201. Efficacy of herbicides to control weeds in potato (Solanum tuberosum L.) under tarai conditions of Uttaranchal

By Tripathi, S. S.; Singh, Govindra
From Pestology (2003), 27(1), 15-17. Language: English, Database: CAPLUS

A field expt. conducted during the winter season of 2000-2001 and 2001-2002 evaluated the efficacy of herbicides against weeds in Potato. Anagallis arvensis and Chenopodium album were the major weeds constituting 32.8 and 19.8% of the total weed population at 60 days after planting. Presence of weeds throughout the growing season caused more than 47% redn. in the tuber yields. All the herbicides at different doses caused significant redn. in the d. and dry matter prodn. of weeds and significant increase in tuber prodn. Chlorimuronethyl at 6 g ha^{-1} produced tuber yield at par with weed-free treatment. Increasing dose of clomazone alone did not influence tuber yield significantly. Pendimethalin and prometryn each at lower doses gave almost similar tuber prodn. Prometryn 500 and 750 g ha^{-1} produced tuber yields at par with pendimethalin at 500 and 1000 g ha^{-1}, resp.

~0 Citings

202. Biotin limitation in Sinorhizobium meliloti strain 1021 alters transcription and translation

By Heinz, Elke B.; Streit, Wolfgang R.
From Applied and Environmental Microbiology (2003), 69(2), 1206-1213. Language: English, Database: CAPLUS, DOI:10.1128/AEM.69.2.1206-1213.2003

Most Sinorhizobium meliloti strains lack several key genes involved in microbial biotin biosynthesis, and it is assumed that this may be a special adaptation which allows the microbe to down-regulate metabolic activities in the absence of a host plant. To further explore this hypothesis, we employed two different strategies. (i) Searches of the S. meliloti genome database in combination with the construction of nine different gusA reporter fusions identified three genes involved in a biotin starvation response in this microbe. A gene coding for a protein-Me carboxyl transferase (pcm) exhibited 13.6-fold-higher transcription under biotin-limiting conditions than cells grown in the presence of 40 nM biotin. Consistent with this observation, biotin-limiting conditions resulted in a significantly decreased survival of pcm mutant cells compared to parental cells or cells grown in the presence of 40 nM biotin. Further studies indicated that the autoinducer synthase gene, sinI, was transcribed at a 4.5-fold-higher level in early stationary phase in biotin-starved cells than in biotin-supplemented cells. Lastly, we obsd. that open reading frame smc02283, which codes for a putative copper resistance protein (CopC), was 21-fold down-regulated in response to biotin starvation. (ii) In a second approach, proteome anal. identified 10 proteins which were significantly down-regulated under the biotin-limiting conditions. Among the proteins identified by using matrix-assisted laser desorption ionization-time of flight mass spectrometry were the subunit of the RNA polymerase and the 50S ribosomal protein L7/L12 (L8) subunit, indicating that biotin-limiting conditions generally affect transcription and translation in S. meliloti.

~7 Citings

203. Genotypic characterization of rhizobia isolated from wild legumes of Egyptian soils by DNA-RAPD PCR fingerprinting and their IEF protein patterns

By El-Bakry, Ahmed A.; Tantawy, Hassan; Abdel-Wahab, Samir M.; El-Batanony, Nadia H.; Ibrahim, Samir A.
From African Journal of Mycology and Biotechnology (2002), 10(2), 47-63. Language: English, Database: CAPLUS

Total genomic DNA isolated from 18 wild rhizobial isolates, obtained from nodules of 12 wild leguminous plant species, grown in different phytogeog. regions of lower Egypt was analyzed by the polymerase chain reaction (PCR) using three arbitrary primers (UBC23, UBC44 and UBC73). The amplified fragment length polymorphisms (amplification profiles) generated by the three primers, effectively differentiated a diverse collection of wild rhizobial isolates. The three primers were also highly discriminatory on the 18 wild isolate DNA and generated unique amplification profiles for each isolates, revealing that those wild isolates may be new strains of rhizobia. Also, the water sol. proteins of the 18 wild isolates were analyzed by the IEF protein banding patterns. It was found that they had great diversity and they were very distinct from each other.

~1 Citing

204. Weed control in rose-scented geranium (Pelargonium spp)

By Kothari, Sushil K.; Singh, Chandra P.; Singh, Kamla
From Pest Management Science (2002), 58(12), 1254-1258. Language: English, Database: CAPLUS, DOI:10.1002/ps.592

Field investigations were carried out during 1999 and 2000 to identify effective chem./cultural methods of weed control in rose-scented geranium (Pelargonium spp). The treatments comprised pre-emergence applications of oxyfluorfen (0.15, 0.20 and 0.25 kg ha^{-1}) and pendimethalin (0.50, 0.75 and 1.00 kg ha^{-1}), successive hand weeding, hoeing and mulching using spent of lemon grass (at 5 tons ha^{-1}) 45 days after planting (DAP), three hand-weedings 30, 60 and 90 DAP, weed-free (frequent manual weeding) and weedy control. Broad-leaf weeds were more predominant than grass and sedge weeds, accounting for 85.8% weed d. and 93.0% weed dry wt. in 1999 and 77.2% weed d. and 93.9% weed dry wt. in 2000. Unrestricted weed growth significantly reduced geranium oil yield, by 61.6% and 70.6% in 1999 and 2000, resp. Pre-emergence application of pendimethalin (0.75-1.00 kg ha^{-1}) or oxyfluorfen (0.25 kg ha^{-1}), successive hand-weeding, hoeing and mulching and three hand-weedings were highly effective in reducing weed d. and dry wt. and gave oil yield comparable to the weed-free check. Application of oxyfluorfen (0.15 or 0.20 kg ha^{-1}) and pendimethalin (0.50 kg ha^{-1}) were less effective in controlling the weed species in geranium. None of the herbicides impaired the quality of rose-scented geranium oil measured in terms of citronellol and geraniol content.

~0 Citings

205. Spectrophotometric determination of cerium with leuco xylene cyanol FF

By Revanasiddappa, Hosakere D.; Kiran Kumar, Telangusadhushetty N.
From Analytical Sciences (2002), 18(11), 1275-1278. Language: English, Database: CAPLUS, DOI:10.2116/analsci.18.1275

A simple, inexpensive, highly sensitive and specific spectrophotometric detn. of cerium using leuco xylene cyanol FF is reported. The method was successfully applied to the detn. of cerium in high-purity rare earth oxides, soil, natural water, plant tissues, hair, and rock samples.

~10 Citings

206. A comparison of ecotoxicological tests

By Botsford, James L.
From ATLA, Alternatives to Laboratory Animals (2002), 30(5), 539-550. Language: English, Database: CAPLUS

A simple, inexpensive and rapid method of detg. toxicity by using a bacterium as the indicator organism was developed and compared with 23 other tests. The av. correlation coeff. when comparing these 23 tests with the present test was 0.800, ranging from 0.580 to 0.950. Eleven of the tests were compared in detail by using 35 of the chems. on the Multicentre Evaluation of In Vitro Cytotoxicity list of test chems. Comparing results from the present test with test results for these 35 chems. with Microtox, Biotox, Daphnia magna, rat hepatocytes and ascites tumor cell resulted in correlation coeffs. ranging from 0.871 to 0.933. Comparisons of the test data with rodent LD50 values, human LD ests. from autopsies and human LDs obtained from the literature provided correlation coeffs. ranging from 0.580 to 0.770, indicating that the test compares less favorably with these methods. This test provides data comparable to data from other ecotoxicol. tests.

~11 Citings

207. Symbiotic characterization of isoleucine + valine and leucine auxotrophs of Sinorhizobium meliloti

By Hassani, Raad; Prasad, C. Krishna; Vineetha, K. E.; Vij, Neeraj; Singh, Prachi; Sud, Reeteka; Yadav, Sangeeta; Randhawa, Gursharn S.
From Indian Journal of Experimental Biology (2002), 40(10), 1110-1120. Language: English, Database: CAPLUS

Ten isoleucine+valine and three leucine auxotrophs of Sinorhizobium meliloti Rmd201 were obtained by random mutagenesis with transposon Tn5 followed by screening of Tn5 derivs. on minimal medium supplemented with modified Holliday pools. Based on intermediate feeding, intermediate accumulation and cross-feeding studies, isoleucine+valine and leucine auxotrophs were designated as ilvB/ilvG, ilvC and ilvD, and leuC/leuD and leuB mutants, resp. Symbiotic properties of all ilvD mutants with alfalfa plants were similar to those of the parental strain. The ilvB/ilvG and ilvC mutants were Nod^-. Inoculation of alfalfa plants with ilvB/ilvG mutant did not result in root hair curling and infection thread formation. The ilvC mutants were capable of curling root hairs but did not induce infection thread formation. All leucine auxotrophs were Nod^+ Fix^-. Supplementation of leucine to the plant nutrient medium did not restore symbiotic effectiveness to the auxotrophs. Histol. studies revealed that the nodules induced by the leucine auxotrophs did not develop fully like those induced by the parental strain. Nod factors. The nodules induced by leuB mutants were structurally more advanced than the leuC/leuD mutant induced nodules. These results indicate that ilvB/ilvG, ilvC and one or two leu genes of S. meliloti may have a role in symbiosis. The position of ilv genes on the chromosomal map of S. meliloti was found to be near ade-15 marker.

~4 Citings

208. Efficacy of sulfosulfuron against weeds in wheat in relation to irrigation frequency

By Kumar, S.; Tyagi, R. C.; Malik, R. K.
From Tests of Agrochemicals and Cultivars (2001), 22, 20-21. Language: English, Database: CAPLUS

To overcome the problem of wheat crop infestation with grassy weeds, a selective weedicide, called sulfosulfuron, is proposed as an alternative to isoproturon because of its broad spectrum weed control, low dose and low mammalian toxicity. A field investigation was conducted to test sulfosulfuron under different irrigation frequency in wheat crops. On the av., wheat irrigated four and six times yielded 16.3% and 18.2% higher, resp., as compared to crops given two irrigations, which might be attributed to better growth and development in terms of yield attributes because of better moisture availability. At all rates, sulfosulfuron produced significantly higher yield of wheat as compared to weedy check. Based on these results, sulfosulfuron at 20 g a.i. ha^{-1} has proven to be an effective alternative to control grassy as well as broad leaved weeds in wheat.

~0 Citings

209. Sequencing and annotation of the megaplasmid pSymB of the nitrogen-fixing endosymbiont Sinorhizobium meliloti

By Weidner, S.; Buhrmester, J.; Sharypova, L.; Vorholter, F.-J.; Becker, A.; Puhler, A.
Edited By:Finan, Turlough M
From Nitrogen Fixation: Global Perspectives, Proceedings of the International Congress on Nitrogen Fixation, 13th, Hamilton, ON, Canada, July 2-7, 2001 (2002), 46-49. Language: English, Database: CAPLUS

An international consortium was formed to sequence the complete genome of the nitrogen-fixing endosymbiont Sinorhizobium meliloti strain 1021, which is composed of a chromosome and two megaplasmids, pSymA and pSymB. The sequence of the megaplasmid pSymB was established as a collaborative project of the Bielefeld group and in the group of T.M. Finan from the McMaster University. Results of the project indicate that the megaplasmid pSymB is a second chromosome in S. meliloti. In addn. to pSymB being comparable in size, the gene regions of pSymB coding for the arginine-tRNA and MinCDE are essential for the growth of the S. meliloti. Also, the G+C content of pSymB and of the chromosome of S. meliloti are almost identical.

~0 Citings

210. Functional analysis of Sinorhizobium meliloti genes involved in biotin synthesis and transport

By Entcheva, Plamena; Phillips, Donald A.; Streit, Wolfgang R.
From Applied and Environmental Microbiology (2002), 68(6), 2843-2848. Language: English, Database: CAPLUS, DOI:10.1128/AEM.68.6.2843-2848.2002

External biotin greatly stimulates bacterial growth and alfalfa root colonization by Sinorhizobium meliloti strain 1021. Several genes involved in responses to plant-derived biotin have been identified in this bacterium, but no genes required for biotin transport are known, and not all loci required for biotin synthesis have been assigned. Searches of the S. meliloti genome database in combination with complementation tests of Escherichia coli biotin auxotrophs indicate that biotin synthesis probably is limited in S. meliloti 1021 by the poor functioning or complete absence of several key genes. Although several open reading frames with significant similarities to genes required for synthesis of biotin in gram-pos. and gram-neg. bacteria were found, only bioB, bioF, and bioH were demonstrably functional in complementation tests with known E. coli mutants. No sequence or complementation evidence was found for bioA, bioC, bioD, or bioZ. In contrast to other microorganisms, the S. meliloti bioB and bioF genes are not localized in a biotin synthesis operon, but bioB is co-transcribed with two genes coding for ABC transporter-like proteins, designated here bioM and bioN. Mutations in bioM and bioN eliminated growth on alfalfa roots and reduced bacterial capacity to maintain normal intracellular levels of biotin. Taken together, these data suggest that S. meliloti normally grows on exogenous biotin using bioM and bioN to conserve biotin assimilated from external sources.

~36 Citings

211. Effect of dose and mode of metribuzin application on Phalaris minor and yield of wheat (Triticum aestivum)

By Pandey, Jitendra
From Indian Journal of Agricultural Sciences (2002), 72(1), 11-13. Language: English, Database: CAPLUS

A study was conducted during winter (Rabi) season of 1998-2000 to find out optimum dose and mode of metribuzin application on its effect on Phalaris minor (Retz) and yield of wheat (Triticum aestivum L. emend. Fiori and Paol). There was severe competition between wheat and little canary grass (Phalaris minor). Competition by yellow sweet clover (Melilotus indica), swincress (Coronopus didymus) and wood sorrel (Rumex sp.) which also invaded the field was insignificant. The av. redn. in grain yield due to P. minor competition was 36%. Weed control treatments lowered weed population and weed biomass accumulation and boosted up crop yield. Application of metribuzin as post-emergence resulted in better control of weeds than its pre-emergence application. At 200 g/ha, it killed all the plants of swincress, yellow sweet clover and wood sorrel (Rumex sp.) and gave excellent control of Phalaris minor (94%). At 150 g/ha, its effect on C. didymus and Rumex sp. was almost similar to that of 200 g/ha, but slightly lower on P. minor (86%) and poor on M. indica. Pendimethalin gave moderate control of P. minor and good control of M. indica, C. didymus and Rumex sp. The highest yield was recorded in hand weeding which was significantly superior to all other treatments. Metribuzin as post-emergence at 100 and 150 g/ha caused significantly higher increase compared to its application at 200 g/ha pre and post emergence and 150 g/ha pre emergence. It caused marked increase in productive tillers and yield attributes. The increase in yield attributes in pendimethalin was similar to that of metribuzin 100 g/ha pre-emergence.

~1 Citing

212. Performance of metsulfuron methyl and pendimethalin alone and their mixtures with isoproturon on weed control in wheat (Triticum aestivum) seed crop

By Chopra, Nisha; Singh, Harpal; Tripathi, H. P.; Chopra, N. K.
From Indian Journal of Agronomy (2001), 46(2), 239-245. Language: English, Database: CAPLUS

A field expt. was conducted during the winter seasons of 1996-97 and 1997-98 to study the comparative performance of different herbicides, their combinations and their reduced doses for weed control in wheat (Triticum aestivum L. emend. Fiori & Paol.) seed crop. Unchecked weeds caused nearly 37.7% seed yield loss. Maximum seed yield of 39.9 and 33.66 q/ha was recorded in weed-free treatment resp. during both the years. This high-yielding treatment was significantly at par with sequential application of herbicides and herbicide mixt. but was statistically significant to full and half doses of Pendimethalin and Metsulfuron Me in both the years. Pendimethalin @ 1.0 kg a.i./ha and Metsulfuron @ 0.008 kg a.i./ha significantly increased seed yield over unweeded control. Reduced dose of Isoproturon @ 0.5 kg a.i./ha, Pendimethalin @ 0.5 kg a.i./ha and Metsulfuron @ 0.004 kg a.i./ha was least effective in controlling weeds and had min. impact on enhancing seed yield over the control.

~1 Citing

213. The Sinorhizobium meliloti stringent response affects multiple aspects of symbiosis

By Wells, Derek H.; Long, Sharon R.
From Molecular Microbiology (2002), 43(5), 1115-1127. Language: English, Database: CAPLUS, DOI:10.1046/j.1365-2958.2002.02826.x

Sinorhizobium meliloti and host legumes enter into a nitrogen-fixing, symbiotic relationship triggered by an exchange of signals between bacteria and plant. S. meliloti produces Nod factor, which elicits the formation of nodules on plant roots, and succinoglycan, an exopolysaccharide that allows for bacterial invasion and colonization of the host. The biosynthesis of these mols. is well defined, but the specific regulation of these compds. is not completely understood. Bacteria control complex regulatory networks by the prodn. of ppGpp, the effector mol. of the stringent response, which induces physiol. change in response to adverse growth conditions and can also control bacterial development and virulence. Through detailed anal. of an S. meliloti mutant incapable of producing ppGpp, we show that the stringent response is required for nodule formation and regulates the prodn. of succinoglycan. Although it remains unknown whether these phenotypes are connected, we have isolated suppressor strains that restore both defects and potentially identify key downstream regulatory genes. These results indicate that the S. meliloti stringent response has roles in both succinoglycan prodn. and nodule formation and, more importantly, that control of bacterial physiol. in response to the plant and surrounding environment is crit. to the establishment of a successful symbiosis.

~66 Citings

214. Taxonomic significance of chromosome number and seed protein electrophoretic analysis in some taxa of tribe Trifolieae (Papilionoideae)

By George, N. M.; Hussein, H. A.
From Egyptian Journal of Biotechnology (2002), 11, 323-329. Language: English, Database: CAPLUS

Chromosome no. and the seed protein electrophoretic anal. of nine species and one variety of tribe Trifolieae were investigated. The diploid chromosome no. (2n) showed variation being; 2n = 14, 16, 18, 28 and 30. Addnl., the data obtained from the numerical anal. of the seed protein electrophoretic profiles coupled with the chromosome counts add an addnl. evidence that largely accords to the previous sepn. of the genus Ononis from the tribe Trifolieae. Furthermore, the seed protein anal. and/or the chromosome counts proved their value as reliable characters for delimitation of the examd. taxa at the generic and specific levels resp.

~1 Citing

215. Influence of herbicides on weed management in true potato

By Pandey, J.; Sing, R.; Verma, A. K.
From Acta Agronomica Hungarica (2001), 49(2), 183-187. Language: English, Database: CAPLUS, DOI:10.1556/AAgr.49.2001.2.9

Severe competition was shown between potato and the predominant weed species Coronopus didymus, Chenopodium album, Fumaria parviflora, Melilotus indica and Spergula arvensis. Competition by other weed species was nominal. The max. redn. in tuber yield due to weed competition was 50.5% in 1997-98 and 63.4% in 1998-99. Weed control treatments lowered the weed d. and weed biomass and scaled up tuber yield in both the years, but their effect on weed species differed. Metribuzin killed all the Chenopodium album plants and gave excellent control of Coronopus didymus (94%) and effective control of other weed species. Pendimethalin inhibited the germination of Chenopodium album, gave good control of arvensis and lowered the d. of other weed species. Fluchloralin completely inhibited the germination of Fumaria parviflora and gave good control of Chenopodium album and Spergula arvensis, but was least effective against other weed species. The highest yield was recorded in the weed-free treatment, which was significantly superior to all other treatments. Hand weeding + earthing up, isoproturon (1.0 kg/ha), metribuzin and pendimethalin caused an identical increase in tuber yield, which was significantly higher than the increase in the rest of the treatments. Atrazine at 0.25 kg ha^{-1} resulted in a higher increase than when applied at 0.5 kg ha^{-1}. Fluchloralin, paraquat and paddy straw mulch boosted up prodn., but the increase in tuber yield was not significant.

~1 Citing

216. Cloning and characterization of the pyruvate carboxylase from Sinorhizobium meliloti Rm1021

By Dunn, Michael F.; Araiza, Gisela; Finan, Turlough M.
From Archives of Microbiology (2001), 176(5), 355-363. Language: English, Database: CAPLUS, DOI:10.1007/s002030100336

The gene encoding pyruvate carboxylase (pyc) was isolated from a Sinorhizobium meliloti Rm1021 cosmid bank by complementation of a Rhizobium tropici pyc mutant. PYC-neg. mutants of S. meliloti Rm1021 were isolated by transposon mutagenesis and were unable to grow with glucose or pyruvate as sole carbon sources, but were symbiotically competent in combination with alfalfa plants. PYC activity assays, pyc::lacZ gene fusion studies and an in vivo biotinylation assay showed that PYC activity in S. meliloti was dependent mainly on biotin availability and not on changes in gene transcription. The subunit and holo-enzyme mol. masses of the S. meliloti PYC indicated that the enzyme was an α_4 homotetramer. The S. meliloti PYC had a high apparent K_a (0.23 mM) for the allosteric activator acetyl-CoA and was product-inhibited by sub-millimolar concns. of oxaloacetate. In contrast to other bacterial α_4-PYCs which have been characterized, the S. meliloti enzyme was not strongly inhibited by L-aspartate.

~19 Citings

217. Skin care preparation for applicating body part for lean figure/Cosmetic or pharmaceutical composition for external application on skin to treat obesity of the application site

By Fujii, Masashi
From Jpn. Kokai Tokkyo Koho (2001), JP 2001302527 A 20011031, Language: Japanese, Database: CAPLUS

A cosmetic or pharmaceutical compn. for external application on skin to treat obesity of the application site comprises Melilotus officinalis ext. (0.01-80wt%) and/or Aesculus hippocastanum L. seed ext. (0.01-80wt%), activated milk-derived inactive cytokine-like substances (0.01-10wt%), and a cooling agent of 1-menthyl glyceryl ether (0.01-10wt%) and/or 1-menthol (0.01-10wt%) as the obesity indicator. The cosmetic or pharmaceutical compn. is effective on obesity caused by intercellular edema complicated with retention of lymph and obesity caused by intake of fats in the fat cells. It is capable of controlling the obesity of a body part so as to form an attractive figure as desired by women.

~0 Citings

218. Composition for hair/A hair tonic composition containing plant extract and rutin or its derivative

By Tanaka, Hiroshi
From Jpn. Kokai Tokkyo Koho (2001), JP 2001294516 A 20011023, Language: Japanese, Database: CAPLUS

A hair tonic compn. comprises an ext. of at least one plant selected from genera of Stellaria, Echinacea, Anthriscus, Primula, Trifolium, Cassia, Melilotus, Astragalus, Crataegus, Ligustrum, Atractylodes and Cistanche, such as Stellaria media L.VILL., Echinacea angustifolia DC., Anthriscus cerefolium L. HOFFM., Primula vulgaris HUDS., Trifolium pratense L., Cassia angustifolia VAHL., Melilotus officinalis (L.) PALL., Astragalus membranaceus (FISCH.) BUNGE, Crataegus cuneata SIEB.et ZUCC., Ligustrum lucidum AITON, Atractylodes lancea DC., and Cistanche salsa MEYER (C. A.); and rutin or its deriv. (perferably G rutin PS-C). Other materials such as oils, alc., surfactant, colorant, antioxidant, antiseptics, pH regulator, thickener, perfume, other plant or animal ext., etc. can be optionally blended. The compn. has effect in promoting melanin prodn. and is effective for preventing gray hair. The following herbs may also be used: Stellaria herba, Stellaria neglecta WEIHE., Stellaria paniculigera MAKINO., Stellaria dichotomae radix, Stellaria alsine GKIMM., Stellaria saxatilis BUCH.-HAM., Stellaria yunnanesis FRANCH., Anthriscus sylvestris (L.) HOFFM., Primula faberi OLIV., Primula patens TURCZ., Primula vittata BUR. et FRANCH., Primula sikkimensis HOOK., Trifolium repens L., Cassia torae semen, Melilotus suaveolens LEDEB., Melilotus indicus (L.) ALL., Melilotus alba DESR., Astragalus mongholicus BUNGE, Crataegus pinnatifida BUNGE, and Atractylodes ovata DC..

~1 Citing

219. Temporal effects on the composition of a population of Sinorhizobium meliloti associated with Medicago sativa and Melilotus alba

By Bromfield, Eden S. P.; Butler, Gail; Barran, Leslie R.
From Canadian Journal of Microbiology (2001), 47(6), 567-573. Language: English, Database: CAPLUS, DOI:10.1139/w01-034

An assessment was made of the impact of temporal sepn. on the compn. of a population of Sinorhizobium meliloti assocd. with Medicago sativa (alfalfa) and Melilotus alba (sweet clover) grown at a single site that had no known history.of alfalfa cultivation. Root nodules were sampled on six occasions over two seasons, and a total of 1620 isolates of S. meliloti were characterized on the basis of phage sensitivity using 16 typing phages. Plant infection tests indicated that symbiotic S. meliloti were deficient in the soil at the time of planting and that these bacteria were present at low d. during the first season ($<10^2$/g of soil); m the second season nos. increased markedly to about 10^5/g of soil. Overall, 37 and 51 phage types, resp., were encountered among the nodule isolates from M. sativa and M. alba. The data indicate significant temporal shifts in the frequency and diversity of types assocd. with the two legume species. Apparent temporal variation with respect to the frequency of types appeared largely unpredictable and was not attributable to any one sampling time. The results indicate an apparent redn. in phenotypic diversity over the course of the expt. Differential host plant selection of specific types with respect to nodule occupancy was indicated by significant interactions between legume species and either the frequency or diversity of phage types. Isolates from M. sativa that were resistant to lysis by all typing phages (type 14) were unusual in that they were predominant on this host at all sampling times (between 53% and 82% nodule occupancy) and were relatively homogeneous on the basis of DNA hybridization with 98% of the isolates analyzed sharing the same nod EFG hybridization profile. In contrast, those isolates from M. alba comprising type 14 were encountered at low total frequency (2%) and were genetically heterogeneous on the basis of Southern hybridization. The implications of the obsd. temporal and host plant variation for ecol. studies are discussed.

~11 Citings

220. Identification and structure of the Rhizobium galegae common nodulation genes: evidence for horizontal gene transfer

By Suominen, Leena; Roos, Christophe; Lortet, Gilles; Paulin, Lars; Lindstrom, Kristina
From Molecular Biology and Evolution (2001), 18(6), 907-916. Language: English, Database: CAPLUS, DOI:10.1093/oxfordjournals.molbev.a003891

Rhizobia are soil bacteria able to fix atm. nitrogen in symbiosis with leguminous plants. In response to a signal cascade coded by genes of both symbiotic partners, a specific plant organ, the nodule, is formed. Rhizobial nodulation (nod) genes trigger nodule formation through the synthesis of Nod factors, a family of chitolipooligosaccharides that are specifically recognized by the host plant at the first stages of the nodulation process. Here, we present the organization and sequence of the common nod genes from Rhizobium galegae, a symbiotic member of the Rhizobiaceae. This species has an intriguing phylogenetic position, being symbiotic among pathogenic agro-bacteria, which induce tumors instead of nodules in plant shoots or roots. This apparent incongruence raises special interest in the origin of the symbiotic app. of R. galegae. Our anal. of DNA sequence data indicated that the organization of the common nod gene region of R. galegae was similar to that of Sinorhizobium meliloti and Rhizobium leguminosarum, with nodIJ downstream of nodABC and the regulatory nodD gene closely linked to the common nod operon. Moreover, phylogenetic analyses of the nod gene sequences showed a close relationship esp. between the common nodA sequences of R. galegae, S. meliloti, and R. leguminosarum biovars viciae and trifolii. This relationship in structure and sequence contrasts with the phylogeny based on 16S rRNA, which groups R. galegae close to agrobacteria and sep. from most other rhizobia. The topol. of the nodA tree was similar to that of the corresponding host plant tree. Taken together, these observations indicate that lateral nod gene transfer occurred from fast-growing rhizobia toward agrobacteria, after which the symbiotic app. evolved under host plant constraint.

~32 Citings

221. Two RpoH homologs responsible for the expression of heat shock protein genes in Sinorhizobium meliloti

By Ono, Y.; Mitsui, H.; Sato, T.; Minamisawa, K.
From Molecular and General Genetics (2001), 264(6), 902-912. Language: English, Database: CAPLUS, DOI:10.1007/s004380000380

We identified two rpoH-related genes encoding σ^{32}-like proteins from Sinorhizobium meliloti, a nitrogen-fixing root-nodule symbiont of alfalfa. The genes, $rpoH_1$ and $rpoH_2$, are functionally similar to rpoH of Escherichia coli because they partially complemented an E. coli rpoH null mutant. We obtained evidence indicating that these genes are involved in the heat shock response in S. meliloti. Following an increase in temp., synthesis of several putative heat shock proteins (Hsps) was induced in cultures of wild-type cells: the most prominent were 66- and 60-kDa proteins, both of which are suggested to represent GroEL species. The other Hsps could divided into two groups based on differences in synthesis kinetics: synthesis of the first group peaked 5-10 min, and expression of the other group 30 min, after temp. upshift. In the $rpoH_1$ mutant, inducible synthesis of the former group was markedly reduced, whereas that of the latter group was not affected. Synthesis of both the 66- and 60-kDa proteins was partially reduced. While no appreciable effect was obsd. in the $rpoH_2$ single mutant, the $rpoH_2$ mutation had a synergistic effect on the 60-kDa protein in the $rpoH_1^-$ background. The results indicate that two distinct mechanisms are involved in the heat shock response of S. meliloti: one requires the $rpoH_1$ function, while $rpoH_2$ can substitute in part for the $rpoH_1$ function. Moreover, the $rpoH_1$ mutant and $rpoH_1$ $rpoH_2$ double mutant exhibited Nod^+ Fix^- and Nod^- phenotypes, resp., on alfalfa.

~22 Citings

222. Sugar-binding activity of pea lectin enhances heterologous infection of transgenic alfalfa plants by Rhizobium leguminosarum biovar viciae

By Van Rhijn, Pieternel; Fujishige, Nancy A.; Lim, Pyung Ok; Hirsch, Ann M.
From Plant Physiology (2001), 126(1), 133-144. Language: English, Database: CAPLUS, DOI:10.1104/pp.126.1.133

Transgenic alfalfa (Medicago sativa L. cv Regen) roots carrying genes encoding soybean lectin or pea (Pisum sativum) seed lectin (PSL) were inoculated with Bradyrhizobium japonicum or Rhizobium leguminosarum bv viciae, resp., and their responses were compared with those of comparably inoculated control plants. We found that nodule-like structures formed on alfalfa roots only when the rhizobial strains produced Nod factor from the alfalfa-nodulating strain, Sinorhizobium meliloti. Uninfected nodule-like structures developed on the soybean lectin-transgenic plant roots at very low inoculum concns., but bona fide infection threads were not detected even when B. japonicum produced the appropriate S. meliloti Nod factor. In contrast, the PSL-transgenic plants were not only well nodulated but also exhibited infection thread formation in response to R. leguminosarum bv viciae, but only when the bacteria expressed the complete set of S. meliloti nod genes. A few nodules from the PSL-transgenic plant roots were even found to be colonized by R. leguminosarum bv viciae expressing S. meliloti nod genes, but the plants were yellow and senescent, indicating that nitrogen fixation did not take place. Exopolysaccharide appears to be absolutely required for both nodule development and infection thread formation because neither occurred in PSL-transgenic plant roots following inoculation with an Exo- R. leguminosarum bv viciae strain that produced S. meliloti Nod factor.

~48 Citings

223. Ultrastructural studies on nodules induced by pyrimidine auxotrophs of Sinorhizobium meliloti

By Vineetha, K. E.; Vij, Neeraj; Prasad, C. Krishna; Hassani, Raad; Randhawa, Gursharn S.
From Indian Journal of Experimental Biology (2001), 39(4), 371-377. Language: English, Database: CAPLUS

Twenty three pyrimidine auxotrophs of Sinorhizobium meliloti Rmd201 were generated by random mutagenesis with transposon Tn5. On the basis of biochem. characters these auxotrophic mutants were classified into car, pyrC and pyrE/pyrF categories. All auxotrophs induced white nodules which were ineffective in nitrogen fixation. Light and electron microscopic studies revealed that the nodules induced by pyrC mutants were more developed than the nodules of car mutants. Similarly the nodules induced by pyrE/pyrF mutants had more advanced structural features than the nodules of pyrC mutants. The nodule development in case of pyrE/pyrF mutants was not to the extent obsd. in the parental strain. These results indicated that some of the intermediates and/or enzymes of pyrimidine biosynthetic pathway of S. meliloti play a key role in bacteroidal transformation and nodule development.

~11 Citings

224. glnD and mviN are genes of an essential operon in Sinorhizobium meliloti

By Rudnick, Paul A.; Arcondeguy, Tania; Kennedy, Christina K.; Kahn, Daniel
From Journal of Bacteriology (2001), 183(8), 2682-2685. Language: English, Database: CAPLUS, DOI:10.1128/JB.183.8.2682-2685.2001

To evaluate the role of uridylyltransferase, the Sinorhizobium meliloti glnD gene was isolated by heterologous complementation in Azotobacter vinelandii. The glnD gene is cotranscribed with a gene homologous to Salmonella mviN. GlnD1::Ω or mviN1::Ω mutants could not be isolated by a powerful sucrose counterselection procedure unless a complementing cosmid was provided, indicating that glnD and mviN are members of an indispensable operon in S. meliloti.

~24 Citings

225. A simple, inexpensive, and rapid method to determine toxicity using a bacterial indicator organism

By Botsford, J. L.
From Proceedings of the Conference on Hazardous Waste Research: Environmental Challenges and Solutions to Resource Development, Production, and Use, Denver, CO, United States, May 23-25, 2000 (2000), 22-35. Language: English, Database: CAPLUS

A simple, inexpensive and rapid method to det. the toxicity of compds., isolated chems., soil samples, and water samples has been developed. The test uses the bacterium, Rhizobium meliloti, as the indicator organism. Toxicity values obtained with this test are comparable to those obtained with more familiar tests like the sand flea Daphnia magna, Microtox, and tests using animal and human cells grown in culture. No specialized equipment is required, only a spectrophotometer and a water bath. No specialized training is required. Only rudimentary chem. skills are required to perform the assay which takes less than an hour. The test could be adopted in developing nations without sophisticated labs., with very modest budgets and with relatively unskilled personnel. It could be included as an alternative test for toxicity in sophisticated labs. A patent has been obtained and we are seeking a firm to market the assay. However, the test could be used by any lab. able to grow bacteria. Detailed information is available in the published literature.

~0 Citings

226. Suppression of plant defense reactions in alfalfa cell cultures by Sinorhizobium meliloti surface carbohydrates

By Niehaus, K.; Albus, U.; Baier, R.; Becker, A.; Schiene, Karin; Puhler, A.
From Current Plant Science and Biotechnology in Agriculture (2000), 38(Nitrogen Fixation: From Molecules to Crop Productivity), 233-234. Language: English, Database: CAPLUS

The soil bacterium Sinorhizobium meliloti is able to establish a symbiosis with its host plant alfalfa (Medicago sativa) as well as with the model legume Medicago truncatula. During the establishment of this symbiosis, bacterial cells infect plant roots and induce a new organ, the root nodule. The bacterial nod genes, code for the synthesis and excretion of the nodulation factors (Nod factors), which are able to induce nodule organogenesis in the legume. A study was conducted to det. whether Nod factors may stimulate the plant defense system of M. sativa. Findings indicated that S. meliloti nodulation factors did not induce plant defense reaction in M. sativa cell suspension cultures. Also, S. meliloti lipopolysaccharide (LPS) was able to suppress plant defense reactions induced by yeast elicitors. It is proposed that S. meliloti LPS actively suppress plant defense reactions in the host plant M. sativa.

~1 Citing

227. Changes of soil and plant tissue selenium status in an upland grassland contaminated by selenium-rich agricultural drainage sediment after ten years transformed from a wetland habitat

By Wu, Lin; Banuelos, Gary; Guo, Xun
From Ecotoxicology and Environmental Safety (2000), 47(2), 201-209. Language: English, Database: CAPLUS, DOI:10.1006/eesa.2000.1948

A field survey was conducted in 1989, 1994, and 1999 in order to monitor the soil and vegetation Se concns. at the Kesterson upland grassland contaminated by Se-rich drainage sediment. The rate of Se dissipation estd. by the change of soil Se concn., via volatilization, was 1.1% per yr. Soil water-extractable Se increased in 1994, but was greatly reduced in 1999. The increase of soil Se concn. in the top 15 cm of soil at the fresh-soil fill sites indicates that the plants were able to effectively take up the sol. soil Se from the lower soil profile and to deposit it on the top of the field. This process may reduce the rate of leaching of soil Se. The concn. of soil water-sol. Se was relatively low and it is unlikely that problems of transport of Se from the Kesterson soil to the adjacent uncontaminated environment by leaching can occur. Plant tissue Se concn. was found to coincide with the soil water-extractable Se concn. The av. plant tissue Se concn. and soil water-extractable Se detected in 1999 was about 10 μg Se g^{-1} and 110 μg Se kg^{-1} dry wt., resp., and the estd. bioaccumulation value of this upland grassland is less than 10% of the previous wetland habitat. Therefore, the existing Kesterson grassland should not be at high risk to the environment. (c) 2000 Academic Press.

~9 Citings

228. Mycorrhizal associations with some plant species in a soil strip of different successional stages in Egypt

By Ramadan, T.; Omar, S. A.
From Journal of Plant Nutrition (2000), 23(8), 1153-1166. Language: English, Database: CAPLUS, DOI:10.1080/01904160009382089

In this study, soil and plant samples were collected from a strip of soil comprising four successional stages from the eastern desert plateau to the Nile Valley, Egypt. Some essential elements [i.e., potassium (K), calcium (Ca), magnesium (Mg), and sulfur (S)] decreased on transition from the reclaimed soil in the desert to the Nile Valley. Soil nitrite content was the highest in Nile Valley soil and decreased toward desert soil. Water content increased with the transition from sandy soil to clay soil, whereas pH values of the soils did not strongly differ and were moderately alk. Root colonization with arbuscular-mycorrhizal (AM) fungi of 33 plant species (11 cultivated and 22 wild) collected from the study area was highest in eastern desert plateau and decreased toward the Nile Valley. Mycorrhizal spore counts reflected the root colonization data. The decrease in mycorrhizal colonization was explained on the basis of difference in soil porosity, soil water contents, and toxicity of nitrite. Contents of K, Ca or Mg in some species were increased by increasing the colonization percentage of roots by AM fungi. Increasing the infection percentage of roots decreased or maintained the ratio of Na/(K + Ca + Mg) (in mequiv) in the shoots of investigated plants. The contents of chlorophyll, sol. sugars, and protein significantly increased as a result of increasing colonization value. Also, mycorrhizal root colonization improved the water status of most plant species. These results suggest that increasing infection by AM fungi in the newly reclaimed soil may enable the plants to maintain internal water status and mineral balance through decreasing the ratio of distressing ions to the nutrient ones.

~1 Citing

229. Effect of field inoculation with Sinorhizobium meliloti L33 on the composition of bacterial communities in rhizospheres of a target plant (Medicago sativa) and a non-target plant (Chenopodium album)-linking of 16S rRNA gene-based single-strand conformation polymorphism community profiles to the diversity of cultivated bacteria

By Schwieger, Frank; Tebbe, Christoph C.
From Applied and Environmental Microbiology (2000), 66(8), 3556-3565. Language: English, Database: CAPLUS, DOI:10.1128/AEM.66.8.3556-3565.2000

Fourteen weeks after field release of luciferase gene-tagged Sinorhizobium meliloti L33 in field plots seeded with Medicago sativa, we found that the inoculant also occurred in bulk soil from noninoculated control plots. In rhizospheres of M. sativa plants, S. meliloti L33 could be detected in noninoculated plots 12 wk after inoculation, indicating that growth in the rhizosphere preceded spread into bulk soil. To det. whether inoculation affected bacterial diversity, 1,119 bacteria were isolated from the rhizospheres of M. sativa and Chenopodium album, which was the dominant weed in the field plots. Amplified ribosomal DNA restriction anal. (ARDRA) revealed plant-specific fragment size frequencies. Dominant ARDRA groups were identified by 16S rRNA gene nucleotide sequencing. Database comparisons indicated that the rhizospheres contained members of the Proteobacteria (α, β, and γ subgroups), members of the Cytophage-Flavobacterium group, and Gram-pos. bacteria with high G+C DNA contents. The levels of many groups were affected by the plant species and, in the case of M. sativa, by inoculation. The most abundant isolates were related to Variovorax sp., Arthrobacter ramosus, and Acinetobacter calcoaceticus. In the rhizosphere of M. sativa, inoculation reduced the nos. of cells of A. calcoaceticus and members of the genus Pseudomonas and increased the no. of rhizobia. Cultivation-independent PCR-single-strand conformation polymorphism (SSCP) profiles of a 16S rRNA gene region confirmed the existence of plant-specific rhizosphere communities and the effect of the inoculant. All dominant ARDRA groups except Variovorax species could be detected. On the other hand, the SSCP profiles revealed products which could not be assigned to the dominant cultured isolates, indicating that the bacterial diversity was greater than the diversity suggested by cultivation.

~62 Citings

230. Sinorhizobium meliloti putA gene regulation: a new model within the family Rhizobiaceae

By Soto, Maria Jose; Jimenez-Zurdo, Jose Ignacio; Van Dillewijn, Pieter; Toro, Nicolas
From Journal of Bacteriology (2000), 182(7), 1935-1941. Language: English, Database: CAPLUS, DOI:10.1128/JB.182.7.1935-1941.2000

Proline dehydrogenase (PutA) is a bifunctional enzyme that catalyzes the oxidn. of proline to glutamate. In Sinorhizobium meliloti, as in other microorganisms, the putA gene is transcriptionally activated in response to proline. In Rhodobacter capsulatus, Agrobacterium, and most probably in Bradyrhizobium, this activation is dependent on an Lrp-like protein encoded by the putR gene, located immediately upstream of putA. Interestingly, sequence and genetic anal. of the region upstream of the S. meliloti putA gene did not reveal such a putR locus or any other encoded transcriptional activator of putA. Furthermore, results obtained with an S. meliloti putA null mutation indicate the absence of any proline-responsive transcriptional activator and that PutA serves as an autogenous repressor. Therefore, the model of S. meliloti putA regulation completely diverges from that of its Rhizobiaceae relatives and resembles more that of enteric bacteria. However, some differences have been found with the latter model: (i) S. meliloti putA gene is not catabolite repressed, and (ii) the gene encoding for the major proline permease (putP) does not form part of an operon with the putA gene.

~12 Citings

231. Lipochitin oligosaccharides from Rhizobium leguminosarum bv. viciae reduce auxin transport capacity in Vicia sativa subsp. nigra roots

By Boot, Kees J. M.; Van Brussel, Anton A. N.; Tak, Teun; Spaink, Herman P.; Kijne, Jan W.
From Molecular Plant-Microbe Interactions (1999), 12(10), 839-844. Language: English, Database: CAPLUS, DOI:10.1094/MPMI.1999.12.10.839

Induction of the formation of root nodule primordia in legume roots by symbiotic rhizobia is probably preceded by a change in plant hormone physiol. A Vicia sativa (vetch) split root system was used to study the effect of inoculation with rhizobia or purified Nod factors (lipochitin oligosaccharides, LCOs) on polar auxin transport in roots. Addn. of R. leguminosarum bv. viciae, the infective symbiote of vetch, to roots of its host plant reduced polar auxin transport capacity of these roots within 24 h, in contrast to addn. of non-nodulating, Sym plasmid-cured rhizobia. Addn. of purified vetch-specific LCOs (NodRlv-IV/V[18:4,Ac]) caused a transient redn. in as little as 4 h after application, while after 16 h a second, stronger, and prolonged inhibition was obsd. that lasted at least 48 h. This redn. of auxin transport capacity was in the same order of magnitude as inhibition by N-(1-naphthyl)phthalamic acid (NPA). Purified LCOs (NodRm-IV[16:2,Ac,S]) from Sinorhizobium meliloti, the symbiote of alfalfa, and chitopentaose were inactive, which indicates a specific effect of LCOs produced by R. leguminosarum bv. viciae. Auxin transport inhibition was restricted to the apical nodulation-susceptible part of the roots, whereas the upper parts of the roots showed no difference in auxin transport after treatment. The effect could be obsd. with as low as 10^{-9} M NodRlv-IV/V[18:4,Ac] LCOs. Redn. of auxin transport by LCOs could not be inhibited by nitrate. Since inhibition of auxin transport capacity preceded the first root cortical cell divisions that result in root primordium formation, our results suggest a direct relationship between LCOs, polar auxin transport, and root nodule initiation, consistent with the hypothesis of U. Mathesius, H. R. M. Schlaman, H. P. Spaink, C. Sautter, B. G. Rolfe, and M. A. Djordjevic (Plant J. 14:23-34, 1998). However, nonmitogenic NodRlv-IV/V[18:1,Ac] showed a similar effect, which suggests that mitogenicity results from addnl. effects, in concert with auxin transport inhibition.

~70 Citings

232. Biosynthesis of trehalose from maltooligosaccharides in rhizobia

By Streeter, John G.; Bhagwat, Arvind
From Canadian Journal of Microbiology (1999), 45(8), 716-721. Language: English, Database: CAPLUS, DOI:10.1139/w99-050

Previously, the enzymes for trehalose synthesis that are present in Escherichia coli were demonstrated in Bradyrhizobium japonicum and B. elkanii. An alternative mechanism recently reported for the synthesis of trehalose from maltooligosaccharides was considered based on the fact that high concns. of sugars in liq. culture stimulated the accumulation of trehalose. An assay for the synthesis of trehalose from maltooligosaccharides using crude, gel-filtered protein prepns. was developed. Anal. of a variety of the Rhizobiaceae indicates that the "maltooligosaccharide mechanism" is present in B. japonicum, B. elkanii, Rhizobium sp. NGR234, Sinorhizobium meliloti, R. tropici A, R. leguminosarum bv viciae, R. l. bv trifolii, and Azorhizobium caulinodans. Synthesis of trehalose from maltooligosaccharide could not be detected in R. tropici B or R. etli. With these two exceptions, it is suggested that rhizobia have two mechanisms for the biosynthesis of trehalose.

~19 Citings

233. Characterization of an atypical superoxide dismutase from Sinorhizobium meliloti

By Santos, Renata; Bocquet, Stephane; Puppo, Alain; Touati, Daniele
From Journal of Bacteriology (1999), 181(15), 4509-4516. Language: English, Database: CAPLUS

Sinorhizobium meliloti Rm5000 is an aerobic bacterium that can live free in the soil or in symbiosis with the roots of leguminous plants. A single detectable superoxide dismutase (SOD) was found in free-living growth conditions. The corresponding gene was isolated from a genomic library by using a sod fragment amplified by PCR from degenerate primers as a probe. The sodA gene was located in the chromosome. It is transcribed monocistronically and encodes a 200-amino-acid protein with a theor. M_r of 22,430 and pI of 5.8. S. meliloti SOD complemented a deficient Escherichia coli mutant, restoring aerobic growth of a sodA sodB recA strain, when the gene was expressed from the synthetic tac promoter but not from its own promoter. Amino acid sequence alignment showed great similarity with Fe-contg. SODs (FeSODs), but the enzyme was not inactivated by H_2O_2. The native enzyme was purified and found to be a dimeric protein, with a specific activity of 4000 U/mg. Despite its Fe-type sequence, at. absorption spectroscopy showed manganese to be the cofactor (0.75 mol of manganese and 0.24 mol of iron per mol of monomer). The apoenzyme was prepd. from crude exts. of S. meliloti. Activity was restored by dialysis against either $MnCl_2$ or $Fe(NH_4)_2(SO_4)_2$, demonstrating the cambialistic nature of the S. meliloti SOD. The recovered activity with manganese was sevenfold higher than with iron. Both reconstituted enzymes were resistant to H_2O_2. Sequence comparison with 70 FeSODs and MnSODs indicates that S. meliloti SOD contains several atypical residues at specific sites that might account for the activation by manganese and resistance to H_2O_2 of this unusual Fe-type SOD.

~43 Citings

234. Technical methods section: a simple method for determining the toxicity of chemicals using a bacterial indicator organism

By Botsford, James L.
From Environmental Toxicology (1999), 14(2), 285-289. Language: English, Database: CAPLUS, DOI:10.1002/(SICI)1522-7278(199905)14:2<285::AID-TOX10>3.0.CO;2-G

The toxicity of chems. was detd. using Rhizobium meliloti as the indicator organism and monitored by spectrophotometrically following dye redn. Examples using 3-phenoxybenzoic acid, cyanide, and trichlorophenol were reported.

~7 Citings

235. Characterization of symbiotically efficient alfalfa-nodulating rhizobia isolated from acid soils of Argentina and Uruguay

By Segundo, E.; Martinez-Abarca, F.; van Dillewijn, P.; Fernandez-Lopez, M.; Lagares, A.; Martinez-Drets, G.; Niehaus, K.; Puhler, A.; Toro, N.
From FEMS Microbiology Ecology (1999), 28(2), 169-176. Language: English, Database: CAPLUS, DOI:10.1111/j.1574-6941.1999.tb00572.x

The diversity, growth and symbiotic behavior of symbiotically efficient alfalfa-nodulating rhizobia isolated from acid soils of Argentina and Uruguay were analyzed. Partial sequencing of the 16S rDNA indicated that these isolates belong to Sinorhizobium meliloti species. IS-fingerprinting anal. revealed a high diversity among the isolates but some of them appear related to inoculant strains currently used in the region. The S. meliloti isolates showed a decreased growth rate with increasing acidity. They were, however, able to nodulate alfalfa at pH 5.6, but showed a delayed nodulation and decreased nodule no. typical of S. meliloti strains. The impaired nodulation of S. meliloti at pH 5.6 did not result in a redn. of alfalfa dry matter prodn. or nitrogen content. However, significant differences were obsd. for the relative symbiotic effectiveness of the strains analyzed. LPU63 (Argentina) was the most effective among the isolates and exhibited a high nodulation competitiveness at both neutral and acidic pH. These results suggest that the isolate LPU63 may be a potential efficient inoculant for alfalfa in acid soils.

~13 Citings

236. Efficacy of tralkoxydim with and without isoproturon on two grassy and three broad-leaf weeds in spring wheat

By Kumar, Subhash; Singh, Govindra
From International Journal of Tropical Agriculture (1997), 15(1-4), 203-210. Language: English, Database: CAPLUS

Field studies indicated that the tank mixt. of tralkoxydim, at 0.25, with isoproturon, at 0.5 kg/ha, controlled Phalaris minor, Avena ludoviciana, Chenopodium album and Melilotus indica completely and produced the grain yield comparable to the weed-free conditions. Tralkoxydim, at 0.3-0.4 kg/ha, only provided complete control of the grassy weeds, like P. minor and A. ludoviciana, and it was not effective against the broad-leaf weeds, like C. album, M. indica or Vicia sativa. Isoproturon at 1.0 kg/ha provided only 47 % control of A. ludoviciana. None of the treatments was effective against V. sativa.

~1 Citing

237. Mutational analysis of the Rhizobium etli recA operator

By Tapias, Angels; Barbe, Jordi
From Journal of Bacteriology (1998), 180(23), 6325-6331. Language: English, Database: CAPLUS

Based upon our earlier studies (A. Tapias, A. R. Fernandez de Henestrosa, and J. Barbe, J. Bacteriol. 179:1573-1579, 1997) we hypothesized that the regulatory sequence of the Rhizobium etli recA gene was $TTGN_{11}CAA$. However, further detailed anal. of the R. etli recA operator described in the present work suggests that it may in fact be $GAACN_7GTAC$. This new conclusion is based upon PCR mutagenesis anal. carried out in the R. etli recA operator, which indicates that the GAAC and GTAC submotifs found in the sequence $GAACN_7GTAC$ are required for the maximal stimulation of in vivo transcription and in vitro DNA-protein complex formation. This DNA-protein complex is also detected when the $GAACN_7GTAC$ wild-type sequence is modified to obtain $GAACN_7GAAC$, $GTACN_7GTAC$, or $GAACN_7GTTC$. The wild-type promoters of the Rhizobium meliloti and Agrobacterium tumefaciens recA genes, which also contain the $GAACN_7GTAC$ sequence, compete with the R. etli recA promoter for the DNA-protein complex formation but not with mutant derivs. in any of these motifs, indicating that the R. etli, R. meliloti, and A. tumefaciens recA genes present the same regulatory sequence.

~12 Citings

238. Accumulation of nickel in selected forage species

By Singh, S. P.; Nayyar, V. K.
From Journal of the Indian Society of Soil Science (1998), 46(3), 479-481. Language: English, Database: CAPLUS

Ni concns. in all forage species increased with increasing rates of Ni addn. Plant species differed markedly with respect to their Ni accumulation capacity; Gramineae accumulated 2 times Ni than legumes.

~2 Citings

239. Biosynthetic control of molecular weight in the polymerization of the octasaccharide subunits of succinoglycan, a symbiotically important exopolysaccharide of Rhizobium meliloti

By Gonzalez, Juan E.; Semino, Carlos E.; Wang, Lai-Xi; Castellano-Torres, Laura E.; Walker, Graham C.
From Proceedings of the National Academy of Sciences of the United States of America (1998), 95(23), 13477-13482. Language: English, Database: CAPLUS, DOI:10.1073/pnas.95.23.13477

Succinoglycan, a symbiotically important exopolysaccharide of Rhizobium meliloti, is composed of polymd. octasaccharide subunits, each of which consists of one galactose and seven glucoses with succinyl, acetyl, and pyruvyl modifications. Prodn. of specific low mol. wt. forms of R. meliloti exported and surface polysaccharides, including succinoglycan, appears to be important for nodule invasion. In a previous study of the roles of the various exo gene products in succinoglycan biosynthesis, exoP, exoQ, and exoT mutants were found to synthesize undecaprenol-linked fully modified succinoglycan octasaccharide subunits, suggesting possible roles for their gene products in polymn. or transport. Using improved techniques for analyzing succinoglycan biosynthesis by these mutants, we have obtained evidence indicating that R. meliloti has genetically separable systems for the synthesis of high mol. wt. succinoglycan and the synthesis of a specific class of low mol. wt. oligosaccharides consisting of dimers and trimers of the octasaccharide subunit. Models to account for these unexpected findings are discussed. Possible roles for the ExoP, ExoQ, and ExoT proteins are compared and contrasted with roles that have been suggested on the basis of homologies to key proteins involved in the biosynthesis of O-antigens and of certain exported or capsular cell surface polysaccharides.

~65 Citings

240. A simple assay for toxic chemicals using a bacterial indicator

By Botsford, J. L.
From World Journal of Microbiology & Biotechnology (1998), 14(3), 369-376. Language: English, Database: CAPLUS

A simple, inexpensive and rapid technique to measure toxicity has been developed using Rhizobium meliloti as the indicator organism and its rapid redn. of MTT. Toxic chems. inhibited the redn. in this bacterium, but not in others. Nearly 50 org. chems. and 14 minerals were tested; inhibition was proportional to the concn. of the toxic chem. The mechanism to account for both the redn. of the dye and the inhibition of redn. is uncertain. This method provides a simple and inexpensive way to det. the crit. concn. of toxic compds. The assay provides values comparable to those provided by the fat head minnow (Pimephales promelas). Results are also comparable to those obtained with the Microtox and Polytox assays, two com. assays that use bacteria as indicator organisms.

~12 Citings

241. The nos (nitrous oxide reductase) gene cluster from the soil bacterium Achromobacter cycloclastes: cloning, sequence analysis, and expression

By McGuirl, Michele A.; Nelson, Laura K.; Bollinger, John A.; Chan, Yiu-Kwok; Dooley, David M.
From Journal of Inorganic Biochemistry (1998), 70(3,4), 155-169. Language: English, Database: CAPLUS, DOI:10.1016/S0162-0134(98)10001-6

The nitrous oxide (N_2O) reductase (nos) gene cluster from Archromobacter cycloclastes has been cloned and sequenced. Seven protein coding regions corresponding to nosR, nosZ (structural N_2O reductase gene), nosD, nosF, nosY, nosL, and nosX are detected, indicating a genetic organization similar to that of Rhizobium meliloti. To aid homol. studies, nosR from R. meliloti has also been sequenced. Comparison of the deduced amino acid sequences with corresponding sequences from other organisms has also allowed structural and functional inferences to be made. The heterologous expression of NosD, NosZ (N_2O reductase), and NosL is also reported. A model of the Cu_A site in N_2O reductase, based on the crystal structure of this site in bovine heart cytochrome c oxidase, is presented. The model suggests that a His residue of the Cu_A domain may be a ligand to the catalytic Cu_Z site. In addn., the origin of the spectroscopically-obsd. Cys coordination to Cu_Z is discussed in terms of the sequence alignment of seven N_2O reductases.

~19 Citings

242. High-temperature effects on germination and viability of weed seeds in soil

By Arora, A.; Yaduraju, N. T.
From Journal of Agronomy and Crop Science (1998), 181(1), 35-43. Language: English, Database: CAPLUS, DOI:10.1111/j.1439-037X.1998.tb00395.x

The control of weeds by solar heating of the soil using transparent polyethylene (PE) sheets was studied in the field during the summers of 1994 and 1995. The max. soil temp. under plastic cover at 5 cm depth averaged 53°. At 5 cm soil depth, solarization increased temp. by about 9°. In the non-solarized soils, such high-temp. days were fewer. A temp. of 55° at 5 cm soil depths was recorded both in irrigated and non-irrigated mulched soils. However, mulched soil recorded 70% of the treatment period compared with 43% in unirrigated and mulched soils. Lower depths of 10 and 15 cm did not attain a temp. 55° or 60° on any day during the exptl. period. Solarization treatment with PE sheets significantly increased NO_3^--N and NH_4^+-N in comparison with non-solarized plots. While uncovered plots showed significant increase in available phosphorus and marginally increased in potassium and elec. cond. Org. carbon content and pH did not vary under different treatments. PE mulching for 30 days significantly reduced the no. of weed seeds, specifically Avena fatua and Phalaris minor, while Trianthema monogyna and Asphodelus tenuifolius were not affected much in comparison with the former. Melilotus indica was not at all affected by the solarization treatment studied. The solarization redn. index (SRI) was calcd. for each weed species studied and it was concluded that weeds having a low SRI can be controlled more electively than weeds with high SRI values. The heating effect from solarization decreased with soil depth. The 30 days' soil solarization treatment in moist soil was more effective than the 10 and 20 days' heating treatment in moist and dry soils for weed control.

~2 Citings

243. Honey bees as indicators of radionuclide contamination: comparative studies of contaminant levels in forager and nurse bees and in the flowers of three plant species

By Haarmann, T. K.
From Archives of Environmental Contamination and Toxicology (1998), 35(2), 287-294. Language: English, Database: CAPLUS, DOI:10.1007/s002449900378

Two sep. field expts. were conducted as part of ongoing research concerning the use of honeybees (Apis mellifera) as indicators of environmental radionuclide contamination. The expts. were conducted in a study site contg. radionuclide contamination above background levels. The first expt. compared levels of radionuclides found in forager bees to levels found in nurse bees. Bees were collected from colonies, analyzed for concns. of radionuclides, and the results were compared using statistical methods. Results indicated that there is no significant difference between the contaminant levels in forager and nurse bees. A second expt. compared the levels of radionuclides found in the flowers of three plant species growing in the study site: salt cedar (Tamarix ramosissima), white sweet clover (Melilotus albus), and rabbit brush (Chrysothamnus nauseosus). Results indicated that there is no significant difference in the amts. of radionuclides found in the flowers of these three plants.

~2 Citings

244. Tn5 mutants of Rhizobium meliloti with an altered composition of polysaccharides and analysis of their symbiotic properties

By Zatovskaya, T. V.; Ushakov, K. V.; Yurgel, S. N.; Kosenko, L. V.; Zakharova, I. Ya.; Simarov, B. V.
From Russian Journal of Genetics (Translation of Genetika (Moscow)) (1998), 34(6), 606-611. Language: English, Database: CAPLUS

Four mutants with an altered compn. of lipopolysaccharides (LPSs) were isolated by means of random Tn5 mutagenesis of the CXM1-188 strain of Rhizobium. The parental SKhM1-188 strain was electrophoresed in SDS-polyacrylamide gels. The strain was shown to synthesize two types of LPS: high-mol. wt. (LPS1) and low-mol. wt. (LPS2). Mutants Tb29 and Ts22 were shown to synthesize only LPS2 and not LPS1, while mutants Ts32 and Tb9 retained the ability to synthesize both LPS forms. However, as shown by SDS-PAGE electrophoregrams, LPS1 zones of these mutants differed from the LPS1 zone of the parental strain. According to results of transduction of kanamycin resistance from mutant strains to the parental strain, the obsd. modifications of lipopolysaccharides in all four mutants were caused by single Tn5 insertions in the SKhM1-188 genome. The symbiotic properties of bacteria were analyzed in sterile plant tube tests with Medicago sativa L. Mutants did not differ from the original strain with respect to symbiotic effectiveness, but they had altered competitiveness, which was evaluated by the method of coinoculation with an nonactive strain, R. meliloti SKhM1-48. Mutants Tb29 and Ts22, which lacked the ability to synthesize LPS1, manifested a sharp decrease in competitiveness compared to the original strain. Mutants Ts32 and Tb29 synthesizing modified LPS1 were characterized by a less pronounced decrease in competitiveness. These results indicate that the lipopolysaccharides of R. meliloti are important for the expression of competitiveness of these bacteria.

~2 Citings

245. Tn5 mutations of Rhizobium meliloti enhancing the redox potential of free-living cells and the effectiveness of their symbiosis with alfalfa

By Yurgel, S. N.; Sharypova, L. A.; Simarov, B. V.
From Russian Journal of Genetics (Translation of Genetika (Moscow)) (1998), 34(6), 601-605. Language: English, Database: CAPLUS

Twenty-nine transposants with an increased ability to reduce the redox potential indicator 2,3,5-triphenyl-tetrazolium bromide (the Red^{++} phenotype) and six mutants showing enhanced symbiotic effectiveness (the Eff^{++} phenotype) were obtained from the CXM1-188 strain of Rhizohium meliloti. The frequency of the appearance of Tn5 mutants with the Red^{++} phenotype was 3×10^{-3}, which is significantly lower than that of mutants with the Eff^{++} phenotype (2.4×10^{-2}). Twenty-three out of 29 mutations with the Red^{++} phenotype were localized on the megaplasmid 2, while the remaining six were shown to reside in the chromosome. Analyzing the symbiotic properties of the mutants showed that 21 out of 29 transposants exhibit enhanced symbiotic activity.

~2 Citings

246. Characterization and splicing in vivo of a Sinorhizobium meliloti group II intron associated with particular insertion sequences of the IS630-Tc1/IS3 retroposon superfamily

By Martinez-Abarca, Francisco; Zekri, Sanae; Toro, Nicolas
From Molecular Microbiology (1998), 28(6), 1295-1306. Language: English, Database: CAPLUS, DOI:10.1046/j.1365-2958.1998.00894.x

By sequence anal. of Sinorhizobium meliloti strain GR4 plasmid pRmeGR4b, the authors have identified a group II intron named RmInt1 inserted within the insertion sequence ISRm2011-2 of the IS630-Tc1/IS3 retroposon superfamily. Like some other group II introns, RmInt1 possesses, in addn. to the structurally conserved ribozyme core, an open reading frame (ORF) with homol. to reverse transcriptases. Using a T7 expression system in Escherichia coli, the authors show that the intron is active in splicing in vivo and that splicing efficiency requires the intron-encoded ORF, which suggests that the putative intron encoded protein has a maturase function. DNA hybridization studies indicate that intron RmInt1 is widespread within S. meliloti native populations and appears to be mostly located within this IS element. Nevertheless, some S. meliloti strains harbor one copy of RmInt1 at a different location. DNA sequence anal. of the 5' exon of one of these heterologous intron insertion sites revealed the presence of a putative IS element closely related to insertion sequence ISRm2011-2. The intron-binding sites (IBS1 and IBS2 motifs) are conserved, although a transition of a G→A in the IBS1 has occurred. The authors results demonstrate an assocn. of intron RmInt1 with particular insertion sequences of the IS630-Tc1/IS3 retroposon superfamily that may have ensured the spread and maintenance of this group II intron in S. meliloti.

~42 Citings

247. Sequences around the fragmentation sites of the large subunit ribosomal RNA in the family Rhizobiaceae: 23S-like rRNAs in Rhizobiaceae

By Selenska-Pobell, Sonja; Doring, Heidi
From Antonie van Leeuwenhoek (1998), 73(1), 55-67. Language: English, Database: CAPLUS

Representatives of the family Rhizobiaceae possess, instead of one single 23S rRNA mol., 3 different sets of 23S-like rRNA fragments with sizes of about: 135 bases and 2.6 kb (set 1); 135 bases, 400 bases, and 2.2 kb (set 2); 135 bases and 2 mols. of about 1.3 kb (set 3). In 2 of the fragmentations, intervening sequences (IVS I and IVS II) are involved. IVS I is connected to a cleavage of the 23S rRNA primary transcript into two mols. (135 b and 2.6 kb large). IVS II is located at position 543 of the gene, and it leads to an addnl. processing of the 2.6 kb rRNA species into 2 mols. with sizes of about 400 bases and 2.2 kb. In contrast to IVS I, which is a common feature of all rhizobia, IVS II is present in a limited no. of strains only. The primary and secondary structures of the regions of the unmatured 23S rRNA transcript possessing IVS I (helix 9) and IVS II (helix 25) were analyzed. On the basis of these analyses, secondary structure models are proposed for the parts of the matured 23S rRNA-like mols. of rhizobia corresponding to the helixes 9 and 25. The third fragmentation of the rhizobial 23S rRNA represents a break in the central part of the 2.6-kb large rRNA and it leads to an occurrence of 2 fragments with approx. equal size of about 1.3 kb. Thus, the central fragmentation is not connected to the presence of IVSs but probably to a minor change in the nucleotide sequence in the central part of the 2.6 rRNA.

~20 Citings

248. The Rhizobium etli FixL protein differs in structure from other known FixL proteins

By D'hooghe, I.; Michiels, J.; Vanderleyden, J.
From Molecular & General Genetics (1998), 257(5), 576-580. Language: English, Database: CAPLUS, DOI:10.1007/s004380050684

The central heme-binding domain in the FixL proteins of Sinorhizobium meliloti, Bradyrhizobium japonicum, Rhizobium leguminosarum biovar viciae and Azorhizobium caulinodans, is highly conserved. The similarity with the corresponding domain in the Rhizobium etli FixL protein is considerably less. This observation prompted us to analyze the heme-binding capacities of the R. etli FixL protein. The R. etli fixL gene was overexpressed in Escherichia coli. In the presence of S. meliloti FixJ, the overexpressed R. etli FixL protein was able to enhance FixJ-mediated activation of an S. meliloti pnifA-lacZ fusion, indicating that the R. etli FixL protein possesses an active conformation in E. coli. Subsequently, using a non-denaturing gel assay for heme, we analyzed the heme-binding capacity of the R. etli FixL protein expressed in E. coli, taking the S. meliloti FixL protein as a pos. control. The R. etli FixL protein expressed in E. coli does not contain a heme group, in contrast to the S. meliloti FixL protein. Therefore we conclude that the R. etli FixL is a nonheme protein in the nif regulatory cascade.

~16 Citings

249. Distribution of free seleno-amino acids in plant tissue of Melilotus indica L. grown in selenium-laden soils

By Guo, Xun; Wu, Lin
From Ecotoxicology and Environmental Safety (1998), 39(3), 207-214. Language: English, Database: CAPLUS, DOI:10.1006/eesa.1997.1628

Accumulation of specific groups of seleno-amino acids in plant tissue reflects not only the Se tolerance of a plant species, but also Se toxicity to animals. The distribution of seleno-amino acids in a Se-tolerant grassland legume species (Melilotus indica L.) grown in Se-laden soils was studied using high-resoln. gas chromatog.-and gas chromatog.-mass spectrometry. Five seleno-amino acids including selenocystine, seleno-methionine, selenocysteine, Se-methylselenocysteine, and γ-glutamyl-Se-methylselenocysteine were identified and measured for their plant tissue concns. Se-methylselenocysteine, a nonprotein seleno-amino acid, was found in the plant tissue. Its concn. ranged from 15.3 μmol kg^{-1} for the plants growing in soil of low Se concn. to 109.8 μmol kg^{-1} for the plants grown in soil of high Se concn. Accumulation of the nonprotein seleno-amino acid in this species resembles that in Se accumulator plants. γ-Glutamyl-Se-methylselenocysteine was detected in the plant. However, its concn. was very low. It might not become a toxic element in the food chain. Results of plant tissue Se accumulation anal. indicated that there was a five-fold increase in tissue selenocysteine concn. when the total tissue Se increased from 5.07 to 22.02 mg kg^{-1}, but there was no further increase in tissue selenocysteine concn. when the tissue total Se concn. increased from 22.0 to 117.4 mg kg^{-1}. Selenomethinone constituted more than 50% of the total seleno-amino acid in the plant. More research is needed to reveal whether the mechanisms limiting the accumulation of selenocysteine and preferential accumulation of selenomethionine found in this study play any role in Se tolerance in this species.

~29 Citings

250. Characterization of rhizobia homologues of Sinorhizobium meliloti insertion sequences ISRm3 and ISRm4

By Villadas, Pablo J.; Burgos, Pedro; Rodriguez-Navarro, Dulce N.; Temprano, Francisco; Toro, Nicolas
From FEMS Microbiology Ecology (1998), 25(4), 341-348. Language: English, Database: CAPLUS, DOI:10.1111/j.1574-6941.1998.tb00485.x

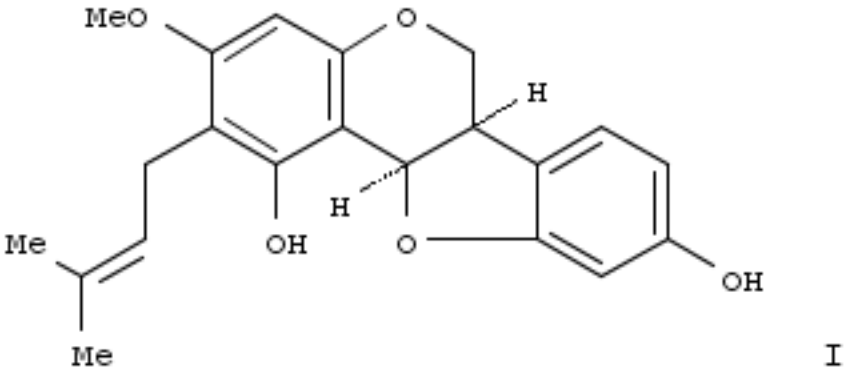
Homologues to Sinorhizobium meliloti insertion sequences ISRm3 and ISRm4 were found within Rhizobium leguminosarum bv. viciae field populations. Similarly, homologous sequences to S. meliloti ISRm4 were found in S. fredii strains. Based on the polymerase chain reaction, some of these putative insertion sequence elements were cloned and partially sequenced. DNA sequence comparisons indicate that S. meliloti and R. leguminosarum ISRm3-type elements are closely related whereas the ISRm4 homologs show distinct relationships. In addn., specific primers for PCR recognition of ISRm3 and ISRm4 elements in rhizobia species and S. meliloti ISRm6 were designed.

~3 Citings

251. A novel prenylated pterocarpan from Melilotus indica

By Saxena, V. K.; Nigam, Swati
From Fitoterapia (1997), 68(5), 403-404. Language: English, Database: CAPLUS

The seeds of M. indica yielded a novel pterocarpan, identified as 1,9-dihydroxy-2-(3-methylbut-2-enyl)-3-methoxypterocarpan (I).



I

~3 Citings

252. Variation of nitrogen fixation among Medicago species in association with Rhizobium meliloti isolates

By Yu, Yongxiong; Fujimoto, Fumihiro; Oba, Sinya
From Grassland Science (1998), 43(4), 391-397. Language: English, Database: CAPLUS

Eleven species or subspecies of Medicago widely distributed in the world were evaluated in assocn. with 6 strains of R. meliloti, isolated from nodules of 6 Medicago species. Significant difference in acetylene redn. ability and in plant dry matter among Medicago species were recognized, indicating considerable genetic variation in the symbiotic nitrogen fixation among species in the genus of Medicago. Perennial species M. sativa ssp. sativa and m. sativa ssp. falcate produced effective nodules to all of the 6 strains of R. meliloti, but annual species M. rigidula, M. arabica, M. aculeate and M. rugosa were effective to only 4 strains, suggesting that the latter was more specific to strains of R. meliloti in nitrogen fixation than the former. The 6 strains of R. meliloti isolated from 6 species of Medicago have differentiated in the compatibility with the plant species; GU 94-1, GU 95-1, GU 96-1 were more specific to host plant species than the other 3 strains. The highest acetylene redn. ability and plant dry matter was obtained when a strain of R. meliloti was inoculated to te Medicago species from which the strain was isolated, indicating that the best compatibility was in the combination of the strain of R. meliloti with the species from which the strain was isolated. It can be estd. that the host plant produced very effective large nodules when assocg. symbiotically with the strain of R. meliloti which has the best compatibility. We can conjecture that it is the start which leads to coevolution of R. meliloti with Medicago species.

~0 Citings

253. Exopolysaccharide II production is regulated by salt in the halotolerant strain Rhizobium meliloti EFB1

By Lloret, Javier; Wulff, Brande B. H.; Rubio, Jose M.; Downie, J. Allan; Bonilla, Ildefonso; Rivilla, Rafael
From Applied and Environmental Microbiology (1998), 64(3), 1024-1028. Language: English, Database: CAPLUS

The halotolerant strain Rhizobium meliloti EFB1 modifies the prodn. of extracellular polysaccharides in response to salt. EFB1 colonies grown in the presence of 0.3 M NaCl show a decrease in mucoidy, and in salt-supplemented liq. medium this organism produces 40% less exopolysaccharides. We isolated transposon-induced mutant that, when grown in the absence of salt, had a colony morphol. (nonmucoid) similar to the colony morphol. of the wild type grown in the presence of salt. Calcofluor fluorescence, proton NMR spectroscopy, and genetic anal. of the mutant indicated that galactoglucan, which is not produced under normal conditions by other R. meliloti strains, is produced by strain EFB1 and that prodn. of this compd. decreases when the organism is grown in the presence of salt. The mutant was found to be affected in a genetic region highly homologous to genes for galactoglucan prodn. in R. meliloti Rm2011 (expE genes). However, sequence divergence occurs in a putative expE promoter region. A transcriptional fusion of the promoter with lacZ demonstrated that, unlike R. meliloti Rm2011, galactoglucan is produced constitutively by EFB1 and that its expression is reduced 10-fold during exponential growth in the presence of salt.

~33 Citings

254. A simple, rapid, inexpensive assay for toxic chemicals using a bacterial indicator

By Botsford, James L.
From Studies in Environmental Science (1997), 66(Global Environmental Biotechnology), 429-443. Language: English, Database: CAPLUS

A simple test for toxic chems. has been developed. Rhizobium meliloti is combined with the toxic chem. A tetrazolium dye, MTT (3-[4,5-Dimethylthiazol-2-yl] 2,5-diphenyl-tetrazolium bromide) is added. The bacterium reduces this dye causing the optical absorbance to increase dramatically. The increase can be detd. with a simple spectrophotometer. Toxic chems. and minerals inhibit the redn. of the dye. Presumably the dye serves as a terminal electron acceptor for electron transport. Toxic substances presumably damage the electron transport system. The assay compares favorably with published results of tests using the Microtox and Polytox assays, two methods using microbial indicators that are available com. This assay, using R. meliloti, offers another method to det. the toxicity of compds., a method that is simple, rapid, and inexpensive. It requires no special equipment. Personnel need no special training. It should be possible to use this assay in a third world situation.

~2 Citings

255. Assay for toxic chemicals using bacteria

By Botsford, J. L.; Rivera, J.; Navarez, J.; Riley, R.; Wright, T.; Baker, R.
From Bulletin of Environmental Contamination and Toxicology (1997), 59(6), 1000-1009. Language: English, Database: CAPLUS, DOI:10.1007/s001289900582

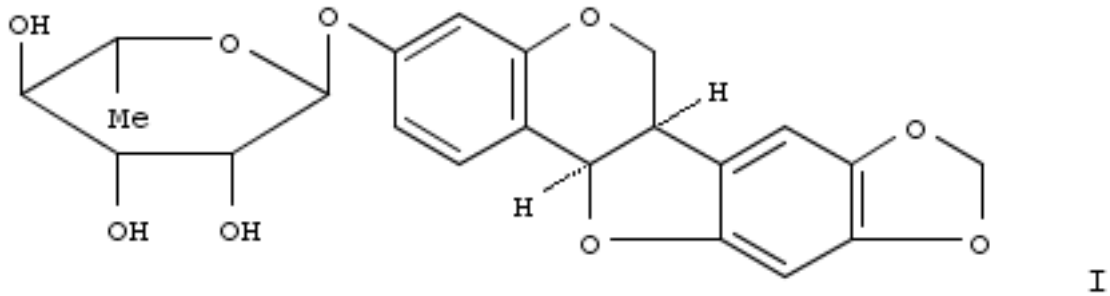
A method to measure the toxicity of chems. is described. Any test for toxic chems. requires an indicator organism. Toxicity is defined by the damage done to living cells. This assay uses the bacterium Rhizobium meliloti as the indicator organism. This assay presents a simple, rapid and inexpensive method to measure toxic chems. without harming animals. Results are comparable to other methods.

~10 Citings

256. A methylenedioxypterocarpan from Melilotus indica

By Saxena, V. K.; Nigam, Swati
From Fitoterapia (1997), 68(4), 343-344. Language: English, Database: CAPLUS

The stem of M. indica yielded a novel pterocarpan identified as 8,9-methylenedioxypterocarpan 3-O-α-L-rhamnopyranoside (I).



I

~2 Citings

257. A new nos gene downstream from nosDFY is essential for dissimilatory reduction of nitrous oxide by Rhizobium (Sinorhizobium) meliloti

By Chan, Yiu-Kwok; Mccormick, Wayne A.; Watson, Robert J.
From Microbiology (Reading, United Kingdom) (1997), 143(8), 2817-2824. Language: English, Database: CAPLUS, DOI:10.1099/00221287-143-8-2817

Rhizobium (Sinorhizobium) meliloti strains capable of dissimilatory nitrous oxide redn. (Nos^+) carry a nosRZDFY gene cluster on a 10.1 kb EcoRI fragment of the nod megaplasmid near the fixGHIS genes. These nos genes are arranged in three complementation groups and the 10.1 kb EcoRI fragment is sufficient to confer Nos activity to R. meliloti strains lacking such activity. An overlapping HindIII fragment contg. the nosRZDFY genes but missing a 0.6 kb HindIII-EcoRI downstream segment was found incapable of imparting Nos activity to strains unable to reduce nitrous oxide, suggesting the presence of other nos gene(s) in this region. Tn5 introduced near the HindIII site resulted in mutants with a Nos^- phenotype. Complete sequence anal. of nosY showed that it was well-conserved with respect to that of Pseudomonas stutzeri. Two previously unreported genes downstream of nosY in R. meliloti were also revealed. Contiguous with nosY was a sequence showing 63% identity with the ORFL protein of P. stutzeri. It appeared to be in the same operon as nosDFY and was predicted to encode a membrane lipoprotein similar to the putative NosL of P. stutzeri. Unlike the latter protein, however, amino acid sequences typical of metal-binding sites and cysteine residues indicative of the active site of protein disulfide isomerase were absent in the predicted NosL of R. meliloti. The Tn5 mutations resulting in a Nos^- phenotype were localized within a 966 nucleotide gene 31 nucleotides downstream of nosDFYL with the same orientation. The new gene, nosX, was detd. to be in a sep. complementation group. It encoded a periplasmic protein with homol. in the C-terminal domain with RnfF of Rhodobacter capsulatus and with a hypothetical Escherichia coli protein, YOJK. It was concluded that there are seven genes constituting the nos cluster in R. meliloti. They are organized in four complementation groups and in the same orientation, spanning a distance of about 9 kb on the nod megaplasmid.

~30 Citings

258. Response of varying doses of tribenuron-methyl on weed control in wheat

By Punia, S. S.; Hooda, R. S.; Malik, R. K.; Singh, B. P.
From Haryana Agricultural University Journal of Research (1996), 26(4), 243-248. Language: English, Database: CAPLUS

Results of the field expts. conducted during rabi 1992-93 and 1993-94 at Hisar and 1993-94 at Karnal revealed that tribenuron-Me at 20 g/ha provided excellent control of Chenopodium album L., Melilotus indica L., Anagallis arvensis L. and Rumex maritimus L. but not of Lathyrus aphaca L. Presence of weeds for the whole season reduced the grain yield of wheat from 4684 to 3788 kg/ha and 5110 to 4014 kg/ha at Hisar and Karnal, resp. Maximum grain yield was obtained in isoproturon treated plots at Karnal but at Hisar, plots treated with tribenuron-Me at the rate of 80 g/ha yielded the max.

~2 Citings

259. Biochemistry and molecular biology of plant sulfotransferases

By Varin, Luc; Marsolais, Frederic; Richard, Martine; Rouleau, Michele
From FASEB Journal (1997), 11(7), 517-525. Language: English, Database: CAPLUS

A review, with 44 refs. It is now well established that, in mammals, sulfate conjugation constitutes an important reaction in the transformation of xenobiotics and in the modulation of the biol. activity of steroid hormones and neurotransmitter. The presence of a sulfate group on some mols. can also be a prerequisite for their biol. function. For example, it is well known that the sulfate groups are directly involved in the mol. interaction between heparin and antithrombin III. In plants, sulfation also seems to play an important role in the intermol. recognition and signaling processes, as indicated by the requirement of a sulfate moiety for the biol. activity of gallic acid glucoside sulfate in the seismonastic and gravitropic movements of plants, and of Nod RM1 in the cortical cell division during early nodule initiation in Rhizobium meliloti-alfalfa interaction. In addn., recent studies indicate that flavonoid conjugates, including the sulfate esters, may play a role in the regulation of plant growth by strongly binding the naphthylphthalamic acid receptor, thus blocking the quercetin-stimulated accumulation of the auxin phytohormone. Although several sulfated metabolites are known to accumulate in a variety of plant species, the study of enzymes that catalyze the sulfation reaction in plants lagged considerably compared to those conducted with their mammalian homologs. This apparent lack of interest may have been because the function of plant-sulfated metabolites is difficult to predict, since their accumulation is often restricted to a limited no. of species. Despite this limitation, several plant sulfotransferases (STs) have been characterized at the biochem. level, and the cDNA clones encoding six plant STs have been isolated. Based on sequence homol., the plant ST coding sequences are grouped under the SULT3 family, also known as the flavonol ST family. This review summarizes our current knowledge of the plant STs and focuses on the functional significance of the sulfate conjugation in plant growth, development, and adaptation to stress.

~64 Citings

260. Ammonia regulated expression of a soybean gene encoding cytosolic glutamine synthetase is not conserved in two heterologous plant systems

By Carrayol, Elisa; Terce-Laforgue, Therese; Desbrosses, Guilhem; Pruvot-Maschio, Gislaine; Poirier, Simone; Ratet, Pascal; Hirel, Bertrand
From Plant Science (Shannon, Ireland) (1997), 125(1), 75-85. Language: English, Database: CAPLUS, DOI:10.1016/S0168-9452(97)00053-8

A 3.5 kb promoter fragment fused to the reporter β-glucuronidase gene (gus) had previously been shown to contain sep. regulatory elements controlling the ammonia-stimulated and organ-specific transcription of GS15, a soybean gene encoding root and root nodule cytosolic glutamine synthetase (GS). In order to det. if the regulatory elements conferring the ammonia-regulated and the organ-specific expression are conserved in different plant species, a GS15 promoter-gus (pGS15GUS) construct was introduced via Agrobacterium-mediated transformation both in tobacco and alfalfa. Histochem. localization of GUS activity revealed that, in both heterologous systems, the cytosolic GS gene was expressed in anthers, theca and pollen at a late stage of flower development. Strong GUS staining was also visible in transgenic alfalfa pulvini and petioles. PGS15GUS was also found to be expressed in roots, however, treatment with ammonia did not increase the expression of the reporter gene either in tobacco or alfalfa. In mutant nodules of alfalfa formed by two different Fix$^-$ strains of Rhizobium meliloti both GUS staining and GUS activity were similar to the Rhizobium wild-type infected nodules indicating that GS15 expression in alfalfa root nodules does not depend on the prodn. of ammonia coming from symbiotically fixed nitrogen. The results are discussed in relation to the possible role of cytosolic GS in different organs of legumes and other plant species.

~8 Citings

261. Growth and nodulation competitiveness of Sinorhizobium meliloti L1 (RecA-) is less than that of its isogenic strain L33 (RecA+) but comparable to that of two S. meliloti wild-type isolates

By Niemann, S.; Puehler, A.; Selbitschka, W.
From Applied Microbiology and Biotechnology (1997), 47(5), 525-529. Language: English, Database: CAPLUS, DOI:10.1007/s002530050967

Gnotobiotic systems were used to assess the competitive abilities of bioluminescent Sinorhizobium meliloti strains L1 (RecA$^-$) and L33 (RecA$^+$) for growth and host plant nodulation in the presence of a reconstructed S. meliloti population. Three wild-type strains belonging to infective subgroups of a natural S. meliloti population were chosen as competitors in microcosm studies. Whereas the RecA$^+$ strain L33 dominated the reconstructed population with respect to growth and alfalfa nodulation, the competitiveness of the RecA$^-$ strain L1 was reduced compared to that of one of the field strains, but comparable to that of the other field isolates. This result indicates that strain L1, despite its recA mutation, has the potential to compete successfully with a resident S. meliloti population after environmental release.

~7 Citings

262. Flavonoids of Melilotus indica

By El Sayed, Nabil H.; Ishak, Moheb S.; Mabry, Tom J.
From Asian Journal of Chemistry (1997), 9(3), 551. Language: English, Database: CAPLUS

Some flavonoids were isolated from the plant Melilotus indica and identified as the known C-glucosides orientin, isoorientin, vitexin, and isovitexin.

~0 Citings

263. Heme compounds as iron sources for nonpathogenic Rhizobium bacteria

By Noya, Francisco; Arias, Alicia; Fabiano, Elena
From Journal of Bacteriology (1997), 179(9), 3076-3078. Language: English, Database: CAPLUS

Many animal-pathogenic bacteria can use heme compds. as iron sources. Like these microorganisms, rhizobium strains interact with host organisms where heme compds. are available. Results presented in this paper indicate that the use of Hb as an iron source is not restricted to animal-pathogenic microorganisms. We also demonstrate that heme, Hb, and legHb can act as iron sources under iron-depleted conditions for Rhizobium meliloti 242. Anal. of iron acquisition mutant strains indicates that siderophore-, heme-, Hb-, and legHb-mediated iron transport systems expressed by R. meliloti 242 share at least one component.

~41 Citings

264. Rhizobium nodulation protein NodC is an important determinant of chitin oligosaccharide chain length in Nod factor biosynthesis

By Kamst, Eric; Pilling, Jens; Raamsdonk, Leonie M.; Lugtenberg, Ben J. J.; Spaink, Herman P.
From Journal of Bacteriology (1997), 179(7), 2103-2108. Language: English, Database: CAPLUS

Synthesis of chitin oligosaccharides by NodC is the first committed step in the biosynthesis of rhizobial lipochitin oligosaccharides (LCOs). The distribution of oligosaccharide chain lengths in LCOs differs between various Rhizobium species. We expressed the cloned nodC genes of Rhizobium meliloti, R. leguminosarum bv. viciae, and R. loti in Escherichia coli. The in vivo activities of the various NodC proteins differed with respect to the length of the major chitin oligosaccharide produced. The clearest difference was obsd. between strains with R. meliloti and R. loti NodC, producing chitintetraose and chitinpentaose, resp. In vitro expts., using UDP-[^{14}C]GlcNAc as a precursor, show that this difference reflects intrinsic properties of these NodC proteins and that it is not influenced by the UDP-GlcNAc concn. Anal. of oligosaccharide chain length in LCOs produced by a R. leguminosarum bv. viciae nodC mutant, expressing the three cloned nodC genes mentioned above, shows that the difference in oligosaccharide chain length in LCOs of R. meliloti and R. leguminosarum bv. viciae is due only to nodC. The exclusive prodn. of LCOs which contain a chitinpentaose backbone by R. loti strains is not due to NodC but to end product selection by Nod proteins involved in further modification of the chitin oligosaccharide. These results indicate that nodC contributes to the host specificity of R. meliloti, a conclusion consistent with the results of several studies which have shown that the lengths of the oligosaccharide backbones of LCOs can strongly influence their activities on host plants.

~36 Citings

265. Plant defense in alfalfa pseudonodules induced by an exopolysaccharide (EPS I)- deficient symbiont (Rhizobium meliloti)

By Niehaus, K.; Kapp, D.; Lorenzen, J.; Meyer-Gattermann, P.; Sieben, S.; Puehler, A.
From Acta Horticulturae (1994), 381(International Symposium on Natural Phenols in Plant Resistance, Vol. 1), 258-264. Language: English, Database: CAPLUS

Mutants of the symbiotic soil bacterium Rhizobium meliloti that fail to synthesize the acidic exopolysaccharide EPS I were unable to induce infected root nodules on the host plant Medicago sativa L. (alfalfa). The pseudonodules induced by EPS I deficient R. meliloti mutants showed a brown, necrotic area on their surface indicating a plant defense reaction. HPLC anal. of pseudonodules revealed an increase of phenolic compds. incorporated into the nodule cell walls when compared with wildtype nodules. An increased enzymic activity of peroxidase (POD) and phenylalanine ammonia-lyase (PAL) was found in noninfected pseudonodules. In contrast to pseudonodules, the activity of these enzymes was not increased in roots inoculated with EPS I deficient R. meliloti mutants, indicating a strictly localized plant response. Hybridization with a phenylalanine ammonia-lyase homologous cDNA probe confirmed that the increased enzymic activity in pseudonodules was the consequence of an enhanced transcription of the PAL-gene. A plant test with more than twenty Medicago species revealed that the inability of EPS I deficient R. meliloti mutants to establish an effective symbiosis is conserved in all tested species. Based on the mechanism of phytopathogenic interactions, EPS I or a related compd. acts as a suppressor of the plant defense system, enabling R. meliloti to infect the plant.

~5 Citings

266. Accumulation of seleno-amino acids in legume and grass plant species grown in selenium-laden soils

By Wu, Lin; Guo, Xun; Banuelos, Gary S.
From Environmental Toxicology and Chemistry (1997), 16(3), 491-497. Language: English, Database: CAPLUS, DOI:10.1002/etc.5620160314

Seleno-amino acid accumulation was studied for two legume and two grass species grown in Se-laden soils. An antagonistic relationship was found between the tissue Se-amino acid concn. and the corresponding sulfur-amino acid concn. This relationship demonstrates a competitive interaction between Se and sulfate at the amino acid synthesis level. The nonsulfur-contg. amino acids were not affected by the increase of tissue Se concn. Sour clover (Melilotus indica L.) was able to accumulate much greater tissue Se concn. than the other three species. Tissue methionine concn. of sour clover, rabbit foot grass (Polypogon monspeliensis L.), and tall fescue (Festuca arundinacea Schreb.) was not affected by the increase of tissue selenomethionine concn., but a highly significant neg. correlation was found in alfalfa (Medicago sativa L.). This discrepancy suggests that a less antagonistic effect on sulfur-amino acids under the increase of Se-amino acid analogs in the tissue might be able to minimize Se toxicity to the plant. Both Se-methylselenocysteine (nonprotein amino acid) and selenomethionine (protein amino acid) accumulated in the plants when grown in Se-laden soils. Possible effects of these Se-amino acids accumulated by plants on animal health should be tested before the plants are used for forage supplementation.

~23 Citings

267. 3,9-Dihydroxypterocarpone: estrogenic component of Melilotus indica

By Saxena, V. K.; Nigam, Swati
From Journal of the Institution of Chemists (India) (1996), 68(4), 122-125. Language: English, Database: CAPLUS

Spectral and chem. degradative studies have led to the structural assignment of a compd. isolated from the seeds of Melilotus indica as 3,9-dihydroxypterocarpone (coumestrol), which was found to possess estrogenic activity.

~0 Citings

268. The common nodABC genes of Rhizobium meliloti are host-range determinants

By Roche, Philippe; Maillet, Fabienne; Plazanet, Claire; Debelle, Frederic; Ferro, Myriam; Truchet, Georges; Prome, Jean-Claude; Denarie, Jean
From Proceedings of the National Academy of Sciences of the United States of America (1996), 93(26), 15305-15310. Language: English, Database: CAPLUS, DOI:10.1073/pnas.93.26.15305

Symbiotic bacteria of the genus rhizobium synthesize lipo-chitooligosaccharides, called Nod factors (NFs), which act as morphogenic signal mols. on legume hosts. The common nodABC genes, present in all rhizobium species, are required for the synthesis of the core structure of NFs. NodC is an N-acetylglucosaminyltransferase, and NodB is a chitooligosaccharide deacetylase; NodA is involved in N-acylation of the aminosugar backbone. Specific nod genes are involved in diverse NF substitutions that confer plant specificity. We transferred to R. tropici, a broad host-range tropical symbiont, the ability to nodulate alfalfa, by introducing nod genes of R. meliloti. In addn. to the specific nodL and nodFE genes, the common nodABC genes of R. meliloti were required for infection and nodulation of alfalfa. Purified NFs of the R. tropici hybrid strain, which contained chitin tetramers and were partly N-acylated with unsatd. C16 fatty acids, were able to elicit nodule formation on alfalfa. Inactivation of the R. meliloti nodABC genes suppressed the ability of the NFs to nodulate alfalfa. Studies of NFs from nodA, nodB, nodC, and nodI mutants indicate that (i) NodA of R. meliloti, in contrast to NodA of R. tropici, is able to transfer unsatd. C16 fatty acids onto the chitin backbone and (ii) NodC of R. meliloti specifies the synthesis of chitin tetramers. These results show that allelic variation of the common nodABC genesis a genetic mechanism that plays an important role in signaling variation and in the control of host range.

~56 Citings

269. Efficacy of sulfonylurea herbicides against broadleaf weeds in wheat

By Balyan, R. S.; Malik, R. K.; Malik, R. S.
From Tests of Agrochemicals and Cultivars (1996), 17, 42-43. Language: English, Database: CAPLUS

Tribenuron at 15 g/ha, metsulfuron at 2 and 4 g/ha, tribenuron + surfactant (Triton AE) at 7.5 or 10 g + 0.1%, metsulfuron + surfactant at 1 or 2 g + 0.1%, and tribenuron + 2,4-D at 7.5 + 250 or 500 g/ha effectively controlled weeds such as Chenopodium album, Melilotus indica, Lathyrus aphaca, and Anagallis arvensis in wheat.

~0 Citings

270. Effects of forage plant and field legume species on soil selenium redistribution, leaching, and bioextraction in soils contaminated by agriculture drain water sediment

By Wu, L.; Van Mantgem, P. J.; Guo, X.
From Archives of Environmental Contamination and Toxicology (1996), 31(3), 329-338. Language: English, Database: CAPLUS, DOI:10.1007/BF00212671

A study was undertaken to assess the potential of tall fescue (Festuca arundinacea Schreb.) and yellow sour clover (Melilotus indica L.) for bioremediation of Se-laden soils. Using soil columns under simulated field soil conditions, the effects of these 2 species were studied on soil Se redistribution, leaching, and Se bioextn. Both leachate vol. and Se concn. in the leachate were greatly influenced by presence of vegetation. The vol. of leachate was considerably lower for columns having either tall fescue or yellow sour clover plantings. Tall fescue had a higher water use rate and greater rooting d. than did in yellow sour clover, indicating the tall fescue will be more practical for bioremediation of Se-laden soils. Soil Se distribution anal. yielded the following patterns: (1) contamination of the lower soil profile of uncontaminated soil occurred at the 1st harvest, but Se concns. at these depths were not at high levels; (2) except for selenite, all forms of water-extractable soil Se concns. showed a clear redn. over time of vegetation harvest; and (3) the redns. of total soil Se were significant, but the differences was relatively small between the forage planting and bare soil treatments. This is due to the fact that only a relatively small fraction of Se inventory was water sol. and available to plants at any one time. A large redn. may become apparent after a longer period of forage plant management.

~22 Citings

271. Sinorhizobium medicae sp. nov., isolated from annual Medicago spp.

By Rome, Sophie; Fernandez, Maria P.; Brunel, Brigitte; Normand, Philippe; Cleyet-Marel, Jean-Claude
From International Journal of Systematic Bacteriology (1996), 46(4), 972-980. Language: English, Database: CAPLUS, DOI:10.1099/00207713-46-4-972

The taxonomic position of isolates of a new genomic species (designated genomic species 2) obtained from several annual Medicago species and originating from different geog. locations was established through the results of phenotypic tests (including the results of auxanog. and biochem. tests and symbiotic properties) and 16S rRNA phylogenetic inferences. A comparison of the complete 16S rRNA sequence of a representative of genomic species 2 (strain A 321^T [T = type strain]) with the 16S rRNA sequences of other members of the Rhizobiaceae and closely related taxa showed that genomic species 2 was phylogenetically related to Sinorhizobium meliloti, Sinorhizobium fredii, Sinorhizobium saheli, and Sinorhizobium teranga. The levels of sequence similarity and obsd. nos. of nucleotide substitutions in Sinorhizobium strains indicated that A 321^T and S. meliloti exhibited the highest level of sequence similarity (99.7%), with four nucleotide substitutions and one deletion. The results of a numerical anal. based on data from 63 auxanog. and biochem. tests clearly sepd. genomic species 2 isolates from S. meliloti. Genomic species 2 isolates nodulated and fixed nitrogen with Medicago polymorpha, whereas S. meliloti isolates were ineffective and formed rudimentary nodules on this host plant. On the basis of phenotypic and 16S sequence anal. data, genomic species 2 isolates cannot be assigned to a previously described species. We propose that these isolates belong to a new species, Sinorhizobium medicae.

~88 Citings

272. Bioextraction of selenium by forage and selected field legume species in selenium-laden soils under minimal field management conditions

By Van Mantgem, Phillip J.; Wu, Lin; Banuelos, Gary S.
From Ecotoxicology and Environmental Safety (1996), 34(3), 228-238. Language: English, Database: CAPLUS, DOI:10.1006/eesa.1996.0068

A forage plant, tall fescue (Festuca arundinacea), and a selected field legume species, sour clover (Melilotus indica), were examd. for their Se bioextn. abilities in Se-laden soils under minimal management conditions. Natural vegetations in a 2-acre plot adjacent to the forage plots were also studied for Se accumulation comparisons. During the dry season, in the fall of 1994, the field plots were either irrigated weekly or without irrigation. No fertilization and weed control were applied. The plants were harvested in May 1995. There were considerable differences in the ability of Se uptake between the forage and the legume species and among the naturally established plant species; the amt. of Se accumulated per land area was largely dependent on their resp. biomass prodn. Comparing Se concn. between preplant and postharvest, there was a detectable redn. in the soil selenate, selenite, and water-extractable org. Se in the tall fescue and melilotus plots. The field irrigation provided more favorable conditions for bioextns. and dissipation of Se by the plants. However, the available soil Se only accounts for less than 10% of the total soil Se and no detectable redn. of total soil Se was found. This may be due to the large inventory and variation of Se concns. in the field soils and therefore obscured the detectable differences. For practical considerations, the forage plants can be repeatedly harvested and used for rangelands of Se deficiency currently seen in some northern California counties.

~7 Citings

273. Effect of glutamate transport and catabolism on symbiotic effectiveness in Rhizobium leguminosarum bv. phaseoli

By Labidi, M.; Lalande, R.; Laberge, S.; Antoun, H.
From Plant and Soil (1996), 182(1), 51-58. Language: English, Database: CAPLUS, DOI:10.1007/BF00010994

Seven Tn5 induced mutants unable to use glutamate as sole carbon and nitrogen source were isolated from the effective Rhizobium leguminosarum bv. phaseoli strain P121-R. As indicated by restriction and hybridization anal., all the mutants arose from a single Tn5 insertion in the chromosome. The ^{14}C-glutamate uptake rate of the mutants was 76-88% lower than that of strain P121-R. Inoculation of Phaseolus vulgaris cv. Labrador with these mutants significantly decreased shoot dry matter yield and the total nitrogen content resp., as compared to inoculation with the parental strain P121-R. All the mutants formed nodules, however they were smaller, white to greenish and approx. 30% less numerous than those formed by strain P121-R. Thus, glutamate transport and catabolism in R. leguminosarum bv. phaseoli P121-R may play an important role in the establishment of an effective symbiosis in field beam. None of the mutants isolated was an auxotroph. All mutants were unable to grow on aspartate suggesting that glutamate and aspartate, probably have the same transporter as indicated in Rhizobium meliloti and in Bacillus subtilis. All mutants readily used glutamine, proline, arginine as sole carbon and nitrogen source, but grew more slowly than the wild type strain. On the other hand, all the mutants were impaired in growth on histidine and γ-aminobutyrate as sole carbon and nitrogen source. As the catabolism of these amino acids occurs predominantly through glutamate. Thus, mutants are also impaired in their ability to use histidine and γ-aminobutyrate as a nitrogen source. Also, other amino acids catabolized through the glutamate pathways may be an addnl. important carbon source for bacterioids in nodules.

~5 Citings

274. mRNAs for flavonoid synthesis and flavonoids accumulate at low levels in alfalfa roots when inoculated with invasive or non-invasive rhizobia.

By Hirsch, A. M.
From Book of Abstracts, 212th ACS National Meeting, Orlando, FL, August 25-29 (1996), AGFD-098. Language: English, Database: CAPLUS

Flavonoids are involved in a no. of crit. events in establishing nitrogen-fixing symbioses. We followed the expression of two nodule-enhanced chalcone synthase (CHS) gene family members and also chalcone isomerase (CHI) and isoflavone reductase (IFR) genes during the interaction between alfalfa and Sinorhizobium meliloti. CHS, CHI, and IFR transcripts increased 2 to 5 days post-inoculation with wildtype rhizobia. Enhanced gene expression was correlated with an increase in root flavonoid content. CHS transcripts were detected in the root hairs and epidermal cells of the root hair zone, and infrequently in nodule primordia. Transcript levels for these genes were also elevated in roots inoculated with a non-invasive (Exo$^-$) mutant of S. meliloti, but not to levels higher than obsd. following inoculation with wild-type rhizobia. However, neither nod gene-inducing flavonoids nor free medicarpin, the phytoalexin of alfalfa, were detected. These results indicate that although invasive and non-invasive S. meliloti trigger the expression of CHS, CHI and IFR in the earliest stages of nodule development, the expression is transient, below the magnitude triggered by pathogenic organisms or elicitor, and is quickly suppressed.

~0 Citings

275. Biotin and other water-soluble vitamins are key growth factors for alfalfa root colonization by Rhizobium meliloti 1021

By Streit, Wolfgang R.; Joseph, Cecillia M.; Phillips, Donald A.
From Molecular Plant-Microbe Interactions (1996), 9(5), 330-338. Language: English, Database: CAPLUS, DOI:10.1094/MPMI-9-0330

Rhizosphere growth limitations imposed on R. meliloti by availability of biotin, thiamin, and riboflavin were overcome by adding nanomolar amts. of these vitamins. Studies done with R. meliloti 1021 showed that both synthesis and uptake of biotin promote colonization of alfalfa roots. Two lines of evidence indicated that plant-derived biotin normally promotes root colonization: adding avidin significantly reduced rhizosphere growth of R. meliloti 1021 and growth of Tn5-induced biotin auxotrophs still increased 10-fold in the rhizosphere. Synthesis, however, is the more important source of biotin for R. meliloti 1021 because in root colonization tests biotin auxotrophs competed very poorly with the parent strain. Mutations conferring biotin auxotrophy were closely linked on a single restriction fragment, and one was complemented with the Escherichia coli bio operon. Initial nucleotide sequencing and DNA-DNA hybridization tests showed the biotin synthesis genes in R. meliloti are quite different from those in E. coli.

~70 Citings

276. Thermoregulation of kpsF, the first region 1 gene in the kps locus for polysialic acid biosynthesis in Escherichia coli K1

By Cieslewicz, Michael; Vimr, Eric
From Journal of Bacteriology (1996), 178(11), 3212-3220. Language: English, Database: CAPLUS

The kps locus for biosynthesis of the capsular polysialic acid virulence factor in Escherichia coli K1 contains at least two convergently transcribed operons, designated region 1 and regions 2 plus 3. On the basis of DNA sequence anal., kpsF appeared to be a good candidate for the first gene of region 1 (M. J. Cieslewicz, S. M. Steenbergern, and E. R. Vimr, J. Bacteriol. 175:8018-8023, 1993). A preliminary indication that kpsF is required for capsule prodn. is the capsule-neg. phenotype of an aphT insertion in the chromosomal copy of kpsF. The present communication describes the isolation and phenotypic characterization of this mutant. Although transcription through kpsF was required for capsule prodn., complementation anal. failed to indicate a clear requirement for the KpsF polypeptide. However, since E. coli contains at least two other open reading frames that could code for homologs of KpsF, the apparent dispensability of KpsF remains provisional. DNA sequence anal. of 1,100 bp upstream from the kpsF translational start site did not reveal any open reading frames longer than 174 nucleotides, consistent with kpsF being the first gene of region 1. Since kpsF appeared to be the first gene of a region whose gene products are required for polysialic acid transport and because capsule prodn. is known to be thermoregulated, primer extension analyses were carried out with total RNA isolated from cells grown at permissive (37°C) and nonpermissive (20°C) temps. The results revealed a potentially complex kpsF promoter-like region that was transcriptionally silent at the nonpermissive temp., suggesting that thermoregulation of region 1 may be exerted through variations in kpsF expression. Addnl. evidence supporting this conclusion was obtained by demonstrating the effects of temp. on expression of the gene kpsE, immediately downstream of kpsF. Chloramphenicol acetyltransferase assays were carried out with constructs contg. the kpsF 5' untranslated region fused to a promoterless cat cassette, providing further evidence that kpsF is thermoregulated. Although the function of KpsF is unclear, primary structure anal. indicated two motifs commonly obsd. in regulatory proteins and homol. with glucosamine synthase from Rhizobium meliloti.

~38 Citings

277. Antifungal studies of pterocarponoids from Melilotus indica

By Saxena, V. K.; Nigam, Swati
From Asian Journal of Chemistry (1996), 8(2), 337-8. Language: English, Database: CAPLUS

Compds. MIS_1 isolated from the seed and MIS_3 isolated from the stem of Melilotus indica are pterocarponoids, which have been found to possess antifungal activity. Activity was tested against Trichophyton mentagrophytes, Epidermophyton floccosum, Aspergillus flavus, Microsporum gypsum and Rhizopus oryzae fungi. The max. inhibitory effects were shown by both compds. against Epidermophyton floccosum and the min. inhibitory effects were obsd. against Rhizopus oryzae.

~3 Citings

278. The auxin transport inhibitor N-(1-naphthyl)phthalamic acid elicits pseudonodules on nonnodulating mutants of white sweetclover

By Wu, Chunfa; Dickstein, Rebecca; Cary, Andrew J.; Norris, Joanna Hanks
From Plant Physiology (1996), 110(2), 501-10. Language: English, Database: CAPLUS

The collection of symbiotic (sym) mutants of white sweetclover (Melilotus alba Desr.) provides a developmental sequence of mutants blocked early in infection or nodule organogenesis. Mutant phenotypes include non-nodulating mutants that exhibit root-hair deformations in response to Rhizobium meliloti, mutants that form ineffective nodules lacking infection threads, and mutants that form infection threads and ineffective nodules. Mutant alleles from both the sym-1 and the syn-3 loci exhibited a non-nodulating phenotype in response to R. meliloti, although one allele in the sym-1 locus formed ineffective nodules at a low frequency. Spot-inoculation expts. on a non-nodulating allele in the sym-3 locus indicated that this mutant lacked cortical cell divisions following inoculation with R. meliloti. The auxin transport inhibitor N-(1-naphthyl)phthalamic acid elicited development of pseudonodules at a high frequency on all of the sweetclover sym mutants, including the nonnodulating mutants, in which the early nodulin ENOD2 was expressed. This suggests that N-(1-naphthyl)phthalamic acid activates cortical cell divisions by circumventing a secondary signal transduction event that is lacking in the non-nodulating sweetclover mutants. The syn-3 locus and possibly the sym-1 locus appear to be essential to early host plant responses essential to nodule organogenesis.

~35 Citings

279. Extension of the Rhizobium meliloti succinoglycan biosynthesis gene cluster: identification of the exsA gene encoding an ABC transporter protein, and the exsB gene which probably codes for a regulator of succinoglycan biosynthesis

By Becker, Anke; Kuester, Helge; Niehaus, Karsten; Puehler, Alfred
From Molecular & General Genetics (1995), 249(5), 487-97. Language: English, Database: CAPLUS, DOI:10.1007/BF00290574

Two new genes, designated exsA and exsB, were identified adjacent to the 24-kb exo gene cluster of R. meliloti, which is involved in succinoglycan (EPS I) biosynthesis. The derived amino acid sequence of ExsA displayed significant homologies to ATP binding cassette (ABC) transporter proteins. R. meliloti strains mutated in exsA were characterized by a decreased ratio of HMW to LMW EPS I, indicating a function for ExsA in EPS I biosynthesis. The R. meliloti NdvA protein, which is involved in the transport of cyclic β-(1,2)-glucans, was identified as the closest homolog of ExsA. R. meliloti exsB mutants produced a 3-fold increased amt. of EPS I in comparison to the wild-type strain. In contrast, a high copy no. of exsB resulted in a decrease in the EPS I level of 20% of wild type, indicating that the exsB gene product can neg. influence EPS I biosynthesis. This influence is not due to transcriptional regulation of the exo genes by the exsB gene product. By plasmid integration it was shown that exsA and exsB represent monocistronic transcription units.

~67 Citings

280. Ferric leghemoglobin in plant-attached leguminous nodules

By Lee, Keuk-ki; Shearman, Linda L.; Erickson, B. Kipp; Klucas, Robert V.
From Plant Physiology (1995), 109(1), 261-7. Language: English, Database: CAPLUS

LegHb (Lb) is essential for nitrogen fixation by intact leguminous nodules. To det. whether ferric Lb (Lb^{3+}) was detectable in nodules under normal or stressed conditions, the status of Lb in intact nodules attached to sweet clover (Melilotus officinalis) and soybean (Glycine max) roots exposed to various conditions was monitored. The effects of N_2 and O_2 were tested to det. whether the spectrophotometric technique was showing the predicted responses of Lb. The soybean and sweet clover nodules' Lb spectra indicated predominantly ferrous Lb and LbO_2 in young (34 day) plants. As the nodule aged beyond 45 days, it was possible to induce Lb^{3+} with a 100% O_2 stream (15 min). At 65 days without inducement, the nodule Lb status indicated the presence of some Lb^{3+} along with ferrous Lb and oxyferrous Lb. Nicotinate and fluoride were used as ligands to identify Lb^{3+}. Computer-calcd. difference spectra were used to demonstrate the changes in Lb spectra under different conditions. Some conditions that increased absorbance in the 626 nm region (indicating Lb^{3+} accumulation) were root-fed ascorbate and dehydroascorbate, plant exposure to darkness, and nodule water immersion.

~15 Citings

281. Identification of nodule-dominant Rhizobium meliloti strains carrying pRmeGR4b-type plasmid within indigenous soil populations by PCR using primers derived from specific DNA sequences

By Villadas, Pablo J.; Velazquez, Encarna; Martinez-Molina, Eustoquio; Toro, Nicolas
From FEMS Microbiology Ecology (1995), 17(3), 161-8. Language: English, Database: CAPLUS, DOI:10.1111/j.1574-6941.1995.tb00139.x

Rhizobium meliloti strain GR4 is a highly infective and competitive bacteria which was isolated in 1975 from a field site in Granada (Spain) and which has a high potential as an inoculant. R. meliloti isolates from alfalfa plants grown in this field site were characterized using polymerase chain reaction. Characterization was based on primers derived from insertion sequence elements (ISRm3 and ISRm4), plasmid origin of replication (pRmeGR4a repC locus) and plasmid pRmeGR4b specific DNA sequences. Soil isolates harboring plasmid type pRmeGR4b represented the major infective population in this field site. A direct correlation between the presence of pRmeGR4b-like plasmid and the competitiveness of the strains was found. In addn., four different R. meliloti field populations isolated from Spanish soils were analyzed for the presence of pRmeGR4b related plasmids. Our results indicate that this plasmid type is widespread among R. meliloti field populations and that its frequency within the infective isolates depends on the host plant.

~22 Citings

282. A homolog of the Rhizobium meliloti nitrogen fixation gene fixN is involved in the production of a microaerobically induced oxidase activity in the phytopathogenic bacterium Agrobacterium tumefaciens

By Schlueter, A.; Rueberg, S.; Kramer, M.; Weidner, S.; Preifer, U. B.
From Molecular & General Genetics (1995), 247(2), 206-15. Language: English, Database: CAPLUS

Hybridization anal. using the Rhizobium meliloti nitrogen fixation gene fixN as a probe revealed the presence of a homologous DNA region in the phytopathogenic bacterium Agrobacterium tumefaciens. Hybridization signals were also detected with total DNAs of Rhizobium leguminosarum bv. phaseoli, Rhodobacter capsulatus and Escherichia coli, but not those of Xanthomonas campestris pv. campestris and Pseudomonas putida. The hybridizing fragment from A. tumefaciens was cloned and sequenced. The predicted gene product of one of the two open reading frames identified on the sequenced fragment shows homol. to FixN of different Rhizobiaceae as well as a low but significant similarity to subunit I of heme copper oxidases from various bacteria. The presence of five strictly conserved histidine residues previously implicated in forming ligands to heme and Cu_B in oxidases and the predicted membrane topol. provide evidence that the A. tumefaciens fixN-like gene product is a component of the heme copper oxidase superfamily. The incomplete open reading frame starting only 8 nucleotides downstream of the fixN-like gene exhibits homol. to Rhizobium fixO. Using an uidA (GUS) gene fusion it could be shown that the A. tumefaciens fixN-like gene is preferentially expressed under microaerobic conditions. Expression of the uidA fusion is abolished in R. meliloti fixJ and fixK mutants, indicating that an Fnr-like protein is involved in transcriptional regulation of the fixN-like gene in A. tumefaciens. The presence of an upstream DNA sequence motif identical to the Fnr-consensus binding site (anaerobox) further supports this hypothesis. A. tumefaciens mutated in the fixN-like gene shows decreased TMPD-specific oxidase activity under microaerobic conditions, indicating that the fixN-like gene or operon codes for proteins involved in respiration under reduced oxygen availability.

~0 Citings

283. Attenuation of symbiotic effectiveness by Rhizobium meliloti SAF22 related to the presence of a cryptic plasmid

By Velazquez, Encarna; Mateos, Pedro F.; Pedrero, Paloma; Dazzo, Frank B.; Martinez-Molina, Eustoquio
From Applied and Environmental Microbiology (1995), 61(5), 2033-6. Language: English, Database: CAPLUS

Several wild-type strains of Rhizobium meliloti isolated from alfalfa nodules exhibited different plasmid profiles, yet did not differ in growth rate in yeast-mannitol medium, utilization of 43 different carbon sources, intrinsic resistance to 14 antibiotics, or detection of 16 enzyme activities. In contrast, three measures of effectiveness in symbiotic nitrogen fixation with alfalfa (shoot length, dry wt., and nitrogen content) indicated that R. meliloti SAF22, whose plasmid profile differs from those of the other strains tested, is significantly less effective than other wild-type strains in symbiotic nitrogen fixation. Light microscopy of nodules infected with strain SAF22 showed an abnormal center of nitrogen fixation zone III, with bacteria occupying a smaller portion of the infected host cells and vacuoles occupying a significantly larger portion of adjacent uninfected host cells. In contrast, the effective nodules infected with other wild types or plasmid pRmSAF22c-cured segregants of SAF22 did not display this cytol. abnormality.

~12 Citings

284. Cloning of the second adenylate cyclase gene (cya2) from Rhizobium meliloti F34: Sequence similarity to eukaryotic cyclases

By Archdeacon, John; Talty, John; Boesten, Bert; Danchin, Antoine; O'Gara, Fergal
From FEMS Microbiology Letters (1995), 128(2), 177-84. Language: English, Database: CAPLUS, DOI:10.1111/j.1574-6968.1995.tb07519.x

A second adenylate cyclase (cya2) gene was isolated from a Rhizobium meliloti F34 gene bank. Complemented E. coli Δcya mutants were capable of utilizing a no. of, but not all, carbon sources known to be regulated by cAMP. DNA hybridization studies showed cya2 to be unique to R. meliloti strains. The cya2 nucleotide sequence was detd. and found to encode a protein of 363 amino acids. Residues were identified within the C-terminal domain which are conserved in both eukaryotic adenylate and guanylate cyclases, including a putative ATP binding site. Similar residues were also found in the prokaryotic R. meliloti Cya1 protein. A R. meliloti cya1/cya2 double mutant was constructed and characterized; however, cAMP prodn. was still obsd. in this strain indicating the presence of a third cya gene.

~10 Citings

285. The cycHJKL genes of Rhizobium meliloti involved in cytochrome c biogenesis are required for "respiratory" nitrate reduction ex planta and for nitrogen fixation during symbiosis

By Kereszt, Attila; Slaska-Kiss, Krystyna; Putnoky, Peter; Banfalvi, Zsofia; Kondorosi, Adam
From Molecular & General Genetics (1995), 247(1), 39-47. Language: English, Database: CAPLUS, DOI:10.1007/BF00425819

The authors report the genetic and biochem. anal. of Rhizobium meliloti mutants defective in symbiotic nitrogen fixation (Fix$^-$) and "respiratory" nitrate redn. (rnr$^-$). The mutations were mapped close to the ade-1 and cys-46 chromosomal markers and the mutated locus proved to be identical to the previously described fix-14 locus. By directed Tn5 mutagenesis, a 4.5 kb segment of the chromosome was delimited in which all mutations resulted in Rnr$^-$ and Fix$^-$ phenotypes. Nucleotide sequence anal. of this region revealed the presence of four open reading frames coding for integral membrane and membrane-anchored proteins. Biochem. anal. of the mutants showed that the four proteins were necessary for the biogenesis of all cellular c-type cytochromes. In agreement with the nomenclature proposed for rhizobial genes involved in the formation of c-type cytochromes, the four genes were designated cycH, cycJ, cycK, and cycL, resp. The predicted protein product of cycH exhibited a high degree of similarity to the Bradyrhizobium japonicum counterpart, while CycK and CycL shared more than 50% amino acid sequence identity with the Rhodobacter capsulatus Cc11 and Cc12 proteins, resp. CycJ encodes a novel membrane anchored protein of 150 amino acids. The authors suggest that this gene cluster codes for (parts of) a multi-subunit cytochrome c haem lyase. Moreover, these results indicate that in R. meliloti c-type cytochromes are required for respiratory nitrate redn. ex planta, as well as for symbiotic nitrogen fixation in root nodules.

~39 Citings

286. A biological containment system for Rhizobium meliloti based on the use of recombination-deficient (recA-) strains

By Selbitschka, Werner; Dresing, Uwe; Hagen, Margit; Niemann, Stefan; Puehler, Alfred
From FEMS Microbiology Ecology (1995), 16(3), 223-32. Language: English, Database: CAPLUS, DOI:10.1111/j.1574-6941.1995.tb00286.x

Using a newly developed integration vector, the Escherichia coli gusA gene conferring β-glucuronidase activity or the firefly (Photinus pyralis) luc gene mediating bioluminescence were integrated into a non-essential site of the chromosome of Rhizobium meliloti 2011. The integration of the constitutively expressed marker genes into the chosen site per se did not affect the strains' ability to perform homologous recombination, its growth characteristics, or its symbiotic nitrogen fixation. Comparative microcosm analyses between the bioluminescent, recombination-proficient (RecA$^+$) R. meliloti strain L33 whose construction is reported in this paper, and its previously described recombination-deficient (RecA$^-$) isogenic counterpart L1 indicate that RecA$^-$ strains of Rhizobium are safe hosts for deliberate release expts.

~30 Citings

287. Complementation of Rhizobium meliloti leucine auxotrophy by the gene bank of Rhizobium leguminosarum bv. Viceae VF39

By Yerko, V. N.; Starchenkov, E. P.
From Fiziologiya i Biokhimiya Kul'turnykh Rastenii (1994), 26(3), 264-8. Language: Russian, Database: CAPLUS

Using a cosmid gene bank of R. leguminosarum bv. viceae VF39, the authors complemented the leucine-requiring mutant R. meliloti T46 and selected prototrophic transconjugants. After transfer of the cosmids sepd. from these transconjugants to R. meliloti T46, they obtained clones which could grow on minimal medium but their symbiotic properties remained identical to those of mutant T46. These data indicate that the leucine biosynthesis gene of R. meliloti T46 is closely linked to DNA responsible for symbiosis with alfalfa.

~0 Citings

288. Interspecies regulation of the recA gene of gram-negative bacteria lacking an E. coli-like SOS operator

By Riera, Joan; Fernandez de Henestrosa, Antonio R.; Garriga, Xavier; Tapias, Angels; Barbe, Jordi
From Molecular & General Genetics (1994), 245(4), 523-7. Language: English, Database: CAPLUS, DOI:10.1007/BF00302266

The recA genes of Agrobacterium tumefaciens, Rhizobium meliloti, Rhizobium phaseoli and Rhodobacter sphaeroides, species belonging to the alpha-group bacteria of the Proteobacteria class, have been fused in vitro to the lacZ gene of Escherichia coli. By using a mini-Tn5 transposon deriv., each of these recA-lacZ fusions was introduced into the chromosome of each of the four species, and into that of E. coli. The recA genes of three of the alpha bacteria are induced by DNA damage when inserted in A. tumefaciens, R. phaseoli or R. meliloti chromosomes. The expression of the recA gene of R. sphaeroides is DNA damage-mediated only when present in its own chromosome; none of the genes is induced in E. coli. Likewise, the recA gene of E. coli is not induced in any of the four alpha species. These data indicate that A. tumefaciens, R. meliloti and R. phaseoli possess a LexA-like repressor, which is able to block the expression of their recA genes, as well as that of R. sphaeroides, but not the recA gene of E. coli. The LexA repressor of R. sphaeroides does not repress the recA gene of A. tumefaciens, R. meliloti, R. phaseoli or E. coli.

~11 Citings

289. Expression vectors for the use of eukaryotic luciferases as bacterial markers with different colors of luminescence

By Cebolla, Angel; Vazquez, M. Enrique; Palomares, Antonio Jose
From Applied and Environmental Microbiology (1995), 61(2), 660-8. Language: English, Database: CAPLUS

An easy way to identify microorganisms is to provide them with gene markers that confer a unique phenotype. Several genetic constructions were developed to use eukaryotic luciferase genes for bacterial tagging. The firefly and click beetle luciferase genes, luc and lucOR, resp., were cloned under constitutive control and regulated control from different transcriptional units driven by P1, λP_R, and Ptrc promoters. Comparison of the expression of each gene in Escherichia coli cells from identical promoters showed that bioluminescence produced by luc could be detected luminometrically in a more sensitive manner. In contrast, luminescence from intact lucOR-expressing cells was much more stable and resistant to high temps. than that from luc-expressing cells. To analyze the behavior of these constructions in other gram-neg. bacteria, gene fusions with luc genes were cloned on broad-host-range vectors. Measurements of light emission from Rhizobium meliloti, Agrobacterium tumefaciens, and Pseudomonas putida cells indicated that both luciferases were poorly expressed from P1 in most bacterial hosts. In contrast, the lambda promoter P_R yielded constitutively high levels of luciferase expression in all bacterial species tested. P_R activity was not regulated by temp. when the thermosensitive repressor cI857 was present in the bacterial species tested, except for E. coli. In contrast, the regulated lacIq-Ptrc::lucOR fusion expression system behaved in a manner similar to that obsd. in E. coli cells. After IPTG (isopropyl-β-D-thiogalactopyranoside) induction, this system produced the highest levels of lucOR expression in all bacterial species tested. As proof of the utility of these constructions, P. putida colonies could be identified with fusions of either luc or lucOR to P_R in a mixed population.

~28 Citings

290. Rhizobium meliloti homologs of Escherichia coli mur genes

By Leach, Francesca; Wacks, Daniel B.; Signer, Ethan R.
From Gene (1994), 148(1), 87-90. Language: English, Database: CAPLUS, DOI:10.1016/0378-1119(94)90238-0

The pectate-lyase-encoding gene pelB of Erwinia chrysanthemi Ec16 was used as a probe for hybridization to Rhizobium meliloti Rm1021 chromosomal DNA under low-stringency conditions. An Rm1021 DNA fragment that hybridized to this probe was cloned and sequenced. Results of RNA hybridization indicate that a portion of the cloned fragment is transcribed in R. meliloti. Although the Rm1021 fragment shares no significant nucleotide sequence identity with Ec16 pelB, it includes an ORF (open reading frame) that shares a high degree of nt sequence identity with the Escherichia coli murD gene. This gene codes for UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase, which catalyzes a step in the synthesis of the E. coli cell wall. The R. meliloti putative murD sequence is preceded by a partial ORF that shares sequence identity with mraY. The orientation of the two ORFs in R. meliloti is similar to that of the E. coli murD and mraY genes.

~2 Citings

291. Identification and cloning of a gene controlling alanine utilization and synthesis of polysaccharides in Rhizobium meliloti

By Yurgens, G. N.; Aronshtam, A. A.
From Genetika (Moscow) (1994), 30(9), 1166-74. Language: Russian, Database: CAPLUS

Three mutants of Rhizobium meliloti strain SKhM1, which were deficient in metab. of alanine, other nitrogen-contg. compds., and synthesis of polysaccharides, were obtained by random transposon mutagenesis with plasmid pSUP2021 as a donor of Tn5. The mutants grew poorly on media in which tryptophan and ammonium were the only sources of nitrogen. In addn., the mutants, as well as mutant-derived transductants and transconjugants, had altered symbiotic nitrogen fixation. The location of Tn5 differed in at least two of the mutants. Complementation of mutants was conducted using a gene bank of Rhizobium meliloti SKhM1 that was developed on the basis of the cosmid vector pLARE5. A 3.5-kb EcoRI fragment of the R. meliloti genome that contained insertions of Tn5 was found in the complementary cosmid by means of Southern blotting. It was shown that this fragment is located on the chromosome. A restriction map of the fragment was constructed and the site of Tn5 insertion detd. Data obtained indicate that genes located in the 3.5-kb EcoRI fragment of the R. meliloti chromosome and involved in assimilation of alanine and other nitrogen-contg. compds. participate in control of nitrogen-fixation symbiosis with alfalfa.

~0 Citings

292. Nodule-specific expression of Rhizobium meliloti symbiotic promoters P1 and P2 in chickpea-Rhizobium sp. symbiosis

By Khanuja, Suman P. S.; Suman, Archna; Singh, Geeta; Kumar, Vinod
From Biology and Fertility of Soils (1994), 18(2), 132-6. Language: English, Database: CAPLUS, DOI:10.1007/BF00336459

Developmentally specific expression of Rhizobium spp. genes involved in symbiotic N_2 fixation is known to operate through cascade regulation of various nif and fix operons. Fusion constructs of lacZ under symbiotic promoters P1 (for nifHDK operon) and P2 (for fixABCX operon) of Rhizobium meliloti were mobilized into Rhizobium spp. (Cicer) strains Rcd301 and RCR13. The assays for β-galactosidase activity to monitor the expression of lacZ under these promoters was performed in host backgrounds of Escherichia coli, R. meliloti, and Rhizobium spp. (Cicer). The enzyme assays indicated significant levels of expression from P1 and P2 promoters in chickpea rhizobia, specifically in symbiotic cells from nodules. However, as in R. meliloti, these promoters did not induce strong expression in free-living cells of Rhizobium spp. (Cicer). This indicates functional homol. of R. meliloti promoters in Rhizobium spp. (Cicer). Functional cross-reactivity of trans regulatory factors like NtrA, NtrC, and NifA between these rhizobia seems evident from the nodule-specific expression of P1 and P2 cis elements.

~1 Citing

293. Response of winter crops to manganese application on a loamy sand soil

By Singh, S. P.; Nayyar, V. K.
From Indian Journal of Agricultural Sciences (1994), 64(9), 627-9. Language: English, Database: CAPLUS

This expt. was conducted to evaluate the response of lentil (Lens culinaris), gobhi sarson (Brassica napus oleifera var. annua), oat (Avena sativa), alfalfa (Medicago sativa), annual yellow sweetclover (Melilotus indica, syn. M. parviflora), and winter maize (Zea mays) to Mn application. The plants growing on normal control soil showed visible symptoms of Mn deficiency. The plants were weak and their stems failed to elongate fully, and shoot biomass was markedly reduced. Manganese application increased the dry-matter yield of all plant species. Mn application to the soil @ 40 kg/ha (Mn_{40}) increased the dry-matter yield (%) of crops, the highest for oat (243), followed by lentil (183), lucerne (96), gobhi sarson (84), annual yellow sweetclover (43), and winter maize (26) compared with the control. This shows that oat is the most sensitive crop and winter maize is the least sensitive to Mn deficiency. Foliar application of Mn also significantly increased the dry-matter yield of all the crops compared with the control and the increase in the yield was almost equal to the yield obtained with the highest rate of Mn (Mn_{40}) applied to soil. Manganese deficiency is thought to generally occur when its concn. in plant tissue is < 20 μg/g dry matter (Jones, J.B., Jr., 1972). In this study, the Mn content of various crops ranged from 8.5 μg/g dry matter of oat to 18.0 μg/g dry matter of winter maize, resulting in max. response of the former and min. response of the latter crop to Mn application. The Mn concn. of different crops increased with increase in Mn level in the growth medium.

~0 Citings

294. A 4.6 kb DNA region of Rhizobium meliloti involved in determining urease and hydrogenase activities carries the structural genes for urease (ureA, ureB, ureC) interrupted by other open reading frames

By Miksch, Gerhard; Arnold, W.; Lentzsch, P.; Priefer, U. B.; Puehler, A.
From Molecular and General Genetics (1994), 242(5), 539-50. Language: English, Database: CAPLUS, DOI:10.1007/BF00285277

A 4.6 kb DNA region of the Rhizobium meliloti strain AK631 was found to contain seven open reading frames (ORFs), all oriented in the same direction. The putative gene products of four of these ORFs were highly homologous to UreA, UreB and UreC of Klebsiella aerogenes, Proteus mirabilis, Proteus vulgaris and Canavalia ensiformis. The overall organization of the DNA region analyzed was ORF1, ureA (ORF-2), ORF3, ureB (ORF4), ORF5, ORF6 and ureC (ORF7), indicating that the organization of the urease structural genes in R. meliloti differs from that of other urease genes so far characterized. ORF1 was incomplete; only the 3' end of the coding region was present. The six complete ORFs coded for polypeptides of 11.1 (UreA), 8.9 (ORF3), 10.8 (UreB), 15.0 (ORF5), 13.8 (ORF6) and 60.7 kDa (UreC). No sequence homol. to known polypeptides could be detected for the gene products of ORF1, ORF3, ORF5 and ORF6. Using a lacZ fusion and insertional mutagenesis it was shown that the seven ORFs identified were all located in the same transcription unit. For mutational anal. a resistance gene cassette was introduced into each of the complete ORFs resulting in apolar mutations. Mutations in ureA, ureB and ureC, but not in ORF3, ORF5 and ORF6, abolished urease activity in R. meliloti. The detn. of hydrogen uptake in these R. meliloti mutants revealed that only ORF6 and ureB are necessary for hydrogen uptake.

~10 Citings

295. An exoB mutant of Rhizobium sp. is effective in indeterminate nodules of Hedysarum coronarium

By Ollero, F. Javier; Valverde, M. Angeles; Sanchez-Palazon, Luis; Villalobo, Eduardo; Espuny, M. Rosario; Bellogin, Ramon A.
From Microbiology (Reading, United Kingdom) (1994), 140(6), 1389-94. Language: English, Database: CAPLUS, DOI:10.1099/00221287-140-6-1389

A Rhizobium sp. (Hedysarum coronarium) calcofluor dark (Cal^-) mutant, named Cal10, was obtained following Tn5mob-insertion mutagenesis. It is affected in the synthesis of exopolysaccharide and presents an altered lipopolysaccharide that is not recognized by a polyclonal antibody against the lipopolysaccharide of the parental strain. The residual exopolysaccharide obtained from the mutant lacks galactose and the high-mol.-mass acidic fraction. This mutant was complemented by plasmid pD56 that restores the prodn. of exopolysaccharide, the alteration of lipopolysaccharide and the Cal^+ phenotype. The data presented indicate that the gene in which the mutant is defective is homologous to the exoB gene of Rhizobium meliloti and fails to synthesize UDP-glucose 4'-epimerase. The Cal10 mutant was Fix^+ on H. coronarium (sulla) although it develops an indeterminate type of nodule, indicating that exopolysaccharide is not essential for a successful nodulation in this symbiotic assocn.

~4 Citings

296. Response of wheat (Triticum aestivum) and associated weeds to application of nitrogen and isoproturon

By Bhagawati, P. C.; Faroda, A. S.; Malik, R. K.
From Indian Journal of Agronomy (1992), 37(4), 721-728. Language: English, Database: CAPLUS

A field expt. was conducted during 1985-86 and 1986-87 to study the response of wheat (Triticum aestivum L. emend. Fiori & Paol.) and assocd. weeds to N and isoproturon. The dominant weeds in the exptl. area were common lambsquarter (Chenopodium album L.), yellow sweet clover [Melilotus indica (L.) All.], scarlet pimpernel (Anagallis arvensis L.), common vetch (Vicia sativa L.) and wild oat (Avena ludoviciana L.). The weed d. at 60 days after sowing was about 43.9, 28.6 and 14.6% more in the unfertilized plots than in the plots fertilized with 120, 80 and 40 kg N/ha resp. Dry wt. of weeds at 60 days after sowing was more in the fertilized plots than in the unfertilized ones. Isoproturon @ 1.0 kg/ha + 2,4-D 0.5 kg/ha was not effective in controlling all types of weeds. Length of ear, no. of spikelets/spike and 1,000-grain wt. were favorably affected by increased N levels and isoproturon. Weeds reduced the grain yield of wheat by 34, 14, 17 and 17% at 9, 40, 80 and 120 kg N/ha resp.

~0 Citings

297. Effects of elevated selenium concentration on selenium accumulation and nitrogen fixation symbiotic activity of Melilotus indica L.

By Wu, Lin; Emberg, Andrew; Biggar, James A.
From Ecotoxicology and Environmental Safety (1994), 27(1), 50-63. Language: English, Database: CAPLUS, DOI:10.1006/eesa.1994.1006

Biol. and soil factors which contribute to the successful colonization of an annual legume species, Melilotus indica, in soils with elevated Se were studied. This species was introduced into the Kesterson Reservoir in the fresh top soil that was brought in under the Kesterson Cleanup Action to fill lowering pond sites and prevent the formation of ephemeral pools contg. hazardous levels of Se. In 4 yr. since its introduction, it has expanded its range of colonization from the fresh soil fill sites to the native soil sites and contributed 10-50% of biomass to the grassland communities. The plant and nodule tissue Se concns. of the field grown plants were found to be neg. correlated with the soil sulfate concn. Nutrient soln. culture studies discovered that M. indica was able to accumulate 500 μg Se g dry wt. without a redn. of growth rate. Plants without nodulation were found to accumulate a greater amt. of Se and more vulnerable to Se toxicity. Acetylene redn. rate measurements indicate that the nitrogen fixation symbiotic activity appears to be more susceptible to an elevated Se concn. than its host plant. M. indica is a winter weed, and it occurs naturally in the Se-rich soils. It growth actively over the winter and spring and complete its life cycle in May. If the root nodules and root tissues are incorporated into the soil, the rate of soil Se volatilization may be accelerated over the warm summer months. For disposal of the Se-rich plant materials the plant shoot tissues may be harvested for Se-deficient forage supplementation. Therefore, this species may be useful for field management and reclamation of Se-contaminated soils.

~7 Citings

298. Succinate metabolism in Rhizobium meliloti

By Driscoll, Brian T.; Osteras, Magne; Finan, Turlough M.
From Current Plant Science and Biotechnology in Agriculture (1993), 17(New Horizons in Nitrogen Fixation), 517-22.
Language: English, Database: CAPLUS

NAD^+ malic enzyme is required for N_2 fixation by R. meliloti. While nodules are Fix^-, they are occupied by large nos. of bacteria enveloped in peribacteroid membrane. While NAD^+ malic enzyme mutants are Fix^-, the dme mutation results in no alteration to the wild-type growth phenotype. Since Pck activity is not detected in R. meliloti bacteroids, studies of NAD^+ malic enzyme indicate that its role in bacteroid metab. may be to channel malate to pyruvate and, hence, to acetyl-CoA through pyruvate dehydrogenase. In addn., the other products of the NAD^+ malic enzyme reaction, specifically NADH and pyruvate, may be important in the energization of N_2 fixation. The symbiotic phenotype of the dme mutants suggests that the $NADP^+$ malic enzyme does not play a large role in C_4-dicarboxylate metab. in bacteroids. This enzyme may have a more important role in maintenance metab.

~1 Citing

299. The role of Rhizobium meliloti surface polysaccharides in nodule development

By Puehler, A.; Arnold, W.; Becker, A.; Roxlau, A.; Keller, M.; Kapp, D.; Lagares, A.; Lorenzen, J.; Niehaus, K.
From Current Plant Science and Biotechnology in Agriculture (1993), 17(New Horizons in Nitrogen Fixation), 207-12.
Language: English, Database: CAPLUS

Expts. are described that indicate that R. meliloti exopolysaccharides as well as lipopolysaccharides are involved in different steps of nodule development. EPS I prodn. was found to be essential for the infection of alfalfa nodules. The data support the model that EPS I is involved in the suppression of plant defense reactions. R. meliloti lipopolysaccharides appear to be less important for the infection process; they, however, play a role for the establishment of an effective symbiosis in Medicago truncatula.

~0 Citings

300. The transcriptional activator HlyU of Vibrio cholerae: nucleotide sequence and role in virulence gene expression

By Williams, S. G.; Attridge, S. R.; Manning, P. A.
From Molecular Microbiology (1993), 9(4), 751-60. Language: English, Database: CAPLUS, DOI:10.1111/j.1365-2958.1993.tb01735.x

HlyU upregulates expression of the hemolysin, HlyA, of Vibrio cholerae. DNA sequence anal. indicates that HlyU is an 11.9-kDa protein contg. a putative helix-turn-helix motif and belonging to a family of small regulatory proteins, including NolR (Rhizobium meliloti), SmtB (Synechococcus PCC 7942), and ArsR (plasmids R773, Escherichia coli; pI258, Staphylococcus aureus; and pSX267, Staphylococcus xylosus). An hlyU mutant was constructed by insertional inactivation, and found to be deficient in the prodn. of both the hemolysin and a 28-kDa secreted protein. The mutant was assessed for virulence in the infant mouse cholera model, revealing a 100-fold increase in the LD_{50}. This suggests that HlyU promotes expression of virulence determinant(s) in vivo.

~49 Citings