strongly reduced by a range of divalent cations. Increasing the Ca concentration in the medium from 25 microM to 10 mM inhibited 63Ni influx by more than 85%. 63Ni influx was also inhibited by 85% by reducing the pH from 7 to 4. Computation of the activity of Ni at the membrane surface under the various treatment conditions showed that Ni uptake was closely correlated with its activity at the membrane surface but not with its concentration in the bulk medium. It was concluded that the effects on Ni uptake of addition of monovalent, divalent and trivalent cations, and of variations in pH are all consistent with the proposition that the activity of Ni at the membrane surface is the major determinant of the rate of Ni influx into mung bean protoplasts. It is proposed that the surface charge on the plasma membrane will influence the membrane transport of most charged molecules into cells.

PMID: 11678284 [PubMed - indexed for MEDLINE]

70: Microbiol Res. 2001;156(2):139-44.

Two pathogenesis-related peroxidases in greengram (Vigna radiata (L.) wilczek) leaves and cultured cells induced by Macrophomina phaseolina (Tassi) Goid. and its elicitor.

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An elicitor has been isolated from Macrophomina phaseolina, the root rot and leaf blight pathogen of greengram. Suspension-cultured cells of greengram were established which responded to the fungal elicitor. When greengram leaves were inoculated with M. phaseolina two new peroxidases appeared. Similarly, two new peroxidases could be detected in suspension-cultured greengram cells when treated with the fungal elicitor. These peroxidases were purified by column chromatography and their molecular masses were 27 and 38 kDa. The new peroxidases detected in both leaves and cultured cells appear to be similar with the same molecular weights.

PMID: 11572453 [PubMed - indexed for MEDLINE]

71: Biochem Biophys Res Commun. 2001 Sep 21;287(2):468-73.

An investigation of bisphosphonate inhibition of a vacuolar proton-pumping pyrophosphatase.

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We report the results of a three-dimensional quantitative structure-activity

relationship (3D-QSAR)/comparative molecular field analysis (CoMFA) of the activity of 18 bisphosphonates and imidodiphosphate in the inhibition of a mung bean (Vigna radiata L.) vacuolar proton pumping pyrophosphatase (V/H(+)-PPase; EC 3.6.1.1). We find an experimental versus QSAR predicted pK(app)(i) R(2) value of 0.89, a cross-validated R(2) = 0.77, and a bootstrapped R(2) = 0.89 for 18 bisphosphonates plus imidodiphosphate over the 1.3 microM to 425 microM range of K(app)(i) values. We also demonstrate that this approach has predictive utility (a 0.26 pK(app)(i) rms error for three test sets of 3 activity predictions each), corresponding to about a factor of two error in K(app)(i) prediction. The 3D-QSAR/CoMFA approach provides a quantitative method for predicting the activity of V/H(+)-PPase inhibitors and is likely to be of use in the design of novel pharmacological agents since all of the major human disease-causing parasitic protozoa contain large levels of pyrophosphate, together with V-type proton-pumping pyrophosphatases located in plant-like vacuoles (acidocalcisomes), which are absent in their mammalian hosts. Copyright 2001 Academic Press.

PMID: 11554752 [PubMed - indexed for MEDLINE]

72: J Biol Chem. 2001 Nov 16;276(46):42869-80. Epub 2001 Sep 11.

A new yeast metabolon involving at least the two first enzymes of arginine biosynthesis: acetylglutamate synthase activity requires complex formation with acetylglutamate kinase.

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Open reading frame YJL071W of Saccharomyces cerevisiae was shown to be ARG2 and identified as the structural gene for acetylglutamate synthase, first step in arginine biosynthesis. The three Ascomycete acetylglutamate synthases characterized to date appear homologous, but unlike the other enzymes of the yeast arginine biosynthesis pathway, they showed no significant similarity to their prokaryotic equivalents. The measured synthase activity did not increase with the number of ARG2 gene copies unless the number of ARG5,6 gene copies was increased similarly. ARG5,6 encodes a precursor that is maturated in the mitochondria into acetylglutamate kinase and acetylglutamyl-phosphate reductase, catalyzing the second and third steps in the pathway. The results imply that the synthase must interact stoichiometrically in vivo with the kinase, the reductase, or both to be active. Results obtained with synthetic ARG5 and ARG6 genes suggested that both the kinase and the reductase could be needed. This situation, which has completely escaped notice in yeast until now, is reminiscent of the observation in Neurospora crassa that nonsense arg-6 kinase/reductase mutants lack synthase activity (Hinde, R. W., Jacobson, J. A., Weiss, R. L., and Davis, R. H. (1986) J. Biol. Chem. 261, 5848-5852). In immunoprecipitation experiments, hemagglutinin-tagged synthase coprecipitated with a protein proven by microsequencing to be the kinase. Western blot analyses showed that the synthase has reduced stability in the absence of the kinase/reductase. Our data demonstrate the existence of a new yeast arginine metabolon involving at least the first two, and possibly the first three, enzymes of the pathway. Hypotheses regarding the biological significance of this interaction are discussed.

PMID: 11553611 [PubMed - indexed for MEDLINE]

73: Plant Physiol. 1992 Mar;98(3):827-34.

Comparison of developmental gradients for growth, ATPase, and fusicoccin-binding activity in mung bean hypocotyls.

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A comparison has been made of the developmental gradients along a mung bean (Vigna radiata L.) hypocotyl of the growth rate, plasma membrane ATPase, and fusicoccin-binding protein (FCBP) activity to determine whether they are interrelated. The hook and four sequential 7.5 millimeter segments of the hypocotyl below the hook were cut. A plasma membrane-enriched fraction was isolated from each section by aqueous two-phase partitioning and assayed for vanadate-sensitive ATPase and FCBP activity. Each gradient had a distinctive and different pattern. Endogenous growth rate was maximal in the second section and much lower in the others. Vanadate-sensitive ATPase activity was maximal in the third section, but remained high in the older sections. Amounts of ATPase protein, shown by specific antibody binding, did not correlate with the amount of vanadate-sensitive ATPase activity in the three youngest sections. FCBP activity was almost absent in the first section, then increased to a maximum in the oldest sections. These data show that the growth rate is not determined by the ATPase activity, and that there are no fixed ratios between the ATPase and FCBP.

PMID: 11540929 [PubMed - indexed for MEDLINE]

74: J Biol Chem. 2001 Nov 23;276(47):43635-44. Epub 2001 Aug 29.

High affinity association of myo-inositol trisphosphates with phytase and its effect upon the catalytic potential of the enzyme.

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A neutral phytase from germinating mung bean (Vigna radiata) seeds dephosphorylates myo-inositol hexakisphosphate sequentially to myo-inositol. The enzyme also binds with higher affinity to myo-inositol trisphosphates (1,4,5), (2,4,5), and (1,3,4) isomers without catalysis. The high affinity complex elicits Ca(2+) mobilization in vitro from microsomes/vacuoles via the formation of a ternary complex with the receptor for Ins(1,4,5)P(3). As a sequel to our previous report, we have carried out a detailed characterization of the two sites and examined the mutual interactions between them. Presaturation of the high affinity site leads to an increase in the affinity of the enzyme for phytic acid and its rate of dephosphorylation as well. From the products of limited tryptic cleavage of phytase, two peptides, each with one activity, have been isolated. The larger peptide (approximately 66 kDa) contains the catalytic

site, and the smaller peptide (approximately 5 kDa) has the high affinity myo-inositol trisphosphate-binding site. The interaction between the dual activities of phytase has been observed also at the level of the two peptides. A sequence homology search using N-terminal 12 amino acid residues of the 5-kDa fragment has revealed significant homology with the Homer class of proteins implicated in signaling pathways involving metabotropic glutamate receptor and myo-inositol 1,4,5-trisphosphate receptor. These results indicate a second role of phytase in Ca(2+) mobilization during germination of mung been seed via a salvage pathway that involves allosteric activation by myo-inositol trisphosphate.

PMID: 11527980 [PubMed - indexed for MEDLINE]

75: J Environ Biol. 2001 Apr;22(2):79-81.

Metalaxyl effect on nitrogenase activity (acetylene reduction) and yield of mungbean (Vigna radiata (L.) wilzek).

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In an experiment, application of different levels of metalaxyl to a sandy loam soil significantly affected the nodulation and nitrogenase activity of mungbean. In both the compost amended and unamended soils, 0.5 mg kg(-1) of metalaxyl enhanced acetylene reduction activity and yield of mungbean, where as higher concentrations (1 mg and 2.5 mg kg(-1) of fungicide) inhibited the nodulation traits as well as economic traits of mungbean.

PMID: 11500021 [PubMed - indexed for MEDLINE]

76: Arch Latinoam Nutr. 2000 Dec;50(4):374-9.

Nutritional value of mung bean (Vigna radiata) as effected by cooking and supplementation.

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The study was conducted to improve the nutritional value of Mung (Vigna radiata) by supplementation with different kinds of meat. Diets were prepared using raw and cooked Mung and then cooked Mung was supplemented with poultry, mutton and beef at 10, 15, and 20 percent levels. Nutritional value of Mung was determined by chemical analysis as well as by rat assay. Mung had 25 percent protein and minor losses were observed during cooking. It had 1.21 percent lysine which was reduced by 43 percent on cooking. Other amino acids also showed losses during cooking. The Protein Efficiency Ratio (PER) of diet containing Mung was significantly reduced on cooking (1.86 vs 1.40). On the contrary cooking resulted in some improvement of Net Protein utilization (NPU) and True

Digestibility (TD) of the Mung based diets. Twenty percent level of different meats showed better results in terms of PER, NPU and TD.

PMID: 11464669 [PubMed - indexed for MEDLINE]

77: Plant Sci. 2001 Jul;161(2):239-247.

Agrobacterium tumefaciens-mediated genetic transformation of mungbean (Vigna radiata L. Wilczek) - a recalcitrant grain legume.

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Agrobacterium-mediated transformation of Vigna radiata L. Wilczek has been achieved. Hypocotyl and primary leaves excised from 2-day-old in-vitro grown seedlings produced transgenic calli on B(5) basal medium supplemented with 5x10(-6) M BAP, 2.5x10(-6) M each of 2,4-D and NAA and 50 mg l(-1) kanamycin after co-cultivation with Agrobacterium tumefaciens strains, LBA4404 (pTOK233), EHA105 (pBin9GusInt) and C58C1 (pIG121Hm) all containing beta-glucuronidase (gusA) and neomycin phosphotransferase II (nptII) marker genes. Transformed calli were found resistant to kanamycin up to 1000 mg(.)l(-1). Gene expression of kanamycin resistance (nptII) and gusA in transformed calli was demonstrated by nptII assay and GUS histochemical analysis, respectively. Stable integration of T-DNA into the genome of transformed calli of mungbean was confirmed by Southern blot analysis. Transgenic calli could not regenerate shoots on B(5) or B(5) containing different cytokinins or auxins alone or in combination. However, for the first time, transformed green shoots showing strong GUS activity were regenerated directly from cotyledonary node explants cultured after co-cultivation with LBA4404 (pTOK233) on B(5) medium containing 6-benzylaminopurine (5x10(-7) M) and 75 mg l(-1) kanamycin. The putative transformed shoots were rooted on B(5)+indole-3-butyric acid (5x10(-6) M) within 10-14 days and resulted plantlets subsequently developed flowers and pods with viable seeds in vitro after 20 days of root induction. The stamens, pollen grains and T(0) seeds showed GUS activity. Molecular analysis of putative transformed plants revealed the integration and expression of transgenes in T(0) plants and their seeds.

PMID: 11448754 [PubMed - as supplied by publisher]

78: Genetica. 2000;109(3):227-34.

Random amplified polymorphic DNA (RAPD) analysis in Indian mung bean (Vigna radiata (L.) Wilczek) cultivars.

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Greengram [Vigna radiata (L.) Wilczek], also known as mung bean, widely cultivated in a large number of countries, is an important pulse crop of Asia

and is considered one of the ancestral species of the genus Vigna. Since yields of greengram have remained low across subtropical and tropical Asia, it is important to estimate genetic diversity in existing cultivars in order to see if the lack of genetic variability might be a constraining factor. In this study, 32 Indian cultivars of greengram were subjected to random amplified polymorphic DNA (RAPD) analysis using 21 decamer primers. A total of 267 amplification products were formed at an average of 12.71 per primer with an overall polymorphism of 64%. The extent of polymorphism was moderate to low. Jaccard similarity coefficient values ranged from 0.65 to 0.92. The cluster analysis resulted in mainly three clusters revealing greater homology between cultivars released from the same source. The results of principal components analysis also substantiated this conclusion. The close genetic similarity between the cultivars could be explained due to the high degree of commonness in their pedigrees. The narrow genetic base of the greengram cultivars revealed in the present analysis emphasises the need to exploit the large germplasm collections having diverse morphoagronomic traits in cultivar improvement programs.

PMID: 11430486 [PubMed - indexed for MEDLINE]

79: Biochim Biophys Acta. 2001 Jul 2;1513(1):38-48.

Transmembrane topography of plasma membrane constituents in mung bean (Vigna radiata L.) hypocotyl cells. I. Transmembrane distribution of phospholipids.

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The transmembrane distribution of phospholipids (PLs) in the plasma membrane (PM) of mung bean (Vigna radiata L.) hypocotyl cells was investigated using annexin V-fluorescein isothiocyanate, porcine pancreas phospholipase A(2), and (31)P-nuclear magnetic resonance (NMR) spectroscopy. Phosphatidylserine was not located on the cell surface of mung bean protoplasts. However, phosphatidylcholine, phosphatidylethanolamine and phosphatidic acid were found to be almost symmetrically distributed across right-side-out PM vesicles obtained by aqueous two-phase partitioning by porcine pancreas phospholipase A(2) assay. (31)P-NMR assay showed that the amount of PLs is about equal in the outer and the inner leaflets of the right-side-out PM vesicles. These results suggest that the topography of PM PLs might not contribute to well-known asymmetrical properties of the outer and inner surfaces of higher plant PMs. It is also indicated that inside-out PM vesicles created by Brij 58-treatment do not retain the native PL topography on dithionate reduction of 7-nitro-2,1,3-benzoxadiazol-4-yl-labeled PLs incorporated in the PM vesicles.

PMID: 11427192 [PubMed - indexed for MEDLINE]

80: Biochim Biophys Acta. 2001 Jul 2;1506(1):12-22.

Inhibition of plant vacuolar H(+)-ATPase by diethylpyrocarbonate.

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Treatment of the tonoplast H(+)-ATPase from mung bean seedlings (Vigna radiata L.) with histidine-specific modifier, diethyl pyrocarbonate (DEP), caused a marked loss of the ATP hydrolysis activity and the proton translocation in a concentration-dependent manner. The reaction order of inhibition was calculated to be 0.98, suggesting that at least one histidine residue of vacuolar H(+)-ATPase was modified by DEP. The absorbance of the vacuolar H(+)-ATPase at 240 nm was progressively increased after incubation with DEP, suggesting that N-carbethoxyhistidine had been formed. Hydroxylamine, which could break N-carbethoxyhistidine, reversed the absorbance change and partially restored the enzymic activity. The pK(a) of modified residues of vacuolar H(+)-ATPase was kinetically determined to be 6.73, a value close to that of histidine. Thus, it is assuredly concluded that histidine residues of the vacuolar H(+)-ATPase were modified by DEP. Kinetic analysis showed that V(max) but not K(m) of vacuolar H(+)-ATPase was decreased by DEP. This result is interpreted as that the residual activity after DEP inhibition was primarily due to the unmodified enzyme molecules. Moreover, simultaneous presence of DEP and DCCD (N,N'-dicyclohexyl-carbodiimide), an inhibitor modified at proteolipid subunit of vacuolar H(+)-ATPase, did not induce synergistic inhibition, indicating their independent effects. The stoichiometry studies further demonstrate that only one out of four histidine residues modified was involved in the inhibition of vacuolar H(+)-ATPase by DEP. Mg(2+)-ATP, the physiological substrate of vacuolar H(+)-ATPase, but not its analogs, exerted preferentially partial protection against DEP, indicating that the histidine residue involved in the inhibition of enzymatic activity may locate at/or near the active site and directly participate in the binding of the substrate.

PMID: 11418093 [PubMed - indexed for MEDLINE]

81: Indian J Exp Biol. 2000 Dec;38(12):1241-4.

Somatic embryogenesis in Vigna radiata (L.) Wilczek.

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Somatic embryogenesis was achieved from immature cotyledon derived callus of mungbean, V.radiata (L.) Wilczek in MS liquid medium. Embryogenic callus was induced on MS medium with NAA (5 mg/L). Differentiation of somatic embryos was observed when embryogenic callus was transferred to MS liquid medium containing 2,4-D (1.5 mg/L) and L-proline (50 mg/L). The torpedo shaped embryos were transferred to MS liquid medium with BAP and ABA (1 mg/L each) for maturation and germination. Fifty per cent of torpedo shaped embryos were converted into tiny plants (8-9 plants out of 17) after one week of culture. The germinated embryos were isolated and transferred to MS half strength basal (solid) medium for further development.

PMID: 11411047 [PubMed - indexed for MEDLINE]

82: Phytochemistry. 2001 Jun;57(3):349-59.

Purification and characterization of isoforms of beta-galactosidases in mung bean seedlings.

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Five isoforms of beta-galactosidase (EC 3.2.1.23), designated as beta-galactosidases I-V, were isolated from five-day-old mung bean (Vigna radiata) seedlings. Beta-galactosidases II and III were purified to electrophoretic homogeneity by a procedure involving acid precipitation, ammonium sulfate fractionation, chromatography on diethylaminoethyl-cellulose (DEAE-Cellulose) and con A-Sepharose. and chromatofocusing. Beta-galactosidases I, II and III have the same molecular mass of 87 kDa. comprising two nonidentical subunits with molecular masses of 38 and 48 kDa, while beta-galactosidases IV and V have molecular masses of 45 and 73 kDa, respectively. All the enzymes were active against p-nitrophenyl-beta-D-galactoside, and to a lesser extent, p-nitrophenyl-alpha-L-arabinoside and p-nitrophenyl-beta-D-fucoside. The enzymes were inhibited by D-galactono-1,4-lactone, D-galactose, Hg2+, Ag+ and sodium dodecyl sulfate (SDS). Beta-galactosidases I, II and III were shown to be competitively inhibited by either D-galactono-1, 4-lactone or D-galactose. Isoforms I, II and III have a common optimal pH of 3.6, while isoforms IV and V have pH optima at 3.8 and 4.0, respectively. Isoelectric points of isoforms I, II and III were 7.7, 7.5 and 7.3, respectively. Double immunodiffusion analysis indicated that beta-galactosidases I, II, III and V are immunologically similar to each other, while beta-galactosidase IV shares partially identical antigenic determinants with the other four isoforms. The purified beta-galactosidases II and III were capable of releasing D-galactose residue from the hemicellulose fraction isolated from mung bean seeds.

PMID: 11393513 [PubMed - indexed for MEDLINE]

83: Nitric Oxide. 2001 Jun;5(3):261-70.

Inhibitory effects of nitric oxide on oxidative phosphorylation in plant mitochondria.

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Plant nitrate reductase (NR) produces nitric oxide (NO) when nitrite is provided as the substrate in the presence of NADH [H. Yamasaki and Y. Sakihama (2000) FEBS Lett. 468, 89-92]. Using a NR-dependent NO producing system, we investigated the effects of NO on the energy transduction system in plant mitochondria isolated from mung bean (Vigna radiata). Plant mitochondria are known to possess two respiratory electron transport pathways-the cytochrome and

alternative pathways. When the alternative pathway was inhibited by n-propyl gallate, the addition of NR strongly suppressed respiratory O(2) consumption driven by the cytochrome pathway. In contrast, the alternative pathway measured in the presence of antimycin A was not affected by NO. The extent of the steady-state membrane potential (Deltapsi) generated by respiratory electron transport rapidly declined in response to NO production. The addition of bovine hemoglobin, a quencher of NO, resulted in the recovery of Deltapsi to the uninhibited level. Consistent with its inhibition of Deltapsi, NO produced by NR strongly suppressed ATP synthesis in the mitochondria. These results provide substantial evidence to confirm that the plant alternative pathway is resistant to NO and support the idea that the alternative pathway may lower respiration-dependent production of active oxygens under conditions where NO is overproduced. Copyright 2001 Academic Press.

PMID: 11384199 [PubMed - indexed for MEDLINE]

84: J Agric Food Chem. 2001 Mar;49(3):1552-8.

Mungbean [Vigna radiata (L.) Wilczek] globulins: purification and characterization.

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Vicilin type (8S) and basic 7S globulins and legumin type (11S) globulins were isolated from mungbean [Vigna radiata (L.) Wilczek]. The native molecular weights of the different globulin types were 360000 for legumin, 200000 for vicilin, and 135000 for basic 7S. Some of the 8S globulin apparently complexed and coeluted with the 11S on gel filtration. On SDS-PAGE, 11S was composed of two bands of 40000 and 24000, 8S was composed of 60000, 48000, 32000, and 26000 bands, and basic 7S was composed of 28000 and 16000 bands. The percent composition of total globulins was estimated to be as follow: 8S, 89%; basic 7S, 3.4%; and 11S, 7.6%. The basic 7S and 11S but not the 8S globulins were found to have disulfide bonds. The presence of carbohydrates by conjugated peroxidase reaction was observed in all bands of 8S, the acidic polypeptide of basic 7S, and its complex but not in 11S. The 28000 basic 7S band and its 42000 complex and the first three major bands of 8S cross-reacted with antibodies to all types of soybean conglycinin subunits (alpha, alpha', and beta), whereas the fourth band cross-reacted only with the anti-beta subunit. None of the mungbean globulins cross-reacted with anti-soybean glycinin. Basic 7S was found to be easily extracted with 0.15 M NaCl, 11S was extracted with 0.35 M NaCl,and 8S was extracted over a wide range of NaCl concentrations. The N-terminal sequences of the different subunits/fragments of the globulins were determined and found to have strong homology with storage proteins of other legumes and crops.

PMID: 11312895 [PubMed - indexed for MEDLINE]

85: J Biol Chem. 2001 Mar 23;276(12):8841-7. Epub 2000 Dec 18.

Control of Mung bean pectinmethylesterase isoform activities. Influence of pH

and carboxyl group distribution along the pectic chains.

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Well-characterized pectin samples with a wide range of degrees of esterification (39-74%) were incubated with the solubilized pure alpha and gamma isoforms of pectinmethylesterase, from mung bean hypocotyl (Vigna radiata). Enzyme activity was determined at regular intervals along the deesterification pathway at pH 5.6 and pH 7.6. It has been demonstrated that the distribution of the carboxyl units along the pectin backbone controls the activity of the cell wall pectinmethylesterases to a much greater extent than the methylation degree, with a random distribution leading to the strongest activity. Polygalacturonic acid was shown to be a competitive inhibitor of the alpha isoform activity at pH 5.6 and to inhibit the gamma isoform activity at both pH 5.6 and pH 7.6. Under these conditions, the drop in enzyme activity was shown to be correlated to the formation of deesterified blocks of 19 +/- 1 galacturonic acid residues through simulations of the enzymatic digestion according to the mechanisms established previously (Catoire, L., Pierron, M., Morvan, C., Herve du Penhoat, C., and Goldberg, R. (1998) J. Biol. Chem. 273, 33150-33156). However, even in the absence of inhibition by the reaction product, activity dropped to negligible levels long before the substrate had been totally deesterified. Comparison of alpha and gamma isoform cDNAs suggests that the N-terminal region of catalytic domains might explain their subtle differences in activity revealed in this study. The role of pectinmethylesterase in the cell wall stiffening process along the growth gradient is discussed.

PMID: 11120736 [PubMed - indexed for MEDLINE]

86: J Exp Bot. 2000 Apr;51(345):713-9.

A complex containing both trypsin inhibitor and dehydroascorbate reductase activities isolated from mitochondria of etiolated mung bean (Vigna radiata L. (Wilczek) cv. Tainan no. 5) seedlings.

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A complex containing trypsin inhibitor (TI) activity was extracted with 0.1 M TRIS buffer (pH 7.9) from trypsin-treated mitochondria of etiolated mung bean seedlings, and further purified with a Superdex 200 FPLC column. This partially purified complex with an M(r) about 820 kDa exhibited additional dehydroascorbate (DHA) reductase activity with specific activities of 0.21, 1.53 and 1.54 mumol ascorbate formed min-1 mg-1 protein at pH 6.0, 6.5 and 7.0, respectively, when glutathione was added. Much lower DHA reductase activity (0.013 and 0.026 mumol ascorbate formed min-1 mg-1 protein at pH 6.5 and 7.0, respectively) was found when glutathione was omitted. The isolated complex gave positive results when it was tested by TI activity staining after SDS-PAGE, and could be recognized by a polyclonal antibody which was raised against 38 kDa

sweet potato Kunitz-type TI, one of the root storage proteins of sweet potato. The possible physiological functions of this complex with both TI and DHA reductase activities were discussed.

PMID: 10938863 [PubMed - indexed for MEDLINE]

87: J Exp Bot. 2000 Jul;51(348):1221-8.

Protein modification by Amadori and Maillard reactions during seed storage: roles of sugar hydrolysis and lipid peroxidation.

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The non-enzymatic modifications of proteins through Amadori and Maillard reactions play an important role in the loss of seed viability during storage. In the present study, the contribution of sugar hydrolysis and lipid peroxidation to Amadori and Maillard reactions, and to seed deterioration was investigated in mung-bean (Vigna radiata Wilczek). The contents of glucose and lipid peroxidation products in seed axes increased significantly during storage. The accumulation of Amadori products in seed axes was correlated to the lipid peroxidation, whereas the accumulation of Maillard products was closely correlated to sugar hydrolysis. The rate of accumulation of Maillard products was not well correlated to the content of Amadori products in both seed axes and protein/glucose model system, reflecting the complex nature of Amadori and Maillard reactions. The content of Amadori products in seed axes increased during the early stages of seed ageing, whereas the content of Maillard products increased steadily during the entire period of storage. The accumulation of Maillard products in seed axes was associated with the decline of seed vigour. These data suggest that, during seed ageing, sugar hydrolysis and lipid peroxidation are coupled with non-enzymatic protein modification through Amadori and Maillard reactions.

PMID: 10937697 [PubMed - indexed for MEDLINE]

88: Hereditas. 2000;132(1):43-8.

The chloroplast genomes of azuki bean and its close relatives: a deletion mutation found in weed azuki bean.

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A physical map of the azuki bean (Vigna angularis cv. Erimo-shozu) chloroplast DNA (cpDNA) was constructed by localising the cleavage sites of PstI, SalI, SmaI, SacI, KpnI, PvuII and XhoI. The resulting map is more similar to the cpDNA-maps of two Vigna species (mung bean, V. radiata, and V. nakashimae) than to common bean (Phaseolus vulgaris) cpDNA map. Azuki bean was originally classified in the genus Phaseolus, and the inclusion of this taxon in the genus Vigna is a recent taxonomic decision. Our result is thus in favour of the

taxonomic placement of azuki bean in the same genus as V. nakashimae and mung bean. We also found that a weed-form accession of azuki bean has a 96-bp deletion relative to the cultivar Erimo-shozu. The 96-bp deletion is located between the trnS-UGA and psbC genes in the large single-copy region of the chloroplast genome. This deletion is flanked by imperfect 9-bp direct repeats, suggesting that the deletion was a result of intra-molecular recombination mediated by these direct repeats.

PMID: 10857258 [PubMed - indexed for MEDLINE]

89: Plant Mol Biol. 2000 Mar;42(4):547-57.

Characterization and developmental expression of single-stranded telomeric DNA-binding proteins from mung bean (Vigna radiata).

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We have identified and characterized protein factors from mung bean (Vigna radiata) nuclear extracts that specifically bind the single-stranded G-rich telomeric DNA repeats. Nuclear extracts were prepared from three different types of plant tissue, radicle, hypocotyl, and root, in order to examine changes in the expression patterns of telomere-binding proteins during the development of mung bean. At least three types of specific complexes (A, B, and C) were detected by gel retardation assays with synthetic telomere and nuclear extract from radicle tissue, whereas the two major faster-migrating complexes (A and B) were formed with nuclear extracts from hypocotyl and root tissues. Gel retardation assays also revealed differences in relative amount of each complex forming activity in radicle, hypocotyl, and root nuclear extracts. These data suggest that the expression of telomere-binding proteins is developmentally regulated in plants, and that the factor involved in the formation of complex C may be required during the early stages of development. The binding factors have properties of proteins and are hence designated as mung bean G-rich telomere-binding proteins (MGBP). MGBPs bind DNA substrates with three or more single-stranded TTTAGGG repeats, while none of them show binding affinity to either double-stranded or single-stranded C-rich telomeric DNA. These proteins have a lower affinity to human telomeric sequences than to plant telomeric sequences and do not exhibit a significant binding activity to Tetrahymena telomeric sequence or mutated plant telomeric sequences, indicating that their binding activities are specific to plant telomere. Furthermore, RNase treatment of the nuclear extracts did not affect the complex formation activities. This result indicates that the single-stranded telomere-binding activities may be attributed to a simple protein but not a ribonucleoprotein. The ability of MGBPs to bind specifically the single-stranded TTTAGGG repeats may suggest their in vivo functions in the chromosome ends of plants.

PMID: 10809001 [PubMed - indexed for MEDLINE]

90: Plant Mol Biol. 1999 Nov;41(4):443-54.

Auxin and brassinosteroid differentially regulate the expression of three

members of the 1-aminocyclopropane-1-carboxylate synthase gene family in mung bean (Vigna radiata L.).

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Indole-3-acetic acid (IAA) markedly increased ethylene production by inducing the expression of three 1aminocyclopropane-1-carboxylate (ACC) synthase cDNAs (pVR-ACS1, pVR-ACS6 and pVR-ACS7) in mung bean hypocotyls. Results from nuclear run-on transcription assay and RNA gel blot studies revealed that all three genes were transcriptionally active displaying unique patterns of induction by IAA and various hormones in etiolated hypocotyls. Particularly, 24-epibrassinolide (BR), an active brassinosteroid, specifically enhanced the expression of VR-ACS7 by a distinct temporal induction mechanism compared to that of IAA. In addition, BR synergistically increased the IAA-induced VR-ACS6 and VR-ACS7 transcript levels, while it effectively abolished both the IAA- and kinetin-induced accumulation of VR-ACS1 mRNA. In light-grown plants, VR-ACS1 was induced by IAA in roots, and VR-ACS6 in epicotyls. IAA- and BR-treatments were not able to increase the VR-ACS7 transcript in the light-grown tissues. These results indicate that the expression of ACC synthase multigene family is regulated by complex hormonal and developmental networks in a gene- and tissue-specific manner in mung bean plants. The VR-ACS7 gene was isolated, and chimeric fusion between the 2.4 kb 5'-upstream region and the beta-glucuronidase (GUS) reporter gene was constructed and introduced into Nicotiana tabacum. Analysis of transgenic tobacco plants revealed the VR-ACS7 promoter-driven GUS activity at a highly localized region of the hypocotyl-root junction of control seedlings, while a marked induction of GUS activity was detected only in the hypocotyl region of the IAA-treated transgenic seedlings where rapid cell elongation occurs. Although there was a modest synergistic effect of BR on the IAA-induced GUS activity, BR alone failed to increase the GUS activity, suggesting that induction of VR-ACS7 occurs via separate signaling pathways in response to IAA and BR. A scheme of the multiple regulatory pathways for the expression of ACC synthase multigene family by auxin and BR is presented.

PMID: 10608655 [PubMed - indexed for MEDLINE]

91: J Agric Food Chem. 1999 Feb;47(2):462-7.

Enhancement of beta-glucosidase and beta-galactosidase of Trigonella foenum-graecum by exposure to the allelochemical mimosine.

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Glycohydrolases assume significance in the metabolism of biological systems and have important industrial applications in the areas of pharmaceuticals, food, and medicine. Glycosidases were screened in germinating seeds, and attempts were made to enhance their levels. Screening of glycosidases in the seedlings during a 72 h germination period revealed higher levels of beta-glucosidase and beta-galactosidase in Trigonella foenum-graecum compared to Cicer arietinum and Vigna radiata. Activity of beta-galactosidase was in general higher than that of beta-glucosidase in all the seedlings tested. During growth, exposure of the

seedlings to an allelochemical, mimosine, at 0.1 mM resulted in the enhancement of enzyme levels by 50% in the seedlings of T. foenum-graecum, whereas the addition of mimosine to the assay medium in vitro did not affect the enzyme activities. Hydrolytic activity was enhanced by addition of glycerol in the medium up to 0.1 M in the case of beta-glucosidase and with 0.05 M in the case of beta-galactosidase. In general, the hydrolytic rate was higher by about 30% in the seedlings exposed to mimosine compared to that of the control. Concomitant enhancement in the rates of transgalactosidation by 51% and transglucosidation by 23% was also noted, underscoring the relevance of plant glycohydrolases for appropriate applications.

PMID: 10563917 [PubMed - indexed for MEDLINE]

92: Plant Physiol. 1999 Nov;121(3):879-88.

Glutathione and homoglutathione synthesis in legume root nodules.

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High-performance liquid chromatography (HPLC) with fluorescence detection was used to study thiol metabolism in legume nodules. Glutathione (GSH) was the major non-protein thiol in all indeterminate nodules examined, as well as in the determinate nodules of cowpea (Vigna unguiculata), whereas homoglutathione (hGSH) predominated in soybean (Glycine max), bean (Phaseolus vulgaris), and mungbean (Vigna radiata) nodules. All nodules had greater thiol concentrations than the leaves and roots of the same plants because of active thiol synthesis in nodule tissue. The correlation between thiol tripeptides and the activities of glutathione synthetase (GSHS) and homoglutathione synthetase (hGSHS) in the nodules of eight legumes, and the contrasting thiol contents and activities in alfalfa (Medicago sativa) leaves (98% hGSH, 100% hGSHS) and nodules (72% GSH, 80% GSHS) indicated that the distribution of GSH and hGSH is determined by specific synthetases. Thiol contents and synthesis decreased with both natural and induced nodule senescence, and were also reduced in the senescent zone of indeterminate nodules. Thiols and GSHS were especially abundant in the meristematic and infected zones of pea (Pisum sativum) nodules. Thiols and gamma-glutamylcysteinyl synthetase were also more abundant in the infected zone of bean nodules, but hGSHS was predominant in the cortex. Isolation of full-length cDNA sequences coding for gamma-glutamylcysteinyl synthetase from legume nodules revealed that they are highly homologous to those from other higher plants.

PMID: 10557236 [PubMed - indexed for MEDLINE]

93: Yeast. 1999 Sep 15;15(12):1269-74.

A strong carbon source effect is mediated by pUC plasmid sequences in a series of classical yeast vectors designed for promoter characterization.

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While using YIp356 and YEp356R lacZ reporter plasmids, we found lacZ expression driven by the ARG2 promoter to be much higher in cells grown on a non-glucose carbon source than in glucose-grown cells (5-10-fold higher on galactose and up to 40-fold higher on ethanol). Furthermore, expression increased 30-fold upon shifting from a high-glucose to a low-glucose medium. This carbon source regulation requires Snf1p and possibly Ssn6p. It appears, however, to be artefactually mediated by plasmid sequences located upstream from the multicloning site. This emerged from the following observations: (a) the derepressive effect disappears if any extra piece of DNA is inserted upstream from the ARG2 promoter; and (b) similar derepression on low glucose is observed with another yeast promoter (ARG11), provided that the flanking 5' region is short. We determined that the cis-elements responsible for this physiologically irrelevant glucose regulation are located between positions 636 and 879 of the pUC18 DNA sequence.

PMID: 10487929 [PubMed - indexed for MEDLINE]

94: Biochem J. 1999 Sep 15;342 Pt 3:641-6.

Localization of a carboxylic residue possibly involved in the inhibition of vacuolar H+-pyrophosphatase by N, N'-dicyclohexylcarbodi-imide.

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A vacuolar H(+)-pyrophosphatase (EC 3.6.1.1) that catalyses PP(i) hydrolysis and the electrogenic translocation of protons from the cytosol to the vacuole lumen, was purified from etiolated hypocotyls of mung bean seedlings (Vigna radiata L.). Group-specific modification was used to identify a carboxylic residue involved in the inhibition of vacuolar H(+)-pyrophosphatase. Carbodi-imides, such as N,N'-dicyclohexylcarbodi-imide (DCCD) and 1-ethyl-3-(3-dimethylamino-propyl)carbodi-imide, and Woodward's reagent K caused a progressive decline in the enzymic activity of vacuolar H(+)-pyrophosphatase in a time- and concentration-dependent manner. The stoichiometry of labelling of the vacuolar H(+)-pyrophosphatase by [(14)C]DCCD determined that DCCD modifies one carboxylic residue per subunit of the enzyme. Protection studies suggest that the DCCD-reactive carboxylic residue resides at or near the substrate-binding site. Furthermore, peptide mapping analysis reveals that Asp(283), located in the putative loop V of a tentative topological model of vacuolar H(+)-pyrophosphatase on the cytosolic side, was labelled by radioactive [(14)C]DCCD. Cytosolic loop V contains both DCCD-sensitive Asp(283) and a conserved motif sequence, rendering it a candidate for the catalytic site of vacuolar H(+)-pyrophosphatase. A topological picture of the active domain of vacuolar H(+)-pyrophosphatase is tentatively proposed.

PMID: 10477275 [PubMed - indexed for MEDLINE]

95: Plant Foods Hum Nutr. 1999;53(2):99-102.

Variability in the antinutritional constituents in greengram Vigna radiata.

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District Hospital Palakkad, Kerala, India.

Five greengram varieties, viz. Mg 161, M3, Co2, Pusa 8793 and Pusa baisakhi, were analyzed for phytic acid, tannic acid and trypsin activity. Significant varietal variation in tannin (310 to 400 mg percent), phytic acid (201.33 to 265.33 mg percent) and trypsin inhibitor activity (55.74 to 97.70 TIU/mg) were observed.

PMID: 10472786 [PubMed - indexed for MEDLINE]

96: Chem Biol Interact. 1999 May 14;119-120:399-404.

Organophosphorus acid anhydrolase in slime mold, duckweed and mung bean: a continuing search for a physiological role and a natural substrate.

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Recently, and for the first time, a diisopropylphosphorofluoridate (DFP)-hydrolyzing enzyme, i.e. an organophosphorus acid anhydrolase (OPAA), has been reported in a plant-source. Based on this and other suggestive evidence, the ability of three plant sources and a protist to hydrolyze DFP and 1,2,2-trimethylpropyl methylphosphonofluoridate (Soman) were tested, and the effects of Mn2+ and ethylenediamine tetraacetate (EDTA) on this activity. The plants are duckweed (Lemna minor), giant duckweed (Spirodela oligorhiza), and germinated mung bean (Vigna radiata); the protist is a slime mold (Dictyostelium discoidium). The tests are based on a crude classification of OPAAs as 'squid type' (DFP hydrolyzed more rapidly than Soman) and all of the others termed by us, with questionable justification, as 'Mazur type' (Soman hydrolyzed more rapidly than DFP). Of the two duckweeds, Spirodela oligorhiza hydrolyzes Soman but not DFP, and Lemna minor does not hydrolyze either substrate. In contrast to the report of Yu and Sakurai, mung bean does not hydrolyze DFP and hydrolyzes Soman with a 5-fold stimulation by Mn2+ and a marked inhibition by EDTA. The slime mold hydrolyzes Soman more rapidly than DFP (but does hydrolyze DFP) and the hydrolysis is Mn2+ stimulated. The failure of these plant sources to hydrolyze DFP is similar to the behavior of OPAA from Bacillus stearothermophilus.

PMID: 10421476 [PubMed - indexed for MEDLINE]

97: Plant Physiol. 1999 Jul;120(3):765-72.

The effect of growth and measurement temperature on the activity of the

alternative respiratory pathway

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A postulated role of the CN-resistant alternative respiratory pathway in plants is the maintenance of mitochondrial electron transport at low temperatures that would otherwise inhibit the main phosphorylating pathway and prevent the formation of toxic reactive oxygen species. This role is supported by the observation that alternative oxidase protein levels often increase when plants are subjected to growth at low temperatures. We used oxygen isotope fractionation to measure the distribution of electrons between the main and alternative pathways in mung bean (Vigna radiata) and soybean (Glycine max) following growth at low temperature. The amount of alternative oxidase protein in mung bean grown at 19 degrees C increased over 2-fold in both hypocotyls and leaves compared with plants grown at 28 degrees C but was unchanged in soybean cotyledons grown at 14 degrees C compared with plants grown at 28 degrees C. When the short-term response of tissue respiration was measured over the temperature range of 35 degrees C to 9 degrees C, decreases in the activities of both main and alternative pathway respiration were observed regardless of the growth temperature, and the relative partitioning of electrons to the alternative pathway generally decreased as the temperature was lowered. However, cold-grown mung bean plants that up-regulated the level of alternative oxidase protein maintained a greater electron partitioning to the alternative oxidase when measured at temperatures below 19 degrees C supporting a role for the alternative pathway in response to low temperatures in mung bean. This response was not observed in soybean cotyledons, in which high levels of alternative pathway activity were seen at both high and low temperatures.

PMID: 0010398711 [PubMed - as supplied by publisher]

98: Plant Cell Physiol. 1999 Apr;40(4):431-8.

Characterization of an auxin-inducible 1-aminocyclopropane-1-carboxylate synthase gene, VR-ACS6, of mungbean (Vigna radiata (L.) Wilczek) and hormonal interactions on the promoter activity in transgenic tobacco.

Yoon IS, Park DH, Mori H, Imaseki H, Kang BG.

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A genomic clone for VR-ACS6, an isozyme of auxin-inducible ACC synthase of mungbean, was isolated, and its promoter activity was examined in transgenic tobacco. The clone contained 1,612 bp long 5' untranscribed region and its coding sequence consisted of three exons and two introns. Genomic Southern hybridization indicated that VR-ACS6 is a single copy gene. The transcription initiation site was a cytosine present at 231-base upstream the translation start codon. The VR-ACS6 promoter contained DNA sequences homologous to various functionally identified auxin-responsive elements. To demonstrate hormonal response of the promoter region, transgenic tobacco plants carrying the 1,719 bp VR-ACS6 promoter/-glucuronidase (GUS) fusion gene were generated. Strong GUS expression occurred by auxin treatment of leaves of T0 transformants and

hypocotyls of T1 etiolated seedlings. Magnitude of the response to auxin was dose-dependent, and the increased GUS activity was detected at 0.1 microM and higher concentrations of IAA. Other plant hormones did not induce GUS activity, but greatly modified the response to auxin. Cytokinin enhanced the IAA-induced expression of GUS reporter gene, whereas ABA and ethylene suppressed the expression. These characteristics of VR-ACS6 promoter activity in transgenic tobacco are in good accordance with the expression patterns of the gene in mungbean hypocotyls. Histochemical staining showed that GUS activity was evident in both etiolated and light grown seedings treated with IAA. Cytokinin enhanced the intensity of auxin-induced GUS stain and also expanded the stained area, whereas ABA and ethylene reduced both intensity and area of the stain.

PMID: 10394636 [PubMed - indexed for MEDLINE]

99: Adv Exp Med Biol. 1999;463:249-54.

Characterization of an aldehyde dehydrogenase gene fragment from mung bean (Vigna radiata) using the polymerase chain reaction.

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PMID: 10352693 [PubMed - indexed for MEDLINE]

100: Biochem Mol Biol Int. 1999 Apr;47(4):547-54.

Orthophosphate is a non-essential activator of Vigna radiata flavokinase.

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The ATP-dependent phosphorylation of riboflavin to FMN by flavokinase from Vigna radiata was activated by orthophosphate (Pi) in a concentration dependent manner. Pi affected both the K(m) and Vmax, indicating that it is a non-essential, mixed type activator. The extent of activation by Pi was dependent on the cation (Mg2+ or Zn2+). Activation by other anions could be correlated to similarity to Pi in molecular size and structure. These observations suggest the presence of a binding site(s) for a phosphate-like anion on flavokinase.

PMID: 10319405 [PubMed - indexed for MEDLINE]

101: Plant Cell Physiol. 1998 Dec;39(12):1337-41.

An increase in apparent affinity for sucrose of mung bean sucrose synthase is caused by in vitro phosphorylation or directed mutagenesis of Ser11.

Nakai T, Konishi T, Zhang XQ, Chollet R, Tonouchi N, Tsuchida T, Yoshinaga F, Mori H, Sakai F, Hayashi T.

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A mutational analysis of mung bean (Vigna radiata Wilczek) sucrose synthase was performed by site-directed mutagenesis of the recombinant protein expressed in Escherichia coli, in which two different acidic amino acid residues (Asp or Glu) were introduced at Ser11 (S11D, S11E). Only the wild-type enzyme (Ser11) was phosphorylated in vitro by a Ca(2+)-dependent protein kinase from soybean root nodules, suggesting that this is the specific target residue in mung bean sucrose synthase. The apparent affinity for sucrose was increased in this phosphorylated enzyme and also in the S11D and S11E mutant enzymes, although the affinities for UDP-glucose and fructose were similar in the wild-type, phosphorylated wild-type, and mutant enzymes. These results suggest that a monoanionic (1-) side chain at position 11 mimics the Ser11-P2- residue to bind and cleave sucrose for the synthesis of UDP-glucose. Since the S11E mutant enzyme showed the lowest K(m) (sucrose) and the highest catalytic efficiency of the recombinant proteins, the enzymic properties of this S11E mutant were further characterized. The results showed that replacement of Ser11 with Glu11 modestly protected the sucrose synthesis activity against phenolic glycosides and altered the enzyme nucleotide specificity. We postulate that the introduction of negative charge at Ser11 is possibly involved in the enzymatic perturbation of sucrose synthase.

PMID: 10050318 [PubMed - indexed for MEDLINE]

102: Plant Physiol. 1999 Feb;119(2):621-6.

Purification and characterization of a NADPH-dependent aldehyde reductase from mung bean that detoxifies eutypine, a toxin from eutypa lata1

Colrat S, Latche A, Guis M, Pech JC, Bouzayen M, Fallot J, Roustan JP.

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Eutypine (4-hydroxy-3-[3-methyl-3-butene-1-ynyl] benzaldehyde) is a toxin produced by Eutypa lata, the causal agent of eutypa dieback in the grapevine (Vitis vinifera). Eutypine is enzymatically converted by numerous plant tissues into eutypinol (4-hydroxy-3-[3-methyl-3-butene-1-ynyl] benzyl alcohol), a metabolite that is nontoxic to grapevine. We report a four-step procedure for the purification to apparent electrophoretic homogeneity of a eutypine-reducing enzyme (ERE) from etiolated mung bean (Vigna radiata) hypocotyls. The purified protein is a monomer of 36 kD, uses NADPH as a cofactor, and exhibits a Km value of 6.3 &mgr;M for eutypine and a high affinity for 3- and 4-nitro-benzaldehyde. The enzyme failed to catalyze the reverse reaction using eutypinol as a substrate. ERE detoxifies eutypine efficiently over a pH range from 6.2 to 7.5. These data strongly suggest that ERE is an aldehyde reductase that could probably be classified into the aldo-keto reductase superfamily. We discuss the possible role of this enzyme in eutypine detoxification.

PMID: 0009952458 [PubMed - as supplied by publisher]

103: Electrophoresis. 1998 Dec;19(18):3110-3.

Comparative analysis of genus Vigna seeds using antiserum against a synthesized multiple antigenic peptide.

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Antiserum for 33 kDa vicilin-like seed proteins in V. angularis was prepared using a synthesized multiple antigenic peptide (MAP). The anti-MAP antiserum was applied to the protein analysis of all of genus Vigna seeds which are stored in the Gene Bank at the National Institute of Agrobiological Resources, Tsukuba, Japan. The anti-MAP antiserum specifically reacted with 33 kDa vicilin-like proteins and weakly with 55 kDa vicilin-like proteins of V. angularis by immunoblotting and could distinguish between these two types of vicilin-like 7 S proteins. Anti-MAP antiserum reacted with 33 kDa band both in wild and cultivated types of V. angularis (4 spots) and half species of V. radiata (2 spots). The N-terminal amino acid sequence of the major immunoreacting spot in V. radiata seeds was analyzed. A partially homologous amino acid sequence with MAP was found in immunoreacted protein and the anti-MAP antiserum was able to be applied as a probe to identify homologous amino acid sequence in other proteomes. V. radiata species could be divided by their immunoreactivities into two groups: the group from Southeast Asia and Australia, which reacted with the anti-MAP antiserum, and the group from West Asia and Madagascar, which did not. The abundant proteins in V. mungo seeds at 55 kDa showed strong reactivity signals with anti-MAP antiserum. The existence of a homologous amino acid sequence with MAP was suggested in the 55 kDa proteins. The seed proteins in V. aconitifolia, V. umbellata, V. vexillata, V. marina, V. unguiculata, and V. oblongifolia did not show any reactions and they do not possess the homologous amino acid sequence with MAP in their seed proteins.

PMID: 9932803 [PubMed - indexed for MEDLINE]

104: Isotopes Environ Health Stud. 1998;34(3):291-6.

Biokinetic studies in humans with stable isotopes as tracers. Part 1: A methodology for incorporation of trace metals into vegetables.

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The metabolism and biokinetics of trace metals in humans can be successfully studied employing stable isotopes of the investigated elements as tracers. For the estimation of the bioavailability and the intestinal absorption from solid food, materials are required which have been intrinsically labelled with the chosen stable tracer, since the use of an extrinsic label may lead to erroneous results. Here a technique for producing intrinsically labelled vegetables is

presented and optimized with regard to molybdenum, gadolinium and ruthenium, elements of interest in the field of radiation protection and/or nutrition. These feasibility studies were aimed to determine the most favourable conditions for the production of vegetables containing the selected tracers in amounts high enough to enable successful biokinetic studies in humans. In this optimization study the natural elements were used instead of the more expensive stable isotopes. Mo is readily absorbed both into cress (Lepidium sativum) and into french beans (Phaseolus vulg. var. nanus). Gd uptake into cress is moderate, while Ru may be easily and successfully incorporated only into sprouts of mung beans (Vigna radiata).

PMID: 9919681 [PubMed - indexed for MEDLINE]

105: Plant J. 1998 Nov;16(3):335-43.

A novel NADPH-dependent aldehyde reductase gene from Vigna radiata confers resistance to the grapevine fungal toxin eutypine.

Guillen P, Guis M, Martinez-Reina G, Colrat S, Dalmayrac S, Deswarte C, Bouzayen M, Roustan JP, Fallot J, Pech JC, Latche A.

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Eutypine, 4-hydroxy-3-(3-methyl-3-butene-1-ynyl) benzyl aldehyde, is a toxin produced by Eutypa lata, the causal agent of eutypa dieback of grapevines. It has previously been demonstrated that tolerance of some cultivars to this disease was correlated with their capacity to convert eutypine to the corresponding alcohol, eutypinol, which lacks phytotoxicity. We have thus purified to homogeneity a protein from Vigna radiata that exhibited eutypine-reducing activity and have isolated the corresponding cDNA. This encodes an NADPH-dependent reductase of 36 kDa that we have named Vigna radiata eutypine-reducing enzyme (VR-ERE), based on the capacity of a recombinant form of the protein to reduce eutypine into eutypinol. The strongest homologies (86.8%) of VR-ERE at the amino acid level were found with CPRD14, a drought-inducible gene of unknown function, isolated from Vigna unguiculata and with an aromatic alcohol dehydrogenase (71.7%) from Eucalyptus gunnii. Biochemical characterization of VR-ERE revealed that a variety of compounds containing an aldehyde group can act as substrates. However, the highest affinity was observed with 3-substituted benzaldehydes. Expression of a VR-ERE transgene in Vitis vinifera cells cultured in vitro conferred resistance to the toxin. This discovery opens up new biotechnological approaches for the generation of grapevines resistant to eutypa dieback.

PMID: 9881154 [PubMed - indexed for MEDLINE]

106: Eur J Biochem. 1998 Dec 1;258(2):794-802.

Purification and cDNA cloning of cytokinin-specific binding protein from mung bean (Vigna radiata).

Fujimoto Y, Nagata R, Fukasawa H, Yano K, Azuma M, Iida A, Sugimoto S, Shudo K, Hashimoto Y.

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Synthetic urea derivatives such as N-phenyl-N'-(4-pyridyl)urea (4PU) and N-(2-chloro-4-pyridyl)-N'-phenylurea (4PU30) have strong cytokinin activities. Using tritiated 4PU30 as a probe, we previously established the presence of a cytokinin-specific binding protein (CSBP) of high affinity (Ka for 4PU30 = 4x10(10) M(-1)) in the soluble fraction of etiolated mung bean seedlings [Nagata, R., Kawachi, E., Hashimoto, Y. & Shudo, K. (1993) Biochem. Biophys. Res. Commun. 191, 543-549]. In this report, we purified CSBP by the use of 4PU-Sepharose 4B, an affinity gel liganded with 4PU. We determined partial amino acid sequences of CSBP and isolated its cDNA by reverse-transcription (RT) PCR. The cDNA encoded a protein with a calculated molecular mass of 17 kDa. A data base homology search revealed that CSBP is a novel member of a major pollen allergen/pathogenesis-related protein family. Recombinant CSBP was expressed in Escherichia coli and was confirmed to bind specifically to cytokinins.

PMID: 9874249 [PubMed - indexed for MEDLINE]

107: Biol Trace Elem Res. 1998 Summer;64(1-3):247-58.

Selenium-mediated differential response of beta-glucosidase and beta-galactosidase of germinating Trigonella foenum-graecum.

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Beta-glucosidase and beta-galactosidase activity profile tested in different seeds during 24 h germination revealed reasonably high levels of activity in Vigna radiata, Cicer arietinum, and Trigonella foenum-graecum. In all seeds tested, beta-galactosidase activity was, in general, higher than that of beta-glucosidase. T. foenum-graecum seedlings exhibited maximal total and specific activities for both the enzymes during 72 h germination. Se supplementation as Na2SeO3 up to 0.75 ppm was found to be beneficial to growth and revealed selective enhancement of beta-galactosidase activity by 40% at 0.5 ppm Se. The activities of both the enzymes drastically decreased at 1.0 ppm level of Se supplementation. On the contrary, addition of Na2SeO3 in vitro up to 1 ppm to the enzyme extracts did not influence these activities. Hydrolytic rates of beta-glucosidase in both control and Se-supplemented groups were enhanced by 20% with 0.05 M glycerol in the medium and 30% at 0.1 M glycerol. The rates were marginally higher in Se-supplemented seedlings than the controls, irrespective of added glycerol in the medium. In contrast, hydrolysis by beta-galactosidase showed a trend of decrease in Se-supplemented seedlings compared to the control, when glycerol was present in the medium. Addition of Se in vitro in the assay medium showed no difference in the hydrolytic rate by beta-galactosidase when compared to control, while the activity of beta-glucosidase declined by 50%. Se-grown seedlings showed an enhancement of transglucosidation rate by 40% in the presence of 0.1 M glycerol. The study reveals a differential response to Se among the beta-galactosidase and beta-glucosidase of T. foenum-graecum with increase in the levels of beta-galactosidase activity.

PMID: 9845479 [PubMed - indexed for MEDLINE]

108: J Biol Chem. 1998 Dec 11;273(50):33150-6.

Investigation of the action patterns of pectinmethylesterase isoforms through kinetic analyses and NMR spectroscopy. Implications In cell wall expansion.

Catoire L, Pierron M, Morvan C, du Penhoat CH, Goldberg R.

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Well characterized pectin samples were incubated with cell wall-bound and -solubilized pure isoforms of pectinmethylesterase from mung bean hypocotyls (Vigna radiata). Both enzyme activity and average product structure were determined at intervals along the deesterification pathway at pH 5.6 and 7.6. The latter analyses were performed by 13C NMR spectroscopy, and the degree of esterification was probed by both 13C NMR and potentiometric measurements. A dichotomy was observed in the behavior of the alpha and gamma isoforms when compared with that of the beta isoenzyme. Ideal blockwise deesterification mechanisms reproduced the experimental average structures (methylester distribution) throughout the course of the reaction. In the case of the alpha and gamma isoforms, a single chain mechanism associated with a free carboxyl group at the second nearest neighbor position could be postulated at pH 5.6, whereas some multiple attack character was required to reproduce the data at pH 7.6. Several mechanisms that differed from the preceding ones were compatible with the data for the beta isoform at the two pH values. Both the nature of the polysaccharides produced in these reactions and the role of pectinmethylesterase in the cell wall-stiffening process along the growth gradient are discussed.

PMID: 9837882 [PubMed - indexed for MEDLINE]

109: Biochim Biophys Acta. 1998 Sep 16;1425(1):245-54.

Protein stability in the amorphous carbohydrate matrix: relevance to anhydrobiosis.

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The formation of intracellular glass is proposed to be relevant to protein stabilization and survival of anhydrobiotic organisms in the dry state. The stability of proteins in the amorphous carbohydrate matrix and its relevance to seed survival have been investigated in the present study. Glucose-6-phosphate dehydrogenase (G6PDH) was preserved in the amorphous glucose/sucrose (1:10, w/w) matrix by freeze-drying. The stability of freeze-dried G6PDH was examined at temperatures above and below the glass transition temperature (Tg). The rate of G6PDH inactivation in the amorphous carbohydrate matrix deviated significantly from the Arrhenius kinetics, and conformed to the Williams-Landel-Ferry (WLF) relationship. The temperature dependence of G6PDH inactivation in two sets of samples with different Tg values was compared. Identical temperature dependence

of G6PDH inactivation was observed after temperature normalization by (T-Tg). Seed survival of Vigna radiata Wilczek (mung bean) showed a similar WLF kinetics at storage temperatures T > or = Tg. In situ protein stability in mung bean embryonic axes was studied using differential scanning calorimetry (DSC). Thermal stability of seed proteins exhibited a strong dependence on the Tg of intracellular glass. These results indicate an important role of the glassy state in protein stabilization. Our data suggest an association between protein stability in intracellular glass and seed survival during storage.

PMID: 9813351 [PubMed - indexed for MEDLINE]

110: Tsitologiia. 1998;40(6):579-84.

[Characterization of aldehyde dehydrogenase gene fragment from mung bean Vigna radiata using the polymerase chain reaction]

[Article in Russian]

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Two degenerate oligonucleotide sequence primers and polymerase chain reactions on total DNA have been utilized to clone on 651--bp gene fragment coding the central part of amino acid sequence of an earlier unknown aldehyde dehydrogenase (ALDH) from mung bean. The deduced partial amino acid sequence for this aldehyde dehydrogenase shows about 65% sequence identity to ALDHs of Vibrio cholerae Rhodococcus sp., Alcaligenes eutrophus and about 45% sequence identity to mammalian ALDHs 1 and 2, ALDHs of Aspergillus niger and A, nidulans, the betain aldehyde dehydrogenase from spinach. Alignment of the mung bean aldehyde dehydrogenase partial amino acid sequence with the sequence of 16 NAD(P)(+)-dependent aldehyde dehydrogenases has demonstrated that all strictly conserved amino acid residues and all three conservative regions are identical.

PMID: 9778740 [PubMed - indexed for MEDLINE]

111: Mol Gen Genet. 1998 May;258(4):378-84.

Genetic localization of a bruchid resistance gene and its relationship to insecticidal cyclopeptide alkaloids, the vignatic acids, in mungbean (Vigna radiata L. Wilczek).

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Bruchid resistance, controlled by a single dominant gene (Br) in a wild mungbean accession (TC1966), has been incorporated into cultivated mungbean (Vigna radiata). The resistance gene simultaneously confers inhibitory activity against the bean bug, Riptortus clavatus Thunberg (Hemiptera: Alydidae). The resultant

isogenic line (BC20 generation) was characterized by the presence of a group of novel cyclopeptide alkaloids, called vignatic acids. A linkage map was constructed for Br and the vignatic acid gene (Va) using restriction fragment length polymorphism (RFLP) markers and a segregating BC20F2 population. By screening resistant and susceptible parental lines with 479 primers, eight randomly amplified polymorphic DNA (RAPD) markers linked to Br were identified and cloned for use as RFLP probes. All eight RAPD-based markers, one mungbean, and four common bean genomic clones were effectively integrated around Br within a 3.7-cM interval. Br was mapped to a 0.7-cM segment between a cluster consisting of six markers and a common bean RFLP marker, Bng110. The six markers are closest to the bruchid resistance gene, approximately 0.2 cM away. The vignatic acid gene, Va, cosegregated with bruchid resistance. However, one individual was identified in the BC20F2 population that retained vignatic acids in spite of its bruchid susceptibility. Consequently, Va was mapped to a single locus at the same position as the cluster of markers and 0.2 cM away from Br. These results suggest that the vignatic acids are not the principal factors responsible for bruchid resistance in V. radiata but will facilitate the use of map-based cloning strategies to isolate the Br gene.

PMID: 9648742 [PubMed - indexed for MEDLINE]

112: Biochem J. 1998 Apr 15;331 (Pt 2):395-402.

Subunit interaction of vacuolar H+-pyrophosphatase as determined by high hydrostatic pressure.

Yang SJ, Ko SJ, Tsai YR, Jiang SS, Kuo SY, Hung SH, Pan RL.

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Vacuolar H+-pyrophosphatase (H+-PPase) from etiolated hypocotyls of mung bean (Vigna radiata L.) is a homodimer with a molecular mass of 145 kDa. The vacuolar H+-PPase was subjected to high hydrostatic pressure to investigate its structure and function. The inhibition of H+-PPase activity by high hydrostatic pressure has a pressure-, time- and protein-concentration-dependent manner. The Vmax value of vacuolar H+-PPase was dramatically decreased by pressurization from 293.9 to 70.2 micromol of PPi (pyrophosphate) consumed/h per mg of protein, while the Km value decreased from 0.35 to 0.08 mM, implying that the pressure treatment increased the affinity of PPi to vacuolar H+-PPase but decreased its hydrolysis. The physiological substrate and its analogues enhance high pressure inhibition of vacuolar H+-PPase. The HPLC profile reveals high pressure treatment of H+-PPase provokes the subunit dissociation from an active into inactive form. High hydrostatic pressure also induces the conformational change of vacuolar H+-PPase as determined by spectroscopic techniques. Our results indicate the importance of protein-protein interaction for this novel proton-translocating enzyme. Working models are proposed to interpret the pressure inactivation of vacuolar H+-PPase. We also suggest that association of identical subunits of vacuolar H+-PPase is not random but proceeds in a specific manner.

PMID: 9531476 [PubMed - indexed for MEDLINE]

113: Plant Physiol. 1998 Apr;116(4):1527-32.

Evidence for 1-(Malonylamino)cyclopropane-1-carboxylic acid being the major conjugate of aminocyclopropane-1-carboxylic acid in tomato fruit

Peiser G, Fa Yang S.

Tomato (Lycopersicon esculentum Miller) fruit discs fed with [2, 3-14C]1-aminocyclopropane-1-carboxylic acid (ACC) formed 1-malonyl-ACC (MACC) as the major conjugate of ACC in fruit throughout all ripening stages, from immature-green through the red-ripe stage. Another conjugate of ACC, gamma-glutamyl-ACC (GACC), was formed only in mature-green fruit in an amount about 10% of that of MACC; conjugation of ACC into GACC was not detected in fruits at other ripening stages. No GACC formation was observed from etiolated mung bean (Vigna radiata [L.] Wilczek) hypocotyls, etiolated common vetch (Vicia sativum L.) epicotyls, or pea (Pisum sativum L.) root tips, etiolated epicotyls, and green stem tissue, where active conversion of ACC into MACC was observed. GACC was, however, formed in vitro in extracts from fruit of all ripening stages. GACC formation in an extract from red fruit at pH 7.15 was only about 3% of that at pH 8.0, the pH at which most assays were run. Our present in vivo data support the previous contention that MACC is the major conjugate of ACC in plant tissues, whereas GACC is a minor, if any, conjugate of ACC. Thus, our data do not support the proposal that GACC formation could be more important than MACC formation in tomato fruit.

PMID: 0009536071 [PubMed - as supplied by publisher]

114: J Protein Chem. 1998 Feb;17(2):161-72.

High-pressure effects on vacuolar H+-ATPase from etiolated mung bean seedlings.

Tsai YR, Yang SJ, Jiang SS, Ko SJ, Hung SH, Kuo SY, Pan RL.

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A high-hydrostatic-pressure technique was employed to study the structure-function relationship of plant vacuolar H+-ATPase from etiolated mung bean seedlings (Vigna radiata L.). When isolated vacuolar H+-ATPase was subjected to hydrostatic pressure, the activity of ATP hydrolysis was markedly inhibited in a time-, protein concentration- and pressure-dependent manner. The pressure treatment decreased both Vmax and Km of solubilized vacuolar H+-ATPase, implying an increase in ATP binding affinity, but a decrease in the ATP hydrolysis activity. Physiological substrate, Mg2+-ATP, augmented the loss of enzymatic activity upon pressure treatment. However, ADP, AMP, and Pi exerted substantial protective effects against pressurization. Steady-state ATP hydrolysis was more sensitive to pressurization than single-site ATPase activity. The inactivation of solubilized vacuolar H+-ATPase by pressure may result from changes in protein-protein interaction. The conformational change of solubilized vacuolar H+-ATPase induced by hydrostatic pressure was further determined by spectroscopic techniques. The inhibition of vacuolar H+-ATPase under pressurization involved at least two steps. Taken together, our work indicates that subunit-subunit interaction is crucial for the integrity and the function of plant vacuolar H+-ATPase. It is also suggested that the assembly of

the vacuolar H+-ATPase complex is probably not random, but follows a sequestered pathway.

PMID: 9535278 [PubMed - indexed for MEDLINE]

115: Biochim Biophys Acta. 1998 Feb 2;1379(2):207-16.

Legume vicilins (7S storage globulins) inhibit yeast growth and glucose stimulated acidification of the medium by yeast cells.

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Vicilin (7S storage proteins) isolated from different legume seeds were shown to inhibit yeast growth and glucose stimulated acidification of the medium by yeast cells. The degree of growth inhibition varied with the origin of vicilins. It was more than 90% for vicilins from cowpea (Vigna unguiculata, cultivar pitiuba) and equal to 65% for vicilins from Vigna radiata, in the case of Saccharomyces cerevisae. Vicilins from cowpea seeds inhibited the glucose stimulated acidification of the medium by S. cerevisae up to 60%. We have also observed that vicilins bind to yeast cells. We suggest that vicilins bind to chitin-containing structures of yeast cells and that such association could result in inhibition of H+ pumping, cell growth and spore formation. A final consequence of the yeast growth inhibition by vicilins is (probably) the formation of spores.

PMID: 9528656 [PubMed - indexed for MEDLINE]

116: Plant Physiol. 1998 Feb;116(2):589-97.

Molecular cloning of vacuolar H(+)-pyrophosphatase and its developmental expression in growing hypocotyl of mung bean.

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Vacuolar proton-translocating inorganic pyrophosphatase and H(+)-ATPase acidify the vacuoles and power the vacuolar secondary active transport systems in plants. Developmental changes in the transcription of the pyrophosphatase in growing hypocotyls of mung bean (Vigna radiata) were investigated. The cDNA clone for the mung bean enzyme contains an uninterrupted open reading frame of 2298 bp, coding for a polypeptide of 766 amino acids. Hypocotyls were divided into elongating and mature regions. RNA analysis revealed that the transcript level of the pyrophosphatase was high in the elongating region of the 3-d-old hypocotyl but was extremely low in the mature region of the 5-d-old hypocotyl. The level of transcript of the 68-kD subunit of H(+)-ATPase also decreased after cell maturation. In the elongating region, the proton-pumping activity of pyrophosphatase on the basis of membrane protein was 3 times higher than that of

H(+)-ATPase. After cell maturation, the pyrophosphatase activity decreased to 30% of that in the elongating region. The decline in the pyrophosphatase activity was in parallel with a decrease in the enzyme protein content. These findings indicate that the level of the pyrophosphatase, a main vacuolar proton pump in growing cells, is negatively regulated after cell maturation at the transcriptional level.

PMID: 9489011 [PubMed - indexed for MEDLINE]

117: Plant Foods Hum Nutr. 1997;50(3):211-22.

Characteristics of two major lectins from mungbean (Vigna radiata) seeds.

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Two major lectins, MBL-I and MBL-II, were purified from Vigna radiata L. seeds using ion-exchange and gel filtration chromatography techniques. MBL-I was found to be a tetramer with native M.W. of 132 kDa and subunit M.W. of 33 kDa having alpha-galactosidase activity. MBL-II consisted of two monomeric lectins with M.W. of 94 kDa and 89 kDa which were associated mainly with beta-galactosidase activity. Both MBL-I and MBL-II are D-galactose-specific lectins.

PMID: 9373872 [PubMed - indexed for MEDLINE]

118: Anal Biochem. 1997 Oct 15;252(2):271-6.

Perils of partitioning: A case study of flavins and flavokinase.

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Partitioning is a common procedure for the separation of two solutes from a solution based on their differential solubility in an immiscible solvent. This has been widely used to quantitate riboflavin, flavin mononucleotide (FMN), and flavin adenine dinucleotide in aqueous samples by extraction with water-saturated benzyl alcohol. Here we report that the partitioning of riboflavin and FMN is affected by the presence of each other in a concentration-dependent manner, thus rendering this procedure unsuitable for quantitation. Direct quantitation of FMN formed in assays for flavokinase from Vigna radiata shows that kinetic analyses using a partition-based assay lead to erroneous conclusions. Copyright 1997 Academic Press.

PMID: 9344413 [PubMed - indexed for MEDLINE]

119: Biosci Biotechnol Biochem. 1997 Sep;61(9):1500-3.

Expression and characterization of sucrose synthase from mung bean seedlings in

Escherichia coli.

Nakai T, Tonouchi N, Tsuchida T, Mori H, Sakai F, Hayashi T.

Wood Research Institute, Kyoto University, Japan.

The cDNA fragment coding for mung bean (Vigna radiata Wilczek) sucrose synthase was introduced into the expression vector pET-20b resulting in the construction of plasmid pEB-01. After transformation of Escherichia coli strain BL21(DE3) cells by pEB-01 and induction with isopropyl thio-beta-galactoside, high level expression of the recombinant enzyme was obtained. The enzyme had a tetrameric form that conserved the activity of sucrose synthase. Although the Km and Vmax of the recombinant enzyme acting on either UDP-glucose or fructose were very close to those of the native enzyme isolated from mung bean seedlings, the Km for sucrose was higher by a factor of 10 for the recombinant enzyme. This suggests that the recombinant sucrose synthase has a tendency to synthesize sucrose, although the native enzyme catalyzes a freely reversible reaction.

PMID: 9339551 [PubMed - indexed for MEDLINE]

120: Phytochemistry. 1997 Jun;45(4):689-93.

Vacuolar uptake of the phytoalexin medicarpin by the glutathione conjugate pump.

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We have studied the uptake of [3H]-medicarpin and its glutathione conjugate(s) into vacuolar membrane vesicles from etiolated hypocotyls of mung bean (Vigna radiata). Unconjugated medicarpin is taken up at a low rate in the presence or absence of MgATP. However, [3H]-medicarpin-glutathione conjugate(s), prepared by incubation of medicarpin with a total maize glutathione S-transferase preparation, is taken up more than four-fold faster than medicarpin in the presence of MgATP, and this uptake is MgATP-dependent. Uptake of medicarpin-glutathione was not significantly inhibited by the ionophore gramicidin-D, but was strongly inhibited by vanadate and the alternative transport substrate S-(2,4-dinitrophenyl) glutathione. Our results demonstrate, in a model system, the potential utilization of the high affinity, high capacity, uncoupler-insensitive glutathione conjugate pump for the vacuolar transport of an isoflavonoid phytoalexin.

PMID: 9195760 [PubMed - indexed for MEDLINE]

121: Clin Exp Allergy. 1997 Apr;27(4):424-30.

Purification and characterization of a soybean hull allergen responsible for the Barcelona asthma outbreaks. II. Purification and sequencing of the Gly m 2 allergen.

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BACKGROUND: A low MW allergen from soybean hull, Gly m 1, with two isoallergens, Gly m 1 A and Gly m 1 B, was associated with the asthma outbreaks that occurred in Cartagena, Spain. Using sera of asthmatic epidemic patients (AEP) from Barcelona, three main soybean hull allergens, two of them with MWs and pIs identical to those reported for Gly m 1 A and Gly m 1 B, were identified. OBJECTIVE: The purpose of this study was to purify and to study the N-terminal amino acid sequence of the third allergen, which has a MW of 8 kDa. METHOD: The purification procedure combined the double dialysis method and preparative isoelectofocusing (IEF). Specific IgE determination to the fractions obtained demonstrated three peaks, one of them corresponding to the 8 kDa allergen. The pooled fractions containing this allergen were studied by sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE), SDS-PAGE/Western blot and IEF/Western blot. Only a band with a MW of 8 kDa and a pI of 6 was obtained. Its allergenic activity was measured and it was demonstrated that the allergenicity of soybean hull correlates with the presence of the 8 kDa allergen. The N-terminal amino acid sequence of the first 20 amino acids, which was registered at the PIR Data Submission as the N-terminal partial sequence of Gly m 2, was determined according the Edman degradation method. RESULTS: Gly m 2 N-terminal amino acid sequence lacks homology with that reported for the allergen Gly m 1 but has a homology of 71% with a storage protein from cotyledon of Vigna radiata (cow pea) and 64% with a "disease response protein' from Pisum sativum (green pea). These results suggest that Gly m 2 in soybeans could protect against diseases which affect soybean plants. CONCLUSION: This study demonstrates the existence of another soybean hull allergen, Gly m 2, partially responsible for the soybean asthma outbreaks that occurred in Barcelona, Spain.

PMID: 9146936 [PubMed - indexed for MEDLINE]

122: Plant Cell Physiol. 1997 Mar;38(3):290-6.

Accumulation of a glycoprotein that is homologous to a seed storage protein in mung bean hypocotyls at the late stage of tissue elongation.

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Physiological changes were examined in the amount of a 50-kDa glycoprotein (gp50) that was recovered in a nuclear fraction from hypocotyls of mung bean (Vigna radiata) seedlings. Immunoblot analysis indicated that the glycoprotein was present in hypocotyls and epicotyls from 4- and 5-day-old seedlings but not in hypocotyls from 2-day-old seedlings. The glycoprotein was not detected in leaves or roots. When we divided hypocotyls of 3-day-old seedlings into elongating region (0 to 1.5 cm below the cotyledon) and the mature region, we found gp50 in the mature region only. The results suggest that the 50-kDa glycoprotein is synthesized de novo and accumulates at the late stage during elongation of cells in the hypocotyl. Furthermore, an antibody specific to gp50 reacted with a major 50-kDa protein in cotyledons, which is known as a storage protein in mung bean cotyledon. Eighteen amino acid residues among 22 amino-terminal residues of gp50 were identical to those of the storage protein from cotyledon. A peptide map of the glycoprotein after digestion with V8 protease was similar to that of the storage protein. Overall, our findings

suggest that the glycoprotein recovered in the nuclear fraction is an isoform of the seed storage protein that is expressed only in the mature cells of hypocotyls and epicotyls.

PMID: 9150602 [PubMed - indexed for MEDLINE]

123: Plant Cell Physiol. 1997 Mar;38(3):217-24.

VR-ACS6 is an auxin-inducible 1-aminocyclopropane-1-carboxylate synthase gene in mungbean (Vigna radiata).

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We have isolated four cDNA clones of ACC synthase from etiolated mungbean seedlings treated with auxin. pVR-ACS2, pVR-ACS3 and pVR-ACS6 contained the same sequences as the previously reported DNA fragments, pMAC2, pMAC3 (Botella et al. 1992b) and pMBA1 (Kim et al. 1992), respectively. pVR-ACS1 was identical with pAIM-1 (Botella et al. 1992a). VR-ACS6 was specifically induced in response to the auxin signal. The IAA-induction of VR-ACS6 was very rapid (within 30 min) and insensitive to cycloheximide treatment at concentrations up to 100 microM. Significant accumulation of VR-ACS6 mRNA was detected at 1 microM IAA. The IAA-induced expression of VR-ACS6 was suppressed by ABA and ethylene, but enhanced by BA. These characteristics of VR-ACS6 expression were well correlated with the physiological data of auxin-induced ethylene production in mungbean hypocotyls. VR-ACS1 was strongly induced by cycloheximide, but was found to be not auxin-specific. Inhibitors of either ethylene biosynthesis (AOA) or action (NBD) increased the basal level of VR-ACS1 mRNA.

PMID: 9150600 [PubMed - indexed for MEDLINE]

124: Plant Physiol. 1997 Jan;113(1):119-26.

Immunopurification and characterization of a 40-kD 1-aminocyclopropane-1-carboxylic acid N-malonyltransferase from mung bean seedling hypocotyls.

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1-Aminocyclopropane-1-carboxylic acid (ACC) N-malonyltransferase catalyzes the transfer of the malonyl group from malonyl coenzyme A to ACC to form malonyl ACC. Using partially purified ACC N-malonyltransferase from the hypocotyls of mung bean (Vigna radiata) seedlings, we produced two mouse monoclonal antibodies (1H5 and 2G3) to this enzyme. These antibodies bind to sites other than the active site of the enzyme because monoclonal antibody-bound ACC N-malonyltransferase still exhibits full catalytic activity. A monoclonal antibody column was constructed using 1H5 and protein G Sepharose. The ACC N-malonyltransferase purified from this monoclonal antibody column has a molecular mass of 40 kD, which is different from that reported previously. The

enzyme has a higher electrophoretic mobility on sodium dodecyl sulfate-polyacrylamide gel electrophoresis in the absence of the reducing agent dithiothreitol. The optimum temperature of this 40-kD ACC N-malonyltransferase is 45 degrees C and the apparent Kms for ACC and malonyl coenzyme A are 66.7 and 40 microns, respectively.

PMID: 9008392 [PubMed - indexed for MEDLINE]

125: Plant Mol Biol. 1996 Aug;31(5):1039-49.

Pectinmethylesterase isoforms from Vigna radiata hypocotyl cell walls: kinetic properties and molecular cloning of a cDNA encoding the most alkaline isoform.

Bordenave M, Breton C, Goldberg R, Huet JC, Perez S, Pernollet JC.

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Peptide maps and partial amino acid sequences of the 3 main pectinmethylesterases (PMEs) solubilized from mung bean hypocotyl cell walls demonstrated that these proteins were different isozymes originating from a small multigene family. A cDNA clone encoding the most alkaline PME (PE gamma) have been obtained by PCR using degenerate oligonucleotide primers. Combining the protein and nucleotide sequencing data, the complete amino acid sequence of PE gamma was determined. The nature protein is composed of 318 amino acids with a calculated Mtau of 34 677 and an estimated pI of 9.84 consistent with the values previously obtained by SDS-PAGE and IEF. It shares most of the conserved regions of previously known PMEs. Enzymatic activities of the three isoforms were differently affected by the presence of cations in the incubation medium but, in all cases, infra-optimal cation concentrations induced two opposite effects: a decrease in the Vmax and an increase in the affinity of the enzymes for their substrate. The presence of cations in the assay modulates both the number of enzyme molecules available to the demethylation reaction and the conformation of the pectin and, in turn, the affinity of the PMEs for their substrate.

PMID: 8843946 [PubMed - indexed for MEDLINE]

126: FEBS Lett. 1996 Jun 17;388(2-3):139-42.

PCR cloning and expression analysis of a cDNA encoding a pectinacetylesterase from Vigna radiata L.

Breton C, Bordenave M, Richard L, Pernollet JC, Huet JC, Perez S, Goldberg R.

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A cDNA clone encoding a pectinacetylesterase (PAE) was isolated from 3-day-old mung bean seedlings using PCR-based techniques. Degenerate oligonucleotide primers were designed according to the N-terminus and internal peptides from the purified PAE. The full-length clone of 1453 bp codes for a signal peptide of 24 amino acids and a mature protein of 375 amino acids. The Mr and the pI of the cDNA-deduced amino acid sequence agree with the values estimated for the

purified enzyme. No significant sequence identity between the PAE and any known protein could be found in the databases. Northern analysis revealed developmentally regulated expression of the mRNA in mung been seedlings.

PMID: 8690073 [PubMed - indexed for MEDLINE]

127: Indian J Biochem Biophys. 1996 Jun;33(3):184-94.

Purification, characterisation and steady state kinetic properties of cytosolic pyruvate kinase free of phosphoenol pyruvate phosphatase activity from germinating mung beans (Vigna radiata L.)

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Mung bean pyruvate kinase (PK) practically free from PEP-phosphatase has been purified about 36 fold. The enzyme is irreversibly inactivated on desalting by gel filtration or dialysis (without EDTA). The inactivation is also observed in the presence of ATP, Mg2+ or thiols but is prevented by a non-proteinous, heat stable, small molecular mass factor present in the mung bean extract. Mung bean PK has a molecular mass of 210 kDa. It shows single exponential decay of activity at various temperatures (-4 to 60 degrees C). The Km of PEP and ADP are found to be 0.12 and 0.24 mM, respectively at pH 6.5, when the enzyme is saturated with the second substrate. The Km values for PEP and ADP are 0.05 and 0.16 mM, at pH 8.5 and 0.09 and 0.17 mM, respectively at pH 7.5. The optimum pH is 7.5. The enzyme shows an absolute requirement for Mg2+ (Km 0.43 mM) or Mn2+ ions (Km 0.125 mM). Potassium ions are not essential but activate the enzyme in the presence of Mg2+ or Mn2+ ions. ATP shows competitive inhibition with ADP and non-competitive with PEP. Kinetic studies at different pHs and effects of ATP suggest the formation of a ternary complex (E.ADP.PEP) by a combination of random and compulsory ordered pathways depending on the experimental conditions.

PMID: 8828288 [PubMed - indexed for MEDLINE]

128: Plant Mol Biol. 1996 Mar;30(6):1129-37.

Calcium-dependent protein kinase gene expression in response to physical and chemical stimuli in mungbean (Vigna radiata).

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Protein kinases are important in eukaryotic signal transduction pathways. In this study we designed degenerate oligonucleotides corresponding to two conserved regions of protein kinases and using the polymerase chain reaction (PCR) have amplified a 141 bp fragment of DNA from mungbeans (Vigna radiata Rwilcz cv. Berken). Sequence analysis of the PCR products indicates that they encode several putative protein kinases with respect to their identity with

other known plant protein kinases. Using one of the six fragments (CPK3-8), we isolated a 2022 bp cDNA (VrCDPK-1) from a Vigna radiata lambda gt11 library. VrCDPK-1 has a 96 bp 5'-untranslated region and a 465 bp 3'-untranslated region and an open reading frame of 1461 bp. VrCDPK-1 contains all of the conserved regions commonly found in calcium dependent protein kinases (CDPK). VrCDPK-1 shares 24 to 89% sequence identity with previously reported sequences for plant CDPKs at the protein level. Southern analysis revealed the presence of several copies of the CDPK gene. VrCDPK-1 expression was stimulated when mungbean cuttings were treated with CaCl2, while treatment with MgCl2 had no effect. We are reporting for the first time a CDPK gene in mungbean which is inducible by mechanical strain. Cuttings treated with indole-3-acetic acid (IAA) or subjected to salt stress showed an increase in VrCDPK-1 expression. There was a dramatic stimulation in VrCDPK-1 expression 6 h after cuttings were treated with cycloheximide.

PMID: 8704124 [PubMed - indexed for MEDLINE]

129: Plant Cell Physiol. 1995 Dec;36(8):1531-9.

Molecular cloning and analysis of the cDNA for an auxin-regulated calmodulin gene.

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An auxin-regulated calmodulin cDNA (arCaM) were isolated by differential screening from a mung bean (Vigna radiata) cDNA library. The expression of the arCaM transcript in the etiolated mung bean hypocotyl was examined by RNA gel blot analysis. The arCaM transcript was induced depending on indole-3-acetic acid (IAA) concentrations. An increase in level of the arCaM transcript upon treatment of hypocotyl segments with 10 microM IAA was detected after 1 h and a maximum level was detected at 2 h. Induction of the arCaM transcript occurred upon treatment with 10 microM 2,4-dichlorophenoxyacetic acid (2,4-D) or naphthalene-1-acetic acid (NAA) as well as with IAA, while treatment with 10 microM p-chlorophenoxyisobutyric acid (PCIB) as an anti-auxin, prevented the induction. Ethylene did not have any effect. Other stress conditions, such as exposure to salt stress, heavy metal ions and heat shock, also had no effect on the induction. The levels of the arCaM transcript in leaves of light-grown mung bean plants treated with IAA showed steady but small increases with time.

PMID: 8589930 [PubMed - indexed for MEDLINE]

130: Bull Environ Contam Toxicol. 1995 Oct;55(4):562-7.

Dissipation of deltamethrin and fenvalerate residues in green gram (Vigna radiata (L.) Wilczek) under Indian climatic condition.

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PMID: 8555681 [PubMed - indexed for MEDLINE]

131: Biol Trace Elem Res. 1995 May;48(2):141-60.

Subcellular distribution of selenium during uptake and its influence on mitochondrial oxidations in germinating Vigna radiata L.

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The metabolic significance of Se in plants is not well documented, though the presence of many selenoenzymes in bacteria and the essentiality of Se in higher animals is established. Since germination is an active process in plant growth and metabolism, the effect of Se was investigated in germinating Vigna radiata L, a nonaccumulating Se-deficient legume. Growth and protein were enhanced in seedlings supplemented with selenium (Se) as sodium selenite in the medium up to 1 microgram/mL. The pattern of uptake of 75Se in the differentiating tissues and the subcellular distribution were investigated. The percentage of incorporation of 75Se was greater in the mitochondria at the lowest level (0.5 micrograms/mL) of Se supplementation compared to higher levels of Se exposure. Proteins precipitated from the postmitochondrial supernatant fractions, when separated by means of polyacrylamide gel electrophoresis (PAGE), indicated a major selenoprotein in the seedlings germinated at 2.0 micrograms/mL Se. In seedlings grown with supplemented Se, enhanced respiratory control ratio and succinate dehydrogenase activity were observed in the mitochondria of tissues, indicative of a role for Se in mitochondrial membrane functions.

PMID: 7662500 [PubMed - indexed for MEDLINE]

132: Biochem Biophys Res Commun. 1995 Apr 6;209(1):1-5.

Proline accumulates in plants exposed to UV radiation and protects them against UV induced peroxidation.

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Proline accumulated in the shoots of seedlings of rice (Oryza sativa), mustard (Brassica juncea) and mung bean (Vigna radiata) exposed to UV radiations. The level of proline in the seedlings increased significantly with increase in UV exposure time. The production of malondialdehyde (an indice of lipid peroxidation) was also higher in the shoots of seedlings exposed to UV radiation as compared to controls, suggesting that UV radiations promote lipid peroxidation. The extent of UV radiation promoted enhancement in the levels of proline as well as that of malondialdehyde was higher in the seedlings of rice than those of mung bean or mustard. This lead us to believe that UV radiation induced proline accumulation protects plants against UV radiation promoted peroxidative processes. UV radiations also promoted peroxidation in linolenic acid micelles. The presence of proline along with linolenic acid micelles during

UV exposure caused a considerable reduction in the production of malondialdehyde. This study, for the first time shows that plants exposed to UV radiations accumulate proline and proline can protect plant cells against UV radiation induced peroxidative processes.

PMID: 7726821 [PubMed - indexed for MEDLINE]

133: Biol Trace Elem Res. 1995 Apr;48(1):67-89.

Kinetic analysis of 75selenium uptake by mitochondria of germinating Vigna radiata of different selenium status.

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Earlier studies in our laboratory demonstrated the beneficial role of Se in Vigna radiata, a Se-deficient legume, during germination, as reflected in growth-related parameters and specific uptake of 75Se. Uptake of Na2(75)SeO3, added in vitro by mitochondria isolated from seedlings germinated in control (without Se), and Se-supplemented groups (0.5, 1.0, and 2.0 ppm Se) indicated a proportional increase in the uptake with added Na2(75)SeO3, in concentrations up to 25 microM. The uptake of 75Se, increased linearly with time up to 15 min and a definite efflux followed at 30 min. The results were indicative of cooperative effects during Se transport. Kinetic analyses of the uptake of 75Se during time intervals of 15 and 30 min were carried out both in the whole mitochondria and the mitochondrial protein fractions. Graphical analyses using Lineweaver-Burk plot, Hill plot, log [v] vs log [A] and Scatchard plot confirmed the existence of negative cooperativity during 75Se uptake. Hill coefficient (nH) values were estimated to be around 0.7-0.8. Scatchard plots for 75Se uptake were biphasic, suggesting the probable presence of two classes of binding sites. The number of high and low affinity binding sites were estimated to be around 4-7 and 26-30 nmol/mg protein, respectively. Studies with mitochondrial respiratory inhibitors indicated about 10-20% of the total 75Se uptake to be energy dependent. Inhibition of 75Se uptake by about 60-70% by sulfate and sulfite (5-25 microM) implies the involvement of dicarboxylate port in Se transport. A decrease in the uptake of 75Se by 40-60% effected by CdCl2, HgCl2, mersalyl, and NEM confirmed the interaction of thiols in the process. Evidence for the regulatory nature of 75Se uptake by mitochondria of V. radiata emerges from the present study.

PMID: 7626374 [PubMed - indexed for MEDLINE]

134: Biochem J. 1995 Mar 15;306 (Pt 3):631-6.

Receptor for myo-inositol trisphosphate from the microsomal fraction of Vigna radiata.

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The microsomal fraction from mung-bean (Vigna radiata) hypocotyl was found to

contain Ins (1,4,5)P3- and Ins(2,4,5)P3-binding activity. Preincubation of the microsomal fraction with thiol-containing reagents reduced specific InsP3 binding. A single class of binding site with a Kd value of 1.5 nM and Bmax. of 1.1 pmol/mg of protein was detected. Other myo-inositol phosphates exhibited little affinity for this protein. The binding protein was purified to homogeneity and the molecular mass of the native form recorded as 400 kDa. However, under denaturing conditions the molecular mass was 110 kDa, suggesting that the protein is a homotetramer. That this protein is associated with Ca2+ release was confirmed by including it in proteoliposomes and adding Ins(1,4,5)P3 or Ins(2,4,5)P3. The affinity of Ins(1,4,5)P3 is 3-fold higher than that of Ins(2,4,5)P3. The binding affinity of InsP3 is also reflected in the extent of Ca2+ released from the microsomal fraction. Heparin inhibits binding of InsP3 to the protein, the K1/2 being 0.26 microM. It is also shown that the protein acts as a receptor for InsP3 with characteristics of high affinity and low density.

PMID: 7702554 [PubMed - indexed for MEDLINE]

135: Proc Natl Acad Sci U S A. 1995 Feb 28;92(5):1595-8.

A mechanical strain-induced 1-aminocyclopropane-1-carboxylic acid synthase gene.

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Ethylene production is observed in all higher plants, where it is involved in numerous aspects of growth, development, and senescence. 1-Aminocyclopropane-1-carboxylic acid synthase (ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase, EC 4.4.1.14) is the key regulatory enzyme in the ethylene biosynthetic pathway. We are reporting an ACC synthase gene in Vigna radiata (mung bean) that is inducible by mechanical strain. The ACC synthase cDNA AIM-1 was induced by mechanical strain within 10 min, reaching a maximum at 30 min, showing a dramatic reduction after 60 min, and showing no detectable message by 3 hr. The kinetics of induction for AIM-1 was similar to a mechanical strain-induced calmodulin (MBCaM-1) in V. radiata, whereas the kinetics of its decline from maximum was different. When plants were subjected to calcium-deficient conditions, supplemental calcium, calcium chelators, calcium storage releasers, calcium ionophore, or calmodulin antagonists, there was no effect on AIM-1, indicating that the mechanical strain-induced AIM-1 expression is a calcium-independent process. Induction of MBCaM-1 in all cases behaved in the same way as AIM-1, suggesting that they share similar mechanically activated cis- and/or trans-acting elements in their promoter.

PMID: 7878024 [PubMed - indexed for MEDLINE]

136: Plant Foods Hum Nutr. 1995 Feb;47(2):173-9.

Improvement in HC1-extractability of minerals in home made weaning foods.

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Three weaning foods were formulated from locally available cereals and pulses such as rice (Oryza sativa), kangini (Setaria italica), sanwak (Echinochloa frumentacea), green gram (Vigna radiata) and jaggery. Cereals and pulses were mixed in the proportion of 7:3. Nutrient composition of developed weaning foods was within range prescribed by Indian Standard Institute and was found to be acceptable. Roasting was the processing technique employed in developing weaning foods which resulted in significant increase in HC1-extractable minerals, an index of their bioavailability to humans. The higher HC1-extractability of the minerals may be ascribed to the decreased phytic acid in the processed home made weaning foods.

PMID: 7792266 [PubMed - indexed for MEDLINE]

137: Nahrung. 1995;39(2):132-8.

Effect of processing on the composition of dietary fibre and starch in some legumes.

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The effect of processing on the total dietary fibre (TDF) insoluble (IDF) and water-soluble (SDF) fractions as well as total (TS), available (AS) and resistant (RS) starch were studied in three legumes, viz. bengalgram (Cicer arietinum L.), Cowpea (Vigna unguiculata) and greengram (Vigna radiata). The processes studied were fermentation, germination, pressure-cooking and roasting. The dietary fibre (DF) content and its components were determined using the enzymatic-gravimetric method. The TS content was determined by the enzymatic method after solubilization with KOH. The DF content ranged from 23.2 to 25.6 g/100 g in the raw and 16.0 to 31.5 g/100 g in the processed legumes. All the processing treatments significantly decreased the SDF content and increased the IDF content of all the three legumes. The mean TS, AS and RS content of the raw legumes were similar, 46.9, 36.7 and 10.2 g/100 g respectively. AS content of all the legumes was reduced by the processing treatments, except pressure cooking. Correspondingly, higher amounts of RS were observed in the processed legumes, except pressure cooked, resulting in an increase in the TDF content.

PMID: 7783778 [PubMed - indexed for MEDLINE]

138: Plant Physiol. 1994 Oct;106(2):697-702.

Purification and characterization of two ferredoxin-NADP+ oxidoreductase isoforms from the first foliage leaves of mung bean (Vigna radiata) seedlings.

Jin T, Morigasaki S, Wada K.

PMID: 7991687 [PubMed - indexed for MEDLINE]

139: Plant Foods Hum Nutr. 1994 Oct;46(3):245-53.

Protein quality of weaning foods based on locally available cereal and pulse combination.

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Locally available cereals and pulses such as rice (Oryza sativa), kangini (Setaria italica), sanwak (Echinochloa frumentacea), green gram (Vigna radiata) and jaggery were used to formulate three weaning foods. Cereal, pulse and jaggery were mixed in the ratio of 70:30:25. Roasting was the main processing technique used in the formulation of these weaning foods. The developed weaning foods had 5.06 to 5.68 g moisture, 10.28 to 13.71 g protein, 2.91 to 3.77 g ash, 1.08 to 1.87 g fat, 14.42 to 14.98 mg iron, 1.03 to 1.27 g crude fibre, and 357 to 374 Kcal. The weaning foods had a nutrient composition within the range prescribed by the Indian Standard Institute for processed weaning foods. The study indicated that the weaning foods obtained from locally available food stuffs have the potential of being produced locally, adaptable for household consumption and can be good substitute for commercial formulae.

PMID: 7855096 [PubMed - indexed for MEDLINE]

140: FEBS Lett. 1994 Aug 22;350(2-3):323-7.

Oxygen exchange reactions catalyzed by vacuolar H(+)-translocating pyrophosphatase. Evidence for reversible formation of enzyme-bound pyrophosphate.

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Vacuolar membrane-derived vesicles isolated from Vigna radiata catalyze oxygen exchange between medium phosphate and water. On the basis of the inhibitor sensitivity and cation requirements of the exchange activity, it is almost exclusively attributable to the vacuolar H(+)-pyrophosphatase (V-PPase). The invariance of the partition coefficient and the results of kinetic modeling indicate that exchange proceeds via a single reaction pathway and results from the reversal of enzyme-bound pyrophosphate synthesis. Comparison of the exchange reactions catalyzed by V-PPase and soluble PPases suggests that the two classes of enzyme mediate P(i)-HOH exchange by the same mechanism and that the intrinsic reversibility of the V-PPase is no greater than that of soluble PPases.

PMID: 8070586 [PubMed - indexed for MEDLINE]

141: Plant Foods Hum Nutr. 1994 Jun;45(4):349-55.

Shelf life of weaning foods developed from locally available food stuffs.

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Four weaning foods were formulated using locally available cereals and pulses such as wheat (Triticum aestivum), barley (Hordeum vulgare), green gram (Vigna radiata) and jaggery. Cereal, pulse and jaggery were used in the proportion of 70:30:25. Roasting and malting were two processing techniques used. The developed weaning foods were evaluated for their nutritional characteristics and shelf life. All the formulations had a nutrient composition within the range prescribed by the Indian Standard Institute (ISI) for processed weaning foods. Peroxide value and fat acidity of weaning foods increased with increase in storage period. Malting of weaning foods resulted in higher increase of peroxide value and fat acidity as compared to roasted ones during the period of storage. All the blends were found to be acceptable up to 60 days of storage. The results, indicated that weaning foods developed from locally available less inexpensive foods may be used as good supplements for infants.

PMID: 7971776 [PubMed - indexed for MEDLINE]

142: Plant Mol Biol. 1994 Mar;24(5):757-66.

Differential expression of two calmodulin genes in response to physical and chemical stimuli.

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Two different calmodulin (CaM) cDNAs (MBCaM-1 and MBCaM-2) were isolated from a vigna radiata lambda gt11 library by screening with a heterologous Arabidopsis cDNA probe (TCH-1). Both cDNAs are 85% homologous inside the coding region but are highly divergent outside this region. The polypeptides encoded by MBCaM-1 and MBCaM-2 are identical except for two conservative substitutions at positions 7 and 10. Southern analysis revealed that both cDNAs are encoded by different genes. Expression studies revealed different patterns of expression of both genes. MBCaM-1 mRNA exhibited a dramatic transient increase in response to touch, while MBCaM-2 expression showed a steady but small increase as compared to MBCaM-1. When plants were grown in complete darkness MBCaM-1 was undetectable and MBCaM-2 exhibited very low levels of expression. One hour after exposure of etiolated seedlings to light MBCaM-1 showed no change, while MBCaM-2 expression was increased. After a 6 h exposure to light there was an induction of both MBCaM-1 and MBCaM-2; however, the magnitude of this increase was much greater for MBCaM-2. When plants were grown under a 16 h light/8 h dark cycle the mRNA levels for MBCaM-1 were lower during the light period and increased during the beginning of the night cycle, while MBCaM-2 showed no change. Plants treated with indole-3-acetic acid had a peak in MBCaM-1 expression 6 h after treatment initiation with a slight decline 3 h after the peak, while MBCaM-2 showed a

steady but small increase over time as compared to MBCaM-1. When plants were subjected to salt stress they showed an increase in MBCaM-1 expression 2 h after treatment initiation reaching a maximum after 4 h with no further increase after 6 h, while MBCaM-2 remained unchanged over the time course.

PMID: 8193300 [PubMed - indexed for MEDLINE]

143: Plant Foods Hum Nutr. 1994 Feb;45(2):165-73.

In vitro starch and protein digestibility and iron availability in weaning foods as affected by processing methods.

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In the present investigation, four weaning foods were formulated using locally available cereals and pulses such as wheat (Triticum aestivum), barley (Hordeum vulgare) and green gram (Vigna radiata). Cereal, pulse and jaggery were used in the proportion of 70:30:25. Domestic processing technique like roasting and malting were used to process cereals and pulses for development of weaning foods. All the four blends had a nutrient composition within the range prescribed by the Indian Standard Institute (ISI) for processed weaning foods. The processing of grains resulted in 16-20% increase in starch digestibility and 17-32% increase in protein digestibility. Also 16-32% increase in iron availability was observed on processing. The effect was more remarkable in malted weaning foods as compared to roasted ones.

PMID: 8153067 [PubMed - indexed for MEDLINE]

144: Plant Physiol. 1994 Jan;104(1):127-33.

Characterization of a soybean beta-conglycinin-degrading protease cleavage site.

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Protease C1, an enzyme from soybean (Glycine max [L.] Merrill cv Amsoy 71) seedling cotyledons, was previously determined to be the enzyme responsible for the initial degradation of the alpha' and alpha subunits, but not the beta subunit, of beta-conglycinin storage protein. The sizes of the proteolytic products generated by the action of protease C1 suggest that the cleavage sites on the alpha' and alpha subunits of beta-conglycinin may be located in their N-terminal domain, which is not found in the beta subunit of beta-conglycinin. To check this hypothesis, storage proteins from other plant species that are homologous to either the alpha'/alpha or the beta subunit of beta-conglycinin were tested as substrates. As expected, the convicilin from pea (Pisum sativum), a protein homologous to the alpha' and alpha subunits of beta-conglycinin, was digested by protease C1. The vicilins from pea as well as vicilins from adzuki bean (Vigna angularis), garden bean (Phaseolus vulgaris), black-eyed pea (Vigna

unguiculata), and mung bean (Vigna radiata), storage proteins that are homologous to the beta subunit of soybean beta-conglycinin, were not degraded by protease C1. Degradation of soybean beta-conglycinin involves a sequential attack of the alpha subunit at multiple sites, culminating in the formation of a stable intermediate of 53.5 kD and a final product of 48.0 kD. The cleavage sites resulting in this formation of the intermediates and final product were determined by N-terminal analysis. These were compared to the known amino acid sequences of the three beta-conglycinin subunits. Results showed these two polypeptides to be generated by proteolysis of the alpha subunit at regions bearing long strings of acidic amino acid residues.

PMID: 8115542 [PubMed - indexed for MEDLINE]

145: Planta. 1994;194(2):223-9.

Structure and expression of cDNAs encoding 1-aminocyclopropane-1-carboxylate oxidase homologs isolated from excised mung bean hypocotyls.

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By screening a mung bean (Vigna radiata L.) hypocotyl cDNA library using a combination of apple (pAE12) and tomato (pTOM13) 1-aminocyclopropane 1-carboxylate (ACC)-oxidase cDNAs as probes, putative ACC-oxidase clones were isolated. Based on restriction-enzyme map and DNA-sequencing analyses, they can be divided into two homology classes, represented by pVR-ACO1 and pVR-ACO2. While pVR-ACO1 and pVR-ACO2 exhibit close homology in their coding regions, their 3'-noncoding regions are divergent. pVR-ACO1 is a 1312-bp full-length clone and contains a single open reading frame encoding 317 amino acids (MW = 35.8 kDa), while pVR-ACO2 is 1172 bp long and is a partial cDNA clone encoding 308 amino acids. These two deduced amino-acid sequences share 83% identity, and display considerable sequence conservation (73-86%) to other ACC oxidases from various plant species. Northern blot analyses of RNAs isolated from hypocotyl, leaf, and stem tissues using gene-specific probes indicate that the pVR-ACO1 transcript is present in all parts of the seedling and that the expression in hypocotyls is further increased following excision. The maximum induction of ACC-oxidase transcripts occurred at about 6 h after excision, while the maximum enzyme activity was observed at 24 h. When excised hypocotyls were treated with ethylene a further enhanced level of transcripts was observed. Aminooxyacetic acid, an inhibitor of ACC-synthase activity, and 2,5-norbornadiene, an inhibitor of ethylene action, suppressed the wound-induced accumulation of ACC-oxidase mRNA, while an addition of ethylene in these tissues restored the accumulation of ACC-oxidase mRNA.(ABSTRACT TRUNCATED AT 250 WORDS)

PMID: 7765118 [PubMed - indexed for MEDLINE]

146: Planta. 1994;192(3):359-64.

Further characterization of auxin-regulated mRNAs in hypocotyl sections of mung bean [Vigna radiata (L.) Wilczek]: sequence homology to genes for fatty-acid

desaturases and atypical late-embryogenesis-abundant protein, and the mode of expression of the mRNAs.

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The amino-acid sequence deduced from the nucleotide sequence of an auxin-regulated gene, ARG1, isolated from auxin-treated sections of mung-bean hypocotyls (Yamamoto et al. 1992, Plant Cell Physiol. 33, 13-20), is 69% identical to that of a delta 15 fatty-acid desaturase from Brassica napus L. that is localized in the endoplasmic reticulum. The ARG1 message is present at high levels in the hook portion of the hypocotyl, the plumule and the root tip of 3-d-old etiolated seedlings. The amino-acid sequence encoded by another auxin-regulated gene, ARG2, is 39% identical to that of an atypical late-embryogenesis-abundant (LEA) protein of cotton, LEA5-A. The ARG2 message is localized in the upper part of hypocotyls. Its abundance increases upon treatment of hypocotyl sections with fusicoccin, as well as with auxin. Determination of the distribution and kinetics of induction of mRNAs transcribed from the five auxin-regulated genes of mung bean, which include Aux22s and SAUR as well as ARG1 and ARG2, shows that they are heterogeneous in their mode of gene expression. The physiological implications of the homology between the two auxin-regulated genes and the genes for previously identified proteins are discussed in the context of auxin-induced elongation of the hypocotyl.

PMID: 7764402 [PubMed - indexed for MEDLINE]

147: Mol Gen Genet. 1993 Dec;241(5-6):531-41.

A novel response-regulator is able to suppress the nodulation defect of a Bradyrhizobium japonicum nodW mutant.

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The two-component regulatory system Nod-VW of Bradyrhizobium japonicum is essential for the nodulation of the legume host plants Vigna radiata, V. unguiculata and Macroptilium atropurpureum. The NodV protein shares homology with the sensor-kinases, whereas the NodW protein is a member of the response-regulator class. We report here the identification of a new B. japonicum DNA region that is able to suppress the phenotypic defect of a nodW mutant, provided that this region is expressed from a foreign promoter. The minimal complementing region, which itself is not essential for nodulation in a nodW+ background, consists of one gene designated nwsB (nodW-suppressor). The deduced amino acid sequence of the nwsB gene product shows a high degree of homology to NodW. The nws B gene is preceded by a long open reading frame, nwsA, whose putative product appears to be a sensor-kinase. Downstream of nwsB, an open reading frame encoding a second putative response-regulator was identified. Interspecies hybridization revealed the presence of nwsAB-like DNA also in other Bradyrhizobium strains. Using nwsB'-'lacZ fusions, the nwsB gene was found to be expressed rather weakly in B. japonicum. This low level of expression is obviously not sufficient to compensate for a nodW- defect, whereas strong

overexpression of nwsB is a condition that leads to suppression of the nodW- mutation.

PMID: 8264528 [PubMed - indexed for MEDLINE]

148: Plant Mol Biol. 1993 Dec;23(5):963-79.

Nascent transcript-binding protein of the pea chloroplast transcriptionally active chromosome.

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This study describes the nascent RNA-binding protein of the pea chloroplast transcriptional complex. The protein has been identified by photoaffinity labelling of the transcriptionally active chromosome (TAC) which utilizes the endogenous plastid DNA as template. UV irradiation of lysed chloroplast or the isolated TAC under conditions optimized for transcription photocross-links nascent radiolabelled transcripts (up to 250 nucleotides in length) to a 48 kDa protein. The photoaffinity labelling of the transcript-binding protein is dependent on UV irradiation, is maximal after about 30 min of irradiation, and is completely dependent on transcriptional activity; no cross-linkage has been observed with pre-synthesized RNA. Cross-linkage is influenced by salts and inhibitors in accordance with their effects on transcription. The photoconjugate is composed of protein and RNA moieties, and can be hydrolysed by several proteases. However, the cross-linked transcript is protected from nucleases until the protein is removed. Manganese enhances photoaffinity labelling of the transcript-binding protein, and this is paralleled by an increase in total transcriptional activity of TAC. This protein was isolated by 2-dimensional polyacrylamide gel electrophoresis and the sequence of 15 amino acid residues at the amino terminus was determined. The nascent transcript-binding protein appears to be involved in the transcription of all three classes of chloroplast genes. We also found a polypeptide of identical molecular weight to get cross-linked to nascent transcripts in chloroplasts isolated from other legumes such as Cicer arietenum, Vigna radiata and Phaseolus vulgaris, and monocots like Zea mays, Oryza sativa and Pennisetum americanum.

PMID: 8260634 [PubMed - indexed for MEDLINE]

149: Eur J Biochem. 1993 Oct 15;217(2):755-62.

Steady-state kinetics of substrate hydrolysis by vacuolar H(+)-pyrophosphatase. A simple three-state model.

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The results of analyses of the steady-state kinetics of the vacuolar

H(+)-translocating pyrophosphatase (V-PPase) of native tonoplast vesicles isolated from etiolated hypocotyls of Vigna radiata (mung bean) and purified enzyme from the same source under a wide range of Mg2+, pyrophosphate (PPi) and K+ concentrations are consistent with a minimal reaction scheme in which dimagnesium pyrophosphate is the active substrate species and catalysis is mediated by preformed enzyme-Mg2+ complex. When account is taken of the sensitivity of the V-PPase to ionic strength, additional kinetic interactions are not required to describe the behavior of the enzyme. N-Ethylmaleimide-protection assays show that the dissociation constant for Mg2+ binding in the absence of PPi is an order of magnitude smaller than that estimated from the steady-state kinetics of PPi hydrolysis. Two distinct Mg(2+)-binding sites are therefore invoked. Since the protective action of Mg2+ is independent of the nature of the monovalent cations and Mg2+ and K+ do not compete during substrate hydrolysis, divalent and monovalent cations are concluded to bind at separate sites. The pH dependencies of the kinetic parameters are consistent with the participation of groups of pKa 5.7 and 8.6 in substrate binding and groups of pKa 6.1 and 9.0 in the substrate-conversion step, indicating that at least four ionizable groups are essential for catalysis. These findings are discussed with respect to the reaction mechanism of the V-PPase and the potential regulatory significance of cytosolic free Mg2+ and K+ in vivo.

PMID: 8223618 [PubMed - indexed for MEDLINE]

150: FEBS Lett. 1993 Jul 26;327(2):199-202.

Differential sensitivity of membrane-associated pyrophosphatases to inhibition by diphosphonates and fluoride delineates two classes of enzyme.

Baykov AA, Dubnova EB, Bakuleva NP, Evtushenko OA, Zhen RG, Rea PA.

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1,1-Diphosphonate analogs of pyrophosphate, containing an amino or a hydroxyl group on the bridge carbon atom, are potent inhibitors of the H(+)-translocating pyrophosphatases of chromatophores prepared from the bacterium Rhodospirillum rubrum and vacuolar membrane vesicles prepared from the plant Vigna radiata. The inhibition constant for aminomethylenediphosphonate, which binds competitively with respect to substrate, is below 2 microM. Rat liver mitochondrial pyrophosphatase is two orders of magnitude less sensitive to this compound but extremely sensitive to imidodiphosphate. By contrast, fluoride is highly effective only against the mitochondrial pyrophosphatase. It is concluded that the mitochondrial pyrophosphatase and the H(+)-pyrophosphatases of chromatophores and vacuolar membranes belong to two different classes of enzyme.

PMID: 8392953 [PubMed - indexed for MEDLINE]

151: Plant Physiol. 1993 Jun;102(2):691-2.

cDNA for catalase from etiolated mung bean (Vigna radiata) hypocotyls.

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PMID: 8108520 [PubMed - indexed for MEDLINE]

152: Proc Natl Acad Sci U S A. 1993 Apr 1;90(7):2890-4.

Purification, characterization, and cDNA cloning of an NADPH-cytochrome P450 reductase from mung bean.

Shet MS, Sathasivan K, Arlotto MA, Mehdy MC, Estabrook RW.

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We report here the isolation and deduced amino acid sequence of the flavoprotein, NADPH-cytochrome P450 (cytochrome c) reductase (EC 1.6.2.4), associated with the microsomal fraction of etiolated mung bean seedlings (Vigna radiata var. Berken). An 1150-fold purification of the plant reductase was achieved, and SDS/PAGE showed a predominant protein band with an apparent molecular mass of approximately 82 kDa. The purified plant NADPH-P450 reductase gave a positive reaction as a glycoprotein, exhibited a typical flavoprotein visible absorbance spectrum, and contained almost equimolar quantities of FAD and FMN per mole of enzyme. Specific antibodies revealed the presence of unique epitopes distinguishing the plant and mammalian flavoproteins as demonstrated by Western blot analyses and inhibition studies. Peptide fragments from the purified plant NADPH-P450 reductase were sequenced, and degenerate primers were used in PCR amplification reactions. Overlapping cDNA clones were sequenced, and the deduced amino acid sequence of the mung bean NADPH-P450 reductase was compared with equivalent enzymes from mammalian species. Although common flavin and NADPH-binding sites are recognizable, there is only approximately 38% amino acid sequence identity. Surprisingly, the purified mung bean NADPH-P450 reductase can substitute for purified rat NADPH-P450 reductase in the reconstitution of the mammalian P450-catalyzed 17 alpha-hydroxylation of pregnenolone or progesterone.

PMID: 8464904 [PubMed - indexed for MEDLINE]

153: Biochim Biophys Acta. 1993 Feb 13;1156(2):123-7.

Pyrophosphate: fructose-6-phosphate 1-phosphotransferase and biosynthetic capacity during differentiation of hypocotyls of Vigna seedlings.

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The relationship between the activity of pyrophosphate:fructose-6-phosphate 1-phosphotransferase (PFP) and the capacity for biosynthesis of macromolecules was examined in segments from different parts of hypocotyls of etiolated seedlings of Vigna mungo and V. radiata. The relative ratio of the maximum

activity of PFP to that of ATP-dependent phosphofructokinase (PFK) (PFP/PFK ratio) was high in young tissues and decreased with differentiation and ageing of the tissues. The highest level of fructose-2,6-bisphosphate was observed in the youngest part of hypocotyls of V. mungo. The level was markedly decreased with ageing of tissues. The levels of PPi and ATP were also higher in younger parts than in older parts of the hypocotyls, but the ratio of the level of PPi to that of ATP was almost constant in all parts of the hypocotyl. A good correlation was found between the PFP/PFK ratio and the biosynthetic capacity, as estimated from the rate of incorporation of [U-14C]sucrose into ethanol-insoluble macromolecules.

PMID: 8381302 [PubMed - indexed for MEDLINE]

154: Genetics. 1992 Nov;132(3):841-6.

Evidence for orthologous seed weight genes in cowpea and mung bean based on RFLP mapping.

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A well saturated genomic map is a necessity for a breeding program based on marker assisted selection. To this end, we are developing genomic maps for cowpea (Vigna unguiculata 2N = 22) and mung bean (Vigna radiata 2N = 22) based on restriction fragment length polymorphism (RFLP) markers. Using these maps, we have located major quantitative trait loci (QTLs) for seed weight in both species. Two unlinked genomic regions in cowpea contained QTLs accounting for 52.7% of the variation for seed weight. In mung bean there were four unlinked genomic regions accounting for 49.7% of the variation for seed weight. In both cowpea and mung bean the genomic region with the greatest effect on seed weight spanned the same RFLP markers in the same linkage order. This suggests that the QTLs in this genomic region have remained conserved through evolution. This inference is supported by the observation that a significant interaction (i.e., epistasis) was detected between the QTL(s) in the conserved region and an unlinked RFLP marker locus in both species.

PMID: 1361476 [PubMed - indexed for MEDLINE]

155: J Biol Chem. 1992 Oct 25;267(30):21850-5.

Reconstitution of transport function of vacuolar H(+)-translocating inorganic pyrophosphatase.

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A procedure for reconstitution of the transport function of the vacuolar H(+)-translocating inorganic pyrophosphatase (H(+)-PPase; EC 3.6.1.1) prepared from etiolated hypocotyls of Vigna radiata (mung bean) is described. The method entails sequential extraction of isolated vacuolar membrane (tonoplast) vesicles

with deoxycholate and CHAPS (3-[(3-cholamidopropyl)-dimethylammonio]-1-propanesulfonate), combination of CHAPS-solubilized protein with phospholipid-cholesterol mixtures, dialysis, and glycerol density gradient centrifugation. The final proteoliposome preparation is 9-fold enriched for PPase activity and active in pyrophosphate (PPi)-energized electrogenic H(+)-translocation. Since both PPi hydrolysis and PPi-dependent H(+)-translocation by the proteoliposomes are indistinguishable from the corresponding activities of native tonoplast vesicles, the functional integrity of the H(+)-PPase appears to be conserved during solubilization and reconstitution. The high transport capacity and amenability of the reconstituted enzyme to both radiometric membrane filtration and fluorimetric H(+)-translocation assays, on the other hand, demonstrate its applicability to a broad range of transport studies. SDS-polyacrylamide gel electrophoresis of the proteoliposomes reveals selective enrichment of the M(r) 66,000, substrate-binding subunit of the H(+)-PPase and two additional polypeptides of M(r) 21,000 and 20,000. Although the M(r) 21,000 and 20,000 polypeptides have not been described previously, all attempts to reconstitute H(+)-PPase lacking these components were unsuccessful. It is therefore tentatively proposed that the M(r) 21,000 and 20,000 polypeptides, as well as the M(r) 66,000 subunit, are required for the productive reconstitution of PPi-dependent H(+)-translocation.

PMID: 1328246 [PubMed - indexed for MEDLINE]

156: Biochem J. 1992 Aug 1;285 (Pt 3):737-43.

Inhibition of tonoplast ATPase from etiolated mung bean seedlings by fluorescein 5'-isothiocyanate.

Tzeng CM, Hsu LH, Pan RL.

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Fluorescein 5'-isothiocyanate (FITC) was used to modify the lysine residue in the active site of tonoplast H(+)-ATPase from etiolated mung-bean (Vigna radiata L.) seedlings. FITC caused marked inactivation of the enzyme activities of both membrane-bound and soluble ATPase and its associated H+ translocation. The SDS/PAGE pattern revealed that the FITC-binding site was in the large (A) subunit of ATPase. Inhibition could be substantially prevented by its physiological substrate ATP, pyrophosphate and nucleotides in the decreasing order: ATP greater than pyrophosphate greater than ADP greater than AMP greater than GTP greater than CTP greater than UTP. The mode of inhibition by FITC was competitive with respect to ATP. Loss of ATPase activity followed pseudo-first-order kinetics with a Ki of 0.33 mM, a minimum inactivation half-time of 110 s, and a first-order rate constant of 0.244 s-1. A double-logarithmic plot of apparent rate constant versus FITC concentration gave a slope of 0.913, indicating that inactivation results from reaction of at least one lysine residue at the catalytic site of the large subunit. Labelling studies indicated that the incorporation of approx. 1 mol of FITC/mol of ATPase is sufficient to inhibit ATPase completely. The enhancement and blue shift of emission maxima of FITC after modification of ATPase indicated that the labelled lysine residue was located in a relatively hydrophobic domain.

PMID: 1386733 [PubMed - indexed for MEDLINE]

157: Plant Foods Hum Nutr. 1992 Jul;42(3):239-46.

Protein quality of developed home made weaning foods.

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Home made weaning foods developed from locally available foods like bajra, barley, green gram (Vigna radiata L.), amaranth grain (Amaranthus sp.) and jaggery using household technologies like roasting and malting had a PER ranging from 2.04 to 2.13, BV 79.56 to 80.68, NPU 66.75 to 67.86, NPR 2.13 to 2.76 and PRE 34.18 to 44.18. The values were comparable to that of cerelac--a commercial weaning food.

PMID: 1502125 [PubMed - indexed for MEDLINE]

158: Plant Mol Biol. 1992 Feb;18(4):793-7.

Identification and characterization of three putative genes for 1-aminocyclopropane-1-carboxylate synthase from etiolated mung bean hypocotyl segments.

Botella JR, Schlagnhaufer CD, Arteca RN, Phillips AT.

Department of Horticulture, Pennsylvania State University, University Park 16802.

The polymerase chain reaction (PCR) was used to produce 3 putative clones for ACC synthase from etiolated mung bean (Vigna radiata Rwilcz cv. Berken) hypocotyls. This was accomplished by utilizing genomic DNA from mung bean and degenerate primers made from information derived from highly conserved regions of ACC synthase from different plant tissues. The total length of pMAC-1, pMAC-2 and pMAC-3 are 308, 321, and 326 bp, respectively, all of which code for 68 amino acids. The introns for pMAC-1, pMAC-2 and pMAC-3 are 92, 105, and 110 bp, respectively. The degrees of homology at the DNA level for each of these clones is ca. 80% in their coding region and ca. 50% in their respective introns. This is the first report providing evidence that there are at least 3 genes for ACC synthase in etiolated mung bean.

PMID: 1558953 [PubMed - indexed for MEDLINE]

159: Biochem Biophys Res Commun. 1991 Dec 31;181(3):962-7.

Immunological cross-reactivity between proton-pumping inorganic pyrophosphatases of widely phylogenic separated species.

Nore BF, Sakai-Nore Y, Maeshima M, Baltscheffsky M, Nyren P.

Department of Biochemistry, University of Stockholm, Sweden.

Immunological cross-reactivity among three types of inorganic pyrophosphatases, that is, the proton pumping inorganic pyrophosphate synthase (H(+)-PPi synthase) and the soluble inorganic pyrophosphatase, both from Rhodospirillum rubrum, and the vacuolar membrane inorganic pyrophosphatase (H(+)-PPase) from mung bean (Vigna radiata), were examined by means of immunoblot analyses. Antibodies raised against the mung bean H(+)-PPase cross-reacted with the H(+)-PPi synthase from R. rubrum but not with the soluble PPase from R. rubrum. N,N'-dicyclohexylcarbodiimide (DCCD), which inhibits both synthesis and hydrolysis of PPi catalysed by purified and chromatophore H(+)-PPi synthase, binds to the enzyme as shown by fluorography of [14C]DCCD labelling. These results suggest that the R. rubrum H(+)-PPase share close structural similarities with the vacuolar H(+)-PPase from Mung bean.

PMID: 1662506 [PubMed - indexed for MEDLINE]

160: Indian J Biochem Biophys. 1991 Oct-Dec;28(5-6):449-55.

Transformation and regeneration of mung bean (Vigna radiata).

Pal M, Ghosh U, Chandra M, Pal A, Biswas BB.

Department of Biochemistry, Bose Institute, Calcutta.

The procedure relied on a protocol in which shoot organogenesis was induced on cotyledons of mung bean genotypes selected for susceptibility to agrobacterium seems to work reproducibly if not efficiently. Approximately 4-5% of the shoots produced on the kanamycin selected cotyledons are transgenic based on assays on kanamycin resistance and GUS activity. This demonstrated that transformation and regeneration in mung bean are possible. However, raising the transformed plants in field condition is yet to be perfected.

PMID: 1812081 [PubMed - indexed for MEDLINE]

161: Indian J Biochem Biophys. 1991 Aug;28(4):252-6.

Isolation and characterization of a naturally occurring inhibitor from mung bean (Vigna radiata) seedlings for serine hydroxymethyltransferase.

Vijaya M, Sukanya N, Savithri HS, Rao NA.

Department of Biochemistry, Indian Institute of Science, Bangalore.

A naturally occurring inhibitor of serine hydroxymethyltransferase (EC 2.1.2.1) in mung bean seedlings extracts was purified by ammonium sulphate precipitation, phenyl-Sepharose chromatography followed by heating to release the inhibitor bound to the protein. The inhibitor had an absorption maximum at 200 nm, was not precipitated by trichloroacetic acid, was dialysable and resistant to inactivation by heating at 98 degrees C for 4 hr, protease and ribonuclease digestion; but was acid labile. The chromatographically pure preparation

inhibited both mung bean and sheep liver SHMT. Qualitative and quantitative analyses indicated that it contained a carbohydrate moiety, an O-amino and vicinal diol groups. Paper electrophoresis at pH 4.3 suggested that the inhibitor was positively charged.

PMID: 1752627 [PubMed - indexed for MEDLINE]

162: J Biol Chem. 1991 Jul 25;266(21):13742-5.

beta-Furfuryl-beta-glucoside. An endogenous activator of higher plant UDP-glucose: (1----3)-beta-glucan synthase.

Ohana P, Delmer DP, Steffens JC, Matthews DE, Mayer R, Benziman M.

Department of Biological Chemistry, Hebrew University, Jerusalem, Israel.

We have recently established the existence of endogenous activators of higher plant UDP-glucose: (1----3)-beta-glucan synthase (Callaghan, T., Ross, P., Weinberger-Ohana, P., and Benziman, M. (1988) Plant Physiol. 86, 1099-1103). Here we report the purification and chemical analysis of the most abundant and specific compound, termed Activator I, isolated from Vigna radiata. This compound was extensively purified by a multistep procedure which yielded 0.1 mg of purified activator/g of fresh tissue. Enzyme digestion, neutral sugar analysis, GC/MS of permethylated derivatives, and NMR analysis of native Activator I indicated that the compound contains a single beta-linked glucosyl residue. High resolution FAB-MS indicated an elemental composition of C11H16O7 (Mr = 260), with a calculated Mr of 98 for the aglycone. 13C, DEPT, and COSY NMR spectra showed that the aglycone molecule is an oxygen heterocycle of 5 carbons, consistent with a structure of beta-furfuryl alcohol. Comparison of IR and GC/EI-MS spectra of authentic beta-furfuryl alcohol with native aglycone confirmed the conclusion that Activator I is beta-furfuryl-beta-glucoside. Chemically synthesized beta-furfuryl-beta-glucoside has identical chemical properties and biological activity when compared with the purified endogenous activator (Ka = 50 microM).

PMID: 1830307 [PubMed - indexed for MEDLINE]

163: Biochem Int. 1991 May;24(2):291-7.

Stimulation of nucleic acid and protein synthesis in mungbean (Vigna radiata L.) seeds by uv irradiation.

Padmaker, Singh A, Awasthi CP.

Department of Biophysics, N.D. University of Agriculture and Technology, Faizabad, India.

The effect of a range of ultraviolet (uv) irradiation doses on nucleic acid and protein synthesis has been studied during seed germination and seedling growth in mungbean (Vigna radiata L). The treatment of seeds with low dose irradiation were stimulative for the synthesis of these molecules.

PMID: 1718283 [PubMed - indexed for MEDLINE]

164: Plant Foods Hum Nutr. 1991 Apr;41(2):107-16.

Development, acceptability and nutritional value of weaning mixtures.

Gupta C, Sehgal S.

Department of Foods and Nutrition, Haryana Agricultural University, Hisar, India.

Low cost weaning mixtures were prepared by mixing (i) malted pearl millet (Penicitum typhidium L), roasted amaranth (Amaranthus sp.); roasted green gram (Vigna radiata); jaggery and (ii) malted barley (Dehusked barley); roasted amaranth grain; roasted green gram; jaggery in proportion 60:20:40:45 wt/wt and were nutritionally evaluated. Both the blends had a nutrient composition within the range prescribed by the Indian Standard Institute (ISI) for processed weaning foods. The processing of grains resulted in lower levels of phytic acid, polyphenols and saponins and higher in vitro protein digestibility than those of the raw grains used for preparing mixtures. Both the mixtures were acceptable to trained panelists and children.

PMID: 1852724 [PubMed - indexed for MEDLINE]

165: Gene. 1991 Mar 1;99(1):63-8.

Subrepeats of rDNA intergenic spacer present as prominent independent satellite DNA in Vigna radiata but not in Vigna angularis.

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Lehrstuhl fur Allgemeine Genetik, Biologisches Institut, Universitat Tubingen, F.R.G.

Subrepeats located in the rDNA intergenic spacer are also present as independently occurring, tandemly arranged satellite DNA clusters in the genome of Vigna radiata (mung bean). These 174-bp satellite repeats are identified as non-rDNA repeats by the presence of an AluI site. In the closely related Vigna angularis (adzuki bean), 174-bp repeats characterized by an AluI site occur in the rDNA with high sequence homology to the V. radiata rDNA subrepeats. A part of the 174-bp element that shows high similarity to a Xenopus terminator box (T2/T3) is slightly modified in V. angularis. However, a characteristic stem-loop structure can be formed, as in the case of V. radiata. Two highly conserved 12-bp regions occur within the 174-bp rDNA repeats of the two plants investigated. One of these 12-bp stretches exhibits some sequence identity to an element repeated twice in the 325-bp repeats in the intergenic spacer region of Vicia faba (broad bean).

PMID: 2022324 [PubMed - indexed for MEDLINE]

166: Folia Microbiol (Praha). 1991;36(2):164-8.

Production of Tsr factor by Rhizobium meliloti.

Jain V, Garg N, Nainawatee HS.

Department of Chemistry and Biochemistry, Haryana Agricultural University, Hisar, India.

The root exudates of alfalfa (Medicago sativa) and mungbean (Vigna radiata) induced the Tsr (thick and short roots) factor production in Rhizobium meliloti. The factor caused a 30-40% reduction of root length in alfalfa seedlings. Pea root exudate had no Tsr induction activity. The flavonoid naringenin could replace the roots in inducing Tsr production. Naringenin-induced Tsr factor caused 70% shortening of main roots. The Tsr inducing property of naringenin was specific since quercetin and syringaldehyde had no such effect.

PMID: 1823653 [PubMed - indexed for MEDLINE]

167: Proc Natl Acad Sci U S A. 1990 Apr;87(7):2680-4.

Proposed regulatory pathway encoded by the nodV and nodW genes, determinants of host specificity in Bradyrhizobium japonicum.

Gottfert M, Grob P, Hennecke H.

Mikrobiologisches Institut, Eidgenossische Technische Hochschule, Zurich, Switzerland.

Bradyrhizobium japonicum is the root nodule endosymbiont of soybean (Glycine max), mung bean (Vigna radiata), cowpea (Vigna unguiculata), and Siratro (Macroptilium atropurpureum). We report the characteristics of a nodulation-gene region of B. japonicum that contributes only marginally to the bacterium's ability to nodulate soybean but is essential for the nodulation of the three alternative hosts. This DNA region consists of two open reading frames designated nodV and nodW. The predicted amino acid sequences of the NodV and NodW proteins suggest that they are members of the family of two-component regulatory systems, which supports the hypothesis that NodV responds to an environmental stimulus and, after signal transduction, NodW may be required to positively regulate the transcription of one or several unknown genes involved in the nodulation process. It seems likely that all host plants produce the necessary signal, whereas host specificity may be brought about by the product(s) of the gene(s) activated by NodW.

PMID: 2320582 [PubMed - indexed for MEDLINE]

168: J Invertebr Pathol. 1990 Mar;55(2):147-51.

Influence of media composition on the production of delta-endotoxin by Bacillus thuringiensis var. thuringiensis.

Mummigatti SG, Raghunathan AN.

Infestation Control and Protectants Discipline, Central Food Technological Research Institute, Mysore, India.

Powders of edible leguminous seeds, greengram (Vigna radiata) or soybean (Glycine max), were used as the major protein source with different combinations of soluble starch and/or cane sugar molasses as the major carbohydrate source for the production of delta-endotoxin by Bacillus thuringiensis var. thuringiensis serotype 1 in submerged fermentation. The primary product (lyophilized with 6 g of lactose) yield was 8.7 to 9.1 g/liter from media with dehusked greengram powder and 9.7 to 10.3 g/liter from media with defatted soybean powder in basal medium. The toxicity of primary products was assayed against fifth-instar Bombyx mori larvae by force-feeding. The primary product from the medium containing defatted soybean powder and soluble starch gave a maximum viable spore count of 91.3 x 10(6)/mg, with a corresponding potency of 35,800 IU/mg, whereas the medium containing dehusked greengram powder and cane sugar molasses gave a spore count of 49.5 x 10(6)/mg, with a highest potency of 38,300 IU/mg. Either legume protein in combination with cane sugar molasses yielded primary product 2.1 to 2.4 times more potent than the U.S. standard. The combined carbohydrate source consisting of soluble starch and cane sugar molasses, irrespective of the source of protein in the media, drastically reduced delta-endotoxin production, thereby reducing the potency of the primary products compared to the U.S. standard.

PMID: 2156939 [PubMed - indexed for MEDLINE]

169: Biochem Int. 1990;21(4):667-75.

Purification and characterization of high salt-soluble vicilin from mung bean (Vigna radiata).

Bhattacharyya SP, Biswas BB.

Department of Biochemistry, Bose Institute, Calcutta, India.

We report a method for the purification of vicilin from mung bean (Vigna radiata) mainly on the basis of solubility of mung bean vicilin even in high salt. Mung bean vicilin remains in solution even after 90% relative saturation of ammonium sulphate. The resulting supernatant after dialysis was subjected to gel filtration (Sephadex G-150) to remove other contaminant polypeptides, and finally the protein was purified by DEAE cellulose chromatography. This purified fraction exhibited 3 bands on SDS-PAGE compared with vicilin from other legumes which exhibite more than 3 bands generally. The results raise the possibility that the presence of the two small polypeptides in vicilin preparations is the breakdown product of the major larger one of mol.wt. 52 K and that vicilin may be a tetramer of four subunits of Mr 52000. That the high salt-soluble protein containing 52 K subunit is vicilin has been determined by several criteria.

PMID: 2241993 [PubMed - indexed for MEDLINE]

170: Plant Foods Hum Nutr. 1989 Sep;39(3):257-66.

Antinutrients in amphidiploids (black gram x Mung bean): varietal differences and effect of domestic processing and cooking.

Kataria A, Chauhan BM, Punia D.

Department of Foods and Nutrition, Haryana Agricultural University, Hisar, India.

Phytic acid, saponin and polyphenol contents in grains of various varieties of black gram (Vigna mungo) Mung bean (Vigna radiata L.) amphidiploids ranged from 697 to 750, 2746 to 2972 and 702 to 783 mg/100 g, respectively. Domestic processing and cooking methods including soaking, ordinary and pressure cooking of soaked and unsoaked seeds, and sprouting significantly lowered phytic acid, saponin and polyphenol contents of the amphidiploid seeds. Soaking for 18 h removed 31 to 37% of the phytic acid; the extent of removal was higher with long periods of soaking. Saponins and polyphenols were relatively less affected. Loss of the antinutrients was greater when soaked instead of unsoaked seeds were cooked. Pressure cooking had a greater effect than ordinary cooking. Antinutrient concentrations declined following sprouting; the longer the period of germination the greater was the reduction.

PMID: 2608635 [PubMed - indexed for MEDLINE]

171: Mol Gen Genet. 1989 Aug;218(2):302-7.

Termination of transcription of ribosomal RNA genes of mung bean occurs within a 175 bp repetitive element of the spacer region.

Schiebel K, von Waldburg G, Gerstner J, Hemleben V.

Universitat Tubingen, Institut fur Biologie, Federal Republic of Germany.

In mung bean (Vigna radiata, formerly Phaseolus aureus) one length heterogeneity in the intergenic spacer (IGS) of the ribosomal DNA (rDNA) is due to a variable number of 175-bp subrepeats. This spacer region downstream of the 25S rRNA coding region was characterized by sequencing the 2.4 kb EcoRI/HindIII fragment of a 10.5 kb mung bean rDNA repeat. Within the 175-bp repetitive elements a sequence was detected showing strong similarity to the T2/T3-box (GACTTGC) found in Xenopus rDNA and involved in termination and enhancing transcription. In mung bean this sequence partly forms the stem of a possible stem-loop structure at the 3'end of each subrepeat. Nuclease mapping of transcription termination sites (TTS) results in two signals, 65 bp and 315 bp downstream of the 3'end of the 25S rRNA coding region. The longer transcript terminates 20 bp downstream of the stem-loop structure at the end of the first 175-bp subrepeat. A spacer model is proposed which allows "readthrough enhancement". No cross-hybridization was observed between the 180-bp subrepeats in pea (Pisum sativum) rDNA and the mung bean 175-bp subrepeat.

PMID: 2779517 [PubMed - indexed for MEDLINE]

172: Mol Gen Genet. 1989 Feb;215(3):407-15.

Mutational analysis of the Bradyrhizobium japonicum common nod genes and further nod box-linked genomic DNA regions.

Gottfert M, Lamb JW, Gasser R, Semenza J, Hennecke H.

Mikrobiologisches Institut, Eidgenossische Technische Hochschule, Zurich, Switzerland.

By insertional and deletional marker replacement mutagenesis the common nod region of Bradyrhizobium japonicum was examined for the presence of additional, essential nodulation genes. An open reading frame located in the 800 bp large intergenic region between nodD1 and nodA did not appear to be essential for nodulation of soybean. Furthermore, a strain with a deletion of the nodI- and nodJ-like genes downstream of nodC had a Nod+ phenotype. A mutant with a 1.7 kb deletion immediately downstream of nodD1 considerably delayed the onset of nodulation. This region carried a second copy of nodD (nodD2). A nodD1-nodD2 double mutant had a similar phenotype to the nodD2 mutant. Using a 22-mer oligonucleotide probe partially identical to the nod box sequence, a total of six hybridizing regions were identified in B. japonicum genomic DNA and isolated from a cosmid library. Sequencing of the hybridizing regions revealed that at least three of them represented true nod box sequences whereas the others showed considerable deviations from the consensus sequence. One of the three nod box sequences was the one known to be associated with nodA, whereas the other two were located 60 to 70 kb away from nif cluster I. A deletion of one of these two sequences plus adjacent DNA material (mutant delta 308) led to a reduced nodulation on Vigna radiata but not on soybean. Thus, this region is probably involved in the determination of host specificity.

PMID: 2710106 [PubMed - indexed for MEDLINE]

173: Gene. 1988 Dec 15;73(1):57-66.

Isolation, characterization and sequencing of a novel repetitive DNA from the mung bean Vigna radiata.

Roy P, Bhattacharyya N, Biswas BB.

Department of Biochemistry, Bose Institute, Calcutta, India.

A family of highly reiterated, small (approx. 300 bp) sequences has been identified in DNA of the mung bean Vigna radiata. The members are extensively interspersed throughout the chromosomes with some clustering. They also occur extrachromosomally. There is no tissue-specificity to the repeat family but it is highly species-specific. The repetitive DNA hybridizes to total RNA as well as to polyadenylated RNA isolated from germinated mung beans. It has analogy with the human AluI family in the mode of isolation, size, genomic distribution, copy number and transcribability though they do not share any sequence homology. A repetitive DNA clone was selected from a shotgun genomic library of mung bean DNA in pBR322. The average copy number of the cloned repeat is estimated to be 8 x 10(4) per haploid genome, and thus constitutes approx. 5% of the total mung bean genome. The genomic organization and transcription of the cloned repeat is reported. Sequencing of the cloned repetitive DNA reveals the presence of the number of direct and inverted repeats and some short palindromic sequences.

PMID: 3243436 [PubMed - indexed for MEDLINE]

174: Genome. 1988 Oct;30(5):723-33.

Complex organization of the length heterogeneous 5' external spacer of mung bean (Vigna radiata) ribosomal DNA.

Gerstner J, Schiebel K, von Waldburg G, Hemleben V.

Institut fur Biologie II, Universitat Tubingen, Federal Republic of Germany.

Restriction enzyme analysis and cloning of the 18S, 5.8S, and 25S ribosomal RNA genes (rDNA) of the mung bean (Vigna radiata = Phaseolus aureus) reveal length heterogeneity in the repeating units (10-11 kbp) localized within two different regions in the ribosomal spacer. The 1.5-2.0 kbp region flanking the 3' end of the 25S rRNA contains various numbers (8-10) of tandemly arranged 180 bp subrepeats. After DNA sequencing a complex organized length heterogeneous 5' external spacer built up of different numbers of 340 bp subrepeats, each flanked by 52 bp direct repeats, is detected and described for the first time for plant ribosomal DNA repeating units. Sequences occurring in front of and within this repeated structure (elements II-IV) can be combined with the motifs P1, P2, and P3. These exhibit a strong similarity to transcription initiation sites specific for RNA polymerase I described for other plant and animal rDNA investigated to date. Transcription products complementary to the complex repeated structures are detected by hybridization to total nuclear RNA. The 9 bp element V located in fron of the first 340 bp region appears in duplicated form as a direct repeat with sequence similarity to SV40 (or RNA polymerase II) enhancer sequences.

PMID: 3203889 [PubMed - indexed for MEDLINE]

175: J Chromatogr. 1988 Jan 29;436(1):59-66.

Electrophoretic study of alpha-D-galactosidases from seeds of Glycine soja and Vigna radiata possessing erythroagglutinating activity.

Secova E, Ticha M, Kocourek J, Dey PM.

Department of Biochemistry, Charles University, Albertov, Czechoslovakia.

Polyacrylamide gel electrophoresis in an acidic buffer system was used to study the electrophoretic behaviour of two forms of alpha-D-galactosidase from seeds of soy bean (Glycine soja) and mung bean (Vigna radiata). The interaction of the enzymes with saccharides was monitored by affinity electrophoresis; for the preparation of affinity gels, water-soluble O-glycosyl polyacrylamide copolymers and polysaccharides were used. alpha-D-Galactosidases from both sources interact with immobilized alpha-D-galactosyl residues. On the basis of the results of affinity electrophoresis performed in the presence of various free sugars, dissociation constants for the complexes between alpha-D-galactosidase and free sugars were calculated.

PMID: 2836454 [PubMed - indexed for MEDLINE]

176: Gene. 1988;62(1):165-9.

Sequence organization and putative regulatory elements in the 5S rRNA genes of two higher plants (Vigna radiata and Matthiola incana).

Hemleben V, Werts D.

Department of Genetics, University of Tubingen, F.R.G.

The tandemly arranged and clustered highly repeated 5S rRNA genes are investigated for two plants belonging to different higher plant families: Matthiola incana (Brassicaceae, Dilleniidae, Rosidae; 3600 5S rRNA genes/n) shows a homogeneous repeat size of 510 bp, whereas Vigna radiata (mung bean, former Phaseolus aureus, Fabaceae, Rosidae; approx. 4300 5S rRNA genes) has a repeat size of 215 bp. The mung-bean 5S rRNA coding region starts 5' with AGG and ends with CCT; Matthiola starts with GGG and ends with CCC. Striking is the strict occurrence of a 'TATA' box starting at nucleotide-28 similar to Neurospora crassa 5S rRNA genes. The 3' end is followed by CTTTT or GTTT stretches present in different numbers in the non-transcribed spacer suggesting a function in termination.

PMID: 3371663 [PubMed - indexed for MEDLINE]

177: Plant Foods Hum Nutr. 1988;38(1):75-81.

Proximate composition and antinutritional factors in rice bean (Vigna umbellata).

Malhotra S, Malik D, Dhindsa KS.

Department of Chemistry and Biochemistry, Haryana Agricultural University, Hisar, India.

Thirteen promising strains of Rice bean (Vigna umbellata) were analysed for their proximate compositions and antinutritional factors. Protein content in these varieties ranged from 17.50 to 23.10 per cent, ash from 3.06 to 4.48 per cent, ether extract from 2.4 to 3.9 per cent and crude fibre from 1.70 to 4.25 per cent. Trypsin inhibitor activity ranged from 112.63 to 163.98 units/g and polyphenols ranged from 0.58 to 1.19 per cent. Phytohemagglutinating activity was present in all the strains, except one, RB-32. Oligosaccharides, viz., raffinose, stachyose and verbascose, ranged from 0.32 to 0.91, 0.95 to 1.98 and 1.40 to 2.58 per cent, respectively. Attempts have been made to compare the results with a standard variety each of cowpea (Vigna unguiculata), moong (Vigna radiata) and mash (Vigna mungo).

PMID: 3231596 [PubMed - indexed for MEDLINE]

178: Plant Foods Hum Nutr. 1988;38(1):51-9.

Contents and digestibility of carbohydrates of mung beans (Vigna radiata L.) as

affected by domestic processing and cooking.

Kataria A, Chauhan BM.

Department of Foods and Nutrition, Haryana Agricultural University, Hisar, India.

Effects of common processing and cooking methods on sugar and starch contents and starch digestibility (in vitro) of mung bean (Vigna radiata L.) were investigated. Soaking reduced the level of total soluble sugars, reducing sugars, non-reducing sugars and starch and improved starch digestibility, significantly. Cooking (both ordinary and pressure cooking) increased the concentrations of the sugars and digestibility of starch of soaked as well a unsoaked seeds. Starch contents, however, were decreased. Germination decreased starch thereby raising the level of the soluble sugars. Starch digestibility was increased appreciably.

PMID: 3231594 [PubMed - indexed for MEDLINE]

179: Crit Rev Biotechnol. 1988;8(3):197-216.

The proteolysis of trypsin inhibitors in legume seeds.

Wilson KA.

Department of Biological Sciences, State University of New York, Binghamton.

The seeds of plants often contain large amounts of proteins, which are subjected to extensive proteolytic processing during seed development and subsequent germination. One class of legume seed proteins, the Bowman-Birk-type trypsin inhibitors, has proved especially useful as a subject in studying these events. Sequence studies of the trypsin inhibitors from a number of legume species suggest that many of the inhibitors undergo a limited shortening at the amino terminus during seed development. However, during germination, the inhibitors appear to function as storage proteins. As such, they are subjected to extensive proteolysis, ultimately leading to their destruction. This degradative process has been studied extensively in the mung bean (Vigna radiata [L.] Wilczek). Proteolysis of the mung bean trypsin inhibitor involves, at least initially, an ordered sequence of limited proteolytic cleavages. The two proteases involved in the initial phases of this degradation have been identified and partially characterized.

Publication Types:
Review
Review, Tutorial

PMID: 3063391 [PubMed - indexed for MEDLINE]

180: Biochem Biophys Res Commun. 1986 Jun 13;137(2):788-94.

Construction of a genomic library from germinating seedlings of mung bean (Vigna radiata). Evidence for the presence of a class of repetitive sequences and

selection of beta-tubulin specific recombinant phage.

Sen S, Roy P.

We have constructed a genomic library of Vigna radiata from its total DNA in the phage charon 4A. Recombinant phages were used to hybridize with a family of mung bean repetitive DNA. At least 30% of recombinant phages showed positive hybridization with a specific type of sequences. These phages were also used to screen for beta-tubulin-specific recombinants and a recombinant phage with beta-tubulin gene was identified.

PMID: 3729938 [PubMed - indexed for MEDLINE]

181: Crit Rev Food Sci Nutr. 1986;25(1):73-105.

Chemistry and technology of green gram (Vigna radiata [L.] Wilczek).

Adsule RN, Kadam SS, Salunkhe DK.

Green gram or mung bean (Vigna radiata [L.] Wilczek) is an important food legume grown under tropical and subtropical conditions. It is an excellent source of protein and is almost free from flatulence-causing factors. Because of this, green gram seeds are preferred for feeding babies and those convalescing. The seeds contain a higher proportion of lysine than any other legume seeds. The seeds are processed and consumed as cooked whole beans or splits (dhals), sprouts, immature seeds, and flour and are used in various recipes. The proposed work will incorporate available information on nutritional composition, processing, and utilization of green gram. The results reported in the literature on the above aspects of green gram will be analyzed critically, and future research needs will be defined to improve the utilization of green gram as human food.

Publication Types:
Review

PMID: 3539530 [PubMed - indexed for MEDLINE]

182: Steroids. 1985 Aug-Sep;46(2-3):727-33.

Prostaglandin inhibitors and the development of mung bean seedlings.

Gawienowski AM, Csernus KM, Simon JE, Craker LE.

The effect of cortisol and prostaglandin inhibitors on the growth and development of germinating mung bean, Vigna radiata L. Wilzek, cv. Jumbo was investigated. Cortisol, indomethacin, and a mixture of cortisol with aspirin, or benoxaprofen significantly increased radicle length and the number of lateral roots as compared with non-treated controls. A mixture of cortisol and indomethacin significantly increased growth of hypocotyls.

PMID: 3939270 [PubMed - indexed for MEDLINE]

183: Arch Biochem Biophys. 1984 Dec;235(2):319-25.

Stereoselectivity of 1-aminocyclopropanecarboxylate malonyltransferase toward stereoisomers of 1-amino-2-ethylcyclopropanecarboxylic acid.

Liu Y, Su LY, Yang SF.

A malonyltransferase isolated from mungbean (Vigna radiata L.) hypocotyls catalyzed the malonylation of both 1-aminocyclopropane-1-carboxylic acid (ACC) and D-amino acids. The possibility that ACC was recognized by the enzyme as a D-amino acid was investigated by examining the efficiencies of the four stereoisomers of 1-amino-2-ethylcyclopropane-1-carboxylic acid (AEC) serving as substrates of malonyltransferase and as inhibitors of ACC malonyltransferase. Although all four isomers were malonylated by the enzyme and competitively inhibited the malonylation of ACC to N-malonyl-ACC, (1R,2S)-AEC and (1R,2R)-AEC, both of which have an R-configuration as a D-amino acid, had lower Km and Ki values (0.1 to 0.2 mM) than their enantiomers, (1S,2R)-AEC (Km and Ki values were about 1 mM) and (1S,2S)-AEC (Km and Ki values were higher than 10 mM), which have an S-configuration as an L-amino acid. Similarly, (R)-isovaline (2-amino-2-methylbutanoic acid), which has an R-configuration as a D-amino acid, inhibited more effectively the enzymatic conversion of ACC to malonyl-ACC than did (S)-isovaline, which has an S-configuration as an L-amino acid. In mungbean hypocotyls (1R,2S)-AEC and (1R,2R)-AEC were also more efficiently converted into malonyl conjugates and more efficiently inhibited the conversion of radioactive ACC into malonyl-ACC than their enantiomers, although the differences in efficiency among stereoisomers were smaller in hypocotyls than in enzymatic reactions. These results suggest that ACC is recognized by the enzyme as a D-amino acid.

PMID: 6517594 [PubMed - indexed for MEDLINE]

184: Anal Biochem. 1984 Aug 15;141(1):168-78.

An enzymatic assay for calmodulins based on plant NAD kinase activity.

Harmon AC, Jarrett HW, Cormier MJ.

NAD kinase with increased sensitivity to calmodulin was purified from pea seedlings (Pisum sativum L., Willet Wonder). Assays for calmodulin based on the activities of NAD kinase, bovine brain cyclic nucleotide phosphodiesterase, and human erythrocyte Ca2+-ATPase were compared for their sensitivities to calmodulin and for their abilities to discriminate between calmodulins from different sources. The activities of the three enzymes were determined in the presence of various concentrations of calmodulins from human erythrocyte, bovine brain, sea pansy (Renilla reniformis), mung bean seed (Vigna radiata L. Wilczek), mushroom (Agaricus bisporus), and Tetrahymena pyriformis. The concentrations of calmodulin required for 50% activation of the NAD kinase (K0.5) ranged from 0.520 ng/ml for Tetrahymena to 2.20 ng/ml for bovine brain. The K0.5's ranged from 19.6 ng/ml for bovine brain calmodulin to 73.5 ng/ml for mushroom calmodulin for phosphodiesterase activation. The K0.5's for the activation of Ca2+-ATPase ranged from 36.3 ng/ml for erythrocyte calmodulin to 61.7 ng/ml for mushroom calmodulin. NAD kinase was not stimulated by

phosphatidylcholine, phosphatidylserine, cardiolipin, or palmitoleic acid in the absence or presence of Ca2+. Palmitic acid had a slightly stimulatory effect in the presence of Ca2+ (10% of maximum), but no effect in the absence of Ca2+. Palmitoleic acid inhibited the calmodulin-stimulated activity by 50%. Both the NAD kinase assay and radioimmunoassay were able to detect calmodulin in extracts containing low concentrations of calmodulin. Estimates of calmodulin contents of crude homogenates determined by the NAD kinase assay were consistent with amounts obtained by various purification procedures.

PMID: 6093619 [PubMed - indexed for MEDLINE]

185: Indian J Biochem Biophys. 1983 Dec;20(6):362-8.

Alterations in properties of mung bean (Vigna radiata) serine hydroxymethyltransferase consequent on conformation changes induced by folic acid & L-serine.

Rao DN, Appaji Rao N.

PMID: 6425201 [PubMed - indexed for MEDLINE]

186: Eur J Cell Biol. 1983 Jan;29(2):139-44.

Inhibition of lignin formation by L-alpha-aminooxy-beta-phenylpropionic acid, an inhibitor of phenylalanine ammonia-lyase.

Amrhein N, Frank G, Lemm G, Luhmann HB.

Mungbean (Vigna radiata (L.) Wilczek) seedlings grown for 9 days on filter paper soaked with 0.3 to 1 mM L-alpha-aminooxy-beta-phenylpropionic acid (AOPP), a potent inhibitor of L-phenylalanine ammonia-lyase, had a greatly reduced anthocyanin content, and the cell walls of the xylem vessels did not stain with the phloroglucinol/HCl or safranine/astrablue reagents indicating the absence of lignin-like material. Furthermore, vanillin was detectable in nitro-benzene-oxidized lignin preparations only from control seedlings, but not from AOPP-treated seedlings. Scanning electron microscopy of hypocotyl cross sections revealed collapsed xylem vessels in seedlings grown in the presence of AOPP indicating that lignin is required for resistance against the tensile forces in the conducting cells of the xylem. AOPP enhanced the growth of cultured cells of Lonicera prolifera Rehd. while it inhibited the production of extracellular material that gave a positive reaction with phloroglucinol/HCl.

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187: Acta Biochim Pol. 1983;30(2):139-48.

Proteinases involved in the degradation of trypsin inhibitor in germinating mung beans.

Wilson KA, Tan-Wilson AL.

The mung bean (Vigna radiata (L.) Wilczek) trypsin inhibitor (MBTI) is rapidly modified by limited proteolysis during the early stages of seedling growth. Using an electrophoretic assay that separates the unmodified inhibitor (MBTI-F) and the first two modified species (MBTI-E and -C), a pH optimum of approximately 4 was found for the modification reaction. The inhibitor modifying activity is initially low in ungerminated seeds, with the reaction F leads to E being the primary reaction catalyzed. Activity catalyzing the production of MBTI-C appears on the first day of germination. This activity (F leads to E leads to C) increases up to 6 days after inhibition, at which time the cotyledons begin to abscise. The activity converting MBTI-F and -E to MBTI-C was strongly inhibited by phenylmethylsulfonyl fluoride (3.3 mM) but only weakly by iodoacetate (9 mM) and not at all by pepstatin A (9 microM), leupeptin (18 microM), or EDTA (5 mM). These results suggest the involvement of proteinases other than the major endopeptidase of the germinating seed, vicilin peptidohydrolase. This conclusion is further supported by gel filtration of the extracts of cotyledons on Sephacryl S-200. At least three proteinases are present in germinated cotyledons capable of modifying MBTI-F to MBTI-C and/or -E. All are distinguishable from vicilin peptidohydrolase on the basis of their molecular weight and inhibition by low molecular weight organic reagents.

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188: Eur J Cell Biol. 1981 Jun;24(2):226-35.

Uptake and apparent digestion of cytoplasmic organelles by protein bodies (protein storage vacuoles) in mung bean cotyledons.

Herman EM, Baumgartner B, Chrispeels MJ.

The large protein bodies of the storage parenchyma cells of mung bean (Vigna radiata) cotyledons contain vesicles measuring 0.2 to 2.0 mum in diameter. The vesicles contain ribosomes, ribosomes, membranous elements which may be derived from the endoplasmic reticulum and occasionally Golgi bodies and mitochondria. The vesicles can be seen by transmission electron microscopy in thin sections of plastic embedded specimens and in replicas of freeze-fractured preparations. Serial sections show that the vesicles are completely separated from the protein body membrane and are not invaginations of that membrane. Vesicles with cytoplasmic structures are seen most frequently in 2 to 4 day old seedlings. The vesicles may be formed when undulations of the protein body membrane are so deep as to permit the pinching-off of a portion of the cytoplasm, resulting in its subsequent isolation from the cytoplasm within the protein body. The digestion of the storage protein in the protein body is accompanied by the disappearance of the ribosomes and the membranous elements in the vesicles. We interpret this disappearance of the cytoplasmic structures in the vesicles as being due to their digestion by the protein body hydrolases (ribonuclease, proteinase and lipolytic enzymes). The uptake of cytoplasmic structures by the protein bodies continues after the reverse proteins have been digested. Cytochemical staining shows that the protein bodies and especially the vesicles are rich in acid phosphatase, a known marker of lytic activity in cells. The evidence presented here indicates that the protein bodies are the intracellular sites at which the digestion of cytoplasmic structure occurs. Protein bodies should therefore be considered not only as compartments for the hydrolysis of the stored protein, but also as autophagic organelles involved in the degradation of cytoplasmic

macromolecules. The term protein bodies is well established, but the term protein storage vacuoles may describe these organelles more precisely.

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189: J Sci Food Agric. 1981 Jun;32(6):601-7.

Imitation milks from Cicer arietinum (L.), Vigna unguiculata (L.) Walpers and Vigna radiata (L.) Wilczek and other legumes.

Caygill JC, Jones JA, Ferber CE.

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190: J Cell Sci. 1981 Apr;48:333-43.

Use of purified endopolygalacturonase for a topochemical study of elongating cell walls at the ultrastructural level.

Roland JC, Vian B.

Endopolygalacturonase, a fungal enzyme purified by Albersheim and his group which specifically degrades the galacturonosyl linkages of pectic polysaccharides, was used at the ultrastructural level on intact tissues from differentiated organs. Specimens were taken from the elongating zone of mung bean (Vigna radiata) hypocotyls. Incubation with the enzyme solution was performed en bloc, prior to embedding and to ultrastructural cytochemistry (PATAg test for polysaccharides), or by flotation of ultrathin frozen sections. From the morphological viewpoint, the images obtained are sharp and reproducible. They support the plywood model for the organization of expanding walls. The ordering of walls appears to be built up very early, at the very beginning of elongation, in the upper part of the hypocotyl (hook). The specificity of the enzyme allows a topochemical study of the wall. Data indicate an uneven distribution of polysaccharides of pectic type across a single wall and among the different cells. Outer and inner wall areas are highly resistant to extraction by endopolygalacturonase. In the middle lamella the insolubility of amorphous components probably indicates a local concentration of highly methyl-esterified carboxyl groups not susceptible to endopolygalacturonase attack; conversely, adjacent parts of the middle lamella are regularly extracted, indicating a high concentration of galacturonans. An intense extraction occurs in the bow-shaped zone, revealing the occurrence of a massive embedding of unesterified pectic polysaccharides around the fibrillar subunits responsible for the twisted patterns. In the inner and recent part of the wall, the ordering of fibrillar subunits seems progressive and possibly related to the peptic embedding. This incrusting material could play a role in the morphogenesis of the ordered wall by means of specific assembly and interconnections of wall subunits.

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191: J Mol Evol. 1981;17(2):78-84.

Evolutionary sequence divergence within repeated DNA families of higher plant genomes. I. Analysis of reassociation kinetics.

Preisler RS, Thompson WF.

The higher proportion of repeated DNA sequences in the garden pea (Pisum sativum) than in the mung bean (Vigna radiata), as well as other differences between these legume genomes, are consistent with a higher rate of sequence amplification in the former. This hypothesis leads to a prediction that repeated sequence families in Pisum are mostly heterogeneous, as defined by Bendich and Anderson (1977), while Vigna families are homogeneous. An assay developed by these authors to distinguish between the two types of families, by comparison of reassociation rates at different temperatures, was utilized. The results for Vigna defied the predictions of the assay for either homogeneous or heterogeneous model. Evaluation of the kinetic data in light of the great diversity of repeated family copy numbers in both genomes enabled an interpretation of the results as consistent with heterogeneous families in Pisum and homogeneous families in Vigna. These tentative conclusions were supported by the results of a thermal denaturation (melting) assay described in the accompanying paper.

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192: J Mol Evol. 1981;17(2):85-93.

Evolutionary sequence divergence within repeated DNA families of higher plant genomes. II. Analysis of thermal denaturation.

Preisler RS, Thompson WF.

An assay based on derivative analysis of thermal denaturation (melting) behavior of reassociated DNA was developed in an attempt to characterize the sequence relationships in repeated DNA families according to the homogeneous or heterogeneous models of Bendich and Anderson (1977). The validity of the technique was confirmed by the use of deaminated Escherichia coli DNA models for repetitive families. The melting data for DNA reassociated at two different temperatures provided strong evidence that Pisum sativum repeated families are mostly heterogeneous, while homogeneous families predominate in Vigna radiata. These findings, together with other differences between the two genomes, suggest that the rate of sequence amplification has been higher in the evolutionary history of Pisum DNA. A general trend seems to exist for high amplification rates in large, highly repetitive plant genomes such as Pisum and lower rates in smaller plant genomes such as Vigna, as well as in the generally smaller, less repetitive genomes of most animal species.

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193: J Inorg Biochem. 1980 Jul;12(4):343-51.

Reduction of DL-selenocystine and isolation of L-seleoncysteine.

Burnell JN, Karle JA, Shrift A.

Cystine, selenocytsine, and several analogs were reduced by dithiothreitol (DTT), beta-mercaptoethanol (ME) and sodium borohydride (NaBH4). DTT was the most effective; DTT to cystine ratios from 10 to 80 were equally effective. With selenocysteine, however, absorption was considerably reduced at all ratios. Selenocysteine was identified as the reduction product by reaction with Gaitonde's reagent, comparison of absorption spectra, paper chromatograhy, utilization by cysteinyl-tRNA synthetase fro Paracoccus denitrificans and Vigna radiata, changes in solubility after DTT treatment, and comparison of infrared spectra. During the ATP-PPi exchange assay, DTT and ME convert cysteine and selenocysteine derivatives to cysteine and selenocysteine which serve as substrates for cysteinyl-tRNA synthetase.

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194: J Cell Biol. 1978 Oct;79(1):10-9.

Localization of vicilin peptidohydrolase in the cotyledons of mung bean seedlings by immunofluorescence microscopy.

Baumgartner B, Tokuyasu KT, Chrispeels MJ.

Vicilin peptidohydrolase, the protease that hydrolyzes the reserve proteins in the cotyledons of mung bean (Vigna radiata) seedlings, has been localized intracellularly by immunofluorescence microscopy using monospecific antibodies against the enzyme and rhodamine-coupled goat-anti-rabbit immunoglobulin G's. The enzyme can first be visualized after 3 days of seedling growth and is associated with small foci within the cytoplasm of the storage parenchyma cells farthest from the vascular bundles. On the 4th day of growth, the protease is also present in the numerous large protein bodies within these cells. Vicilin peptidohydrolase is known to be synthesized de novo starting on the 3rd day of growth. Our observations are therefore consistent with the interpretation that the enzyme is synthesized in the cytoplasm and subsequently transported to the protein bodies.

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