301. Luteolin absorption in Rhizobium meliloti wild-type and mutant strains

By Hubac, C.; Ferran, J.; Guerrier, D.; Tremolieres, A.; Kondorosi, A.
From Journal of General Microbiology (1993), 139(7), 1571-8. Language: English, Database: CAPLUS, DOI:10.1099/00221287-139-7-1571

Luteolin is a flavonoid produced by plants which is required for induction of nod genes in Rhizobium meliloti. R. meliloti absorbed luteolin at higher rate than all other bacteria tested, including R. leguminosarum. The flavonoids naringenin and quercetin, which do not induce the expression of nodulation genes of R. meliloti, were absorbed at a lower rate by this species, suggesting a certain degree of species specificity of flavonoid absorption. Luteolin accumulated preferentially in the outer membrane, but a small amt. was always found in the inner membrane. Luteolin strongly inhibited NADH oxidase, an enzyme of the respiratory chain, raising the possibility that the site of luteolin absorption in the outer membrane allows the protection of the respiratory chain located in the inner membrane from an excess of flavonoids. The incorporation of luteolin was affected in some exo or nod mutants of R. meliloti. The exoB mutant, which does not produce exopolysaccharides, accumulated lower amts. of luteolin in the outer membrane than the exo$^+$ parent. Among the nod mutants affected in nodulation genes, those not expressing any of the three nodD genes accumulated luteolin at a significantly lower level in both the outer and the inner membrane. A strain overexpressing the nod genes, particularly the nodD genes, absorbed luteolin at a higher level in both membranes. These results indicate that absorption of luteolin by R. meliloti involves several gene products, including the NodD protein.

~9 Citings

302. Plant defence and delayed infection of alfalfa pseudonodules induced by an exopolysaccharide (EPS I)-deficient Rhizobium meliloti mutant

By Niehaus, K.; Kapp, D.; Puehler, A.
From Planta (1993), 190(3), 415-25. Language: English, Database: CAPLUS, DOI:10.1007/BF00196971

Mutants of the symbiotic soil bacterium R. meliloti that fail to synthesize the acidic exopolysaccharide EPS I were unable to induce infected root nodules on Medicago sativa (alfalfa). These strains, however, elicited pseudonodules that contained no infection threads or bacteroids. The cortical cell walls of the pseudonodules were abnormally thick and incrusted with an autofluorescent material. Parts of these cell walls and wall appositions contained callose. Biochem. anal. of nodules induced by the EPS I-deficient R. meliloti mutant revealed an increase of phenolic compds. bound to the nodule cell walls when compared with the wild-type strain. These microscopic and biochem. data indicated that a general plant defense response against the EPS I-deficient mutant of R. meliloti was induced in alfalfa pseudonodules. Following prolonged incubation with the EPS I-deficient R. meliloti mutant, the defense system of the alfalfa plant could be overcome by the rhizobium mutant. In the case of the delayed infections, the mutants colonized lobes of the pseudonodules, but the infection threads in these nodules had an abnormal morphol. They were greatly enlarged and did not contain the typical gum-like matrix inside. The bacteria were tightly packed. EPS I or a related compd. may act as a suppressor of the alfalfa plant defense system, enabling R. meliloti to infect the plant.

~125 Citings

303. The use of a Rhizobium meliloti cosmid genebank for molecular cloning of the leucine biosynthesis gene involved in genetic control of nitrogen fixing symbiosis with alfalfa

By Aronstam, A. A.; Umarov, B. R.; Yerko, V. N.; Andronov, E. E.; Simarov, B. V.
From Genetika (Moscow) (1993), 29(2), 235-45. Language: Russian, Database: CAPLUS

Using random Tn5 mutagenesis the leucine auxotrophic mutant of Rhizobium meliloti CXM1 was obtained which formed nodules incapable of nitrogen fixation on alfalfa. A cosmid gene bank of R. meliloti on vector pLAFR5 was constructed. Using this bank and the helper plasmid pRK2013 the leucine requiring mutant T46 was complemented and prototrophic exconjugants which formed normal nitrogen fixing nodules were selected. However, anal. of rhizobia isolated from the nodules revealed that the loss of the recombinant cosmid harboring the leu$^+$ gene could occur during bacterial proliferation inside root tissue and in the free living state. These data indicate that the leucine biosynthesis genes of R. meliloti are involved in symbiosis development.

~0 Citings

304. Cloning and characterization of multiple groEL chaperonin-encoding genes in Rhizobium meliloti

By Rusanganwa, Emmy; Gupta, Radhey S.
From Gene (1993), 126(1), 67-75. Language: English, Database: CAPLUS, DOI:10.1016/0378-1119(93)90591-P

Heat-shock treatment of R. meliloti cells causes major enhancement in the synthesis of several proteins with apparent mol. wts. in the range of 58-60 kDa. Using the polymerase chain reaction and degenerate oligodeoxyribonucleotide primers for conserved regions of the 60-kDa heat-shock protein (HSP60) or GroEL protein family, a 0.6-kb probe for the R. meliloti hsp60 gene was prepd. Southern blot anal. of R. meliloti DNA digested with different restriction enzymes and hybridized to R. meliloti hsp60 probes indicated the presence of between 4 and 5 hsp60 or groEL in this species. The complete nucleotide sequences of 3 groEL genes in R. meliloti were detd. The deduced amino acid (aa) sequences of these proteins show extensive similarity to each other (78-85% aa identity) and to other GroEL homologs. In the upstream regions of two of the groEL, but not the third, open reading frames corresponding to GroES proteins were also identified. Anal. of various prokaryotic GroEL sequences suggests that the multiple groEL or R. meliloti have evolved by means of gene duplication events within this or a related group of organisms. Some of the groEL in R. meliloti are located on the 2 megaplasmids present in these cells. The presence of multiple GroEL homologs in R. meliloti suggests a possible role of the GroEL or HSP60 chaperonins in the nodulation (symbiosis) and nitrogen fixation processes.

~38 Citings

305. Alfalfa (Medicago sativa L.) root exudates contain isoflavonoids in the presence of Rhizobium meliloti

By Dakora, Felix D.; Joseph, Cecillia M.; Phillips, Donal A.
From Plant Physiology (1993), 101(3), 819-24. Language: English, Database: CAPLUS

Root exudates of alfalfa (M. sativa) inoculated with symbiotic R. meliloti bacteria contained three isoflavonoids that were not found in exudates of uninoculated plants. Data from proton NMR, mass spectrometry, and UV-visible absorbance analyses indicated that root exudates of inoculated plants contained aglycon and glycoside forms of the phytoalexin medicarpin and a formononetin-7-O-(6''-O-malonylglycoside), a conjugated from of the medicarpin precursor formononetin. The medicarpin mols. did not induce nod gene transcription in R. meliloti, but the formononetin-7-O-(6''-o-malonylglycoside) induced nod genes regulated by both NodD1 and NodD2 proteins in R. meliloti. Hydrolysis of either the malonyl or the glycosyl linkage from the formononetin conjugate eliminated nod gene-inducing activity. The nod gene-inducing activity of crude root exudates was increased 200 and 65% upon inoculation with R. meliloti or R. leguminosarum bv phaseoli, resp. When root exudate from uninoculated alfalfa was incubated with R. meliloti, high performance liq. chromatog. analyses showed no evidence that bacterial metab. produced medicarpin. These results indicate that alfalfa responds to symbiotic R. meliloti by exuding a phytoalexin normally elicited by pathogens and that the microsymbiont can use a precursor of the phytoalexin as a signal for inducing symbiotic nod genes.

~57 Citings

306. Natural establishment and selenium accumulation of herbaceous plant species in soils with elevated concentrations of selenium and salinity under irrigation and tillage practices

By Wu, Lin; Enberg, Andrew; Tanji, Kenneth K.
From Ecotoxicology and Environmental Safety (1993), 25(2), 127-40. Language: English, Database: CAPLUS, DOI:10.1006/eesa.1993.1012

The effects of irrigation and tillage practices were studied on species richness, biomass, and Se accumulation of naturally established herbaceous plants in soils with elevated levels of Se and salinity at Kesterson Reservoir, Merced County, California. The irrigation-tillage practice combinations were (1) no irrigation, no tillage; (2) irrigation, no tillage; (3) no irrigation, tillage; and (4) irrigation, tillage. The fields were allowed to become colonized naturally by herbaceous plant species. For the Mediterranean climate in the study site, irrigation was conducted biweekly through the summer months, and tillage was done in 3-mo intervals. Biomass and Se accumulation of Atriplex patula, Bassia hyssopifolia, Melilotus indica, and Salsola kali were substantially affected by irrigation. The degree and direction of the effects were species dependent. The field plots which were tilled at 3-mo intervals remained bare throughout the expt. The total soil Se concns. in the top 15 cm soil horizon ranged 40-70 mg/kg dry wt. Soil Se concns. <25 cm soil depth were much lower and within a range of 2-4 mg/kg. Less that 1/10th of the total soil Se inventory in the top soil horizons was water extractable, and the distribution of the Se inventory did not change significantly over the period of 1990 and 1991 despite the irrigation and tillage practices, suggesting that a large portion of the Se inventory was not remobilized. The water-extractable soil Se concn. was significantly lower in soils with the greatest biomass prodn., suggesting an effective bioextn. of soil Se by the native herbaceous plants.

~15 Citings

307. Analyses of the roles of R. meliloti exopolysaccharides in nodulation

By Reuber, T. L.; Reed, J. W.; Glazebrook, J.; Urzainqui, A.; Walker, G. C.
From Current Plant Science and Biotechnology in Agriculture (1991), 10(Adv. Mol. Genet. Plant-Microbe Interact., Vol. 1), 182-8. Language: English, Database: CAPLUS

Genetic expts. have indicated that succinoglycan (EPS I), the acidic Calcofluor-binding exopolysaccharide of the N_2-fixing bacterium Rhizobium meliloti strain Rm1021, is required for nodule invasion and possibly for later events in nodule development on alfalfa and other hosts. Thirteen exo loci on the 2nd megaplasmid were identified that are required for, or affect, the synthesis of EPS I. Mutations in certain of these loci completely abolish the prodn. of EPS I and result in mutants that form empty Fix$^-$ nodules. Two loci, exoR and exoS, were identified that are involved in the regulation of EPS I synthesis in the free-living state. Certain exo mutations which completely abolish EPS I prodn. are lethal in an exoR95 or exoS96 background. Histochem. analyses of the expression of exo genes during nodulation using exo::TnphoA fusions have indicated that the exo genes are expressed most strongly in the invasion zone. In addn., R. meliloti has a latent capacity to synthesize a 2nd exopolysaccharide (EPS II) that can substitute for the role(s) of EPS I in nodulation of alfalfa but not of other hosts. Possible roles for exopolysaccharides in symbiosis are discussed. Evidence indicating that the R. meliloti exoD gene encodes a novel function needed for nodule invasion is summarized.

~2 Citings

308. Siderophore-mediated iron transport correlates with the presence of specific iron-regulated proteins in the outer membrane of Rhizobium meliloti

By Reigh, Geraldine; O'Connell, Michael
From Journal of Bacteriology (1993), 175(1), 94-102. Language: English, Database: CAPLUS

A universal chem. assay used to detect the prodn. of siderophores in a range of Rhizobium strains showed that prodn. is strain-specific. Fe nutrition bioassays carried out on R. meliloti strains to det. cross-utilization of their siderophores showed that R. meliloti 2011, 220-5, and 220-3 could each use the siderophores produced by the other 2 but not the siderophore produced by R. meliloti DM4 (and vice versa). Mutants of R. meliloti 2011 and 220-5 defective in siderophore prodn. were isolated by Tn5-mob mutagenesis. The Tn5-mob-contg. EcoRI fragment of mutant R. meliloti 220-5-1 was cloned into pUC19. By using this fragment as a probe, the presence of a homologous region was obsd. in R. meliloti 2011 and 220-3 but not in R. meliloti DM4. A complementing cosmid from a gene bank of R. meliloti 2011 was identified by using the same probe. Introduction of this cosmid into R. meliloti 102F34, a strain not producing a siderophore, resulted in the ability of this strain to produce a siderophore and also in the ability to utilize the siderophores produced by R. meliloti 2011, 220-5, and 220-3 but not the siderophore produced by R. meliloti DM4. A comparative anal. of the outer membrane proteins prepd. from Fe-deficient cultures of R. meliloti 102F34 and 102F34 harboring the cosmid revealed the presence, in the latter, of a low-Fe-induced outer membrane protein corresponding to a low-Fe-induced protein in R. meliloti 2011, 220-5, and 220-3. This protein is not present in R. meliloti DM4. The results suggest that R. meliloti 220-5, 2011, and 220-3 produce siderophores that are identical or sufficiently similar in structure to be transported by the membrane transport system of each strain, while also indicating that utilization of a particular siderophore is correlated with the presence of specific outer membrane proteins.

~20 Citings

309. The Rhizobium leguminosarum FnrN protein is functionally similar to Escherichia coli Fnr and promotes heterologous oxygen-dependent activation of transcription

By Schlueter, A.; Patschkowski, T.; Unden, G.; Preifer, U. B.
From Molecular Microbiology (1992), 6(22), 3395-404. Language: English, Database: CAPLUS, DOI:10.1111/j.1365-2958.1992.tb02207.x

An open reading frame from R. leguminosarum bv. viciae strain VF39, previously identified and found to be similar to E. coli fnr and Rhizobium meliloti fixK (orf240, thereafter called fnrN), was further analyzed. Anal. of the expression of an fnrN-lacZ transcriptional fusion revealed that fnrN is preferentially expressed under oxygen limitation. Using R. meliloti fixN-lacZ fusions it was shown that the fnrN gene product only mediates transcriptional activation under microaerobiosis, indicating that the FnrN protein responds, directly or indirectly, to oxygen. Plasmids which expressed fnrN under the control of an E. coli promoter were able to complement an E. coli fnr mutant with respect to anaerobic growth on nitrate but not fumarate, and to promote anaerobic but not aerobic activation of the Fnr-dependent E. coli genes narGHJI, nirB and fdnGHI coding for nitrate reductase, NADH-dependent nitrite reductase and formate dehydrogenase-N, resp. Fumarate and DMSO reductase activities were not induced by FnrN. The E. coli fnr gene substituted for fnrN in oxygen-regulated transcription of nirB- and fixN-lacZ fusions in R. leguminosarum. The results indicate that Fnr and FnrN are functionally very similar and share a common mode of oxygen-dependent transcriptional activation. From hybridization studies, it appeared that fnrN-like genes are present in a no. of different R. leguminosarum strains.

~0 Citings

310. Physiological characteristics of Rhizobium meliloti 1021 Tn5 mutants with altered rhizobactin activities

By Barton, Larry L.; Fekete, Frank A.; Vester, Craig R.; Gill, Paul R., Jr.; Neilands, J. B.
From Journal of Plant Nutrition (1992), 15(10), 2145-56. Language: English, Database: CAPLUS, DOI:10.1080/01904169209364464

R. meliloti 1021 and several Tn5-generated mutants were examd. for physiol. activities which would reflect the capacity of these strains for efficient iron metab. Rhizobactin prodn. in liq. culture, as measured by CAS reactivity, was greatest in R. meliloti 1021, with lesser amts. formed by strains PRR 63 and PRR 62. Examn. of the various strains of R. meliloti grown under different levels of iron revealed that all strains tested were constitutive for ferric reductase. Evaluation of Medicago saliva cultivated in peat pots and inoculated with R. meliloti revealed that greatest levels of growth was with R. meliloti 1021, the only strain in this study with an efficient rhizobactin system. Evaluation of dinitrogen fixed by nodulated plants grown in a hydroponic system indicated that the amt. of nitrogen fixed per bacteroid in the nodule was not const. but was correlated with the rhizobactin-producing capability of the R. meliloti strains. Levels of dinitrogen fixed per unit of viable bacteroids was greater with R. meliloti 1021 than with PRR 29 or PRR 30.

~4 Citings

311. Acid-tolerant species of Medicago produce root exudates at low pH which induce the expression of nodulation genes in Rhizobium meliloti

By Howieson, J. G.; Robson, A. D.; Abbott, L. K.
From Australian Journal of Plant Physiology (1992), 19(3), 287-96. Language: English, Database: CAPLUS, DOI:10.1071/PP9920287

An acid rhizosphere may interfere with the transcription of nodulation genes in Rhizobium spp. by modifying the prodn. of legume root exudates, or the rhizobial response to them. Certain annual species of Medicago (M. murex, M. polymorpha) can nodulate better in acid soils and solns. than other species (M. truncatula, M. littoralis). The mechanisms of this acid tolerance in nodulation are poorly understood. Root exudates collected at pH 5.8 and pH 6.0 from acid-tolerant species of annual medics induced the expression of nodulation genes in R. meliloti as indicated from a lacZ gene fusion, whereas exudates from acid-sensitive species grown at these pH values displayed decreased induction activity. For the acid-sensitive host, M. truncatula, increasing the Ca concn. from 0.5 to 5.0 mM at pH 5.8 increased the nod-gene induction activity of its exudates, but there was no effect at higher pH. There was no effect of Ca or pH on the nod-gene induction activity of exudates collected from M. murex. These results indicate a likely mechanism underlying differences in ability to nodulate under acid stress among annual species of Medicago.

~15 Citings

312. Synthesis of the ferredoxin-like protein FdxN from Rhizobium meliloti bacteroids as a fusion protein in Escherichia coli

By Riedel, Kai Uwe; Masepohl, Bernd; Klipp, Werner; Puehler, Alfred
From Canadian Journal of Microbiology (1992), 38(6), 534-40. Language: English, Database: CAPLUS, DOI:10.1139/m92-088

To analyze the overexpression of the Rhizobium meliloti fdxN gene in Escherichia coli, different translational and transcriptional fusions were constructed. The translational signals of R. meliloti fdxN were recognized in E. coli as demonstrated by the use of in-frame lac fusions. Translational fusions consisting of the lacZ or the lpp gene fused in frame to the 3' end of the entire fdxN gene were expressed at high levels in E. coli. In contrast, the wild-type R. meliloti FdxN protein without a C-terminal fusion could only be detected using the very sensitive T7 promoter-polymerase system and not in immunoblots with antibodies against an FdxN-LacZ hybrid protein. Evidently, translational fusions to the 3' end of fdxN had a stabilizing effect on the expression of the fdxN gene. A constitutively expressed transcriptional fdxN fusion, which did not mediate detectable amts. of FdxN protein either in E. coli or in free-living R. meliloti cells, complemented the Fix$^-$ phenotype of an R. meliloti fdxN::[Tc] mutant strain to wild-type levels. Therefore, either low amts. of the wild-type FdxN protein are sufficient for symbiotic nitrogen fixation or there are stabilizing factors, which are present only in R. meliloti bacteroids but not in free-living R. meliloti cells. Fusion proteins consisting of FdxN and LacZ or a partial Lpp protein restored the Fix$^-$ phenotype of an R. meliloti fdxN mutant to 3 and 11%, resp., indicating that a C-terminal fusion did not completely abolish the function of FdxN.

~0 Citings

313. Functional analysis of the cysteine motifs in the ferredoxin-like protein FdxN of Rhizobium meliloti involved in symbiotic nitrogen fixation

By Masepohl, Bernd; Kutsche, Michael; Riedel, Kai Uwe; Schmehl, Manfred; Klipp, Werner; Puehler, Alfred
From Molecular and General Genetics (1992), 233(1-2), 33-41. Language: English, Database: CAPLUS, DOI:10.1007/BF00587558

The R. meliloti fdxN gene, which is part of the nifA-nifB-fdxN operon, is absolutely required for symbiotic N_2 fixation. The deduced sequence of the FdxN protein is characterized by 2 cysteine motifs typical of bacterial-type ferredoxins. The Fix^- phenotype of an R. meliloti fdxN::[Tc] mutant could be rescued by the R. leguminosarum fdxN gene, whereas no complementation was obsd. with nif-assocd. genes encoding ferredoxins from Bradyrhizobium japonicum, Azotobacter vinelandii, Azotobacter chroococcum, and Rhodobacter capsulatus. In addn. to these heterologous genes, several R. meliloti fdxN mutant genes constructed by site-directed mutagenesis were analyzed. Not only a cysteine residue within the 2nd cysteine motif (position 42), which is known to coordinate the Fe-S cluster in homologous proteins, but also a cysteine located downstream of this motif (position 61), was found to be essential for the activity of the R. meliloti FdxN protein. Changing the amino acid residue proline in position 56 to methionine resulted in a FdxN mutant protein with decreased activity, whereas changes in positions 35 (Asp35Glu) and 45 (Gly45Glu) had no significant effect on the function of the FdxN mutant proteins. In contrast to bacterial-type ferredoxins, which contain 2 identical cysteine motifs of the form C-X_2-C-X_2-C-X_3-C, nif-assocd. ferredoxins, including R. meliloti FdxN, are characterized by 2 different cysteine motifs. Six addnl. amino acids sep. the 2nd (Cys_{42}) and the 3rd cysteines (Cys_{51}) in the C-terminal motif (C-X_2-C-X_8-C-X_3-C). By mol. modeling, it was predicted that these amino acid residues form a loop, which does not alter the relative positions of the neighboring cysteines. Deletion of this loop resulted in an R. meliloti FdxN mutant protein that exhibited almost 70% wild-type activity, indicating that the predicted loop does not affect Fe-S cluster binding and plays no crucial role in activity of the FdxN protein.

~12 Citings

314. Cloning and characterization of a Rhizobium meliloti homolog of the Escherichia coli cell division gene ftsZ

By Margolin, William; Corbo, Joseph C.; Long, Sharon R.
From Journal of Bacteriology (1991), 173(18), 5822-30. Language: English, Database: CAPLUS

The ftsZ gene is essential for initiation of cell division in E. coli and Bacillus subtilis. Studies of division arrest during differentiation of R. meliloti bacteroids were begun by isolating a R. mililoti ftsZ homolog, $ftsZ_{Rm}$. Degenerate primers directed towards a conserved region of ftsZ were used to amplify a segment of R. meliloti DNA by polymerase chain reaction, and the product of this reaction was then used to isolate pos. clones from a bacteriophage library. The DNA sequence of an open reading frame contg. the region of homol. indicated that the R. meliloti FtsZ protein ($FtsZ_{Rm}$) is 50% homologous to the known E. coli and B. subtilis FtsZ proteins, but at 590 amino acids (63 kDa), it is predicted to be nearly 50% larger. Strong expression of an approx. 70-kDa labeled protein in a coupled in vitro transcription-translation system supports this prediction. The addnl. 200 amino acids appear to fall in a single internal domain highly enriched for proline and glutamine residues. When R. meliloti ftsZ ($ftsZ_{Rm}$) expression was regulated on a high-copy-no. plasmid in E. coli with P_{lac} and $lacI^q$, cells were smaller than normal in the presence of low $FtsZ_{Rm}$ levels (with no isopropyl-β-D-thiogalactopyranoside [IPTG]) and filamentous when $FtsZ_{Rm}$ was overproduced (with IPTG). These results suggest that low levels of $FtsZ_{Rm}$ stimulate E. coli cell division, while high levels may be inhibitory.

~42 Citings

315. The biochemical function of the Rhizobium leguminosarum proteins involved in the production of host specific signal molecules

By Spaink, H. P.; Geiger, O.; Sheeley, D. M.; Van Brussel, A. A. N.; York, W. S.; Reinhold, V. N.; Lugtenberg, B. J. J.; Kennedy, E. P.
From Current Plant Science and Biotechnology in Agriculture (1991), 10(Adv. Mol. Genet. Plant-Microbe Interact., Vol. 1), 142-9. Language: English, Database: CAPLUS

In R. leguminosarum and NodF and NodE proteins play an important role in the detn. of host specificity of nodulation. The NodF protein contains a 4'-phosphopantetheine prosthetic group. This result suggests that NodF protein is involved in the synthesis of polyketide derivs. After labeling with ^{14}C-acetate, the compds. produced by this nodulation protein were isolated. The role of the other nodulation proteins were also investigated. In addn. to the regulatory NodD protein, the NodABC and NodFEL proteins appear to be sufficient to produce the five detected wild-type Nod metabolites. Phys. and chem. studies indicate that these R. leguminosarum compds. differ significantly from the reported R. meliloti signal compd. The biol. activity of several Nod metabolites was studied in three different bioassays on Vicia sativa plants showing a biol. functionality of the O-acetyl modification produced by NodL protein.

~1 Citing

316. Chemotaxis of Rhizobium meliloti towards nodulation gene-inducing compounds from alfalfa roots

By Dharmatilake, Amitha J.; Bauer, Wolfgang D.
From Applied and Environmental Microbiology (1992), 58(4), 1153-8. Language: English, Database: CAPLUS

Luteolin, a flavone in seed exudates of alfalfa, induces nodulation genes (nod) in R. meliloti and also serves as a biochem. specific chemoattractant for the bacterium. The present work shows that R. meliloti RCR2011 is capable of very similar chemotactic responses towards 4',7-dihydroxyflavone, 4',7-dihydroxyflavonone, and 4,4'-dihydroxy-2-methoxychalcone, the 3 principal nod gene inducers secreted by alfalfa roots. Chemotactic responses to the root-secreted nod inducers in capillary assays were usually 2-4-fold above background and, for the flavone and flavanone, occurred at concns. lower than those required for half-max. induction of the nodABC genes. Complementation expts. indicated that the lack of chemotactic responsiveness to luteolin seen in nodD1 and nodA mutants of R. meliloti was not due to mutations in the nod genes, as previously thought. Thus, while nod gene induction and flavanoid chemotaxis have the same biochem. specificity, these 2 functions appear to have independent receptors or transduction pathways. The wild-type strain suffered selective, spontaneous loss of chemotaxis towards flavanoids during lab. subculture.

~56 Citings

317. Transcription of the Azospirillum brasilense nifH gene is positively regulated by NifA and NtrA and is negatively controlled by the cellular nitrogen status

By Vande Broek, A.; Michiels, J.; De Faria, S. M.; Milcamps, A.; Vanderleyden, J.
From Molecular and General Genetics (1992), 232(2), 279-83. Language: English, Database: CAPLUS

The expression of a translational A. brasilense nifH-uidA fusion was studied in A. brasilense and in Rhizobium meliloti strains with mutations in nifA, ntrA and ntrC. Induction of the fusion was obsd. in the R. meliloti wild-type and NtrC$^-$ strains on incubation under microaerobic conditions but not in the NifA$^-$ and NtrA$^-$ strains, showing the abs. requirement of both σ^{54} and NifA for activation of the nifH promoter. Histochem. anal. of the root nodules elicited by R. meliloti wild-type showed expression of the fusion in the late symbiotic zone but not in the meristematic and the early symbiotic zones. No induction of the nifH-uidA fusion was obsd. in the R. meliloti wild-type or NifA$^-$ strains incubated aerobically in nitrogen-free medium, indicating that, in contrast to R. meliloti nifH, A. brasilense nifH cannot be activated directly by NtrC. Expression of the nifH gene in A. brasilense only occurs under nitrogen-limiting, microaerobic conditions, suggesting the presence of a nitrogen-dependent control system for nif expression.

~12 Citings

318. Genetic analysis of functional differences among distinct ferredoxins in Rhodobacter capsulatus

By Saeki, Kazuhiko; Suetsugu, Yumi; Tokuda, Kenichiro; Miyatake, Yoshie; Young, Debra A.; Marrs, Barry L.; Matsubara, Hiroshi
From Journal of Biological Chemistry (1991), 266(20), 12889-95. Language: English, Database: CAPLUS

R. capsulatus has been known to possess 2 ferredoxins (I and II) with distinct physicochem. and structural properties: ferredoxin I is a 2[4Fe-4S] type and the other is a [3Fe-4S][4Fe-4S] type. To analyze their possible functional differences, their genes (fdsN and fdxA) were cloned, sequenced, and subjected to interposon mutagenesis expts. The former gene was adjacent to a gene encoding a chloroplast-type [2Fe-2S] ferredoxin (fdxC). Mutants with inactivated fdxN and/or fdxC were obtained, and they showed virtually no growth under nitrogen-fixing conditions. Complementation expts. confirmed that both fdxN and fdxC were required for nitrogen fixation. On the other hand, is was not possible to disrupt fdxA under the screening conditions surveyed, including conditions that do not require nitrogenase activity for growth, suggesting that ferredoxin II could have an unknown essential role(s). These indicate functional differences among multiple ferredoxins in one bacterium other than in cyanobacterial heterocysts and indispensability of certain ferredoxins in nitrogen fixation other than Rhizobium meliloti FdxN.

~30 Citings

319. Species richness and selenium accumulation of plants in soils with elevated concentration of selenium and salinity

By Huang, Zhang Zhi; Wu, Lin
From Ecotoxicology and Environmental Safety (1991), 22(3), 251-66. Language: English, Database: CAPLUS, DOI:10.1016/0147-6513(91)90077-3

Field studies were conducted in bottom soils of ponds which had been used for evapn. of Se-rich agricultural drainage waters at Kesterson, California. Biomass distribution, species richness, and selenium accumulation of plants were examd. for two sites where 15 cm of surface soil was removed and replaced with fill dirt in the fall of 1989, and for two sites that had native soil cover. The Se concns. in the top 15 cm of fill dirt ranged from undetectable to 36 ng g^{-1}. For the native soil sites, Se levels ranged from 75 to 550 ng g^{-1}. Soil Se concn. below 15 cm ranged from 300 to 700 ng g^{-1} and were comparable between the fill dirt and the native soil sites. At least 20 different plant species were brought into the two fill dirt sites with the top soil. However, Avena fatua, Bassia hyssopifolia, Centaurea solstitialis, Erysimum officinale, Franseria acanthicarpa, and Melilotus indica contributed over 60% of the total biomass. Only 5 species were found in the native soil sites, and salt grass (Distichlis spicata) was the predominant species and accounted for over 80% of the total biomass. Between 1989 and 1990, two years after the surface soil replacement, the two fill dirt sites had a 70% redn. in species richness. Plant tissue selenium concns. were quite variable between plant species and between sites of sampling. They were highest in May when the growth was most active and lowest in Dec. At the fill dirt sites, the plant species with deep root systems accumulated greater amts. of selenium than the shallow-rooted species. The soil selenium concn. of the field soil had no neg. effect on pollen fertility, seed set, and seed germination for the plant species examd. However, seedling growth was impaired by the soil selenium concns. This suggests that a selection pressure of soil Se concn. may have been imposed on plant species such as M. indica in an early stage of its life cycle.

~9 Citings

320. Heavy metal effects on soil populations and heavy metal tolerance of Rhizobium meliloti, nodulation, and growth of alfalfa

By Angle, J. S.; Chaney, R. L.
From Water, Air, and Soil Pollution (1991), 57-58, 597-604. Language: English, Database: CAPLUS, DOI:10.1007/BF00282923

Effects of heavy metals on rhizobia and the symbiotic assocn. with leguminous hosts are unclear. To investigate this problem, the authors examd. R. meliloti (microsymbiont) and alfalfa (Medicago sativa) (macrosymbiont) collected from soils contaminated with varying concns. of heavy metals (varying distances from a Zn smelter operating 90 yr.). Soil populations of R. meliloti were not correlated with metal concns. in soil. The lowest rhizobial population was found in the soil with the highest extractable metal concns., but the highest populations were found in soil which was moderately contaminated. A greenhouse study in which alfalfa was grown in the same soils showed no significant trend for nodulation or nitrogenase activity of roots. Highest nodule no. and nitrogenase activity were obsd. in those soils which had the lowest population of R. meliloti. When the heavy metal min. inhibitory concn. (MIC) of individual isolates was examd., no correlation was found between the MIC and soil metal concn. [total, or water or 0.01M $Ca(NO_3)_2$ extractable]. These results indicate that even in highly contaminated soils, metal activity was not high enough to exert an antagonistic influence on the soil rhizobial population or the symbiotic assocn. between alfalfa and R. meliloti.

~11 Citings

321. Metal tolerance of Rhizobium meliloti isolated from heavy-metal contaminated soils

By El-Aziz, R.; Angle, J. S.; Chaney, R. L.
From Soil Biology & Biochemistry (1991), 23(8), 795-8. Language: English, Database: CAPLUS, DOI:10.1016/0038-0717(91)90151-9

Soil populations of rhizobia have been reported to respond to the presence of high concns. of heavy metals by the acquisition of tolerance to specific metals. To examine this possibility, alfalfa plants (Medicago sativa) were collected from soils contg. low to very high concns. of the metals, Cd and Zn. The source of the metals was a Zn smelter in operation for nearly 100 yr. Fifty isolates of Rhizobium meliloti were collected and purified from each soil. All isolates, regardless of their origin, were capable of growing on media contg. very high concns. of the heavy metals, Zn, Cu, Ni and Cd. For example, R. meliloti isolated from soil with extractable [10 mM $Ca(NO_3)_2$] Zn and Cd concns. of 0.025 and 0.003 μg g^{-1}, resp. There was no correlation between extractable soil metal concns. and the ability of the isolates to tolerate metal salts in their growth medium. The greatest no. of metal-tolerant rhizobia were isolated from soil contg. the lowest metal concn. These results indicate that the intrinsic level of metal tolerance of R. meliloti is much higher than metal activities in soil, even highly contaminated soils. This intrinsic level of metal tolerance probably explains the lack of metal response by rhizobia collected from these soils.

~21 Citings

322. Identification of the exo loci required for exopolysaccharide synthesis in Agrobacterium radiobacter NCIB 11883

By Aird, E. L. H.; Brightwell, G.; Jones, M. A.; Johnston, A. W. B.
From Journal of General Microbiology (1991), 137(10), 2287-97. Language: English, Database: CAPLUS, DOI:10.1099/00221287-137-10-2287

A genetic anal. of A. radiobacter NCIB 11883 was initiated with particular ref. to the (exo) genes required for exopolysaccharide synthesis. Following mutagenesis with nitrosoguanidine, several exo mutant strains were isolated and several of the mutations were cor. by DNA cloned in a newly constructed cosmid library. Anal. of various complementing cosmids by genetic and phys. criteria indicated that exo loci were quite widely dispersed in the bacterial genome. Certain exo mutations were cor. by different cosmids that shared no homologous DNA; possible explanations for this are presented. Using phoA fusions, it was shown that some exo genes were, or were closely linked to, genes that specified polypeptides assocd. with the bacterial cell surface. By introducing the cloned exo genes of Rhizobium meliloti it was found that only 1 of 30 exo mutants of A. radiobacter was cor. by a defined exo locus of the former species; further anal. indicated that this particular exo gene corresponded to exoB of R. meliloti. Finally, it was found that several A. radiobacter exo mutants were non-mucoid on media with dicarboxylic acids as sole C source but appeared to be wild-type when sugars were the source of C.

~2 Citings

323. Mutations that affect activity of the Rhizobium meliloti trpE(G) promoter in Rhizobium meliloti and Escherichia coli

By Bae, Young Min; Stauffer, George V.
From Journal of Bacteriology (1991), 173(18), 5831-6. Language: English, Database: CAPLUS

The cloned R. meliloti trpE(G) gene is not expressed in E. coli. Oligonucleotide-directed mutagenesis was used to introduce base substitution mutations in the promoter region of this gene. Three sep. mutations that increased homol. of the putative -10 region of this promoter with the E. coli -10 promoter consensus sequence by 1 bp converted this promoter to an active promoter in E. coli. A deletion extending to position -43 from the 5' side had a minor effect on transcription in R. meliloti. However, transcription was nearly eliminated when a deletion extended to position -33, indicating that the crucial domain of the R. meliloti trpE(G) promoter begins in the region downstream of position -43. The R. meliloti trpE(G) promoter has two regions that show homol. with the E. coli -35 and -10 promoter consensus sequences. Mutations in these putative -35 and -10 regions, but not in the spacer region, affected promoter strength in R. meliloti. By comparing four known R. meliloti promoter sequences, a highly conserved trimer near position -35 (5'-TTG-3') was identified, but no noticeably conserved sequence near position -10.

~2 Citings

324. Cajaflavanone and cajanone released from Cajanus cajan (L. Millsp.) roots induce nod genes of Bradyrhizobium sp

By Dahiya, Jagroop S.
From Plant and Soil (1991), 134(2), 297-304. Language: English, Database: CAPLUS, DOI:10.1007/BF00012049

A broad-host-range plasmid (pEA2-21) contg. a Bradyrhizobium sp (F-4) nod DABC-lacZ translational fusion was constructed and used to monitor nod gene expression in response to pigeonpea root exudate. Two nod-inducing compds. were isolated and identified. Spectral anal. using UV absorption, IR spectra, proton NMR, and mass spectrometry showed that the two inducers were 5,4'-dihydroxy-6-(3'''-methyl-2'''-butenyl)-2''', 2''-di-Me pyrano-[5'', 6'':7, 8]-flavanone (cajaflavanone) and 2,'4',5'-trihydroxy-5-isopentenyl-6,7-dimethylchromene isoflavanone (cajanone). When pEA2-21 was introduced into Rhizobium trifolii and R. meliloti cajanone and cajaflavanone did not induce nod gene indicating that specificity of induction appears to be influenced by the host-strain genome.

~3 Citings

325. Genetic analysis of the attenuator of the Rhizobium meliloti trpE(G) gene

By Bae, Young Min; Stauffer, George V.
From Journal of Bacteriology (1991), 173(11), 3382-8. Language: English, Database: CAPLUS

It was previously reported that transcription of the Rhizobium meliloti trpE(G) gene starts at the adenine residue of the AUG codon of the leader peptide coding sequence (trpL) suggesting that translation of the trpL sequence starts without the Shine-Dalgarno sequence. Mutations replacing the AUG codon of the trpL sequence with AAG or ACG were constructed. These mutations reduced the expression of a trpL'-'lacZ fusion gene to 0.1 and 0.2% of the wild-type level, resp., indicating that the AUG codon is the translation initiation codon for the trpL coding sequence. In addn., these mutations, as well as a mutation converting the eighth codon (UCG) of the trpL sequence to UGA, abolished regulation by attenuation when introduced upstream of the tandem tryptophan codons in a trpE'-'lacZ fusion. Mutations affecting the stability of the probable antiterminator and terminator secondary structures of trpL mRNA were also constructed. Studies using these mutations indicate that the attenuator of R. meliloti functions in a way analogous to that of the Escherichia coli trp attenuator.

~2 Citings

326. Rhizobium meliloti exopolysaccharides: genetic analyses and symbiotic importance

By Reuber, T. Lynne; Reed, Jason; Glazebrook, Jane; Glucksmann, M. Alexandra; Ahmann, Dianne; Marra, Andrea; Walker, Graham C.
From Biochemical Society Transactions (1991), 19(3), 636-41. Language: English, Database: CAPLUS

A review with 54 refs. Genetic expts. have indicated that succinoglycan (EPS I), the acidic Calcofluor-binding exopolysaccharide, of the N-fixing bacterium Rhizobium meliloti strain Rm1021 is required for nodule invasion and possibly for later events in nodule development on alfalfa and other hosts. Fourteen exo loci on the second megaplasmid have been identified that are required for, or affect, the synthesis of EPS 1. Mutations in certain of these loci completely abolish the prodn. of EPS I and result in mutants that form empty Fix$^-$ nodules. Two loci have been identified, exoR and exoS, that are involved in the regulation of EPS I synthesis in the free-living state. Certain exo mutations which completely abolish EPS I prodn. are lethal in an exoR95 or exoS96 background. Histochem. analyses of the expression of exo genes during nodulation using exo::TnphoA fusions have indicated that the exo genes are expressed most strongly in the invasion zone. In addn., R. meliloti has been discovered to have a latent capacity to synthesize a second exopolysaccharide (EPS II) that can substitute for the role(s) of EPS I in nodulation of alfalfa but not of other hosts. Possible roles for exopolysaccharides in symbiosis are discussed.

~3 Citings

327. ndvF, a novel locus located on megaplasmid pRmeSU47b (pEXO) of Rhizobium meliloti, is required for normal nodule development

By Charles, Trevor C.; Newcomb, William; Finan, Turlough M.
From Journal of Bacteriology (1991), 173(13), 3981-92. Language: English, Database: CAPLUS

R. meliloti strains carrying either of 2 overlapping deletions (Δ5408 and ΔF114) of the megaplasmid pRmeSU47b form nodules on alfalfa which fail to fix N_2 (Fix$^-$). Strains carrying these deletions also fail to fluoresce on media contg. calcofluor, indicating a defect in synthesis of the acidic exopolysaccharide (Exo$^-$) of R. meliloti. Cosmid clones (pTH21 and pTH22) were isolated which complement the Fix$^-$ but not the Exo$^-$ phenotype of the strains carrying the Δ5408 and ΔF114 deletions. In addn., cosmid clones which complement the Exo$^-$ phenotype fail to complement the Fix$^-$ phenotype of these deletions; thus, the Exo$^-$ phenotype is not related to the Fix$^-$ phenotype. A 5-kb region within a 7.3-kb BamHI restriction fragment was required for complementation of the Fix$^-$ phenotype of the Δ5408 and ΔF114 deletion strains. Tn5 insertions in the 5-kb region generated a Fix$^-$ phenotype when recombined into the wild-type genome. This locus was designated ndvF, for nodule development. TnphoA mutagenesis of this region generated active alk. phosphatase gene fusions, indicating that ndvF encodes extracytoplasmic protein(s). Induction of nodules by the ndvF mutants was delayed by 2-3 days compared with induction by the wild-type strain. Light microscopy of nodules elicited by strains carrying the large 150-kb ΔF114 deletion, a 12-kb deletion removing ndvF, or an individual ndvF::Tn5 insertion mutation demonstrated that many nodules contained few infected cortical cells, indicating that nodule development was blocked early in the infection process, before the release of bacteria from the infection threads.

~23 Citings

328. Glutamate catabolism in Rhizobium meliloti

By Fitzmaurice, Ann Marie; O'Gara, Fergal
From Archives of Microbiology (1991), 155(5), 422-7. Language: English, Database: CAPLUS, DOI:10.1007/BF00244956

The pathway by which glutamate is degraded as a carbon source has not previously been elucidated, but enzymic anal. of Rhizobium meliloti CMF1 indicated that both glutamate dehydrogenase (GDH) and gamma-aminobutyrate (GABA) bypass activities were present in free living cells. However, when similar studies were performed on R. meliloti CMF1 bacteroids, isolated from alfalfa nodules, only GABA bypass activities were detectable. Both GDH and GABA bypass activities were influenced by the carbon source provided, with max. activities being detected when glutamate was present as sole carbon and nitrogen source. Addn. of a second carbon source, such as succinate, to the growth medium did not influence GDH activity but substantially decreased levels of the first enzyme of the GABA bypass, glutamate decarboxylase (GDC). Cyclic adenosine 3'5'-monophosphate (cAMP) failed to increase GDC activities in R. meliloti CMF1 cells grown in the presence of an addnl. carbon source. It is proposed that the GABA bypass is a major mechanism of glutamate carbon degrdn. in R. meliloti CMF1, a system whose enzymic activities are influenced by the nature of the carbon source present in the growth environment.

~6 Citings

329. Selenium in wetlands and waterfowl foods at Kesterson Reservoir, California, 1984

By Schuler, Carol A.; Anthony, Robert G.; Ohlendorf, Harry M.
From Archives of Environmental Contamination and Toxicology (1990), 19(6), 845-53. Language: English, Database: CAPLUS, DOI:10.1007/BF01055049

Kesterson Reservoir received subsurface agricultural drainwater contg. high levels of salts and Se from farmland in the San Joaquin Valley of California. The accumulation of Se in wetlands and waterfowl foods at Kesterson was investigated during May, August, and Dec. of 1984. High concns. of Se were found in water, sediments, terrestrial and aquatic vegetation, and aquatic insects. Mean Se concns. in aquatic plants and insects were 1.5-170 μg/g dry wt. and were ~11 - 290 times those found at a nearby ref. site. Concns. in some waterfowl food plants and insects at Kesterson were ≤64 times those reported to be a health hazard to birds. Se concns. were more seasonally variable in aquatic plants than in aquatic insects. Few differences in Se accumulation were found among ponds. Deposition of Se in plant parts was not uniform; rhizomes contained higher concns. than seeds and leaves were intermediate. Most biota bioaccumulated max. Se concns. that were 1000 - ~5000 times the concn. in the water.

~25 Citings

330. A biovar-specific signal of Rhizobium leguminosarum bv. viciae induces increased nodulation gene-inducing activity in root exudate of Vicia sativa subsp. nigra

By Van Brussel, Anton A. N.; Recourt, Kees; Pees, Elly; Spaink, Herman P.; Tak, Teun; Wijffelman, Carel A.; Kijne, Jan W.; Lugtenberg, Ben J. J.
From Journal of Bacteriology (1990), 172(9), 5394-401. Language: English, Database: CAPLUS

Flavonoids in root exudate of leguminous plants activate the transcription of Rhizobium genes involved in the formation of root nodules (nod genes). Inoculation with the homologous symbiont R. leguminosarum bv. viciae results in an increased nod gene-inducing activity (Ini) in root exudate of V. sativa subsp. nigra, whereas inoculation with heterologous Rhizobium strains results in exudates with nod gene-inducing activity comparable to that of uninfected plants. Ini can be demonstrated by using either of the isogenic indicator strains contg. an inducible nod promoter fused to the Escherichia coli lacZ reported gene and the regulatory nodD gene of R. leguminosarum bv. vicia, R. leguminosarum bv. trifolii, or R. meliloti. The presence of genes nodDABCEL of R. leguminosarum bv. viciae appeared to be essential for induction of Ini. Mutation of the genes nodI and nodJ causes a delay of Ini, whereas gene nodF appears to be required for both the timely appearance and the max. level of Ini activity. The nodE gene is responsible for the biovar specificity of induction of Ini by Rhizobium spp. Ini is caused by a sol. heat-stable factor of rhizobial origin. This Rhizobium-produced Ini factor has an apparent mol. wt. between 1000 and 10,000 and does not originate from flavonoid precursors.

~28 Citings

331. Functional and evolutionary relatedness of genes for exopolysaccharide synthesis in Rhizobium meliloti and Rhizobium sp. strain NGR234

By Zhan, Hangjun; Gray, James X.; Levery, Steven B.; Rolfe, Barry G.; Leigh, John A.
From Journal of Bacteriology (1990), 172(9), 5245-53. Language: English, Database: CAPLUS

R. meliloti SU47 and Rhizobium sp. strain NGR234 produce distinct exopolysaccharides that have some similarities in structure. R. meliloti has a narrow host range, whereas Rhizobium strain NGR234 has a very broad host range. In cross-species complementation and hybridization expts., it was found that several of the genes required for the prodn. of the two polysaccharides were functionally interchangeable and similar in evolutionary origin. NGR234 exoY corresponded to R. meliloti exoB and exoF, resp. NGR234 exoD was found to be an operon that included genes equiv. to exoM, exoA, and exoL in R. meliloti. Complementation of R. meliloti exoP, -N, and -G by NGR234 R'3222 indicated that addnl. equiv. genes remain to be found on the R-prime. It was not possible to complement NGR234 exoB with R. meliloti DNA. In addn. to functional and evolutionary equivalence of individual genes, the general organization of the exo regions was similar between the two species. It is likely that the same ancestral genes were used in the evolution of both exopolysaccharide biosynthetic pathways and probably of pathways in other species as well.

~9 Citings

332. The rhizobium meliloti trpE(G) gene is regulated by attenuation, and its product, anthranilate synthase, is regulated by feedback inhibition

By Bae, Young Min; Crawford, Irving P.
From Journal of Bacteriology (1990), 172(6), 3318-27. Language: English, Database: CAPLUS

In R. meliloti, the genes involved in biosynthesis of the amino acid tryptophan are found at 3 sep. chromosomal locations. Of the 3 gene clusters, trpE(G), trpDC, and trpFBA, only the trpE(G) gene is regulated by the end product of the pathway, tryptophan. It was found that trpE(G) mRNA contains a leader transcript that terminates at a stem-loop structure in a putative transcription attenuator. The level of this leader transcript that terminates at a stem-loop structure in a putative transcription attenuator. The level of this leader transcript was const. regardless of the amt. of tryptophan in the growth medium. However, the level of full-length trpE(G) mRNA decreased as the amt. of tryptophan increased. The β-galactosidase activity of an R. meliloti strain carrying a trpL'-'lacZ fusion remained const. at different tryptophan concns., but the β-galactosidase activity of the same strain carrying a trpE(G)'-'lacZ fusion decreased as the tryptophan concn. increased. These data indicate that transcription of the R. meliloti trpE(G) gene is regulated only by attenuation. It was also found that the product of the trpE(G) gene, anthranilate synthase, is feedback inhibited by tryptophan.

~16 Citings

333. Rhizobium meliloti glutamate synthase: cloning and initial characterization of the glt locus

By Lewis, Thomas A.; Gonzalez, Rigoberto; Botsford, James L.
From Journal of Bacteriology (1990), 172(5), 2413-20. Language: English, Database: CAPLUS

The genetic locus glt, encoding glutamate synthase from R. melioti 1021, was selected from a pLAFR1 clone bank by complementation of the R. melioti 41 Glt^- mutant AK330. A fragment of cloned DNA complementing this mutant also served to complement the Escherichia coli glt null mutant PA340. Complementation studies using these mutants showed that glutamate synthase expression requires 2 complementation groups present at this locus. Genomic Southern anal. using a probe of the R. meliloti 1021 glt region showed a close resemblance between R. meliloti 1021, 41, and 102f34 at glt, whereas R. meliloti 104A14 showed many differences in restriction fragment length polymorphism patterns at this locus. R. meliloti 102f34, but not other strains, showed an addnl. region with sequence similarity to glt. Insertion alleles contg. transposable kanamycin-resistance elements were constructed and used to derive Glt^- mutants of R. meliloti 1021 and 102f34. These mutants were unable to assimilate ammonia and were NOD^+ Fix^+ on alfalfa seedlings. The mutants also showed poor or no growth on nitrogen sources such as glutamate, aspartate, arginine, and histidine, which are utilized by the wild-type parental strains. Strains that remained auxotrophic but grew nearly as well as the wild type on these nitrogen sources were readily isolated from populations of glt insertion mutants, indicating that degrdn. of these amino acids is neg. regulated in R. meliloti as a result of disruptions of glt.

~10 Citings

334. Genetic analyses of Rhizobium meliloti exopolysaccharides

By Glazebrook, Jane; Reed, Jason W.; Reuber, T. Lynne; Walker, Graham C.
From International Journal of Biological Macromolecules (1990), 12(2), 67-70. Language: English, Database: CAPLUS, DOI:10.1016/0141-8130(90)90055-F

A review with 46 refs. Recently strong genetic evidence indicated that the acidic Calcofluor-binding exopolysaccharide (EPS I) of R. meliloti Rm1021 is required for nodule invasion and possibly for later events in nodule development. Thirteen loci on the second megaplasmid have been identified that are required for, or affect, the development. Thirteen loci on the second megaplasmid have been identified that are required for, or affect, the synthesis of EPS I. Mutations in certain of these loci completely abolish the prodn. of EPS I and result in mutants that form empty Fix$^-$ nodules. exoH Mutants fail to succinylate their EPS I and form empty Fix$^-$ nodules. Two unlinked regulatory loci, exoR and exoS, were identified whose products play neg. roles in the regulation of expression of the exo genes. The authors recently discovered that R. meliloti has a latent capacity to synthesize a second exopolysaccharide (EPS II) that can substitute for the role(s) of EPS I in nodulation of alfalfa but not of other hosts. Possible roles for Rhizobium exopolysaccharides in nodulation are discussed.

~5 Citings

335. Biochemical parameters of seed quality in Trigonella foenum-graecum L

By Benken, I. I.; Bairamov, S. S.; Varich, A. V.
From Rastitel'nye Resursy (1990), 26(1), 80-4. Language: Russian, Database: CAPLUS

Seeds of Trigonella foenum-graecum indica originating from India, China, Afghanistan, and Pakistan contained crude protein 28.7-30.8 and oil 5.5-6.0 dry-wt.%, as a 2-yr av. Resp. values for T. foenum-graecum mediterranea from Syria, Ethiopia, Egypt, Kazakhstan, Libya, Algeria, and England were 29.0-31.6 and 5.6-7.3%. Resp. values in hybrids between the above subspecies were 26.5-30.7 and 5.3-7.1%. The lowest trypsin and chymotrypsin inhibitor activities were found among the hybrids. The frequency of nodulation by Rhizobium meliloti was 78% in indica and 20% in mediterranea.

~0 Citings

336. Symbiotic pseudorevertants of Rhizobium meliloti ndv mutants

By Dylan, Tyler; Nagpal, Punita; Helinski, D. R.; Ditta, Gary S.
From Journal of Bacteriology (1990), 172(3), 1409-17. Language: English, Database: CAPLUS

Nodule development (ndv) mutants of R. melioti cannot invade alfalfa to establish a nitrogen-fixing symbiosis and instead induce the formation of small, white, unoccupied nodules on alfalfa roots. Such mutants also fail to produce the unusual cyclic oligosaccharide β-(1 → 2)-glucan and show defects in several aspects of vegetative growth and function. This report shows that ndv mutants are severely reduced, although not totally deficient, in the ability to attach to and initiate infection threads on alfalfa seedlings, and the symbiotic deficiency can be sepd. from the rest of the mutant phenotype by isolating second-site pseudorevertants. Pseudorevertants selected for restoration of motility, a vegetative property, regained a substantial amt. of attachment capability but only slight infection thread initiation and symbiotic ability. Such strains also regained partial tolerance to growth at low osmolarity, even though they did not recover the ability to synthesize periplasmic β-(1 → 2)-glucan prodn. or any other vegetative property and regained little or no attachment or infection thread initiation capability. These data indicate that wild-type R. meliloti normally has considerable excess capability for both attachment and infection thread initiation and that the symbiotic block in ndv mutants lies further along the developmental pathway than either of these processes, probably at the level of infection thread extension. Further, the fact that neither type of pseudoreverant recovered the ability to produce periplasmic β-(1 → 2)-glucan raises the possibility that this oligosaccharide is not directly required for nodule development.

~30 Citings

337. Expression of the adenyl cyclase-encoding gene (cya) of Rhizobium meliloti F34: existence of two cya genes?

By O'Regan, Michael; Kiely, Barry; O'Gara, Fergal
From Gene (1989), 83(2), 243-9. Language: English, Database: CAPLUS, DOI:10.1016/0378-1119(89)90110-8

To gain insight into the role of cAMP in gram-neg. soil bacteria, the expression of an adenyl cyclase-encoding gene cya of R. meliloti F34 was studied. In both Escherichia coli and Bradyrhizobium japonicum, the gene is expressed from a promoter(s) contained on a 2.6-kb fragment of the cloned insert, which may indicate the presence of a functional cya promoter or the coincidental presence of sequences which can function as promoters in these 2 species. The study of cya-lac fusion activity in R. meliloti indicated that the cya gene is not expressed at detectable levels and, thus, may not contribute to the modulation of cAMP levels under the growth conditions employed. R. meliloti strains carrying defined genomic mutations at the cya locus were still capable of the synthesis of near wild-type levels of cAMP. These results suggest that the cloned cya gene is not the key determinant responsible for cAMP synthesis under the culture conditions employed.

~0 Citings

338. Host restriction and transduction in Rhizobium meliloti

By Williams, Myron N. V.; Klein, Shoshana; Signer, Ethan R.
From Applied and Environmental Microbiology (1989), 55(12), 3229-30. Language: English, Database: CAPLUS

A host restriction difference exists between R. meliloti Rm41 and SU47, as indicated by the reduced plating efficiency of transducing phage M12h1. Restriction can be attenuated by incubating cells at 42° for 3 h; this procedure overcomes a block to transduction from SU47 to Rm41.

~3 Citings

339. Salinity and germination of annual Melilotus from the Guadalquivir delta (SW Spain)

By Maranon, T.; Garcia, L. V.; Troncoso, A.
From Plant and Soil (1989), 119(2), 223-8. Language: English, Database: CAPLUS, DOI:10.1007/BF02370412

The germination response to NaCl treatments has been studied in sweet clover (Melilotus) seed populations collected from saline and nonsaline soils in the Guadalquivir delta. The rank orders for salt tolerance and seed wt. were the same in the 3 Melilotus species living in this area: M. messanensis > M. segetalis > M. indica. Within the species, differences in germination response to salinity were found in M. indica (6 populations) and M. segetalis (8 populations). The relationship between salt tolerance during germination and salinity of maternal habitat is discussed.

~9 Citings

340. Effect of chemical weed control and Rhizobium inoculation on the yield of lentil

By Kumar, Krishan; Kolar, Jaspinder Singh
From Journal of Research (Punjab Agricultural University) (1989), 26(1), 19-24. Language: English, Database: CAPLUS

A field expt. was conducted on loamy sand soil (pH 8.3) to evaluate the performance of terbutryn (0.6 and 1.2 kg/ha), methabenzthiazuron (1.0 and 1.5 kg/ha), and pendimethalin (1.0 and 1.5 kg/ha) for controlling weeds under inoculation and no inoculation in lentil (var. LL 56). Chenopodium album, Medicago denticulata, Melilotus indica, Fumaria parviflora, Rumex dentatus, and Avena ludoviciana were the predominent weed species. Losses in grain yield of lentil due to weeds ranged from 43 to 80%, depending upon the type of weed flora. Manual weeding twice proved effective for controlling all types of weeds. All herbicides proved effective against broad-leaf weeds except M. denticulata. Methabenzthiazuron gave better control of A. ludoviciana than terbutryn and pendimethalin. All the herbicides were inferior to manual weeding twice. Rhizobium inoculation did not affect the lentil yield significantly. None of the herbicides affected the performance of Rhizobium, thereby indicating their compatibility with Rhizobium culture.

~2 Citings

341. Isolation and partial characterization of polypeptides associated with phytotoxin in cultures of the cool-temperature biotype of Stemphylium botryosum pathogenic on alfalfa

By Heiny, Dana Kelly; Gilchrist, David G.
From Physiological and Molecular Plant Pathology (1989), 34(6), 483-505. Language: English, Database: CAPLUS, DOI:10.1016/0885-5765(89)90074-X

S. botryosum pathogenic on alfalfa (Medicago sativa) produced a phytotoxin in a defined liq. medium which caused symptoms similar in sequence and appearance to stemphylium leafspot lesion development on attached alfalfa leaflets. The mol. wt. of the phytotoxin was estd. to be 19,500 by gel filtration chromatog. Treatment of partially purified phytotoxin with proteinase K or subtilisin resulted in loss of phytotoxin activity. Action of the proteases in inducing loss of phytotoxicity was inhibited by phenylmethylsulfonyl fluoride. Concd. cultures filtrates were fractionated by chromatofocusing, HPLC ion-exchange and gel filtration. Gel filtration also was followed by nondenaturing electrophoresis or isoelec. focusing (IEF). Anal. of sequential fractions from each procedure by SDS-PAGE indicated that phytotoxic activity was consistently coincident with the presence of 2 major polypeptides (M_r = 26,900 ± 2%; 19,500 ± 4%) and a triplet of polypeptides (M_r = 15,500). The const. assocn. between the 3 polypeptides suggested an intermol. interaction during fractionation. The phytotoxic activity eluted from the chromatofocusing column between pH 5.79 and 5.43, whereas IEF estd. the isoelec. point to be between 5.40 and 5.02. Immobilized Con A and wheat germ lectin failed to bind phytotoxicity. Proteolytic activity in some phytotoxic gel filtration fractions was reduced by addn. of phenylmethylsulfonyl fluoride and sepd. from phytotoxicity by non-denaturing electrophoresis, indicating that phytotoxicity was not due to serine protease activity. Pathogenicity tests of the cool-temp. biotype on 20 plant species representing 8 plant families resulted in a compatible interaction only on M. sativa and M. polymorpha. In contrast, sensitivity to the phytotoxin was obsd. on both pathogen-resistant and susceptible alfalfa clones along with all other plants tested with the exception of Triticum aestivum, Zea mays, Apium graveolens, and Melilotus officinalis, indicating non-host-specificity of the phytotoxic polypeptides produced by the cool-temp. biotype.

~0 Citings

342. Denitrification activity of phage types representative of two populations of indigenous Rhizobium meliloti

By Chan, Y. K.; Barran, L. R.; Bromfield, E. S. P.
From Canadian Journal of Microbiology (1989), 35(7), 737-40. Language: English, Database: CAPLUS, DOI:10.1139/m89-120

Isolates of R. meliloti from indigenous populations at 2 sites were previously characterized according to phage sensitivity. Isolates representative of the 55 and 65 phage types comprising these 2 populations were tested for denitrification activity with NO_3^- or NO_2^- as substrate. Fifty-seven of the 120 isolates were capable of denitrification, with activities varying considerably between phage types. Only 1 isolate was able to denitrify nitrite but not nitrate, indicating the presence of a truncated denitrification pathway. Each of 5 phage types showed variation in denitrification ability between isolates from different sites, indicating possible adaptation of indigenous R. meliloti to their resp. environments. The estd. frequency of occurrence of denitrifiers in the 2 indigenous populations of R. meliloti (9 and 13%) differed significantly between sites with and without a previous history of Medicago sativa cultivation.

~3 Citings

343. Maintenance of intracellular pH and acid tolerance in Rhizobium meliloti

By O'Hara, Graham W.; Goss, Thomas J.; Dilworth, Michael J.; Glenn, Andrew R.
From Applied and Environmental Microbiology (1989), 55(8), 1870-6. Language: English, Database: CAPLUS

The development and function of the R. meliloti-Medicago sp. symbiosis are sensitive to soil acidity. Physiol. criteria that can be measured in culture which serve to predict acid tolerance in soil would be valuable. The intracellular pH of R. meliloti was measured using either radioactively labeled weak acids (5,5-dimethyloxazolidine-2,4-dione and butyric acid) or pH-sensitive fluorescent compds.; both methods gave similar values. Six acid-tolerant strains (WSM419, WSM533, WSM539, WSM540, WSM852, and WSM870) maintained an alk. intracellular pH when the external pH was between 5.6 and 7.2. In contrast, 2 Australian com. inoculant strains (CC169 and U45) and 4 acid-sensitive strains from alk. soils in Iraq (WSM244, WSM301, WSM365, and WSM367) maintained an alk. intracellular pH when the external pH was ≥6.5, but had intracellular pH values of ≤6.8 when the external pH was ≤6.0. Four transposon Tn5-induced mutants of acid-tolerant strain WSM419, impaired in their ability to grow at pH 5.6, showed limited control over the intracellular pH. The ability to generate a large pH gradient under acid conditions may be a better indicator of acid tolerance in R. meliloti under field conditions that is growth on acidic agar plates.

~55 Citings

344. Studies on selective herbicidal control of Chenopodium and Melilotus spp. in wheat

By Singh, C. P.; Bhardwaj, R. B. L.; Ahuja, K. N.
From Indian Journal of Agronomy (1987), 32(4), 359-61. Language: English, Database: CAPLUS

Applying 0.6 kg fluoroxypyr or 2,4-D/ha 6 wk after seeding wheat, or 0.75 kg isoproturon/ha 4 wk after seeding, increased grain yield to 49.4, 50.4, and 47.6 quintals/ha, resp., from 47.0 quintals/ha in hand-weeded controls, by controlling C. album and M. indica.

~2 Citings

345. Cascade regulation of nif gene expression in Rhizobium meliloti

By David, Michel; Daveran, Marie Line; Batut, Jacques; Dedieu, Annie; Domergue, Odile; Ghai, Jyotsna; Hertig, Cecilia; Boistard, Pierre; Kahn, Daniel
From Cell (Cambridge, MA, United States) (1988), 54(5), 671-83. Language: English, Database: CAPLUS, DOI:10.1016/S0092-8674(88)80012-6

Two genes from R. meliloti, fixL and fixJ, are pos. regulators of symbiotic expression of diverse nitrogen fixation (nif and fix) genes. Gene nif regulation is shown to consist of a cascade. The fixLJ genes activate nifA, which is turn activates nifHDK and fixABCX. Like nifA, fixN can be induced in free-living microaerobic cultures of R. meliloti, indicating a major physiol. role for oxygen in nif and fix gene regulation. Microaerobic expression of fixN and nifA depends on fixL and fixJ. The FixL and FixJ proteins belong to a family of 2-component regulatory systems widely spread among prokaryotes and responsive to the cell environment. It is proposed that FixL, which has features of a trans membrane protein, senses an environmental signal and transduces it to FixJ, a transcriptional activator of nif and fix genes.

~161 Citings

346. A novel exopolysaccharide can function in place of the calcofluor-binding exopolysaccharide in nodulation of alfalfa by Rhizobium meliloti

By Glazebrook, Jane; Walker, Graham C.
From Cell (Cambridge, MA, United States) (1989), 56(4), 661-72. Language: English, Database: CAPLUS, DOI:10.1016/0092-8674(89)90588-6

R. meliloti strain Rm1021, which is known to synthesize a Calcofluor-binding exopolysaccharide (EPS I), also has a cryptic capacity to synthesize a second exopolysaccharide (EPS II). Structural anal. of EPS II has shown that it differs in many respects from EPS I. Genetic anal. indicates that EPS II synthesis requires the products of ≥7 loci on the second symbiotic megaplasmid of R. meliloti, and is induced by a mutation, expR101, which causes increased transcription of these genes. Synthesis of EPS II suppresses the symbiotic defects of EPS I-deficient strains on Medicago sativa (alfalfa), but not on four other plants that are normally hosts for Rm1021. These observations suggest that structural features of bacterial exopolysaccharides are involved in the detn. of host range. The implications of these results for models of exopolysaccharide function, such as serving as signals to the plant or shielding the bacteria from plant defense responses, are discussed.

~127 Citings

347. The DNA-binding domain of the transcriptional activator protein NifA resides in its carboxy terminus, recognizes the upstream activator sequences of nif promoters and can be separated from the positive control function of NifA

By Morett, E.; Cannon, W.; Buck, M.
From Nucleic Acids Research (1988), 16(24), 11469-88. Language: English, Database: CAPLUS, DOI:10.1093/nar/16.24.11469

The pos. control protein NifA activates transcription of nitrogen fixation promoters in Klebsiella pneumoniae. NifA is believed to bind to specific sites, the upstream activator sequences (UAS's), of the nif promoters which it activates. Mutation of the carboxy terminus of NifA showed that this is the DNA-binding domain and that the DNA-binding and pos. activator functions of NifA can be sepd. Mutational anal. of the nifH UAS and in vivo methylation protection anal. of the interaction of NifA with the nifH promoter demonstrates that the UAS is recognized by the carboxy terminus of NifA. The UAS's of K. pneumoniae nif promoters are also required for activation by the Rhizobium meliloti NifA, indicating that this activator also possesses DNA-binding activity.

~25 Citings

348. Rhizobium meliloti host range nodH gene determines production of an alfalfa-specific extracellular signal

By Faucher, Catherine; Maillet, Fabienne; Vasse, Jacques; Rosenberg, Charles; Van Brussel, Anton A. N.; Truchet, Georges; Denarie, Jean
From Journal of Bacteriology (1988), 170(12), 5489-99. Language: English, Database: CAPLUS

The R. meliloti nodH gene is involved in detg. host range specificity. By comparison with the wild-type strain, NodH mutants exhibit a change in host specificity. I.e., although NodH mutants lose the ability to elicit root hair curling (Hac^-), infection threads (Inf^-), and nodule meristem formation (Nod^-) on the homologous host alfalfa, they gain the ability to be Hac^+ Inf^+ Nod^+ on a nonhomologous host such as common vetch. Using root hair deformation (Had) bioassays on alfalfa and vetch, it was demonstrated that sterile supernatant solns. of R. meliloti cultures, in which the nod genes had been induced by the plant flavone luteolin, contained symbiotic extracellular signals. The wild-type strain produced at least one Had signal active on alfalfa (HadA). The $NodH^-$ mutants did not produce this signal but produced at least one factor active on vetch (HadV). Mutants altered in the common nodABC genes produced neither of the Had factors. This result suggests that the nodABC operon dets. the prodn. of a common symbiotic factor which is modified by the NodH product into an alfalfa-specific signal. An abs. correlation was obsd. between the specificity of the symbiotic behavior of rhizobial cells and the Had specificity of their sterile filtrates. This indicates that the R. meliloti nodH gene dets. host range by helping to mediate the prodn. of a specific extracellular signal.

~25 Citings

349. Structure and regulation of fix genes from Rhizobium meliloti

By Kahn, D.; Batut, J.; Daveran, M. L.; David, M.; Boistard, P.
From Comm. Eur. Communities, [Rep.] EUR (1988), (EUR 11517, Physiol. Limitations Genet. Improv. Symbiotic Nitrogen Fixation), 169-74. Language: English, Database: CAPLUS

Genetic anal. of a fix cluster from R. meliloti indicates it extends over 12.5 kb and consists of two fix operons on either side of a fix region duplicated elsewhere on the symbiotic plasmid pSym. Sequence anal. of the fixGHIY operon indicates it encodes a membrane-located cation-pump possibly coupled to a redox process important for symbiotic nitrogen fixation. The duplicated fix region is induced in symbiosis and in free-living microaerobic cultures. Induction depends on two newly described regulatory genes, fixLJ, but not on nifA, the classical nif activator. Loci fixLJ also regulate nif genes in symbiosis via induction of nifA at the PnifA promoter. Therefore, fixLJ regulate most nitrogen fixation genes in R. meliloti: (1) nifA-independent fix genes, such as fixN; and (2) nif genes, by a cascade regulation involving nifA. The sequence of fixLJ shows that the FixL and FixJ proteins belong to a family of two-component regulatory systems widely spread among prokaryotes and sensitive to the external environment. This suggests that fixLJ mediate environmental regulation of nif and fix genes in R. meliloti.

~0 Citings

350. Melanin production encoded by a cryptic plasmid in a Rhizobium leguminosarum strain

By Hynes, Michael F.; Brucksch, Kerstin; Priefer, Ursula
From Archives of Microbiology (1988), 150(4), 326-32. Language: English, Database: CAPLUS, DOI:10.1007/BF00408302

R. leguminosarum Strain VF39, isolated from nodules of field-grown faba beans, contained 6 plasmids ranging in mol. wt. from 90 to 400 Md. Hybridization to nif gene probes, plasmid curing, and mobilization to other strains of Rhizobium and to Agrobacterium showed that the third largest plasmid, pRleVF39d (220 Md), carried genes for nodulation and nitrogen fixation. This plasmid was incompatible with pRL10JI, the Sym plasmid of R. leguminosarum strain JB300. Of the other plasmids, the 2 smallest (pRleVF39a and pRleVF39b, 90 and 160 Md, resp.) were shown to be self-transmissible at a low frequency. Although melanin prodn. is as yet unreported in strains of R. leguminosarum biovar viceae, strain VF39 produced a dark pigment, which, since it was not produced on minimal media and its prodn. was greatly enhanced by the presence of tyrosine in the media, is probably melanin-like. Derivs. of VF39 cured of pRleVF39a no longer produced this pigment, but regained the ability to produce it when this plasmid was transferred into them. Strains of Agrobacterium tumefaciens, R. meliloti, and some strains of R. leguminosarum carrying pRleVF39a did not produce this pigment, indicating perhaps that some genes elsewhere on the VF39 genome are also involved in pigment prodn. Plasmid pRleVF39a appeared to be incompatible with the cryptic Rhizobium plasmids pRle336b and pRL8JI (both ~100 Md), but was compatible with the R. leguminosarum biovar phaseoli Sym plasmids pRP1JI, pRP2JI, and pRph51a, all of which also code for melanin prodn. The absence of pRleVF39a in cured derivs. of VF39 had no effect on the symbiotic performance or competitive ability of this strain.

~28 Citings

351. Enhanced nodule initiation on alfalfa by wild-type Rhizobium meliloti co-inoculated with nod gene mutants and other bacteria

By Caetano-Anolles, Gustavo; Bauer, Wolfgang D.
From Planta (1988), 174(3), 385-95. Language: English, Database: CAPLUS

Nodule formation on alfalfa (Medicago sativa) roots was detd. at different inoculum dosages for wild-type R. meliloti strain RCR2011 and for various mutant derivs. with altered nodulation behavior. The no. of nodules formed on the whole length of the primary roots was essentially const. regardless of initial inoculum dosage or subsequent bacterial multiplication, indicative of homeostatic regulation of total nodule no. In contrast, the no. of nodules formed in just the initial susceptible region of these roots was sigmoidally dependent on the no. of wild-type bacteria added, increasing rapidly at dosages above 5×10^3 bacteria/plant. This behavior indicates the possible existence of a threshold barrier to nodule initiation in the host which the bacteria must overcome. When low dosages of the parent (10^3 cells/plant) were coinoculated with 10^6 cells/plant of mutants lacking functional nodA, nodC, node, nodF or nodH genes, nodule initiation was increased 10-30-fold. Anal. of nodule occupancy indicated that these mutants were able to help the parent (wild-type) strain initiate nodules without themselves occupying the nodules. Coinoculation with R. trifolii or Agrobacterium tumefaciens cured of its Ti plasmid also markedly stimulated nodule initiation by the R. meliloti parent strain. Introduction of a segment of the symbiotic megaplasmid from R. meliloti into A. tumefaciens abolished this stimulation. Bradyrhizobium japonicum And a chromosomal Tn5 nod^- mutant of R. meliloti did not significantly stimulate nodule initiation when coinoculated with wild-type R. meliloti. These results indicate that certain nod gene mutants and members of the Rhizobiaceae may produce extracellular signals that supplement the ability of wild-type R. meliloti cells to induce crucial responses in the host.

~9 Citings

352. Herbicide comprising urea and sulfuric acid

By Young, Donald C.
From Can. (1987), CA 1230236 A1 19871215, Language: English, Database: CAPLUS

Pre- and postemergence weed control is carried out with a soln. comprising urea, H_2SO_4, and optionally a surfactant. A 17-0-0-17 compn. comprising 85% urea + H_2SO_4, applied at 20 gal-acre, at a diln. of 50 gal/acre, totally controlled barnyard grass, morning-glory and thistle in wheat.

~0 Citings

353. Genetic analysis of carbamoylphosphate synthesis in Rhizobium meliloti 104A14

By Kerppola, Tom K.; Kahn, Michael L.
From Journal of General Microbiology (1988), 134(4), 921-9. Language: English, Database: CAPLUS

Ineffective (Fix^-) mutants of Rhizobium. meliloti 104A14 requiring both arginine and uracil, and thus probably defective in carbamoylphosphate synthetase, have been isolated. The mol. and genetic anal. of the R. meliloti genes coding for carbamoylphosphate synthetase is described. Plasmids that complement the mutations were isolated from a R. meliloti gene bank. Restriction anal. of these plasmids indicated that complementation involved two unlinked regions of the R. meliloti chromosome, carA and carB. Genetic complementation between the plasmids and mutants demonstrated a single complementation group for carA, but two overlapping complementation groups for carB. The cloned R. meliloti genes hybridize to the corresponding Escherichia coli carA and carB genes which encodes the two subunits of carbamoylphosphate synthetase. Transposon Tn5 mutagenesis was used to localize the carA and carB genes on the cloned R. meliloti DNA. The cloned R. meliloti carA and carB genes were unable to complement E. coli carA or carB mutants alone or in combination. The mechanism of the unusual pattern of genetic complementation at the R. meliloti carB locus is discussed.

~3 Citings

354. Rhizobium fix genes mediate at least two communication steps in symbiotic nodule development

By Putnoky, Peter; Grosskopf, Erich; Ha, Dang T. Cam; Kiss, Gyorgy B.; Kondorosi, Adam
From Journal of Cell Biology (1988), 106(3), 597-607. Language: English, Database: CAPLUS, DOI:10.1083/jcb.106.3.597

To identify bacterial genes involved in symbiotic nodule development, ineffective nodules of alfalfa (Medicago sativa) induced by 64 different Fix- mutants of R. meliloti were characterized by assaying for symbiotic gene expression and by morphol. studies. The expression of legHb and nodulin-25 genes from alfalfa and of the nifHD genes from R. meliloti were monitored by hybridizing the appropriate DNA probes to RNA samples prepd. from nodules. The mutants were accordingly divided into three groups. In group I none of the genes were expressed, in group II only the plant genes were expressed and in group III all three genes were transcribed. Light and electron microscopical anal. of nodules revealed that nodule development was halted at different stages in nodules induced by different group I mutants. In most cases nodules were empty lacking infection threads and bacteroids or nodules contained infection threads and a few released bacteroids. In nodules induced by a third mutant class bacteria were released into the host cells, however the formation of the peribacteroid membrane was not normal. It is suggested that peribacteroid membrane formation precedes legHb and nodulin-25 induction, moreover, after induction of nodulation by the nod genes at least two communication steps between the bacteria and the host plants are necessary for the development of the mature nodule. By complementing each mutant of group I with a genomic R. meliloti library made in pLAFR1, four new fix loci were identified, indicating that several bacterial genes are involved in late nodule development.

~30 Citings

355. Growth of indigenous Rhizobium leguminosarum and Rhizobium meliloti in soils amended with organic nutrients

By Germida, James J.
From Applied and Environmental Microbiology (1988), 54(1), 257-63. Language: English, Database: CAPLUS

The ability of indigenous R. leguminosarum and R. meliloti to use org. nutrients as growth substrates in soil was assessed by indirect bacteriophage anal. A total of 17 org. compds., including 9 carbohydrates, 3 org. acids, and 5 amino acids, were tested (1000 μg g^{-1}) in three soils with different cropping histories. Four addnl. soils were screened with a glucose amendment. Nutrient amendments stimulated growth of indigenous rhizobia, allowing subsequent replication of indigenous bacteriophages. Phage populations were enumerated by plating soil exts. on 19 R. leguminosarum and 9 R. meliloti indicator strains, including root nodule isolates from the soils assayed. On the basis of indirect phage anal., all soils contained native rhizobia similar to one or more of the indicator strains, although not all indicator strains were detected in soil. All org. compds. stimulated growth of indigenous rhizobia, but the growth response varied for each rhizobial strain depending on the nutrient, the nutrient concn., and the soil. Indigenous rhizobia readily utilized most org. compds. except phenylalanine, glycine, and aspartic acid. The ability of indigenous rhizobia to utilize a wide range of org. compds. as growth substrates in situ indicates their ability to successfully compete with other soil bacteria for nutrients in these soils.

~4 Citings

356. Rhizobium meliloti has three functional copies of the nodD symbiotic regulatory gene

By Honma, Mary A.; Ausubel, Frederick M.
From Proceedings of the National Academy of Sciences of the United States of America (1987), 84(23), 8558-62. Language: English, Database: CAPLUS, DOI:10.1073/pnas.84.23.8558

Two R. meliloti genes ($nodD_2$ and $nodD_3$) were identified that are highly homologous and closely linked to the regulatory gene nodD ($nodD_1$). R. meliloti Strains contg. mutations in the three nodD genes in all possible combinations were constructed, and their nodulation phenotypes were assayed on Medicago sativa (alfalfa) and Melilotus alba (sweet clover). A triple $nodD_1$-$nodD_2$-$nodD_3$ mutant exhibited a Nod- phenotype on alfalfa and sweet clover, indicating that nodD is an essential nodulation gene in R. meliloti. A $nodD_2$ mutant exhibited no discernable defect in nodulation, and $nodD_3$ mutants exhibited a delayed nodulation phenotype of 2-3 days when inoculated onto either host. Alfalfa nodules elicited by a $nodD_1$ mutant appeared 5-6 days after wild-type nodules, and sweet clover nodules elicited by a $nodD_1$ mutant appeared 2-3 days after wild-type nodules. The $nodD_1$-$nodD_2$ double mutants formed nodules with the same delay as single $nodD_1$ mutants on both hosts; $nodD_2$-$nodD_3$ double mutants elicited sweet clover nodules at the same rate as single $nodD_3$ mutants, but this same double mutant was slightly more delayed in alfalfa nodule formation than the $nodD_3$ mutant. The $nodD_1$-$nodD_3$ mutant exhibited an extremely delayed nodulation phenotype on alfalfa and elicited no nodules on sweet clover. These expts. indicate that $nodD_1$ and $nodD_3$ have equiv. roles in nodulating sweet clover but that $nodD_1$ plays a more important role than $nodD_3$ in eliciting nodules on alfalfa. The $nodD_2$ gene appears to have some effect on alfalfa nodulation and none on sweet clover. These results indicate that R. meliloti has three functional nodD genes that modulate the nodulation process in a host-specific manner.

~35 Citings

357. Agrobacterium tumefaciens virulence locus pscA is related to the Rhizobium meliloti exoC locus

By Marks, James R.; Lynch, Tim J.; Karlinsey, Joyce E.; Thomashow, Michael F.
From Journal of Bacteriology (1987), 169(12), 5835-7. Language: English, Database: CAPLUS

A. tumefaciens And R. meliloti carry related genetic loci which have important roles in virulence and symbiosis. Previously, it was shown that 2 virulence loci of A. tumefaciens, chvA and chvB, are related to 2 R. meliloti symbiosis loci, ndvA and ndvB, resp. These 2 phytobacteria possess addnl. related virulence/symbiosis genes. Results of genetic complementation and DNA hybridization expts. indicate that the pscA virulence locus of A. tumefaciens is structurally and functionally related to the exoC symbiosis locus of R. meliloti. Thus, A. tumefaciens and R. meliloti bear at ≥3 related genetic loci that have crucial roles in establishing the interactions that each bacterium has with its resp. host plants.

~3 Citings

358. Variation for activity of nodule nitrogen and carbon assimilating enzymes in alfalfa

By Jessen, D. L.; Barnes, D. K.; Vance, C. P.; Heichel, G. H.
From Crop Science (1987), 27(4), 627-31. Language: English, Database: CAPLUS, DOI:10.2135/cropsci1987.0011183X002700040003x

The nodule enzymes glutamate synthase (GOGAT) and phosphoenolpyruvate carboxylase (PEPC) are important in the assimilation of symbiotically fixed N in alfalfa (Medicago sativa). The objectives of this study were to evaluate several alfalfa germplasm sources for variability in nodule GOGAT and PEPC activities, and to det. the relationships between N_2 fixation and plant yield traits with nodule GOGAT and PEPC enzyme activities. Approx. 160 plants from each of six alfalfa germplasms were grown in sand culture in the glasshouse and assayed for nodule GOGAT and PEPC enzyme activities. Twenty-four genotypes (four from each germplasm) were selected to represent a range in GOGAT and PEPC activities. These genotypes were evaluated in glasshouse and field clonal studies for GOGAT and PEPC activities per g nodule fresh wt., acetylene redn. activity (ARA), nodule mass, nodule color, nodule sol. protein concn., and plant yield. Variability for nodule GOGAT and PEPC activities within each of the six germplasms was large and normally distributed. The 12 high GOGAT genotypes (2 from each germplasm) were 44% greater in GOGAT activity than the 12 low genotypes. The 12 high PEPC genotypes were 27% greater in PEPC activity than the 12 low genotypes. Both groups of high enzyme activity genotypes were significantly greater than the low genotypes in ARA, nodule sol. protein concn. and field shoot yield. Both GOGAT and PEPC activities were pos. correlated (r = 0.61, significant at the 0.01 probability level). Also, GOGAT and PEPC were each correlated with ARA (r = 0.43, significant at the 0.05 probability level, and 0.45, resp.), nodule color score (r = 0.46 and 0.73) and sol. protein concn. (r = 0.77 and 0.90). Plant yield and N_2 fixation measured in the field were not correlated with nodule GOGAT and PEPC activities measured in the glasshouse. The relationships between GOGAT and PEPC with other plant traits indicated that these enzymes are assocd. with the host-Rhizobium meliloti symbiosis and should be explored as possible selection criteria to include in an alfalfa breeding program.

~8 Citings

359. Host-specific regulation of nodulation genes in Rhizobium is mediated by a plant-signal, interacting with the nodD gene product

By Horvath, Beatrix; Bachem, Christian W. B.; Schell, Jeff; Kondorosi, Adam
From EMBO Journal (1987), 6(4), 841-8. Language: English, Database: CAPLUS

A nodD gene was identified from the wide host-range Rhizobium strain MPIK3030 (termed nodD1) which is essential for nodulation on Macroptilium atropurpureum (siratro). Expts. with nodA-lacZ gene fusions demonstrate that the MPIK3030 nodD1 regulates expression of the nodABC genes. Addnl., nodC-lacZ fusions of Rhizobium meliloti were used to show that the MPIK3030 nodD1 gene induces expression of these fusions by interacting with plant factors from siratro and from the non-host Medicago sativa (alfalfa). The R. meliloti nodD genes, however, only interact with alfalfa exudate. In line with these results, no complementation of MPIK3030 nodD1 mutants could be obtained on siratro with the R. meliloti nodD genes, whereas the MPIK3030 nodD1 can complement nodD mutants of R. meliloti on alfalfa. Furthermore, R. meliloti transconjugants harboring the MPIK3030 nodD1 efficiently nodulate the illegitimate host siratro. When compared with other nodD sequences, the amino acid sequence of the MPIK3030 nodD1 shows a conserved amino-terminus, whereas the carboxy-terminus of the putative gene product diverges considerably. Studies on a chimeric MPIK3030-R. meliloti nodD gene indicates that the carboxy-terminal region is responsible for the interaction with plant factor(s) and may have evolved in different rhizobia specifically to interact with plant-host factors.

~29 Citings

360. Identification and characterization of the Rhizobium meliloti ntrC gene: R. meliloti has separate regulatory pathways for activation of nitrogen fixation genes in free-living and symbiotic cells

By Szeto, Wynne W.; Nixon, B. Tracy; Ronson, Clive W.; Ausubel, Frederick M.
From Journal of Bacteriology (1987), 169(4), 1423-32. Language: English, Database: CAPLUS

R. meliloti, The nitrogen-fixing endosymbiont of alfalfa, has a regulatory gene that is structurally homologous to previously characterized ntrC genes in enteric bacteria. DNA sequence anal. showed that R. meliloti ntrC is homologous to previously sequenced ntrC genes from Klebsiella pneumoniae and Bradyrhizobium sp. (Parasponia) and that an ntrB-like gene is situated directly upstream from R. meliloti ntrC. Similar to its counterparts in K. pneumoniae and Escherichia coli, R. meliloti ntrC is expressed when the cells are grown in nitrogen-limiting media. In addn., R. meliloti ntrC is required for growth on media contg. nitrate as the sole nitrogen source and for the ex planta transcription of several R. meliloti nif genes. On the other hand, root nodules elicited by R. meliloti ntrC mutants fix nitrogen as well as nodules elicited by wild-type R. meliloti. These latter results indicate that R. meliloti has sep. regulatory pathways for activating nif gene expression ex planta and during symbiotic nitrogen fixation.

~32 Citings

361. Native pastures of the Guadalquivir river marshes: a worthwhile natural resource

By Murillo, J. M.; Moreno, F.; Barroso, M.; Hernandez, J. M.
From Acta Oecologica, Oecologia Applicata (1986), 7(4), 299-312. Language: English, Database: CAPLUS

Native pastures of the upper zones of the Guadalquivir river marshes (vetas), have a noticeable nutritive value with N, S, P, K, Na, Ca, Fe, Mn, Zn, Cu, K/Na, Ca/P, K/Ca + Mg and digestible dry matter levels adequate, in general, for the indigenous cattle requirements. In these zones, the salinity level of the soil is comparatively low in the top layer after rainy periods and the useful water level is comparatively high, which improves herbage prodn. In general, the phys. properties of the soils of the Guadalquivir river marshes are typical of heavy clay soils.

~0 Citings

362. Effect of rifampin resistance on nodulating competitiveness of Rhizobium meliloti

By Lewis, D. M.; Bromfield, E. S. P.; Barran, L. R.
From Canadian Journal of Microbiology (1987), 33(4), 343-5. Language: English, Database: CAPLUS, DOI:10.1139/m87-059

An assessment was made of the effect of high-concn. rifampin resistance on the nodulating competitiveness of 5 strains of R. meliloti. The results indicate that the acquisition of rifampin resistance by R. meliloti is generally assocd. with a significant loss of nodulating competitiveness and an altered RNA polymerase insensitive to the action of rifampin. All mutants were similar to their parent strains with respect to growth rates, phage sensitivity patterns, and symbiotic effectiveness. The data suggest that rifampin resistance in R. meliloti is unsuitable as a marker for ecol. studies.

~2 Citings

363. Surface properties of Rhizobium meliloti associated with symbiosis

By Kieber, Joseph; Clover, Ralph; Finan, Turlough M.; Signer, Ethan R.
Edited By:Verma, Desh Pal S.; Brisson, Normand
From Mol. Genet. Plant-Microbe Interact., Proc. Int. Symp., 3rd (1987), 182-4. Language: English, Database: CAPLUS

Alterations in membrane proteins of R. melioliti are correlated with bacteroid differentiation. In particular, as may be true for Bradyrhizobium japonicum, the nitrogenase proteins are assocd. with the bacteroid membrane. For wild-type, some bacterial epitopes are found not only in bacteroids but in the peribacteroid membrane as well; for mutant EJ360, bacteroids expose 4 epitopes not displayed in bacteria. Thus, as in R. leguminosarum, differentiation to bacteroids alters the bacterial envelope. Mutants with altered lipopolylysaccharides have been isolated, and the phenotype of at least class 2 mutants suggests that lipopolysaccharide is involved in infection thread elongation, as in R. phaseoli. Dependence of that phenotype on genetic background indicates that for R. meliloti, the role of lipopolysaccharide in symbiosis is complex.

~0 Citings

364. Indigenous plasmids and cultural characteristics of rhizobia nodulating chickpeas (Cicer arietinum L.)

By Cadahia, E.; Leyva, A.; Ruiz-Argueso, T.
From Archives of Microbiology (1986), 146(3), 239-44. Language: English, Database: CAPLUS

This study examd. 27 strains of chickpea rhizobia from different geog. origins for indigenous plasmids, location and organization of nitrogen fixation (nif) genes, and cultural properties currently used to sep. fast- and slow-growing groups of rhizobia. By using an in-well lysis and electrophoresis procedure, one to three plasmids of mol. wts. ranging 35 to >380 Mdal were demonstrated in each of 19 strains, whereas no plasmids were detected in the eight remaining strains. Nitrogenase structural genes homologous to Rhizobium meliloti nifHD, were not detected in plasmids of 26 out of the 27 strains tested. Hybridization of EcoRI digested total DNA from these 26 strains to the nif probe from R. meliloti indicated that the organization of nifHD genes was highly conserved in chickpea rhizobia. The only exception was strain IC-72 M which harbored a plasmid of 140 Mdal with homol. to the R. meliloti nif DNA and exhibited also a unique organization of nifHD genes. The chickpea rhizobia strains showed a wide variation of growth rates (generation times ranged from 4.0 to 14.5 h) in yeast ext.-mannitol medium but appear to be relatively homogeneous in terms of acid prodn. in this medium and acid reaction in litmus milk. Although strains with fast and slow growth rates were identified, DNA/DNA hybridization expts. using a nifHD-specific probe, and the cultural properties examd. so far do not support the sepn. of chickpea rhizobia into two distinct groups of the classical fast- and slow-growing types of rhizobia.

~12 Citings

365. At least two nodD genes are necessary for efficient nodulation of alfalfa by Rhizobium meliloti

By Goettfert, Michael; Horvath, Beatrix; Kondorosi, Eva; Putnoky, Peter; Rodriguez-Quinones, Francisco; Kondorosi, Adam
From Journal of Molecular Biology (1986), 191(3), 411-20. Language: English, Database: CAPLUS, DOI:10.1016/0022-2836(86)90136-1

A R. meliloti DNA region (nodD1) involved in the regulation of other early nodulation genes has been delimited by directed Tn5 mutagenesis and its nucleotide sequence has been detd. The sequence data indicate a large open reading frame with opposite polarity to nodA, -B and -C, coding for a protein of 308 (or 311) amino acid residues. Tn5 insertion within the gene caused a delay in nodulation of Medicago sativa from 4 to 7 days. Hybridization of nodD1 to total DNA of R. meliloti revealed 2 addnl. nodD sequences (nodD2 and nodD3), and both were localized on the megaplasmid pRme41b in the vicinity of the other nod genes. Genetic and DNA hybridization data, combined with nucleotide sequencing showed that nodD2 is a functional gene, whereas the requirement of nodD3 for efficient nodulation of M. sativa could not be detected under these exptl. conditions. The nodD2 gene product consists of 310 amino acid residues and shares 86.4% homol. with the nodD1 protein. Single nodD2 mutants had the same modulation phenotype as the nodD1 mutants, whereas a double nodD1-nodD2 mutant exhibited a more severe delay in nodulation. These results indicate that ≥2 functional copies of the regulatory gene nodD are necessary for the optimal expression of nodulation genes in R. meliloti.

~0 Citings

366. Structure of the D-galacto-D-mannan isolated from the seeds of Melilotus indica all

By Gupta, Ashok K.; Bose, Sukumar
From Carbohydrate Research (1986), 153(1), 69-77. Language: English, Database: CAPLUS, DOI:10.1016/S0008-6215(00)90196-4

A D-galacto-D-mannan ([α] +72.0 and D-galactose-to-D-mannose ratio 1:1.14) was isolated from the seeds of M. indica, syn. M. parviflora. The ^{1}H- and ^{13}C-NMR, and IR spectra indicated the presence of α-D-galactopyranosyl and β-D-mannopyranosyl residues. Methylation of the polysaccharide, followed by hydrolysis, afforded 2,3,4,6-tetra-, 2,3,6-tri-, 2,3-di-, and 3,4-di-O-methyl-D-mannose, and 2,3,4,6-tetra- and 2,3,6-tri-O-methyl-D-galactose in the molar ratios of 1:2:22:6:27:3. Periodate oxidn. of the polysaccharide, followed by redn. and hydrolysis, gave erythritol (1 mol) and glycerol (1.24 mol). Partial acid hydrolysis of the polysaccharide afforded O-β-D-mannopyranosyl-(1→2)-D-mannopyranose, O-β-D-mannopyranosyl-(1→4)-D-mannopyranose, O-α-D-galactopyranosyl-(1→6)-D-mannopyranose, O-α-D-galactopyranosyl-(1→4)-D-galactopyranose, and O-α-D-galactopyranosyl-(1→6)-O-β-D-mannopyranosyl-(1→4)-D-mannopyranose. A highly branched structure having a mannan backbone composed of 36% of (1→4)- and 10% of (1→2)-linked β-D-mannopyranosyl units proposed for the galactomannan.

~2 Citings

367. Identification of host range determinants in the Rhizobium species MPIK3030

By Bachem, Christian W. B.; Banfalvi, Zsofia; Kondorosi, Eva; Schell, Jeff; Kondorosi, Adam
From Molecular and General Genetics (1986), 203(1), 42-8. Language: English, Database: CAPLUS, DOI:10.1007/BF00330382

R. meliloti Primarily nodulates Medicago sativa but cannot nodulate Macroptilium atropurpureum. By introducing an 11.4-kilobase (kb) region into R. meliloti from the Sym-plasmid of Rhizobium strain MPIK3030, the host range of the R. meliloti transconjugants were shown to be extended to M. atropurpureum, 1 of the hosts of MPIK3030 but not normally nodulated by R. meliloti. The region responsible for host-range extension was isolated by mass conjugating a clone bank from MPIK3030 into the R. meliloti wild type, and subsequent screening for nodulation on M. atropurpureum. Using deleted derivs. of a plasmid reisolated from endosymbiotic bacteria, the host-range region was further narrowed down to 3 EcoRI fragments. Tn5 mutagenesis allowed the isolation of 3 discrete regions on the 11.4-kb section which are involved in the extension of host range to M. atropurpureum. Finally, complementation expts. performed with R. meliloti common nod and hsn mutants indicated that none of the genes involved in the early steps of nodulation, including host-range functions, can be complemented by genes carried on the 11.4-kb fragment derived from MPIK3030.

~3 Citings

368. Studies on leguminous seeds. III

By Chowdhury, A. R.; Banerji, R.; Tiwari, S. R.; Misra, G.; Nigam, S. K.
From Fette, Seifen, Anstrichmittel (1986), 88(4), 144-6. Language: English, Database: CAPLUS, DOI:10.1002/lipi.19860880407

The seeds of 20 plant species belonging to Papillonaceae were studied for their fatty acid and mineral compns. The fat and protein contents were 2-30% and 21-45% resp. The seed oils were rich in C-18 unsatd. acid (40.5-77.2%).

~1 Citing

369. Effect of herbicides alone and in combination with weeding on tomato and associated weeds

By Singh, Govindra; Bhan, V. M.; Tripathi, S. S.
From Indian Journal of Weed Science (1984), 16(4), 262-6. Language: English, Database: CAPLUS

Chenopodium album, Anagallis arvensis, Fumaria parviflora, Melilotus indica, And Cyperus rotundus were the major weed species. On an av., weediness resulted in 57.6% redn. in tomato yield when compared with the weed-free condition. Preemergence application of metribuzin [21087-64-9], alachlor [15972-60-8] and nitrofen [1836-75-5] gave significantly increased yield when compared with unweeded controls. All the herbicides, when applied alone, produced yields significantly lower than that of the weed-free treatment. Superimposition of one weeding over the application of herbicides increased tomato yield.

~0 Citings

370. Rhizobium meliloti nodulation genes: identification of nodDABC gene products, purification of nodA protein, and expression of nodA in Rhizobium meliloti

By Egelhoff, T. T.; Long, S. R.
From Journal of Bacteriology (1985), 164(2), 591-9. Language: English, Database: CAPLUS

A set of conserved, or common, bacterial nodulation (nod) loci is required for host plant infection by Rhizobium meliloti and other Rhizobium species. Four such genes, nodDABC, have been indicated in R. meliloti 1021 by genetic anal. and DNA sequencing. An essential step toward understanding the function of these genes is to characterize their protein products. In vitro and maxicell Escherichia coli expression systems, together with gel electrophoresis and autoradiog., were used to detect proteins encoded by nodDABC. Expression of genes on these DNA fragments was facilitated by inserting them downstream of the Salmonella typhimurium trp promoter, both in ColE1 and incP plasmid-based vectors. Use of the incP trp promoter plasmid allowed overexpression of a nodABC gene fragment in R. meliloti. Gene nodA encodes a protein of 21 kilodaltons (kDa), and nodB encodes one of 28 kDa; the nodC product appears as 2 polypeptide bands at 44 and 45 kDa. Expression of the divergently read nodD yields a single polypeptide of 33 kDa. Whether these represent true Rhizobium gene products must be demonstrated by correlating these proteins with genetically defined Rhizobium loci. The 21-kDa putative nodA protein product was purified by gel electrophoresis, selective pptn., and ion-exchange chromatog., and antiserum to the purified gene product was generated. This permitted the immunol. demonstration that the 21-kDa protein is present in wild-type cells and in nodB- or nodC-defective strains, but is absent from nodA::Tn5 mutants, which confirms that the product expressed in E. coli is identical to that produced by R. meliloti nodA. Using antisera detection, it was found that the level of nodA protein is increased by exposure of R. meliloti cells to plant exudate, indicating regulation of the bacterial nod genes by the plant host.

~35 Citings

371. Megaplasmid transfer and incompatibility between plasmids of two different strains of Rhizobium meliloti

By Maoui, K. R.; Bechet, M.; Guillaume, J. B.
From Microbios (1985), 42(171S), 251-62. Language: English, Database: CAPLUS

The conjugal transfer of a megaplasmid between 2 different strains of R. meliloti is reported. This intraspecific transfer was mediated by RP4 which had been previously introduced into the wild-type strain RCR2011. Transfer of plasmid RP4 from this Nod^+ Fix^+ strain to an auxotrophic Nod^+ Fix^- mutant (M5N1m3SR) occurred at frequencies of 3.6×10^{-5}-1.1×10^{-6} or higher. Recombinants reduced acetylene at rates similar to the donor strain. An alteration in the plasmid content was obsd. in Fix^+ recombinants, showing an incompatibility between the incoming megaplasmid and the indigenous middle-sized pRme plasmid of the recipient. These results indicate that simultaneous mobilization and transfer of both chromosomal genes and a megaplasmid can be induced by RP4 between 2 different strains of R. meliloti.

~0 Citings

372. Conservation of symbiotic nitrogen fixation gene sequences in Rhizobium japonicum and Bradyrhizobium japonicum

By Masterson, Robert V.; Prakash, R. K.; Atherly, Alan G.
From Journal of Bacteriology (1985), 163(1), 21-6. Language: English, Database: CAPLUS

Southern hybridization with nif (nitrogen fixation) and nod (nodulation) DNA probes from R. meliloti against intact plasmid DNA of R. japonicum and B. japonicum strains indicated that both nif and nod sequences are on plasmid DNA in most R. japonicum strains. An exception is found with R. japonicum strain USDA194 and all B. japonicum strains where nif and nod sequences are on the chromosome. In R. japonicum strains, with the exception of strain USDA205, both nif and nod sequences are on the same plasmid. In strain USDA205, the nif genes are on a 112-megadalton plasmid, and nod genes are on a 195-megadalton plasmid. Hybridization to EcoRI digests of total DNA to nif and nod probes from R. meliloti show that the nif and nod sequences are conserved in both R. japonicum and B. japonicum strains regardless of the plasmid or chromosomal location of these genes. In addn., nif DNA hybridization patterns were identical among all R. japonicum strains and with most of the B. japonicum strains examd. Similarly, many of the bands that hybridize to the nodulation probe isolated from R. meliloti were found to be common among R. japonicum strains. Under reduced hybridization stringency conditions, strong conservation of nodulation sequences was obsd. in strains of B. japonicum. The plasmid pRjaUSDA193, which possesses nif and nod sequences, does not possess sequence homol. with any plasmid of USDA194, but is homologous to parts of the chromosome of USDA194. Strain USDA194 is unique, since nif and nod sequences are present on the chromosome instead of on a plasmid as obsd. with all other strains examd.

~15 Citings

373. Conserved nodulation genes in Rhizobium meliloti and Rhizobium trifolii

By Fisher, Robert F.; Tu, Janice K.; Long, Sharon R.
From Applied and Environmental Microbiology (1985), 49(6), 1432-5. Language: English, Database: CAPLUS

Plasmids which contained wild-type or mutated R. meliloti nodulation (nod) genes were introduced into Nod- R. trifolii mutants ANU453 and ANU851 and tested for their ability to nodulate clover. Cloned wild-type and mutated R. meliloti nod gene segments restored ANU851 to Nod+, with the exception of nodD mutants. Similarly, wild-type and mutant R. meliloti nod genes complemented ANU453 to Nod+, except for nodCII mutants. Thus, ANU851 identifies the equiv. of the R. meliloti nodD genes, and ANU453 specifies the equiv. of the R. meliloti nodCII genes. In addn., cloned wild-type R. trifolii nod genes were introduced into 7 R. meliloti Nod- mutants. All 7 mutants were restored to Nod+ on alfalfa. The results indicate that these genes represent common nodulation functions and argue for an allelic relationship between nod genes in R. meliloti and R. trifolii.

~5 Citings

374. Effect of calcium on the phosphorus nutrition of Rhizobium meliloti

By Beck, D. P.; Munns, D. N.
From Soil Science Society of America Journal (1985), 49(2), 334-7. Language: English, Database: CAPLUS, DOI:10.2136/sssaj1985.03615995004900020012x

Effects of Ca at 300 and 1500 μM on P nutrition were assessed in 8 strains of R. meliloti in defined liq. medium. Evaluations included: P storage from luxury external concn. (1000 μM P); utilization of stored P after transfer to unreplenished low-P medium (0.06 μM); and growth at low concns. of P buffered at 5, 0.5, and 0.06 μM with an Fe oxide dialysis system. The strains stored P in luxury medium, but unlike other rhizobia, they needed high Ca to utilize the stored P. They either grew or died following transfer to low-P medium, depending on the Ca concn. and the Ca concn. at which they had grown previously. Ability to grow in media buffered at low P, concns. also contrasted with that of other rhizobia, in 2 respects; no strain of R. meliloti grew at 0.06 μM P, regardless of Ca concn., and some strains needed high Ca to grow at 0.5 and 5 μM P. Two isolates from Medicago rugosa and Melilotus indica were less Ca-demanding than 6 isolates from Medicago sativa. Previous reports that R. meliloti has low Ca requirements may be correct only for the luxury P levels that are conventional in defined media. Evidence for high Ca requirement at realistic P concns. agrees with data from soil expts.

~6 Citings

375. Suitability of various legume species and varieties for revegetation of acid surface-mined coal spoils of western Kentucky

By Powell, J. L.; Ellis, M. L.; Armstrong, J. R.; Barnhisel, R. I.
From Univ. Ky., Off. Eng. Serv., [Bull.] UKY BU (1983), (UKY BU133, Symp. Surf. Min. Hydrol. Sedimentol. Reclam.), 121-9. Language: English, Database: CAPLUS

On acid surface-mined coal spoils in western Kentucky during August 1977 and Apr. 1978, 25 selected legume species and varieties of some species were evaluated for yield in small plots with identical fertility management factors. A split-plot exptl. design was used in which there were 2 main plots, the 1st plot where the legumes were seeded alone and the other, N-fertilized plot where the legumes were seeded with Ky. 31 tall fescue. One area was established in the fall and another in the spring. The legumes evaluated consisted of 3 varieties of bird's-foot trefoil, 7 varieties of alfalfa, 4 varieties of red clover, 4 varieties of sericea lespedeza, 2 varieties of annual lespedeza, and single species entries of alsike clover, yellow sweet clover, white clover, hairy vetch, and crown vetch. The above listing of species is, in general, the order of their ranking with respect to yield. Spring seedings also outyielded their counterparts established in the fall. Tempo was the highest yielding alfalfa variety when spring-seeded. Redman was judged as the best overall variety of red clover when fall-seeded. Kenstar and Kenland red clover were judged as the best varieties of red clover for spring seeding for treatments 1 and 2 resp. Among bird's-foot trefoil varieties Dawn was the overall highest yield producer followed closely by the Fergus variety. The data from this expt. in western Kentucky indicated that lespedeza species, alsike clover, yellow sweet clover, white clover, hairy vetch, and crown vetch should not be seeded if success of reclamation is to be judged by predetd. target level yields. N, P, K, Ca, and Mg levels in harvested plant tissues were adequate.

~0 Citings

376. Complementary methods for the differentiation of Rhizobium meliloti isolates

By Fuquay, Janice I.; Bottomley, Peter J.; Jenkins, Michael B.
From Applied and Environmental Microbiology (1984), 47(4), 663-9. Language: English, Database: CAPLUS

The use of serol. methods for differentiation of R. meliloti isolates was studied. One-dimensional SDS-polyacrylamide gel electrophoresis was used to develop protein profiles of 8 field isolates and 1 com. inoculant strain of R. meliloti to choose candidates that were either identical or distinctly different from each other for the prodn. of antisera. The serol. methods of tube agglutination and gel immunodiffusion complemented the SDS-polyacrylamide gel electrophoretic method of identification. On the basis of their agglutination titers and gel immunodiffusion anal., the isolates were placed in 5 serogroups, which were identical to groupings on the basis of protein profiles. Antigenic characteristics of gel immunodiffusion antigens were influenced by the compn. of the growth medium, sonication of whole-cell antigens, and the addn. of formalin. Careful attention should be given to the effects of varying antigen prepn. procedures when examg. R. meliloti, so that exptl. protocols do not complicate the results. The wide range of homologous-antiserum titers obsd. for the 9 isolates indicates different inherent degrees of immunogenicity of R. meliloti which cannot be predicted before serum prodn. The SDS-polyacrylamide gel electrophoresis method is a useful tool for screening a collection of R. meliloti isolates to better ensure that strain-specific antisera representative of different types of organisms will be obtained.

~1 Citing

377. Identification of a Rhizobium trifolii plasmid coding for nitrogen fixation and nodulation genes and its interaction with pJB5JI, a Rhizobium leguminosarum plasmid

By Christensen, Alan H.; Schubert, Karel R.
From Journal of Bacteriology (1983), 156(2), 592-9. Language: English, Database: CAPLUS

R. trifolii T37 contains ≥3 plasmids of >250 megadaltons. Southern blots of agarose gels of these plasmids probed with R. meliloti nif DNA indicated that the smallest plasmid, pRt37a, contains the nif genes. Transfer of the R. leguminosarum plasmid pJB5JI, which codes for pea nodulation and the nif genes and is genetically marked with Tn5, into R. trifolii T37 generated transconjugants contg. a variety of plasmid profiles. The plasmid profiles and symbiotic properties of all of the transconjugants were stably maintained even after reisolation from nodules. The transconjugant strains were placed into 3 groups on the basis of their plasmid profiles and symbiotic properties. The 1st group harbored a plasmid similar in size to pRt37a. These strains formed effective nodules on peas but were unable to nodulate clover and lacked the R. trifolii nif genes. This suggests that genes essential for clover nodulation as well as the R. trifolii nif genes are located on pRt37a and have been deleted. The 2nd group harbored hybrid plasmids formed from pRt37a and pJB5JI which ranged from 140 to ~250 megadaltons. These transconjugants had lost the R. leguminosarum nif genes but retained the R. trifolii nif genes. Strains in this group nodulated both peas and clover but formed effective nodules only on clover. The 3rd group of transconjugants contained a hybrid plasmid similar in size to pRt37b. These strains contained the R. trifolii and R. leguminosarum nif genes and formed N_2-fixing nodules on both peas and clover.

~4 Citings

378. Transfer of an indigenous plasmid of Rhizobium loti to other rhizobia and Agrobacterium tumefaciens

By Pankhurst, C. E.; Broughton, W. J.; Wieneke, U.
From Journal of General Microbiology (1983), 129(8), 2535-43. Language: English, Database: CAPLUS

R. loti Strains NZP2037 and NZP2213 were each found to contain a single large plasmid: pRlo2037a (240 megadaltons) and pRlo2213a (120 megadaltons), resp. Plasmid DNA present in crude cell lysates of each strain and purified pRlo2037a DNA did not hybridize with pID1, a recombinant plasmid contg. part of the N_2 fixation (nif) region of R. meliloti, indicating that nif genes were not present on these plasmids. The transposon Tn5 was inserted into a pRlo2037a and this plasmid was then transferred into R. leguminosarum, R. meliloti, and A. tumefaciens. All transconjugants failed to nodulate Lotus pedunculatus, suggesting that the ability to nodulate this legume was also not carried on pRlo2037a. Transfer of pRlo2037a to R. loti strain NZP2213 did not alter the Nod^+ Fix^- phenotype of this strain for L. pedunculatus. Determinants for flavolan resistance, believed to be necessary for effective nodulation of L. pedunculatus, were not carried on pRlo2037a. Apparently, nodulation, N_2 fixation, and flavolan resistance genes are not present on the large plasmid in R. loti strain NZP2037.

~8 Citings

379. Indication of environmental pollution by mutagenic pesticides from their gametocidal effect on plants

By Kurinnyi, A. I.
From Tsitologiya i Genetika (1983), 17(4), 32-5. Language: Russian, Database: CAPLUS

Fertility of Crepis tectorum pollen decreased with increasing exposure to pesticide pollution, a result indicating the mutagenicity of the pollutants. Other indicator species for quant. detn. and mapping of pollution with mutagenic pesticides are Vicia cracca, V. fenuifolia, Trifolium pratense, and Melilotus albus. Base level of pollen sterility was detd. for these plants with specimens from a nature reserve.

~0 Citings

380. Classification of Rhizobium meliloti by a metabolic property

By Courtois, B.; Hornez, J. P.; Courtois, J.; Derieux, J. C.
From Annales de Microbiologie (Paris) (1983), 134A(2), 141-7. Language: French, Database: CAPLUS

R. meliloti And Agrobacterium strains under conditions of nonproliferation acidified the medium when grown on glucose and metabolized primarily to a polysaccharide. Other Rhizobium species produced approx. as much polysaccharide on glucose as on fructose. These results indicate a closer classification of R. meliloti to the genus Agrobacterium.

~0 Citings

381. Large plasmid in Rhizobium meliloti and Rhizobium lupini

By Ding, Yong; Xu, Qiongfang; Miao, Yuhua; Yang, Taolan
From Yichuan (1982), 4(5), 22-4. Language: Chinese, Database: CAPLUS

On agarose electrophoresis of lysozyme-treated cell prepns. from R. meliloti and R. lupini prepd. according to the method indicated in the EMBO Course (1979), a large plasmid-like band was sepd.; this band appeared behind the chromosomal DNA band and slightly behind the large ref. plasmid pRD1 (101 megadaltons). The large plasmid-like band was further purified by CsCl floatation d. gradient centrifugation. After digestion of the large plasmid prepn. from R. meliloti with restriction endonuclease EcoRI, 8 bands were obsd. in agarose electropherograms; similar amts. and migratory characteristics of the large plasmid bands were obsd. after EcoRI treatment of the R. lupini prepn. Thus, large plasmids of >101 megadaltons appear to be present in R. meliloti and R. lupini.

~0 Citings

382. Effect of inoculation on element uptake by plants grown on saline soils

By Douka, C. E.; Xenoulis, A. C.; Paradellis, T.
From Folia Microbiologica (Prague, Czech Republic) (1982), 27(4), 278-80. Language: English, Database: CAPLUS, DOI:10.1007/BF02877131

A comparison of the elemental concn. in inoculated and control (uninoculated) alfalfa plants showed that Fe, Cu, Zn, and Zr concns. were not affected by inoculation, while Ca, K, Mn, Br, Sr, and Rb concns. were higher in inoculated than control plants. Soil inoculation with Rhizobium meliloti decreased the Mo content of the plants by 58%, indicating that the inoculation efficacy may be measured by the level of Mo in the plants. Root nodulation and plant dry mass after 4 mo of growth were highest in inoculated plants.

~0 Citings

383. Survey of ammonium (methylammonium) transport by aerobic nitrogen-fixing bacteria - the special case of Rhizobium

By Wiegel, Juergen; Kleiner, Diethelm
From FEMS Microbiology Letters (1982), 15(1), 61-3. Language: English, Database: CAPLUS, DOI:10.1111/j.1574-6968.1982.tb00038.x

All 9 strains of N_2-fixing bacteria (Azotobacter vinelandii, Beijerinckia mobilis, Derxia gummosa, Azomonas agilis, Azorhizophilus paspali, Azomonotrichon macrocytogenes, Xanthobacter autotrophicus, Alcaligenes latus, Rhizobium meliloti) studied took up $^{14}CH_3NH_3^+$. With the exception of R. meliloti, this uptake was prevented >90% by 0.2 mM NH_4^+, and part of the accumulated $CH_3NH_3^+$ was released after a pulse with 50 mM NH_4^+. This indicates that all strains possess NH_4^+ transport systems, with the exception of R. meliloti, and support the suggestion that NH_4^+ transport systems are common among free-living N-fixing bacteria. Thus, Rhizobium may be unable to synthesize an NH_4^+ transport system and its membrane may be rather permeable to NH_3.

~1 Citing

384. Toxicity of molybdenum and its trace analysis in animal tissues and plants

By Abbasi, Shahid Abbas
From International Journal of Environmental Analytical Chemistry (1981), 10(3-4), 305-8. Language: English, Database: CAPLUS, DOI:10.1080/03067318108071554

Mo was extd. from goat liver and plants (Melilotus indica and Chloria barbata) with isoamyl alc. and N-o-tolyl-o-methoxybenzohydroxamic acid at pH 1.25-2.5 and detd. spectrophotometrically at 350 nm. Beer's law was obeyed in the 0.5-10.5 μg/mL range. The sensitivity of the technique was 0.010 μg Mo/mL. The technique had a high degree of accuracy in the absence or presence of Cu and Zn.

~1 Citing

385. Influence of 2,4-D on carbon-14 dioxide fixation in Lathyrus aphaca, Melilotus indica and Pisum sativum

By Pathak, A. K.; Bhan, V. M.
From Indian Journal of Weed Science (1980), 12(2), 171-3. Language: English, Database: CAPLUS

Application 2,4-D [94-75-7] (0.5 kg/ha) reduced photosynthetic $^{14}CO_2$ fixation capacity of all 3 species studied. The redn. at 1, 4, and 8 days after 2,4-D treatment was 28.8, 59.4, and 71.2% in L. aphaca, 47.9, 67.3, and 76.9% in M. indica, and 42.7, 74.2, and 87.7% in P. sativum, resp. Susceptibility of these species to 2,4-D may be due to blocking of a photosynthetic mechanism.

~0 Citings

386. Properties of Tn5-induced carbohydrate mutants in Rhizobium meliloti

By Duncan, Margaret J.
From Journal of General Microbiology (1981), 122(1), 61-7. Language: English, Database: CAPLUS

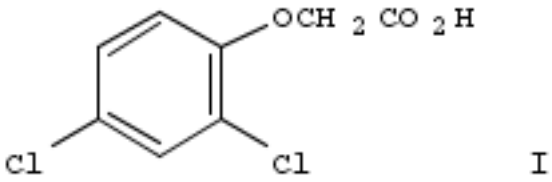
Four carbohydrate mutants isolated from R. meliloti L5-30 by using the translocatable drug-resistance element Tn5 lacked mannitol dehydrogenase, ribose kinase, xylose isomerase, and fructose kinase, resp. An L-arabinose mutant was also isolated. Uptake studies showed that the ribose, xylose, and fructose mutants still utilized the sugars on which they were unable to grow, possibly indicating that R. meliloti has alternative metabolic routes which do not result in growth. All the mutants were able to nodulate alfalfa plants, but the fructose kinase mutant could not fix N, and the L-arabinose mutant showed either late or no N-fixing ability.

~7 Citings

387. Total chlorophyll content of weeds as affected by a triazine and a phenoxy herbicide and its usage as an index of biomass of weeds in the treated plots

By Rao, A. N.; Dubey, P. S.
From Acta Agronomica Academiae Scientiarum Hungaricae (1981), 30(3-4), 425-30. Language: English, Database: CAPLUS

Bladex (cyanazine) [21725-46-2] and 2,4-D (I) [94-75-7] at 0.5, 1.0, and 2.0 kg/ha were applied postemergence to a wheat plot heavily infested by 5 weed species. Redns. in each weed species chlorophyll content per m^2 and biomass (g/m^2) were obsd. 15 days and 1 mo after the herbicide treatments, resp. The av. chlorophyll content of the weeds was linearly correlated with biomass for both herbicidal treatments (r = 0.9749 and 0.9972 for I and Bladex, resp.). Thus, chlorophyll content is an indicator of biomass or dry matter productivity of weeds treated with I and Bladex.



I

~1 Citing

388. Pharmacognostical study of Melilotus indicus (L.) All. var. Tommasinii Jord

By Khafagy, S. M.; Sabri, N. Nazmi; Abou Donia, A. H.
From Egyptian Journal of Pharmaceutical Sciences (1980), 19(1-4), 293-300. Language: English, Database: CAPLUS

Wheat flour was extd. with alc. potash, and coumarin [91-64-5] in the ext. was sepd. by TLC on Silica gel G and detected by fluorescence at 366 nm. The detection threshold was ~0.05% coumarin. M. indicus, The source of coumarin, could also be detected in flour by microscopy. M. indicus Seeds contained coumarin 1.3, β-sitosterol [83-46-5] 0.14, sitosteryl-3β-D-glucoside [474-58-8] 0.014, and choline [62-49-7] 0.28%. Morphol. studies on M. indicus are presented.

~0 Citings

389. Large plasmids of fast-growing rhizobia: homology studies and location of structural nitrogen fixation (nif) genes

By Prakash, Rameswaram K.; Schilperoort, Rob A.; Nuti, Marco P.
From Journal of Bacteriology (1981), 145(3), 1129-36. Language: English, Database: CAPLUS

A single large plasmid was isolated from multiplasmid-harboring strains Rhizobium leguminosarum 1001 and R. trifolii 5. These single plasmids, as well as the largest plasmid detectable in R. phaseoli 3622, hybridized with part of the nif structural genes of Klebsiella pneumoniae. In contrast, the plasmids of R. meliloti strains V7 and L5-30 did not show hybridization with the nif genes of K. pneumoniae, indicating that these genes might be located either on the chromosome or on a much larger plasmid not yet isolated. Studies of the homol. between plasmids of fast-growing Rhizobium species showed that a specific DNA sequence, which carries the structural genes for nitrogenase, is highly conserved on a plasmid in R. leguminosarum, R. trifolii, and R. phaseoli. Furthermore, this type of plasmid in the different species shares extensive DNA homol., suggesting that strains in the R. leguminosarum cluster have preserved a nif plasmid.

~6 Citings

390. Oxygen and mannitol consumption of Rhizobium meliloti in relation to symbiotic nitrogen fixation efficiency

By Bordeleau, L. M.; Lalande, R.; Antoun, H.
From Plant and Soil (1980), 56(3), 439-43. Language: English, Database: CAPLUS, DOI:10.1007/BF02143037

The rates of O and total mannitol consumption were studied with 48 strains of R. meliloti and related to their symbiotic N fixation efficiency (expressed by plant dry-wt. yields) as reported by L.M. Bordeleau et al. (1977). The rate of O consumption is pos. correlated to the total mannitol consumption, and significant inverse relations between these 2 physiol. properties and symbiotic efficiency are apparent. The possibility of using the rate of O consumption as a preselection tool is discussed.

~0 Citings

391. Restriction mapping of DNA of temperate Rhizobium meliloti phage 16-3: comparison of genetic and physical maps indicates a long, genetically silent chromosomal arm

By Dallmann, Geza; Orosz, Laszlo; Sain, Bela
From Molecular and General Genetics (1979), 176(3), 439-48. Language: English, Database: CAPLUS, DOI:10.1007/BF00333109

The complete restriction map of DNA (61.57 kilobases) of temperate R. meliloti phage 16-3 was constructed for enzymes BglII, HindIII, HpaI, KpnI, and a partial map for EcoRI. The strategy employed for mapping included the anal. of double, triple, and partial digests; comparison of wild-type and deletion mutants; and detailed anal. of subfragments, exploiting the presence of cohesive ends of the phage. Comparison of the genetic and phys. maps indicates that one arm of the chromosome is genetically silent and (or) contains nonessential genes.

~4 Citings

392. Weed seed germination responses to some chemical treatments

By Moursi, M. A.; Rizk, T. Y.; El-Deepah, H. R.
From Egyptian Journal of Agronomy (1979), 2(2), 197-209. Language: English, Database: CAPLUS

The effect of urea [57-13-6] at 0.5%, KNO_3 at 0.3%, and thiourea [62-56-6] at 0.2 and 0.25% on the germination of 10 summer weeds and 12 winter weeds was investigated. The response of germination rate index, and length of radicle and plumule of germinated seeds differed greatly according to weed species and chems. used. Whereas these chems. differed in their effect on germination of most weeds studied, they exerted no effect on germination of prickly sida, Swiss chard, and spiny cocklebur. Although urea and KNO_3 had no effect on the germination percentage of pepperweed, sow thistle, and scented trefoil seeds, thiourea increased their germination. On the contrary, both urea and KNO_3 increased the germination percentage of barnyard grass seeds, but thiourea did not. Similar responses were reported in respect to germination rate index and length of radicle and plumule: whereas KNO_3 and thiourea increased the germination rate index of jungle rice seeds, urea did not, moreover KNO_3 increased both radicle and plumule length of jungle rice, but urea and thioure decreased them. Room temp. improved the germination of broad leaf, pigweed, wild mustard, pepperweed, scented trefoil, wild chicory, and sow thistle seeds, but low temp. improved the germination of purslane seeds.

~0 Citings

393. Efficient use of phosphatic fertilizers of varying water solubility for wheat, senji and berseem

By Sadaphal, M. N.; Singh, T.
From Bulletin - Indian Society of Soil Science (1979), 12(Phosphorus Soils, Crops Fert.), 584-8. Language: English, Database: CAPLUS

Field expts. carried out on dwarf wheat, senji (Melilotus parviflora), and berseem (Trifolium alexandrinum) indicated that wheat responded only to the application of phosphate sources having a high degree of water soly., the fertilizers with lower water-sol. P being ineffective. Senji and berseem could utilize phosphate fertilizers having most of the P in the citrate-sol. form, but the magnitude of response was lower than that with a fully water-sol. source. New citrate-sol. products like Pelofos, having a small amt. in water-sol. P, could be recommended for fodder legumes such as senji as well as berseem.

~0 Citings

394. Structure of nodules induced by auxotrophic and ineffective mutants of Rhizobium meliloti strain L5-30 requiring cysteine, arginine + uracil and histidine

By Malek, Wanda; Kowalski, Mieczyslaw
From Acta Microbiologica Polonica (1977), 26(4), 351-9. Language: English, Database: CAPLUS

Nodules produced by ineffective mutants of R. meliloti strain L5-30 requiring arginine + uracil (arg-55) and cysteine-requiring mutants (cys-243, cys-244, cys-246) studied by light microscopy were occupied by bacteria, indicating a defect in transformation of these mutants into N_2-fixing bacteroids. These defects were not assocd. with auxotrophy. In nodules induced by histidine-requiring mutant (his-240) only a few host plant cells were occupied by bacteria. This indicates that the his-240 mutant is defective in liberation from the infection thread and its multiplication since supplementation of the plant growth medium with 50 μg/mL of L-histidine enabled establishment of fully effective assocn. Prototrophic transductants and revertants were fully effective.

~3 Citings

395. Changes in the chemical composition of forages and its relation with in vitro digestibility at different stages of maturity

By Ahuja, S. P.; Chaudhary, K. C.; Sharma, K. C.; Bhatia, I. S.
From Indian Journal of Animal Sciences (1974), 44(10), 725-36. Language: English, Database: CAPLUS

The changes in the crystallinity of cellulose (CC), compn. of cell solubles (CS) and cell-wall constituents of senji (Melilotus indica), metha (Trigonella foenum-graecum), oat (Avena sativa), barley (Hordeum vulgare), sunflower (Helianthus annuus) and Japanese sarson (Brassica campestris) plants during their growth were detd. and correlated with the 48-h in vitro digestion of cellulose (IVCD) and dry matter (IVDMD). The crude protein (CP), true protein (TP) and CS contents decreased, and the lignin, acid-detergent fiber (ADF) contents, except in metha and barley, increased with maturity of the crops. The resp. correlations of IVCD and IVDMD with CP, TP, ADF, CS and CC were 0.60, 0.60, -0.58, 0.54, and -0.69, and 0.49, 0.49, -0.57, 0.40, and -0.38, and were significant. Such correlations of IVCD, IVDMD with lignin and hemicellulose were also established for individual crops, but not for data pooled from all the crops. The roles of CC, lignin, and sugars forming the hemicellulose in depressing the digestion of forages were discussed.

~0 Citings

396. Benzo-1,2-pyrone in Melilotus indicus (L) All

By Silva, Gilberto A. de A. B. e; Saraiva, de Siqueira, Norma Cloris; Sant'Ana, Belkis M. S.; Bauer, Luiz
From Revista Brasileira de Farmacia (1976), 57(3-4), 111-15. Language: Portuguese, Database: CAPLUS

Benzo-1,2-pyrone (I) was isolated from leaves and upper flowers of sweet clover (M. indicus) by thin-layer chromatog. (80:20 C6H6-Me2CO system) using silica gel plates. Leaf and flower samples were macerated prior to extn. with EtOH and C6H6. The C6H6-sol. fraction was used for chromatog. I was purified after the method of E. Guenther (1949), and the identification was confirmed by mass spectroscopy and NMR.

~1 Citing

397. Ammonia assimilation and nitrogen fixation in Rhizobium meliloti

By Kondorosi, A.; Svab, Z.; Kiss, G. B.; Dixon, R. A.
From Molecular and General Genetics (1977), 151(2), 221-6. Language: English, Database: CAPLUS, DOI:10.1007/BF00338698

The enzymes involved in NH3 assimilation by R. meliloti 41 and their role in the regulation of N metab. were studied. Glutamine synthetase (GS) and glutamate synthase (GOGAT) were present at relatively high levels in cells grown in media contg. either low or high concns. of NH3. NADP-linked glutamate dehydrogenase could not be detected. GOGAT and GS mutants were isolated and characterized. A mutant lacking GOGAT activity did not grow even on high concns. of NH3. It was a glutamate auxotroph and was effective in symbiotic N fixation. The GS and assimilatory nitrate reductase activities of this mutant were not repressible by NH3 but still repressible by casamino acids. A mutant with low GS activity required glutamine for optimal growth. It was ineffective and its nitrate reductase was not inducible. These findings indicate that NH3 is assimilated via the GS/GOGAT pathway in free-living R. meliloti and bacterial GOGAT is not important in symbiosis. Furthermore, GS is suggested to be a controlling element in the N metab. of R. meliloti.

~12 Citings

398. Phytoreclamation of technogenic soils and invertase activity

By Keleberda, T. N.
From Pochvovedenie (1976), (10), 126-31. Language: Russian, Database: CAPLUS

Invertase [9001-57-4] activity may serve as an indication of plant efficiency in reclaiming of mine waste soils. Seeding of perennial legumes, sweet clover, and some tree species (pine, false acacia, and European alder) increased the humus and N accumulation, esp. in the 2-10-cm layer, and so increased the invertase activity. The invertase activity was highest in the 0-2-cm layer. On lupine-grown dump soils, the increments in tree (pine, birch, and oak) growth and N and chlorophyll contents of leaves were highly significant.

~0 Citings

399. Effect of canavanine on the growth of cells from suspension cultures and on intergeneric heterokaryocytes of canavanine sensitive and tolerant plants

By Constabel, F.; Kirkpatrick, J. W.; Kao, K. N.; Kartha, K. K.
From Biochemie und Physiologie der Pflanzen (1975), 168(1-4), 319-25. Language: English, Database: CAPLUS

Through application of the polyethylene glycol method, protoplasts of canavanine-sensitive soybean cell cultures were fused with canavanine-tolerant protoplasts from alfalfa, Caragana, and sweet clover. Within several days of culture the fusion products, heterokaryocytes, divided and developed into small cell clusters. The heterokaryocytes exhibited a sensitivity to canavanine as strong as soybean protoplasts. The results indicate that protoplasts from cultured soybean cells and from mature leaves of alfalfa, Caragana, and sweet clover, when fused, do not generate an incompatibility which would prevent cell division. The reaction pattern of the heterokaryocytes appeared to be detd. by the soybean partner.

~0 Citings

400. Genetic studies of induced mutants in Melilotus alba. IV. Inheritance and complementation of six additional chlorophyll-deficient mutants

By Ronnenkamp, R. R.; Gorz, H. J.; Haskins, F. A.
From Crop Science (1975), 15(2), 187-8. Language: English, Database: CAPLUS,
DOI:10.2135/cropsci1975.0011183X001500020013x

Genetic studies of six ethyl methanesulfonate-induced chlorophyll-deficient mutants of sweet clover (M. alba) indicated that each behaved as a monogenic recessive. Genes from 5 of the mutants were nonallelic to each other and to 4 previously reported mutants. The chlorophyll-deficient mutants could be readily distinguished from the normal, were sufficiently vigorous to permit good growth, and produced enough seed for adequate line maintenance.

~0 Citings