

101. The replication origin of a repABC plasmid

By Cervantes-Rivera, Ramon; Pedraza-Lopez, Francisco; Perez-Segura, Gabriela; Cevallos, Miguel A.
From [BMC Microbiology \(2011\), 11, 158](#). Language: English, Database: CAPLUS, DOI:10.1186/1471-2180-11-158

Background: repABC operons are present on large, low copy-no. plasmids and on some secondary chromosomes in at least 19 α -proteobacterial genera, and are responsible for the replication and segregation properties of these replicons. These operons consist, with some variations, of three genes: repA, repB, and repC. RepA and RepB are involved in plasmid partitioning and in the neg. regulation of their own transcription, and RepC is the limiting factor for replication. An antisense RNA encoded between the repB-repC genes modulates repC expression. Results: To identify the minimal region of the *Rhizobium etli* p42d plasmid that is capable of autonomous replication, we amplified different regions of the repABC operon using PCR and cloned the regions into a suicide vector. The resulting vectors were then introduced into *R. etli* strains that did or did not contain p42d. The minimal replicon consisted of a repC open reading frame under the control of a constitutive promoter with a Shine-Dalgarno sequence that we designed. A sequence anal. of repC revealed the presence of a large A+T-rich region but no iterons or DnaA boxes. Silent mutations that modified the A+T content of this region eliminated the replication capability of the plasmid. The minimal replicon could not be introduced into *R. etli* strain contg. p42d, but similar constructs that carried repC from *Sinorhizobium meliloti* pSymA or the linear chromosome of *Agrobacterium tumefaciens* replicated in the presence or absence of p42d, indicating that RepC is an incompatibility factor. A hybrid gene construct expressing a RepC protein with the first 362 amino acid residues from p42d RepC and the last 39 amino acid residues of RepC from SymA was able to replicate in the presence of p42d. Conclusions: RepC is the only element encoded in the repABC operon of the *R. etli* p42d plasmid that is necessary and sufficient for plasmid replication and is probably the initiator protein. The oriV of this plasmid resides within the repC gene and is located close to or inside of a large A+T region. RepC can act as an incompatibility factor, and the last 39 amino acid residues of the carboxy-terminal region of this protein are involved in promoting this phenotype.

~12 Citings

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102. Use of EST database markers from *M. truncatula* in the transferability to other forage legumes

By Chandra, Amaresh
From [Journal of Environmental Biology \(2011\), 32\(3\), 347-354](#). Language: English, Database: CAPLUS

In general tropical forage legumes lack microsatellites or simple sequence repeat (SSR) markers. Development of genic SSR markers from expressed sequence tagged (EST) database is an alternate and efficient approach to generate the std. DNA markers for genome anal. of such crop species. In the present paper a total of 816 EST-SSRs contg. perfect repeats of mono (33.5%), di (14.7%), tri (39.3%), tetra (2.7%), penta (0.7%) and hexa (0.4%) nucleotides were identified from 1,87,763 ESTs of *Medicago truncatula*. Along with, 70 (8.5%) SSRs of a compd. type were also obsd. Seven primer pairs of tri repeats were tested for cross transferability in 19 accessions of forage legumes comprising 11 genera. At two different annealing temps. (55 and 60°C) all primer pairs except AJ410087 reacted with many accessions of forage legumes. A total of 51 alleles were detected with six *M. truncatula* EST-SSRs primer-pairs against DNA from 19 accessions representing 11 genera where no. of alleles ranged from 2 to 13. The cross-transferability of these EST-SSRs was 40.6% at 55°C and 32.3% at 60°C annealing temp. 24 Alleles of the total 50 (48%) at 55°C and 27 of 51 (53%) at 60°C were polymorphic among the accessions. These 27 polymorphic amplicons identified could be used as DNA markers. This study demonstrates the developed SSR markers from *M. truncatula* ESTs as a valuable genetic markers and also proposes the possibility of transferring these markers between species of different genera of the legumes of forage importance. It was evident from the results obtained with a set of *Desmanthus virgatus* accessions where Sequential Agglomerative Hierarchical and Nested (SAHN) cluster anal. based on Dice similarity and Unweighted Pair Group Method with Arithmetic mean Algorithm (UPGMA) revealed significant variability (24 to 74%) among the accessions. High bootstrap values (>30) supported the nodes generated by dendrogram anal. of accessions.

~4 Citings

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103. Medication for treatment of patients with drug hepatitis

By Kolosovskii, E. D.; Radchenko, V. G.; Shabrov, A. V.; Radchenko, D. V.
From [Russ. \(2011\), RU 2419449 C1 20110527](#), Language: Russian, Database: CAPLUS

FIELD: medicine.SUBSTANCE: invention relates to field of pharmacy, in particular to phytotherapy, and can be applied for treatment of drug hepatitis. Medication represents herbal mixture, including 29 herbs: herbal part of woodland strawberry, herbal part of common dandelion, inflorescences of pineapple weed, leaves of stinging nettle, inflorescences of tansy, inflorescences of pot marigold, fruits of common juniper, peppermint leaves, herbal part of St John's wort. Medication additionally contains: lime tree flowers, herbal part of heartsease, herbal part of Centaurium, flax seeds, dill seeds, burdock root, herbal part of common chicory, herbal part of common knotgrass, collective fruits of common hop, herbal part of cornflower, leaves of cowberries, leaves of *Arctostaphylos*, corn stigma, herbal part of immortelle, root and rhizome of *Acorus*, herbal part of *Menyanthes*, garden angelica root, herbal part of yellow [sweet clover](#), Inula root, herbal part of common horsetail.EFFECT: mixture reduces terms of hepatitis treatment, as well as improves clinico-laboratory [indices](#) due to normalisation of liver function tests and functional state of liver.4 ex, 2 tbl.

~0 Citings

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104. Mixed silage of *Melilotus albus* and *Avena sativa*

By Gu, Xueying; Yu, Zhu; Guo, Yanping; Sun, Qizhong; Wu, Yanhong
From [Caoye Kexue \(2011\), 28\(1\), 152-156](#). Language: Chinese, Database: CAPLUS

The fermn. quality and chem. components of the ensiled white **sweet clover** (*Melilotus albus*) and oats (*Avena sativa*) were investigated. The forages was either ensiled solely or ensiled by mixing the **sweet clover** and oats at the rates of 70 : 30, 50 : 50 and 30 : 70 to det. the optimal mixt. between white **sweet clover** and oats. The results indicated that the pH value, content of ammonia nitrogen, content of dry matter and crude protein content of directly ensiling white **sweet clover** were significantly higher ($P < 0.05$) than those of other four groups. The pH value and content of ammonia nitrogen of directly ensiling oats was significantly lower than that of other four groups ($P < 0.05$). There were no differences between directly ensiling oats and mixed silage which had 70% oats in the crude protein content. The contents of lactic acid, neutral detergent fiber and acid detergent fiber content of directly ensiling oats were significantly higher ($P < 0.05$) than those of directly ensiling white **sweet clover**, but there were no differences in mixed silage which had 70% oats. Butyric acid content of directly ensiling white **sweet clover** was markedly higher than that of the mixed silage which had 70% white **sweet clover** ($P < 0.05$). There was no butyric in other three groups. This study suggested that the directly ensiling oats was better feed, and the effectiveness of the mixed silage which had 70% oats was better. It was similar with the mixed silage which had 50% oats.

~0 Citings

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105. Residue analysis of an organophosphate pesticide in wild plants in Lahore area

By Islam, Amjad; Farrukh, Muhammad Akhyar; ur Rahman, Attique; Qureshi, Fahim A.; Ahmed, Sheraz
From [American-Eurasian Journal of Agricultural & Environmental Sciences \(2010\), 9\(5\), 514-518](#). Language: English, Database: CAPLUS

Residue anal. of chlorpyrifos (an organophosphate pesticide) was investigated in different wild plants. Chlorpyrifos was analyzed in different samples of plants collected from different sites of Lahore. Anal. was carried out using High Performance Liq. Chromatog. (HPLC). Et acetate, acetonitrile (HPLC), methanol, dichloromethane are the solvents were used as mobile phase to achieve the best sepn. Investigation of all sample showed that no residue was found in 31.8% samples while 54.54% samples contained chlorpyrifos residue at or below MRL and 13.6% samples contained chlorpyrifos residue above MRL. Chlorpyrifos was detected in 0.02-0.71 mg/kg concn. range and the results showed that concn. of chlorpyrifos varies from 0.02 mg/kg to 0.71 mg/kg. Maximum limit of chlorpyrifos residue in these plants established by either World Health Organization (WHO) or European Union (EU) is 0.05, 0.5, 0.5 mg/kg. The highest concn. of chlorpyrifos residue was 0.71 mg/kg in **Melilotus Indica**. Study of residue anal. of chlorpyrifos in plants has the significant role to solve the environmental problems related to pesticides.

~3 Citings

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106. Heterologous expression of *Anabaena* sp. PCC7120 cyanophycin metabolism genes *cphA1* and *cphB1* in *Sinorhizobium* (Ensifer) *meliloti*** 1021**

By Abd-El-Karem, Yasser; Elbers, Tanja; Reichelt, Rudolf; Steinbuechel, Alexander
From [Applied Microbiology and Biotechnology \(2011\), 89\(4\), 1177-1192](#). Language: English, Database: CAPLUS, DOI:10.1007/s00253-010-2891-x

Sinorhizobium meliloti infects leguminous plants resulting in a nitrogen-fixing symbiosis. Free living cells accumulate poly(3-hydroxybutyrate) (PHB) as carbon and energy source under imbalanced growth conditions. The *cphA1*₇₁₂₀ gene encoding a cyanophycin (CGP) synthetase of *Anabaena* sp. PCC7120 in plasmids pVLT31::cphA1₇₁₂₀ and pBBR1MCS-3::cphA1₇₁₂₀ was expressed in the wild-type *S. meliloti* 1021 and in a *phbC*-neg. mutant generated in this study. Expression of *cphA1*₇₁₂₀ and accumulation of CGP in cells were studied in various media. Yeast mannitol broth (YMB) and pBBR1MCS-3::cphA1₇₁₂₀ yielded the highest CGP contents in both *S. meliloti* 1021 strains. Supplying the YMB medium with isopropyl-β-D-thiogalactopyranoside, aspartic acid, and arginine enhanced CGP contents about 2.5- and 2.8-fold in *S. meliloti* 1021 (pBBR1MCS-3::cphA1₇₁₂₀) and *S. meliloti* 1021 *phbC*ΩKm (pBBR1MCS-3::cphA1₇₁₂₀), resp. Varying the nitrogen-to-carbon ratio in the medium enhanced the CGP content further to 43.8% (wt./wt.) of cell dry wt. (CDW) in recombinant cells of *S. meliloti* 1021 *phbC*ΩKm (pBBR1MCS-3::cphA1₇₁₂₀). Cells of *S. meliloti* 1021 (pBBR1MCS-3::cphA1₇₁₂₀) accumulated CGP up to 39.6% in addn. to 12.1% PHB (wt./wt., of CDW). CGP from the *S. meliloti* strains consisted of equimolar amts. of aspartic acid and arginine and contained no other amino acids even if the medium was supplemented with glutamic acid, citrulline, ornithine, or lysine. CGP isolated from cells of *S. meliloti* 1021 (pBBR1MCS-3::cphA1₇₁₂₀) and *S. meliloti* 1021 *phbC*ΩKm (pBBR1MCS-3::cphA1₇₁₂₀) exhibited av. mol. wts. between 20 and 25 kDa, whereas CGP isolated from *Escherichia coli* S17-1 (pBBR1MCS-3::cphA1₇₁₂₀) exhibited av. mol. wt. between 22 and 30 kDa. Co-expression of cyanophycinase from *Anabaena* sp. PCC7120 encoded by *cphB1*₇₁₂₀ in *cphA1*₇₁₂₀-pos. *E. coli* S17-1, *S. meliloti* 1021, and its *phbC*-neg. mutant gave cyanophycinase activities in crude exts., and no CGP granules occurred. A higher PHB content in *S. meliloti* 1021 (pBBR1MCS-3::cphB1₇₁₂₀::cphA1₇₁₂₀) in comparison to the control indicated that the cells used CGP degrading product (β-aspartate-arginine dipeptide) to fuel PHB biosynthesis.

~3 Citings

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107. The role of sigma factor RpoH1 in The pH stress response of *Sinorhizobium meliloti*

By de Lucena, Daniella K. C.; Puehler, Alfred; Weidner, Stefan

From *BMC Microbiology* (2010), 10, No pp. given. Language: English, Database: CAPLUS, DOI:10.1186/1471-2180-10-265

Environmental pH stress constitutes a limiting factor for *S. meliloti* survival and development. The response to acidic pH stress in *S. meliloti* is versatile and characterized by the differential expression of genes assocd. with various cellular functions. The purpose of this study was to gain detailed insight into the participation of sigma factors in the complex stress response system of *S. meliloti* 1021 using pH stress as an effector. In vitro assessment of *S. meliloti* wild type and sigma factor mutants provided first evidence that the sigma factor RpoH1 plays a major role in the pH stress response. Differential expression of genes related to rhizobactin biosynthesis was obsd. in microarray analyses performed with the *rpoH1* mutant at pH 7.0. The involvement of the sigma factor RpoH1 in the regulation of *S. meliloti* genes upon pH stress was analyzed by comparing time-course expts. of the wild type and the *rpoH1* mutant. Three classes of *S. meliloti* genes could be identified, which were transcriptionally regulated in an RpoH1-independent, an RpoH1-dependent or in a complex manner. The first class of *S. meliloti* genes, regulated in an RpoH1-independent manner, comprises the group of the exopolysaccharide I biosynthesis genes and also the group of genes involved in motility and flagellar biosynthesis. The second class of *S. meliloti* genes, regulated in an RpoH1-dependent manner, is composed of genes known from heat shock studies, like *ibpA*, *grpE* and *groEL5*, as well as genes involved in translation like *tufA* and *rplC*. Finally, the third class of *S. meliloti* genes was regulated in a complex manner, which indicates that besides sigma factor RpoH1, further regulation takes place. This was found to be the case for the genes *dctA*, *ndvA* and *smc01505*. Conclusions: Clustering of time-course microarray data of *S. meliloti* wild type and sigma factor *rpoH1* mutant allowed for the identification of gene clusters, each with a unique time-dependent expression pattern, as well as for the classification of genes according to their dependence on RpoH1 expression and regulation. This study provided clear evidence that the sigma factor RpoH1 plays a major role in pH stress response.

~4 Citings

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108. EPS II-Dependent Autoaggregation of *Sinorhizobium meliloti* Planktonic Cells

By Sorroche, Fernando G.; Rinaudi, Luciana V.; Zorreguieta, Angeles; Giordano, Walter

From *Current Microbiology* (2010), 61(5), 465-470. Language: English, Database: CAPLUS, DOI:10.1007/s00284-010-9639-9

Planktonic cells of *Sinorhizobium meliloti*, a Gram-neg. symbiotic bacterium, display autoaggregation under static conditions. ExpR is a LuxR-type regulator that controls many functions in *S. meliloti*, including synthesis of two exopolysaccharides, EPS I (succinoglycan) and EPS II (galactoglucan). Since exopolysaccharides are important for bacterial attachment, we studied the involvement of EPS I and II in autoaggregation of *S. meliloti*. Presence of an intact copy of the *expR* locus was shown to be necessary for autoaggregation. A mutant incapable of producing EPS I displayed autoaggregation percentage similar to that of parental strain, whereas autoaggregation was significantly lower for a mutant defective in biosynthesis of EPS II. Our findings clearly indicate that EPS II is the essential component involved in autoaggregation of planktonic *S. meliloti* cells, and that EPS I plays no role in such aggregation.

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109. Functional analysis of the fixL/fixJ and fixK genes in *Azospirillum brasilense* Sp7

By Li, Huamin; Xu, Feng; Ren, Xiaojie; Chen, Sanfeng

From [Annals of Microbiology \(Heidelberg, Germany\) \(2010\), 60\(3\), 469-480](#). Language: English, Database: CAPLUS, DOI:10.1007/s13213-010-0065-9

This study demonstrates for the first time that the two-component FixL/FixJ system, activating expression of nitrogen fixation genes in response to low oxygen concn. in rhizobia, also exists in *Azospirillum brasilense* Sp7. A heme staining assay showed that *A. brasilense* FixL contains a heme cofactor like that of rhizobial FixL proteins. *Azospirillum brasilense* FixL and FixJ could activate expression of *Sinorhizobium meliloti* nifA in *S. meliloti* fixL⁻ and fixJ⁻ mutants and in *Escherichia coli*, and that activation was dependent on oxygen concn., indicating that *A. brasilense* FixL and FixJ have the same function as *S. meliloti* FixL and FixJ. *Azospirillum brasilense* FixL and FixJ could activate expression of *A. brasilense* fixK in *E. coli*. *Azospirillum brasilense* FixL, FixJ, and FixK pos. regulated expression of *A. brasilense* nifA in *A. brasilense* strains but not in *E. coli*. The results show that FixL and FixJ can activate the fixK expression, with FixK subsequently activating nifA expression in *A. brasilense*. *Azospirillum brasilense* fixJ was involved in aerotaxis and *S. meliloti* fixJ could restore aerotaxis of the *A. brasilense* fixJ⁻ mutant. Mutations in fixL and fixJ did not affect nitrogen fixation.

~0 Citings

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110. Variation in coumarin content of *Melilotus* species grown in South Australia

By Nair, R. M.; Whittall, A.; Hughes, S. J.; Craig, A. D.; Revell, D. K.; Miller, S. M.; Powell, T.; Auricht, G. C.

From [New Zealand Journal of Agricultural Research \(2010\), 53\(3\), 201-213](#). Language: English, Database: CAPLUS, DOI:10.1080/00288233.2010.495743

This paper describes the range in coumarin concns. at 90% flowering stage in 149 accessions belonging to 15 *Melilotus* species grown in a genetic resources field characterization expt. in Adelaide, South Australia, and detcs. coumarin concns. in *Melilotus* species grown at two contrasting field sites in South Australia (Kybybolite and Keith). In the genetic resources characterization expt., the mean coumarin content ranged from 0.06 to 0.753% of dry matter. *M. segetalis*, *M. dentatus*, *M. sulcatus*, *M. sculus* and *M. infestus* recorded low (0.06 to 0.113%) coumarin levels while moderate levels (0.332-0.753%) were registered in the other species. The coumarin levels at Kybybolite and Keith sites ranged from 0.095 to 0.943% amongst *M. indicus* accessions compared to *M. sculus* (0.007-0.100%) and *M. sulcatus* (0.007-0.810%). No coumarin was detected in a *M. segetalis* accession at these two sites. Accessions of *M. sculus* and an accession of *M. segetalis* (SA 36979) and of *M. sulcatus* (SA 40019) could be potential candidates as pasture legumes that can combine tolerance of both salinity and waterlogging, and acceptably low concns. of coumarin.

~0 Citings

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111. Phylogeny and character evolution in *Medicago* (Leguminosae): evidence from analyses of plastid trnK/matK and nuclear GA3ox1 sequences

By Steele, Kelly P.; Ickert-Bond, Stefanie M.; Zarre, Shahin; Wojciechowski, Martin F.

From [American Journal of Botany \(2010\), 97\(7\), 1142-1155](#). Language: English, Database: CAPLUS, DOI:10.3732/ajb.1000009

The genus *Medicago*, with about 87 species, includes the model legume species *M. truncatula*, and a no. of important forage species such as *M. sativa* (alfalfa), *M. scutellata* (snail medic), and *M. lupulina* (black medic). Relationships within the genus are not yet sufficiently resolved, contributing to difficulty in understanding the evolution of a no. of distinguishing characteristics such as aneuploidy and polyploidy, life history, structure of cotyledons, and no. of seeds per fruit. Phylogenetic relationships of 70-73 species of *Medicago* and its sister genus *Trigonella* (including *Melilotus*) were reconstructed from nucleotide sequences of the plastid trnK/matK region and the nuclear-encoded GA3ox1 gene (gibberellin 3- β -hydroxylase) using max. parsimony and Bayesian inference methods. Our results support certain currently recognized taxonomic groups, e.g., sect. *Medicago* (with *M. sativa*) and sect. *Buceras*. However, other strongly supported clades-the "reduced subsection *Leptospireae* clade" that includes *M. lupulina*, the "polymorpha clade" that includes *M. murex* and *M. polymorpha* and the "subsection *Pachyspireae* clade" that includes *M. truncatula*-each of which includes species presently in different subsections of sect. *Spirocarpos*, contradict the current classification. These results support the hypothesis that some characters considered important in existing taxonomies, for example, single-seeded fruits that have arisen more than once in both *Medicago* and *Trigonella*, are indeed homoplastic. Others, such as the 2n = 14 chromosome no., have also arisen independently within the genus. In addn., we demonstrate support for the utility of GA3ox1 sequences for phylogenetic anal. among and within closely related genera of legumes.

~9 Citings

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112. Residue and Bio-Efficacy Evaluation of Controlled Release Formulations of Metribuzin Against Weeds in Wheat

By Kumar, Jitendra; Nisar, Keyath; Shakil, N. A.; Sharma, Rajvir

From [Bulletin of Environmental Contamination and Toxicology](#) (2010), 85(3), 357-361. Language: English, Database: CAPLUS, DOI:10.1007/s00128-010-0091-0

Controlled release formulations of metribuzin in polyvinyl chloride, (emulsion); carboxy Me cellulose, CMC and carboxy Me cellulose-kaolinite composite, CMC-KAO are reported. The MET-CMC-KAO-3 (T₉) formulation provided a superior control (76.1%) of weeds in field grown wheat in comparison to metribuzin 75 DF (57.14%) at the dose (350 g a.i. ha⁻¹) after 90 days of sowing. The treatment (T₉) reduced the dry wt. of the weed flora after 30 days of sowing (4.0 g m⁻²) and significantly superior over metribuzin 75 DF (6.0 g m⁻²) and control (17.72 g m⁻²). There were nil to negligible metribuzin residue in soil at harvest of wheat crop and were within prescribed limit of 10 mg L⁻¹ in drinking water (EPA).

~1 Citing

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113. The response to nitric oxide of the nitrogen-fixing symbiont *Sinorhizobium meliloti*

By Meilhoc, Eliane; Cam, Yvan; Skapski, Agnes; Bruand, Claude

From [Molecular Plant-Microbe Interactions](#) (2010), 23(6), 748-759. Language: English, Database: CAPLUS, DOI:10.1094/MPMI-23-6-0748

Nitric oxide (NO) is crucial in animal- and plant-pathogen interactions, during which it participates in host defense response and resistance. **Indications** for the presence of NO during the symbiotic interaction between the model legume *Medicago truncatula* and its symbiont *Sinorhizobium meliloti* have been reported but the role of NO in symbiosis is far from being elucidated. The objective here was to understand the role or roles played by NO in symbiosis. First, the authors analyzed the bacterial response to NO in culture, using a transcriptomic approach. They identified approx. 100 bacterial genes whose expression is upregulated in the presence of NO. Most of these genes are regulated by the two-component system FixLJ, known to control the majority of rhizobial genes expressed in planta in mature nodules, or the NO-dedicated regulator NnrR. Among the genes responding to NO is hmp, encoding a putative flavoHb. The authors report that an hmp mutant displays a higher sensitivity toward NO in culture and leads to a reduced nitrogen fixation efficiency in planta. Because flavoHbs are known to detoxify NO in numerous bacterial species, this result is the first **indication** of the importance of the bacterial NO response in symbiosis.

~27 Citings

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114. Characterization of an **indican**-hydrolyzing enzyme from *Sinorhizobium meliloti*

By Kim, Ji-Yun; Lee, Jin-Young; Shin, Youn-Sook; Kim, Geun-Joong

From [Process Biochemistry \(Amsterdam, Netherlands\)](#) (2010), 45(6), 892-896. Language: English, Database: CAPLUS, DOI:10.1016/j.procbio.2010.02.017

A novel β -glucosidase (I) capable of hydrolyzing **indican** to indigo was mined and isolated from *S. meliloti* using a systematic approach. The corresponding gene was amplified by PCR and overexpressed in the sol. fraction as an MBP fusion protein. The resulting enzyme easily purified to apparent homogeneity via a consecutive step in the affinity column. Recombinant I was detd. to be a monomer with a calcd. mol. wt. of 52 kDa and showed max. activity for **indican** at pH 7.0 and 45°. The K_m and V_{max} values of I for **indican** were detd. to be 0.97 mM and 355.6 μ M/min/mg protein, resp., at pH 7.0 and 35°. Addnl., I hydrolyzed both β -(1-4)- and β -(1-6)-glucosidic bonds and revealed a minor activity against α -D-glucosides. Furthermore, I was severely inhibited by dithiothreitol, **indicating** a possibility that the oxidn. of amino acids could play a crucial role in the activity of the enzyme.

~4 Citings

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115. Factors influencing the production of stilbenes by the knotweed, *Reynoutria xbohemica*

By Kovarova, Marcela; Bartunkova, Kristyna; Frantik, Tomas; Koblihova, Helena; Prchalova, Katerina; Vosatka, Miroslav

From [BMC Plant Biology](#) (2010), 10, No pp. given. Language: English, Database: CAPLUS, DOI:10.1186/1471-2229-10-19

Japanese knotweed, *Reynoutria japonica*, is known for its high growth rate, even on adverse substrates, and for contg. org. substances that are beneficial to human health. Its hybrid, *Reynoutria xbohemica*, was described in the Czech Republic in 1983 and has been widespread ever since. We examd. whether *Reynoutria xbohemica* as a medicinal plant providing stilbenes and emodin, can be cultivated in spoil bank substrates and hence in the coalmine spoil banks changed into arable fields. We designed a pot expt. and a field expt. to assess the effects of various factors on the growth efficiency of *Reynoutria xbohemica* on clayish substrates and on the prodn. of stilbenes and emodin in this plant. In the pot expt., plants were grown on different substrates that varied in org. matter and nutrient content, namely the content of nitrogen and phosphorus. Nitrogen was also introduced into the substrates by *melilot*, a leguminous plant with nitrogen-fixing rhizobia. *Melilot* served as a donor of mycorrhizal fungi to knotweed, which did not form any mycorrhiza when grown alone. As expected, the prodn. of knotweed biomass was highest on high-nutrient substrates, namely compost. However, the concn. of the org. constituents studied was higher in plants grown on clayish low-nutrient substrates in the presence of *melilot*. The content of resveratrol including that of its derivs., resveratroloside, piceatannol, piceid and astringin, was significantly higher in the presence of *melilot* on clay, loess and clayCS. Nitrogen supplied to knotweed by *melilot* was correlated with the ratio of resveratrol to resveratrol glucosides, indicating that knotweed bestowed some of its glucose prodn. upon covering part of the energy demanded for nitrogen fixation by *melilot*'s rhizobia, and that there is an exchange of org. substances between these two plant species. The three-year field expt. confirmed the ability of *Reynoutria xbohemica* to grow on vast coalmine spoil banks. The prodn. of this species reached 2.6 t of dry mass per ha. Relationships between nitrogen, phosphorus, emodin, and belowground knotweed biomass belong to the most interesting results of this study. Compared with *melilot* absence, its presence increased the no. of significant relationships by introducing those of resveratrol and its derivs., and phosphorus and nitrogen. Knotweed phosphorus was predominantly taken up from the substrate and was neg. correlated with the content of resveratrol and resveratrol derivs., while knotweed nitrogen was mainly supplied by *melilot* rhizobia and was pos. correlated with the content of resveratrol and resveratrol derivs.

~0 Citings

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116. The enoyl-ACP reductase gene, *fabI1*, of *Sinorhizobium meliloti* is involved in salt tolerance, swarming mobility and nodulation efficiency

By Liu, Ying; Zhu, Jia Bi; Yu, Guan Qiao; Zou, Hua Song

From [Chinese Science Bulletin \(2010\), 55\(3\), 259-262](#). Language: English, Database: CAPLUS, DOI:10.1007/s11434-009-0721-2

Our previous work showed that an enoyl-ACP reductase gene *fabI1* of *Sinorhizobium meliloti* was down-regulated in the *nifA* mutant nodule bacteria. To gain a better understanding of *fabI1* gene, a single site insertion mutant was constructed in this study. The *fabI1* mutant was retarded in cell growth, and its ability to grow on media with high concn. of NaCl was reduced. In addn., the mutant was completely defective in swarming phenotype. During symbiosis, the *fabI1* mutant had delayed nodule formation on host plants. Despite the fact that *FabI1* protein showed 66% identity with another enoyl-ACP reductase *FabI2* in *S. meliloti*, defects in *fabI1* were not rescued by the plasmidborne version of *fabI2*. This indicated the different functions of the two *FabI* proteins in *S. meliloti*.

~2 Citings

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117. Evaluation of Nutritional Composition of Plant Species of Soone Valley in Punjab, Pakistan

By Ahmad, Kafeel; Khan, Zafar Iqbal; Ibrahim, Muhammad; Ashraf, Muhammad; Hussain, Mumtaz

From [Journal of Plant Nutrition \(2010\), 33\(4\), 496-517](#). Language: English, Database: CAPLUS, DOI:10.1080/01904160903506241

The key component for global sustainability is plant diversity, an essential for living sources on this planet. An investigation was carried out in the Soone Valley, Punjab, Pakistan to det. the nutritional value of plant diversity in relation to requirements of grazing ruminants therein. Various parameters such as moisture content, crude protein, mineral matter, fat fiber content, dry matter, nitrogen free extractable substances, and net energy were evaluated in this investigation. Results showed that various plant species studied exhibited fluctuation in all parameters in this valley. Correlation studies also indicated that various parameters showed neg. as well as pos. significant relationships with various parameters of soil in this valley. The information will be useful in further conservation program. *Acacia farnesiana* was neg. correlated (-0.335) with protein and mineral matter (-0.048). Significant correlations of different plant species regarding nitrogen- phosphorus-potassium (NPK) were recorded with net energy. Various variables studied in this investigation demonstrated their importance to be used in further conservation, research, and grazing livestock programs.

~2 Citings

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118. Levels of total amino acids, soluble proteins and phenolic compounds in forages in relation to requirements of ruminants grazing in the salt range (Punjab), Pakistan

By Ahmad, Kafeel; Khan, Zafar Iqbal; Ashraf, Muhammad; Hussain, Mumtaz; Valeem, Ehsan Elahi
From [Pakistan Journal of Botany \(2009\), 41\(3\), 1521-1526](#). Language: English, Database: CAPLUS

Soone Valley (Salt Range) Punjab, Pakistan is a rich habitat of a large no. of plain and animal species. Various leguminous and non-leguminous species are indigenous to this Valley which are grazed by a large no. of ruminants. Levels of total amino acids, sol. proteins and phenolic compds. were appraised in pods and leaves in the leguminous plant species therein, because metabolites are important constituents of nutrition for ruminants. The data obtained after anal. showed that amino acids and sol. proteins varied from 37.18 to 50.87 and 22.27 to 35.47 mg g⁻¹ fresh wt. in leaves resp. whereas in pods they ranged from 50.22 to 53.98 and 30.67 to 35.48 mg g⁻¹ fresh wt. resp. in all species studied. Phenolic compds. ranged from 0.15 to 0.48 mg g⁻¹ dry wt. in leaves while they varied from 0.11 to 0.32 mg g⁻¹ dry wt. in pods, resp., in all species under investigation in all pastures. Based on observations recorded for all the attributes, it was concluded that the forage plant species were palatable because all species, contained sufficient amt. of amino acids and proteins. Furthermore, the effects of high levels of phenolic found in the leguminous species of the range need to be investigated on the grazing livestock therein particularly in relation to the toxicosis of these compds. on animals.

~2 Citings

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119. Soil chemical and biochemical properties of a salt-marsh alluvial Spanish area after long-term reclamation

By Laudicina, Vito Armando; Hurtado, Maria Dolores; Badalucco, Luigi; Delgado, Antonio; Palazzolo, Eristanna; Panno, Michele
From [Biology and Fertility of Soils \(2009\), 45\(7\), 691-700](#). Language: English, Database: CAPLUS,
DOI:10.1007/s00374-009-0380-0

Marisma, one of the largest salt-marsh alluvial areas in SW Spain, has been reclaimed since 1970 by artificial drainage and amendment with phosphogypsum (PG) so as to reduce Na⁺ satn. Within the reclaimed area, two 250- x 20-m plots were treated as follows: (1) amendment with 25 Mg/ha of PG every 2 to 3 years between 1979 and 2003 (plot PY); (2) like PY but PG treatment stopped after 1997 (plot DR). A contiguous virgin Marisma salt-marsh plot (MV), neither drained nor amended, was the control. In MV, soil microbial biomass C, most enzyme activities and total org. C content were much greater than in PY and DR soils, despite the salinity stress. The decrease in soil org. matter content in PY and DR soils was likely due to cotton-cropping practices, which favored the org. C mineralization and nutrients removal by crops. Microbial activity of MV soil, probably stimulated by the rhizodepositions of the natural vegetation, did not suffer from the osmotic effect due to the raising of soil soln. ionic strength. Microbial quotient could be ranked as MV > PY > DR, whereas the metabolic quotient had an opposite trend. Thus, both quotients suggested that the interruption of PG amendment was not favoring microbial activity. Principal component anal. clearly identified the chem. and biochem. soil properties mostly affected by the reclamation and also **indicated** the longer PG amendment in PY plot. Stepwise discriminant anal. identified two physiol. different types of soil microflora, one less active present in the MV virgin soil and another more active present in the reclaimed PY and DR soils.

~9 Citings

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120. Effect of poly-3-hydroxybutyrate synthase mutation on the metabolism of *Ensifer* (formerly *Sinorhizobium*) **meliloti**

By Povoio, Silvana; Casella, Sergio
From [Journal of Basic Microbiology \(2009\), 49\(2\), 178-186](#). Language: English, Database: CAPLUS,
DOI:10.1002/jobm.200800139

In order to investigate the effect of poly-3-hydroxybutyrate synthase mutation (phbC) on the synthesis of exopolysaccharides (EPS) and glycogen, on the symbiotic properties and on the survival under specific conditions of *Ensifer meliloti* (formerly *Sinorhizobium*), a new stable phbC mutant of *Ensifer meliloti* 41 was isolated and characterized. Under poly-3-hydroxybutyrate accumulation conditions, the phbC-minus mutant (strain 41003) accumulates more glycogen and less exopolysaccharides as compared to the wild-type strain, and grows poorly in pyruvate as carbon source. The inactivation of *aniA*, encoding for a global carbon flux regulator, restores in *E. meliloti* 41003 the ability to grow on pyruvate, **indicating** a new role for this gene. Survival studies of *E. meliloti* 41 and 41003 under carbon free medium in both liq. and soil microcosms showed prolonged survival of *E. meliloti* 41 under these adverse conditions as compared to the mutant strain unable to accumulate the polyester. On the other hand, the accumulation of P(3HB) gave no significant advantage in survival under oxygen-limiting conditions. In both strains, *E. meliloti* 41 and 41003, nodule-inducing ability on alfalfa plants and acetylene redn. activity did not significantly differ from each other, although the mutant strain was less competitive in terms of root colonization.

~1 Citing

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121. Distribution of flowering plants and cyanobacteria in relation to soil characters in Bahariya Oasis, Egypt

By Ibraheem, I. B. M.; Al-Sherif, E. A.

From [International Journal of Botany \(2009\), 5\(1\), 36-46](#). Language: English, Database: CAPLUS

Baharia Oasis in one of the famous Oases in western desert of Egypt. This study dealt with the distribution of flowering plants and cyanobacteria in the Oasis in relation to each other and to physicochem. characters of soil. Fifty six species of flowering plants and 29 cyanobacterial species were identified in seven different habitats. The data revealed that the flowering plants and algal taxa were controlled by the edaphic factors and physico-chem. characters of the soil. Both pos. and neg. correlations between flowering plants and cyanobacterial taxa were obtained confirming the controversial effect of cyanobacterial crust on vascular plants.

~0 Citings

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122. Integrated weed management for system productivity and economics in soybean (Glycine max)-wheat (Triticum aestivum) system

By Kumar, Mukesh; Das, T. K.

From [Indian Journal of Agronomy \(2008\), 53\(3\), 189-194](#). Language: English, Database: CAPLUS

A field expt. was conducted at New Delhi during 2006-07 and 2007-08 to find out the effect of soil solarization, deep disking, smother crop (cowpea), glyphosate, imazethapyr, and Sesbania mulch on the infestation of weeds and the productivity and profitability of soybean (Glycine max) wheat (Triticum aestivum) cropping system. Soil solarization followed by (fb) glyphosate at 1.0 kg/ha reduced the d. and dry wt. of weeds by 85% in soybean and 65% in wheat. It, therefore, resulted in considerably higher uptake of nutrients by soybean (92.5 kg N, 11.7 kg P, and 34.3 kg K/ha) with concurrent lower uptake by weeds (2.6 kg N, 0.5 kg P, and 3.3 kg K/ha). It also recorded 61.2% higher soybean seed yield and 28% higher wheat yield compared with those of farmers practice (1 summer ploughing). Two hand weedings among rainy-season treatments proved most superior in terms of lowest d., dry wt. and nutrient uptake (2.4 kg N, 0.45 kg P, and 3.1 kg K/ha) by weeds and highest nutrient uptake (85.5 kg N, 10.5 kg P, and 38.2 kg K/ha) by soybean. It recorded 41.3% more soybean seed yield than the unweeded control, but incurred the highest cost of cultivation (Rs 26,643). On soybean-wheat system basis, soil solarization fb glyphosate at 1.0 kg/ha incurred the highest cost of cultivation (Rs 31,519), but controlled weeds effectively and recorded the highest system productivity. However, the net income (Rs 59,926) and benefit: cost ratio (2.5) were the highest in smother crop (cowpea). Imazethapyr as a follow-up treatment in the rainy season provided the highest benefit: cost ratio (1.66). Thus, soil solarization fb glyphosate at 1.0 kg/ha being superior in weed control and system productivity proved to be a beneficial practice in soybean-wheat system, but owing to its high cost was not as economical as the smother crop.

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123. Characterization of root nodule and rhizobium of a leguminosae ephemeral plant-Trigonella arcuata C.A.Mey in Xinjiang

By You, Tianyu; Tan, Zhi; Gu, Lili; Li, Xiuming; Yao, Shixiang; Lan, Haiyan; Zhang, Fuchun

From [Weishengwu Xuebao \(2008\), 48\(7\), 917-923](#). Language: Chinese, Database: CAPLUS

Objective: We studied root nodule proliferation, nodule microstructure, genetic cluster and stress resistance of the rhizobium of *Trigonella arcuata*. Methods: We characterized root nodule and rhizobium with various soil matrixes cultivation, paraffin section, resin semi-ultrathin section techniques, and 16 S rRNA gene cluster anal. Results: (1) Plants grew in mixed soil (nutritious garden soil : poplar zone soil : desert sands = 1 : 1 : 1), had the most nodule proliferation and bore the most pods; The shapes of nodule were palm- or ginger-like; (2) Microstructure of the nodule revealed five different parts differentiated within the nodule: Epidermis (E), cortex (C), vascular bundle (VB), infected cells (IC) and uninfected cells (UIC); (3) Genetic cluster anal. of the full length 16 S rRNA gene sequence (1377 bp) **indicated** that the rhizobium isolated shared the highest identities with *Sinorhizobium meliloti*; (4) The rhizobium could grow between 4 and 60°C (20 min), pH 6.0-12.0 and 0-2% NaCl. For the antibiotic sensitivity, the rhizobium could not grow normally in medium with 25 µg/mL Kanamycin, Streptomycin or Cephalothin, except for 100 µg/mL Ampicillin. Conclusion: Good conditions of soil matrixes were important for nodulation of *T. arcuata*; A large quantity of cells in fascicular nodules were infected by rhizobia; 16 S rRNA gene sequence of *T. arcuata* shared the highest identities with that of *Sinorhizobium meliloti*, and this strain was able to tolerate relatively higher temp. and alk.

~1 Citing

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124. Mining and identification of a glucosidase family enzyme with high activity toward the plant extract **indicán**

By Kim, Ji-Yun; Lee, Jin-Young; Shin, Youn-Sook; Kim, Geun-Joong

From [Journal of Molecular Catalysis B: Enzymatic](#) (2009), 57(1-4), 284-291. Language: English, Database: CAPLUS, DOI:10.1016/j.molcatb.2008.10.001

The present study described that the systematic mining and identification of potentially active β -glucosidase family enzymes toward **indicán**, which extd. from the plant *Polygonum tinctorium* as one of precursors of prodn. for indigo-blue. Some of the mined enzymes were previously identified as glycosyl hydrolases or putative enzymes with unknown properties. In addn., there were no reports on the hydrolytic activity toward **indicán**. To confirm the activity, we analyzed the activity on **indicán** or related substrates in selective medium and amplified four genes from mined strains using PCR, then cloned into *E. coli*. Using a related fluorescent substrate MUG, we verified successful cloning through checking the expression of genes and comparing characteristics with wild-type strains. Then, using recombinant enzymes and chem. synthesized pure **indicán** or the plant ext., it was confirmed that **indicán** was readily converted into indigo-blue. For the overexpression of an enzyme derived from *Shinorhizobium meliloti*, which was found to be the most active through comparative analyses, we subcloned the gene in pMAL-c2X vector and expressed it as a MBP fusion protein. The resulting enzyme was overexpressed (>35% of whole cell protein) and found mainly in sol. fraction. The purified enzyme was detd. to be a monomer with calcd. mol. mass of 52 kDa and showed a specific activity (0.8 unit/mg protein) on the plant ext. including **indicán**. These results demonstrated that the mined enzymes not only could be an alternative resource for indigo-blue prodn., but also might be useful in the prodn. of indigo from the plant **indicán** by a single process.

~7 Citings

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125. Quantification of indole-3-acetic acid from plant associated *Bacillus* spp. and their phytostimulatory effect on *Vigna radiata* (L.)

By Ali, Basharat; Sabri, Anjum Nasim; Ljung, Karin; Hasnain, Shahida

From [World Journal of Microbiology & Biotechnology](#) (2009), 25(3), 519-526. Language: English, Database: CAPLUS, DOI:10.1007/s11274-008-9918-9

Sixteen *Bacillus* strains isolated from rhizosphere, histoplane and phyllosphere of different plant species were identified by 16S rDNA gene sequencing and evaluated for in vitro auxin prodn. as well as growth stimulation of *Vigna radiata* (L.) Wilczek. Auxin prodn. by *Bacillus* spp. in L-broth medium supplemented with 1000 $\mu\text{g ml}^{-1}$ L-tryptophan ranges from 0.60 to 3.0 $\mu\text{g IAA ml}^{-1}$ as revealed by gas chromatog. and mass spectrometric (GC-MS) anal. Rhizospheric isolates exhibit relatively more IAA synthesis than histoplane and phyllosphere isolates. Plant microbe interaction expts. conducted under gnotobiotic conditions recorded 55.55, 46.46 and 46.20% increase in shoot length with *Bacillus megaterium* MiR-4, *B. pumilus* NpR-1 and *B. subtilis* TpP-1, resp., over control. *Bacillus* inoculations also increased shoot fresh wt. with *B. megaterium* MiR-4 (60.94%) and *B. pumilus* NpR-1 (37.76%). Highly significant pos. correlation between auxin prodn. analyzed by GC-MS and shoot length ($r = 0.687^{**}$, $P = 0.01$) and shoot fresh wt. ($r = 0.703^{**}$, $P = 0.01$) was noted under gnotobiotic conditions. Similarly, significant correlation was also found between auxin prodn. by *Bacillus* spp. (GC-MS anal.) and different growth parameters such as shoot length ($r = 0.495^*$, $P = 0.05$), no. of pods ($r = 0.498^*$, $P = 0.05$) and grain wt. ($r = 0.537^*$, $P = 0.05$) at full maturity under natural wire house conditions. Auxin prodn. potential of plant assocd. *Bacillus* spp. can be effectively exploited to enhance the growth and yield of *V. radiata*.

~23 Citings

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126. Evaluation of mulching, stale seedbed, hand weeding and hoeing for weed control in organic garden pea (*Pisum sativum* sub sp. Hortens L.)

By Gopinath, K. A.; Kumar, Narendra; Mina, Banshi L.; Srivastva, Anil K.; Gupta, H. S.

From [Archives of Agronomy and Soil Science](#) (2009), 55(1), 115-123. Language: English, Database: CAPLUS, DOI:10.1080/03650340802287026

A field expt. was conducted during the winter season of 2003-2004 and 2004-2005 in the Indian Himalayas to evaluate the effect of mulching, stale seedbed, hand weeding and hoeing on weeds and yield of org. garden pea (*Pisum sativum* sub sp. Hortens L.). The weed population ranged from 249-477 m^{-2} , and *Polygonum plebejum* L. (34%), *Melilotus indica* L. (31%) and *Avena ludoviciana* Dur. (17%) were the predominant weeds in the exptl. field. Season long weed-crop competition reduced the green pod yield of garden pea by 74% in 2003-2004 and 93% in 2004-2005. All the weed control treatments significantly reduced the population and biomass of weeds resulting in significant increase in green pod yield of garden pea compared to unweeded control. The highest weed control efficiency (84% redn. in weed biomass) was achieved with hand weeding 30 and 60 days after sowing (DAS) closely followed by stale seedbed coupled with one hand weeding (77%). Both these treatments produced significantly higher green pod yield compared to other treatments in both the years. In 2003-2004, hand weeding (30 and 60 DAS) recorded the highest gross margin (Indian Rupees 115,400 ha^{-1}) closely followed by stale seedbed coupled with one hand weeding (Indian Rupees 109,700 ha^{-1}). In the second year, however, the latter treatment gave the highest gross margin (Indian Rupees 56,900 ha^{-1}) compared to other treatments.

~0 Citings

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127. Mechanism of infection thread elongation in root hairs of *Medicago truncatula* and dynamic interplay with associated rhizobial colonization

By Fournier, Joelle; Timmers, Antonius C. J.; Sieberer, Bjorn J.; Jauneau, Alain; Chabaud, Mireille; Barker, David G.
From [Plant Physiology](#) (2008), 148(4), 1985-1995. Language: English, Database: CAPLUS,
DOI:10.1104/pp.108.125674

In temperate legumes, endosymbiotic nitrogen-fixing rhizobia gain access to inner root tissues via a specialized transcellular apoplastic compartment known as the infection thread (IT). To study IT development in living root hairs, a protocol has been established for *Medicago truncatula* that allows confocal microscopic observations of the intracellular dynamics assocd. with IT growth. Fluorescent labeling of both the IT envelope (AtPIP2;1-green fluorescent protein) and the host endoplasmic reticulum (green fluorescent protein-HDEL) has revealed that IT growth is a fundamentally discontinuous process and that the variable rate of root hair invagination is reflected in changes in the host cell cytoarchitecture. The concomitant use of fluorescently labeled *Sinorhizobium meliloti* has further revealed that a bacteria-free zone is frequently present at the growing tip of the IT, thus **indicating** that bacterial contact is not essential for thread progression. Finally, these *in vivo* studies have shown that gaps within the bacterial file are a common feature during the early stages of IT development, and that segments of the file are able to slide collectively down the thread. Taken together, these observations suggest that (1) IT growth involves a host-driven cellular mechanism analogous to that described for intracellular infection by arbuscular mycorrhizal fungi; (2) the non-regular growth of the thread is a consequence of the rate-limiting colonization by the infecting rhizobia; and (3) bacterial colonization involves a combination of bacterial cell division and sliding movement within the extracellular matrix of the apoplastic compartment.

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128. Evaluation of available sugars in plant species indigenous to Soone valley (Punjab) Pakistan

By Ahmad, Kafeel; Khan, Zafar Iqbal; Shah, Zahid Ali; Ibrahim, Muhammad; Mustafa, Irfan; Valeem, Ehsan Elahi
From [Pakistan Journal of Botany](#) (2008), 40(5), 1877-1883. Language: English, Database: CAPLUS

Soone Valley (Salt Range) in Pakistan is a habitat of a large no. of flora and fauna. Various grasses and leguminous species are indigenous to this valley and are grazed by ruminants. Leguminous plant species were characterized for carbohydrates, starch and total sugar contents in pods and leaves as well. The data obtained after anal. showed that carbohydrates ranged from 54.37 to 64.43; starch contents varied from 30.85 to 40.55 mg g⁻¹ dry wt. in leaves while it ranged from 61.65 to 69.09 and 32.55 to 36.11 mg g⁻¹ in pods resp. Overall values of sol. sugars range from 23.88 to 31.42 in leaves and 35.65 to 40.70 in pods in species under investigation in different pastures. Based on observation recorded for total sol. sugars estn., it was concluded that the forage plant species studied were found to be palatable and had significant amt. of those elements required for the needs of livestock reared in that specific rangeland. The results of the present investigation provide key information regarding sufficient amt. of sugars in forages, which seems to be excellent. Furthermore, investigations for toxicosis, if any of sugars on grazing livestock of the range are urgently needed.

~0 Citings

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129. Rapid identification and discrimination among Egyptian genotypes of *Rhizobium leguminosarum* bv. *viciae* and *Sinorhizobium meliloti* nodulating faba bean (*Vicia faba* L.) by analysis of nodC, ARDRA, and rDNA sequence analysis

By Shamseldin, Abdelaal; El-Saadani, Muhammad; Sadowsky, Michael J.; An, Chung Sun
From [Soil Biology & Biochemistry](#) (2008), 41(1), 45-53. Language: English, Database: CAPLUS,
DOI:10.1016/j.soilbio.2008.09.014

Twenty-eight *Rhizobium* strains were isolated from the root nodules of faba bean (*Vicia faba* L.) collected from 11 governorates in Egypt. A majority of these strains (57%) were identified as *Rhizobium leguminosarum* bv. *viciae* (Rlv) based on anal. of a *nodC* gene fragment amplified using specific primers for these faba bean symbionts. The strains were characterized using a polyphasic approach, including nodulation pattern, tolerance to environmental stresses, and genetic diversity based on amplified ribosomal DNA-restriction anal. (ARDRA) of both 16S and 23S rDNA. Anal. of tolerance to environmental stresses revealed that some of these strains can survive in the presence of 1% NaCl and a majority of them survived well at 37 °C. ARDRA indicated that the strains could be divided into six 16S rDNA genotypes and five 23S rDNA genotypes. Sequence anal. of 16S rDNA indicated that 57% were Rlv, two strains were *Rhizobium etli*, one strain was taxonomically related to *Rhizobium rubi*, and a group of strains were most closely related to *Sinorhizobium meliloti*. Results of these studies indicate that genetically diverse rhizobial strains are capable of forming N₂-fixing symbiotic assocns. with faba bean and PCR done using *nodC* primers allows for the rapid identification of *V. faba* symbionts.

~7 Citings

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130. Symbiotic phenotype of a membrane-bound glucose dehydrogenase mutant of *Sinorhizobium meliloti*

By Bernardelli, Cecilia E.; Luna, Maria F.; Galar, Maria L.; Boiardi, Jose L.

From [Plant and Soil \(2008\), 313\(1-2\), 217-225](#). Language: English, Database: CAPLUS, DOI:10.1007/s11104-008-9694-1

The authors have previously reported detection of significant pyrroloquinoline quinone-linked glucose dehydrogenase activity in *Sinorhizobium meliloti* cells isolated from alfalfa (*Medicago sativa* L.) nodules. Here, they report the expression of the *gcd* gene (SMc00110) during root nodule development and characterize the symbiotic phenotype of *S. meliloti gcd* mutant RmH580. Using a *S. meliloti* strain carrying a *gcd-lacZ* transcriptional fusion, *gcd* expression was detected from very early stages of plant-bacteria interactions, at the rhizosphere level, and during further stages of nodule development. Alfalfa plants inoculated with RmH580 showed a delay in nodule emergence and a reduced ability for nodulation at various inoculum dosages. RmH580 was also deficient in its competitive ability; in coinoculation expts. a mutant:wild-type inoculum ratio higher than 100:1 was necessary to obtain an equal ratio of nodule occupancy. These results indicate that PQQ-linked glucose dehydrogenase is required by *S. meliloti* for optimal nodulation efficiency and competitiveness on alfalfa roots.

~7 Citings

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131. Influence of biofertilizer, fertility level and weed management practice on weed growth and yield of late sown chickpea (*Cicer arietinum* L.)

By Singh, Rajesh Kumar

From [Environment and Ecology \(2008\), 26\(3A\), 1306-1309](#). Language: English, Database: CAPLUS

A field expt. was conducted during 2000-02 in winter (rabi) season to find out an effective biofertilizer, fertility level and weed management practice on weed growth and yield of late sown chickpea. Application of VAM exhibited significantly higher weed dry matter accumulation than the application of other biofertilizer sources. However, max. seed and straw yield were recorded with the combined application of *Rhizobium* and VAM which was at par with single inoculation of *Rhizobium* but significantly higher than the VAM alone in both the years. Application of 75% recommended NPK dose recorded the lowest weed dry wt. than rest of other fertility levels, but the highest chickpea seed and straw yields were obsd. under 125% of recommended NPK dose. Pre-emergence application of pendimethalin 0.5 kg a.i./ha coupled with one hoeing at 40 days after sowing significantly reduced the weed dry wt. which resulted in 16.5 and 15.3% higher seed yield over unweeded check in 2000-01 and 2001-02, resp.

~0 Citings

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132. Forage evaluation for some trace elements: A case study in the Soone Valley, Pakistan

By Ahmad, Kafeel; Khan, Zafar Iqbal; Ashraf, Muhammad Yasin; Ashraf, Muhammad; Valeem, Ehsan Elahi

From [Pakistan Journal of Botany \(2008\), 40\(3\), 999-1004](#). Language: English, Database: CAPLUS

A survey was conducted in the Soone Valley in the north-west of the Punjab Province of Pakistan to assess the concns. of some essential minerals during the period of whole year in forages for livestock grazing therein. Samples of dominant species of forage plants were taken, which consisted chiefly of legumes, after following the animals. The samples were analyzed for Cu, Mn, Fe and Zn. Micro mineral concns. in the forages for Mn ranged between 3.92-5.09 and 5.90-6.83; Zn; 0.027-0.076 and 0.028-0.064, Fe; 20.72-25.43 and 25.35-32.94, Cu; 0.38-0.54 and 0.34-0.51 mg g⁻¹ in the leaves and pods, resp. The forage species had varying mineral compn. in both leaves and pods. The plants showed significant differences for Zn and Mn contents of leaves and non-significant differences for pods, while Fe exhibited non-significant difference for the plant parts. Based on investigation recorded for Mn, Zn, and Fe contents, it was concluded that the forage plant species studied were found to be palatable and had much higher concns. of those elements required for the needs of grazing livestock in that specific range and warranted no urgent need of supplementation. The results of the present investigation provide information of reasonable amts. of Mn, Fe, Zn and Cu in forages, which seems to be considerably high. Further investigations for the detn. and prevention of toxicosis, if any of these trace elements on animals of the range are urgently needed.

~5 Citings

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133. Genetic identification and symbiotic efficiency of *Sinorhizobium meliloti* indigenous to Saudi Arabian soils

By Abdel-Aziz, R. A.; Al-Barakah, F. N.; Al-Asmary, H. M.

From *African Journal of Biotechnology* (2008), 7(16), 2803-2809. Language: English, Database: CAPLUS

Soil bacteria *Sinorhizobium meliloti* are of enormous agricultural value, because of their ability to fix atm. nitrogen in symbiosis with an important forage crop legume-alfalfa. The main aim of this study was (i) to isolate indigenous *S. meliloti* strains from different field sites in Saudi Arabia, (ii) to assess genetic diversity and genetic relationships amongst strains of natural populations and (iii) to provide information about nodulation and symbiotic efficiency of indigenous *S. meliloti* strains. Nineteen strains isolated from alfalfa nodules collected from different field sites and one ref. strain were analyzed. Genetic characterization by rep-PCR and RAPD-PCR was applied to study the status of *S. meliloti* populations inhabiting nodules of alfalfa. Cluster anal. of rep-PCR profiles showed significant differences among *S. meliloti* isolates. Both methods resulted in almost identical grouping of strains. Among indigenous strains two divergent groups could be detd. The biggest differences were detected among the ref. strains along with two local isolates and all field isolates. Quant. expression of symbiotic efficiency was evaluated by measurement of total nitrogen in plants and dry matter yield of plants. All strains nodulated alfalfa cultivar CAF 101 but with different efficiency. Significant differences in dry mater yield of alfalfa as well as total nitrogen content were detd. depending on the strain used. The results indicate that sixty one percent of indigenous *S. meliloti* strains can be characterized as low efficient strains.

~1 Citing

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134. Genome sequence of the β -rhizobium *Cupriavidus taiwanensis* and comparative genomics of rhizobia

By Amadou, Claire; Pascal, Geraldine; Mangenot, Sophie; Glew, Michelle; Bontemps, Cyril; Capela, Delphine; Carrere, Sebastien; Cruveiller, Stephane; Dossat, Carole; Lajus, Aurelie; et al

From *Genome Research* (2008), 18(9), 1472-1483. Language: English, Database: CAPLUS, DOI:10.1101/gr.076448.108

The first complete genome sequence of a β -proteobacterial nitrogen-fixing symbiont of legumes, *Cupriavidus taiwanensis* LMG19424, was detd. The genome consists of 2 chromosomes of size 3.42 Mb and 2.50 Mb, and a large symbiotic plasmid of 0.56 Mb. The *C. taiwanensis* genome displays an unexpected high similarity with the genome of the saprophytic bacterium *C. eutrophus* H16, despite being 0.94 Mb smaller. Both organisms harbor two chromosomes with large regions of synteny interspersed by specific regions. In contrast, the 2 species host highly divergent plasmids, with the consequence that *C. taiwanensis* is symbiotically proficient and less metabolically versatile. Altogether, specific regions in *C. taiwanensis* compared with *C. eutrophus* cover 1.02 Mb and are enriched in genes assocd. with symbiosis or virulence in other bacteria. *C. taiwanensis* reveals characteristics of a minimal rhizobium, including the most compact (35-kb) symbiotic island (nod and nif) identified so far in any rhizobium. The atypical phylogenetic position of *C. taiwanensis* allowed insightful comparative genomics of all available rhizobium genomes. No genes were found that were both common and specific to all rhizobia, thus suggesting that a unique shared genetic strategy does not support symbiosis of rhizobia with legumes. Instead, phylodistribution anal. of >200 *Sinorhizobium meliloti* known symbiotic genes indicated large and complex variations of their occurrence in rhizobia and non-rhizobia. This led to an in silico method to ext. genes preferentially assocd. with rhizobia. How the novel genes identified may contribute to symbiotic adaptation is discussed. The complete genome sequence with gene annotation is deposited in GenBank/EMBL/DDBJ with accession nos. CU633749 (chromosome I), CU633750 (chromosome II), and CU633751 (plasmid pRalta).

~56 Citings

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135. Conjugal properties of the *Sinorhizobium meliloti* plasmid mobilome

By Pistorio, Mariano; Giusti, Maria A.; Del Papa, Maria F.; Draghi, Walter O.; Lozano, Mauricio J.; Tejerizo, Gonzalo Torres; Lagares, Antonio

From [FEMS Microbiology Ecology](#) (2008), 65(3), 372-382. Language: English, Database: CAPLUS, DOI:10.1111/j.1574-6941.2008.00509.x

The biol. and biochem. of plasmid transfer in soil bacteria is currently under active investigation because of its central role in prokaryote adaptation and evolution. In this work, the authors examd. the conjugal properties of the cryptic plasmids present in a collection of the N₂-fixing legume-symbiont *Sinorhizobium meliloti*. The study was performed on 65 *S. meliloti* isolates recovered from 25 humic soils of Argentina, which were grouped into 22 plasmid-profile types [i.e. plasmid operational taxonomic units (OTUs)]. The cumulative Shannon index calcd. for the obsd. plasmid profiles showed a clear satn. plateau, thus **indicating** an adequate representation of the *S. meliloti* plasmid-profile types in the isolates studied. The results show that isolates of nearly 14% of the plasmid OTUs hosted transmissible plasmids and that isolates of 29% of the plasmid OTUs were able to retransfer the previously characterized mobilizable-cryptic plasmid pSmelPU88b to a third recipient strain. It is noteworthy that isolates belonging to 14% of the plasmid OTUs proved to be refractory to the entrance of the model plasmid pSmelPU88b, suggesting either the presence of surface exclusion phenomena or the occurrence of restriction incompatibility with the incoming replicon. Incompatibility for replication between resident plasmids and plasmid pSmelPU88b was obsd. in c. 20% of the OTUs. The results reported here reveal a widespread compatibility among the conjugal functions of the cryptic plasmids in *S. meliloti*, and this fact, together with the obsd. high proportion of existing donor genotypes, points to the extrachromosomal compartment of the species as being an extremely active plasmid mobilome.

~9 Citings

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136. The periplasmic regulator ExoS/ChvI inhibits ExoS/ChvI two-component signalling in *Sinorhizobium meliloti*

By Chen, Esther J.; Sabio, Erich A.; Long, Sharon R.

From [Molecular Microbiology](#) (2008), 69(5), 1290-1303. Language: English, Database: CAPLUS, DOI:10.1111/j.1365-2958.2008.06362.x

Sinorhizobium meliloti requires ExoS/ChvI two-component signaling to establish a nitrogen-fixing symbiosis with legume hosts. The importance of ExoS/ChvI signaling in microbe-host interactions is underscored by the requirement of ExoS/ChvI orthologs for virulence of the related α -proteobacteria *Agrobacterium tumefaciens* and *Brucella abortus*. In *S. meliloti*, ExoS/ChvI is a key regulator of gene expression for exopolysaccharide synthesis, biofilm formation, motility, nutrient utilization and free-living viability. Previously, we showed that the novel conserved regulator ExoR interacts genetically with both ExoS and ChvI, and localizes to the periplasm of *S. meliloti*. Here, we show that ExoR phys. assoc. with ExoS and that this assocn. is important for regulating ExoS/ChvI signaling. We have identified point mutations in the Sel1-like repeat region of ExoR that disrupt binding to ExoS and cause a dramatic increase in ExoS/ChvI-dependent gene expression. Furthermore, we have found that phys. interaction with ExoS stabilizes the ExoR protein. Together, our results **indicate** that ExoR binds to ExoS in the periplasm of *S. meliloti* to inhibit ExoS/ChvI activity, and that ExoR represents a novel periplasmic inhibitor of two-component signaling.

~22 Citings

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137. Chemical fertilizers could offer a real solution for minimizing over consumption of herbicides for controlling weeds in faba bean (*Vicia faba* L.)

By El-Shahawy, Tarek A.

From [Trends in Applied Sciences Research](#) (2008), 3(2), 142-153. Language: English, Database: CAPLUS, DOI:10.3923/tasr.2008.142.153

The effect of the different fertilizers on enhancing the herbicidal efficacy of certain herbicides for controlling weeds in faba bean was studied under greenhouse conditions. Two herbicides (bentazon and fluazifop-P-butyl) and three fertilizers (urea, diammonium phosphate and super phosphate) were used. The two herbicides were applied subsequently in combination with the different fertilizers at different rates of concn. (0.288, 0.403 and 0.576 kg a.i. ha⁻¹ bentazon; 0.151, 0.300 and 0.451 kg fluazifop-P-butyl). The fertilizers were in 0.75 and 1% of the total soln. at the basis of NP active compn. Applying the two herbicides alone at the recommended doses was good enough for controlling both types of weeds, broad and narrow leaved ones. However, using both of them in combination with the different fertilizers (i.e., urea and diammonium phosphate) was much more effective. The 1% addn. was almost the best. Applying bentazon and fluazifop-P-Bu in combination with urea gave similar results to those applying under diammonium phosphate addn., either for controlling weeds or increasing yield productivity. Superphosphate-fertilized herbicides were the lowest in comparison; virtually not recommended as in opinion of mine. The crop growth was pos. affected in response, recording the best results with applying the two herbicides in combination with urea and diammonium phosphate too. The seed content of NPK elements was also significantly increased. Thus, using herbicides with fertilizers is highly recommended and 1% addn. is to be the best. To be used precisely at the moderate concn. and in combination with urea or diammonium phosphate is the best chosen overall not only for controlling weeds and increasing yield productivity, but also for preserving our health and environments from overdoses of herbicides consumption.

~1 Citing

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138. Evaluation of macro-mineral concentrations of forages in relation to ruminants requirements: a case study in Soone valley, Punjab, Pakistan

By Ahmad, Kafeel; Ashraf, Muhammad; Khan, Zafar I.; Valeem, Ehsan Elahi
From [Pakistan Journal of Botany \(2008\), 40\(1\), 295-299](#). Language: English, Database: CAPLUS

This manuscript reports the essential macro-mineral compn. of different plant species in the Soone Valley located in the Salt Range within the province of Punjab, Pakistan. The climate of this Range is characterized by a relatively low annual rainfall (508 mm) and temp. varying from 1° C to 36° C in winter and summer, resp. Hot dry winds and prolonged periods of drought are frequent in the Range. Grazing animals were followed and forage plants consumed by the livestock, were collected during the study period in the year 2004. The forage plants consisted of legumes and grasses. Different plant parts such as leaves, leaflets and pods, which were lavishly grazed by the grazing animals were sep'd. and analyzed for macro-minerals, Na, P, K, Ca and Mg. On the basis of observations it can be concluded that most of the forage samples were sufficient in Na, P, K, Ca and Mg for the requirements of ruminants grazing therein. Comparatively, the macro-mineral concns. in pods were higher than those found in the leaves and leaflets showing no need of mineral supplementation. However, it seems most interesting to elucidate the phenomenon of antagonism among minerals, which may adversely affect the availability of minerals in the bodies of animals.

~4 Citings

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139. Influence of new broadleaf herbicides on weed control, seed yield and quality of some wheat (*Triticum aestivum*) cultivars

By Chopra, Neelam Kumar; Chopra, Nisha; Sinha, S. N.
From [Indian Journal of Agricultural Sciences \(2008\), 78\(5\), 405-407](#). Language: English, Database: CAPLUS

A field expt. was conducted at Karnal. Haryana during winter (rabi) seasons of 2000-01 and 2001-02 to evaluate the effect of new broadleaf herbicides, viz. carfentrazone Et and metsulfuron Me for weed control, yield and quality of different wheat (*Triticum aestivum* L.emend. Fiori & Paol.) cultivars raised for seed prodn. Cultivars 'HD 2687', 'HD 2643' and 'HD 2733' smother the weeds more efficiently than the 'HDR 77', 'HD 2380' and 'HD 2329'. 'HD 2687' recorded max. grain yield (4.22 tonnes/ha) across weed control levels which was significantly higher than the 'HDR 77', 'HD 2380' and 'HD 2329'. Both carfentrazone and metsulfuron did not affect the spike morphol. of different wheat cultivars compared to 2,4-D. Carfentrazone 20g/ha and metsulfuron 4 g/ha reduced the weed d. and weed dry wt. significantly over the weed check, carfentrazone 10g/ha and 2,4-D 500 g/ha. Carfentrazone 20 g/ha and metsulfuron 4 g/ha controlled 83.7 and 84.1% of broadleaf weeds-resp. and increased the seed yield significantly over the other treatments. Carfentrazone at 10 and 20g/ha and metsulfuron 4g/ha did not cause any adverse effect on seed germination and seed vigour hence can be safely used in seed prodn. plots of wheat.

~0 Citings

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140. Stable low molecular weight RNA profiling showed variations within *Sinorhizobium meliloti* and *Sinorhizobium medicae* nodulating different legumes from the alfalfa cross-inoculation group

By del Villar, Maria; Rivas, Raul; Peix, Alvaro; Mateos, Pedro F.; Martinez-Molina, Eustoquio; van Berkum, Peter; Willems, Anne; Velazquez, Encarna
From [FEMS Microbiology Letters \(2008\), 282\(2\), 273-281](#). Language: English, Database: CAPLUS,
DOI:10.1111/j.1574-6968.2008.01139.x

Four different low mol. wt. (LMW) RNA profiles, designated I-IV, among 179 isolates from Medicago, *Melilotus* and *Trigonella* species growing in a field site in Northern Spain were identified. From sequence anal. of the 16S rRNA, *atpD* and *recA* genes as well as DNA-DNA hybridization anal. with representatives of each LMW RNA profile it was evident that isolates with LMW RNA profiles I and II belonged to *Sinorhizobium meliloti* and those displaying profiles III and IV to *Sinorhizobium medicae*. Therefore, two distinct LMW RNA electrophoretic mobility profiles were found within each of these two species. Collectively, LMW RNA profiles I and II (identified as *S. meliloti*) were predominant in *Melilotus alba*, *Melilotus officinalis* and *Medicago sativa*. Profiles III and IV (identified as *S. medicae*) were predominant in *Melilotus parviflora*, *Medicago sphaerocarpa*, *Medicago lupulina* and *Trigonella foenum-graecum*. All the four LMW RNA profiles were identified among isolates from *Trigonella monspeliaca* nodules. These results revealed a different specificity by the hosts of the alfalfa cross-inoculation group towards the two bacterial species found in this study.

~5 Citings

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141. Ecological studies on *Typha domingensis* growing in Wadi Darnah, Libya

By Abu Ziada, M. E.

From [Journal of Environmental Sciences \(Mansoura, Egypt\) \(2008\), 35, 185-202](#). Language: English, Database: CAPLUS

The ecol. characteristics of *T. domingensis* Pers., the most frequently occurring swamp plant in Wadi Darnah, at north east of Libyan arab jamahiriya were investigated. Environmental conditions (edaphic and water characteristics) and floristic compn. of ten stands representing *Typha* community type were studied in details. Fifty assoc. species were recorded in these stands. The soil consisted mainly of fine sand. Anions are mainly chlorides, sulfates and bicarbonates whereas, calcium and magnesium ions were the major cations. The concns. of Ca^{2+} and Mg^{2+} ions were relatively higher than potassium and sodium ions. The growth characteristics and mineralomass of the plant exhibit seasonal variations coincided with the fluctuation in the environmental factors. The max. vegetative yield of 3692.4 g dry wt./m² was obtained during Nov. with leaf phytomass of 3065.4 g dry wt./m². Moreover, succulence was relatively high during the study period.

~0 Citings

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142. Autecology and phytochemistry of genus *Amaranthus* in the Nile Delta, Egypt

By Abu Ziada, M. E.; El-Halawany, E. F.; Mashaly, I. A.; Masoud, G. F.

From [Asian Journal of Plant Sciences \(2008\), 7\(2\), 119-129](#). Language: English, Database: CAPLUS,
DOI:10.3923/ajps.2008.119.129

The present study deals with the ecol. and phytochem. of three *Amaranthus* species, namely: *Amaranthus graecizans*, *A. lividus* and *A. viridis*. The components of weed vegetation in the present investigation are classified by cluster anal. into four groups: group A is codominated by *Amaranthus graecizans* and *Portulaca oleracea*, group B is codominated by *Amaranthus lividus* and *Cynodon dactylon*, group C is codominated by *Alternanthera sessilis* and *Echinochloa crus-galli* and group D is codominated by *Aster squamatus*, *Conyza bonariensis* and *Paspalum disticum*. The ordination of the sampled stands applied by Detrended Correspondence Anal. (DCA) indicated that, the recognized vegetation groups are markedly distinguishable and having a clear pattern of segregation on the ordination planes. Also, the application of the Canonical Correspondence Anal. (CCA) showed that, soil texture, porosity, water-holding capacity, bicarbonate, sodium, soil reaction (pH), org. matter and elec. cond. are the most effective soil variables which correlate with the distribution and abundance of weed vegetation in the study area. The seed germination under different levels of salinity, light, temp. and humidity is studied for the three investigated species. Phytochem., the mean values of moisture, ash, total nitrogen, protein, total lipids, sol. sugars, glucose, sucrose, polysaccharides and total carbohydrates were detd. The elementary analyses together with qual. and quant. analyses of 16 amino acids were also carried out in the investigated plant species.

~1 Citing

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143. Method for manufacturing canned food "hen with sweet pepper sauce" of special indication

By Kvasenkov, O. I.

From [Russ. \(2008\), RU 2322116 C1 20080420](#), Language: Russian, Database: CAPLUS

Method for manufg. canned food "hen with sweet pepper sauce" of special indication comprises freezing and cutting leek and thyme upon a chopper; cutting brown onions and sweet pepper, frying in melted butter and cutting upon a chopper; blanching carrots and cutting upon a chopper, blanching parsnip and washing; frying wheat flour in melted butter, cutting hen meat upon a chopper; mixing the above-mentioned components with dry white wine, whisky, cream, bone broth, common salt, red sweet pepper and CO₂-exts. of clove, laurel leaf, hot black pepper and nutmeg; packing into aluminum tubes, sealing and sterilizing. This method increases digestibility of canned food.

~0 Citings

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144. Effect of Al on the growth, nodulation and root hair deformation of Medicago sativa L.

By Yang, Min; Li, Xiaofeng; Yu, Yongxiong; Gu, Minghua; Ling, Guizhi; Chen, Peiqiong; Qing, Dongjin
From [Nongye Huanjing Kexue Xuebao \(2007\), 26\(1\), 202-206](#). Language: Chinese, Database: CAPLUS

To elucidate the mechanisms of the toxicity of Al to leguminous plants at initial stages of symbiotic nodulation, the effects of Al on the growth of primary root, root hair deformation (RHD), nodulation of *Medicago sativa* L. and the growth of *Rhizobium meliloti* (R. *meliloti*) were investigated in this study. After treatment with 3, 6, and 9 $\mu\text{mol/L}^{-1}$ Al for 24 h, the relative elongation of primary roots was just 78.4%, 43.1%, and 26.8% of the contrast (-Al), moreover, the live R. *meliloti* cells reduced by 47.37%, 63.16%, and 84.21%, resp. Furthermore, in the absence of R. *meliloti* and in the presence of Nod factors (NF), the RHD, which indicated root hairs response to nodulation signal at initial stages of nodulation on *Medicago sativa* L., was depressed by 44.6%, 71.4%, and 80.1%, resp. However, in the absence of NF, there was no prominent effect on RHD by Al. The RHD reduced by 24.54%, 33.18%, 51.82%, 63.05%, and 67.86%, resp., after the roots inoculated R. *meliloti* were treated for 48 h with 2, 3, 4, 5, and 6 $\mu\text{mol/L}^{-1}$ Al. These results suggested that the inhibition of RHD might be the result of Al suppressing the transduction of nodulation signal.

~0 Citings

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145. Rhizobium gallicum as an efficient symbiont for bean cultivation

By Mnasri, Bacem; Tajini, Fatma; Trabelsi, Mustapha; Aouani, Mohamed Elarbi; Mhamdi, Ridha
From [Agronomy for Sustainable Development \(2007\), 27\(4\), 331-336](#). Language: English, Database: CAPLUS, DOI:10.1051/agro:2007024

Rhizobia are soil bacteria that fix atm. nitrogen in symbiosis with legumes in specialized organs called nodules. The legumes thus acquire the autonomy to grow in nitrogen-deficient soils. When nitrogen fixation by indigenous rhizobia is limited, field inoculation with efficient and competitive strains is an economically feasible way to increase prodn. When the inoculant is made from native strains of rhizobia the success of inoculation should be increased, since local strains are better adapted than com. inoculants. Here, a *Rhizobium gallicum* strain, 8a3, previously selected for its competitiveness and symbiotic effectiveness with common bean under lab. conditions, was tested in field trials in Tunisia. The expts. were conducted in six fields using three common bean cultivars. The majority of the fields showed a low d. of the native rhizobia and inefficient nodulation by *Sinorhizobium meliloti*, a known symbiont of *Medicago*. Our results show that inoculation with R. *gallicum* strain 8a3 induced an increase in nodule nos. accompanied by a more than twofold increase in shoot dry yield. Monitoring of the nodulation occupancy through the fingerprinting of the repetitive extragenic palindromic sequences (REP-PCR) showed that strain 8a3 was competitive even in the soil showing a high population d. of indigenous R. *gallicum*, and occupied more than 40% of the nodules. Moreover, in vitro antibiosis assays indicated that strain 8a3 produces antimicrobial activity on agar medium against indigenous common bean rhizobia, including the inefficient strains of S. *meliloti*. These results point out the benefits that could be achieved by selecting efficient and competitive strains among natural populations of rhizobia.

~9 Citings

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146. Herbicidal substance from Streptomyces lavendulae with antibiotic, insecticidal and mitogenic activities

By Aly, M. M.; El-Sabbagh, S. M.; El Shanshoury, A. R.
From [Egyptian Journal of Biotechnology \(2006\), 22, 16-36](#). Language: English, Database: CAPLUS

Of twenty five strains of actinomycetes isolated from marine water of Mediterranean sea (Alexandria, Egypt), on starch nitrate agar contg. 25 µg/mL nystatin and streptomycin. Screening of microbial fermn. broths for herbicidal activity against *Medicago sativa* led to the discovery of new secondary metabolite, from an actinomycete isolate. The isolate was recognized as spore former with aerial mycelia contg. LL-DAP (diaminopimelic acid) and glycine. The vegetative hyphae are not fragmented and the spores are borne on sporophores. These criteria in addn. to other physiol. and biochem. characteristics for identification suggested that the isolate could be affiliated to the genus *Streptomyces* and the name *Streptomyces lavendulae* was suggested. The herbicidal substance in the cell free ext. of this isolate proved to be active against different weeds assocd. with wheat plants. It was extd. and purified using different column chromatog. The purified material has excellent antibacterial activities against both Gram pos. and Gram neg. bacteria with MIC ranging from 25-75 µg/mL. It has no antifungal or antitumor activities. Insecticidal activity against ants, lice and house fly was demonstrated. It showed also mitogenic activity with human cell lymphoma. Phys. characters and chem. structure of the purified bioactive substance, in addn. to its toxicity were elucidated and discussed.

~0 Citings

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147. A preparation method of canned food

By Kvasenkov, O. I.

From [Russ. \(2008\), RU 2313985 C1 20080110](#), Language: Russian, Database: CAPLUS

A prepn. method of canned food, hen fricassee with meadow mushrooms, comprises cutting mushroom, and parching in melted oil; cutting onion, and precooking; precooking walnut kernel, garlic, Tamarindi *Indicae*, dried chili, lemon, horseradish and *Rhizoma Bletilla*, and pounding; parching wheat flour in melted oil; pounding sardine; pounding fresh green peas; mixing the above components with egg powder, milk, lemon juice, sweet white wine, tomato saucem acetic acid, starch, sugar, table salt, clove, black pepper, laurel leaf, curry, pricklyash peel, ginger, nutmeg and tarragon under anaerobic condition; cutting chicken; and packaging chicken, the mixt. and bone soup, sealing, and sterilizing. The canned food has improved absorptivity.

~0 Citings

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148. Disruption of nifA gene influences multiple cellular processes in *Sinorhizobium meliloti*

By Gong, Ziyong; Zhu, Jiabi; Yu, Guanqiao; Zou, Huasong

From [Journal of Genetics and Genomics \(2007\), 34\(9\), 783-789](#). Language: English, Database: CAPLUS, DOI:10.1016/S1673-8527(07)60089-7

Sinorhizobium meliloti nifA is important in fixing nitrogen during symbiosis. A nifA null mutant induces small white invalid nodules in the roots of host plant. The addnl. phenotypic alterations assocd. with the disruption of the nifA gene are reported in this study. Under a free-living state, *S. meliloti* nifA mutant reduces its ability to swarm on a half-solid plate. Interestingly, the AHL (Acylhomoserine lactones) contents in the nifA mutant are lower than that of the wild type during the lag phase, whereas it is reversed in the logarithmic and stationary phases. Quant. spectrophotometric assays reveal that the total amt. of extracellular proteins of the nifA mutant are lower than that of the wild type. In addn., the mutant abolishes its nodulation competitive ability during symbiosis. These findings indicate that NifA plays a regulatory role in multiple cellular processes in *S. meliloti*.

~4 Citings

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149. Effect of salt stress on the expression of NHX-type ion transporters in *Medicago intertexta* and *Melilotus indicus* plants

By Zahran, Hamdi H.; Marin-Manzano, M. Carmen; Sanchez-Raya, A. Juan; Bedmar, Eulogio J.; Venema, Kees; Rodriguez-Rosales, M. Pilar

From [Physiologia Plantarum \(2007\), 131\(1\), 122-130](#). Language: English, Database: CAPLUS, DOI:10.1111/j.1399-3054.2007.00940.x

Medicago intertexta and *Melilotus indicus*, two wild leguminous herbs with different tolerance to salinity were investigated for NaCl-induced changes in the expression level of some Na⁺ transporters. *M. indicus* plants grew well at NaCl concn. from 0 to 400 mM, whereas growth of *M. intertexta* plants was severely inhibited at NaCl concns. higher than 100 mM. In *M. intertexta*, increasing NaCl in the growth media caused a strong increase in Na⁺ content concomitant with a decrease in K⁺ content in leaves and, above all, roots. In comparison, *M. indicus* plants cultivated in the presence of NaCl accumulated much less Na⁺ in leaves and roots and no differences in K⁺ content among plants grown in nutrient soln. contg. 100-400 mM NaCl were detected. The expression levels of four genes coding for NHX-type Na⁺/H⁺ antiporters in the above two wild legumes were studied in plants cultivated under the different NaCl concns. Expression levels of the genes were higher in *M. intertexta* as compared with *M. indicus* plants. In *M. intertexta*, salt treatments increased MtNHX1, MtNHX3 and MtNHX4 transcript levels in leaves and roots. However, in *M. indicus* NaCl treatments only induced the expression of MtNHX1 in roots. Apparently, two different mechanisms, Na⁺ avoidance or accumulation into cellular compartments, and developed by the two wild legumes to cope with salt stress, and that expression of NHX antiporters is linked to the accumulator phenotype.

~16 Citings

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150. Effects of Ca²⁺ on acid tolerance of *Medicago sativa* and *Rhizobium meliloti*

By Zhang, Qin; Zhang, Lei; Wei, Shi-qing; Li, Yan-bin; Zhang, Chao

From *Yingyong Shengtai Xuebao* (2007), 18(6), 1231-1236. Language: Chinese, Database: CAPLUS

Soil acidity was an important environmental factor hampering the effective symbiotic nitrogen fixation of *Rhizobium meliloti* and its host plant *Medicago sativa*. The study on the effects of Ca²⁺ on the acid tolerance of *M. sativa* and *R. meliloti* showed that applying 5 and 10 mmol/L⁻¹ of Ca²⁺ could promote the growth of *R. meliloti* and advance its log growth phase. Under neutral pH condition, applying Ca²⁺ didn't have any significant effects on root hair deformation, while under low pH condition, Ca²⁺ demonstrated pos. functions. The higher the Ca²⁺ concn. was, the more significantly it affected, indicating that Ca²⁺ might play an important role in the recognition between *R. meliloti* and its host plant. Applying Ca²⁺ under low pH made the nodulation ahead of time and the nodulation rate enhanced. Definite concn. of Ca²⁺ could increase the no. of nodules in the same period, which was more obvious at anaphase stage or under lower pH condition.

~0 Citings

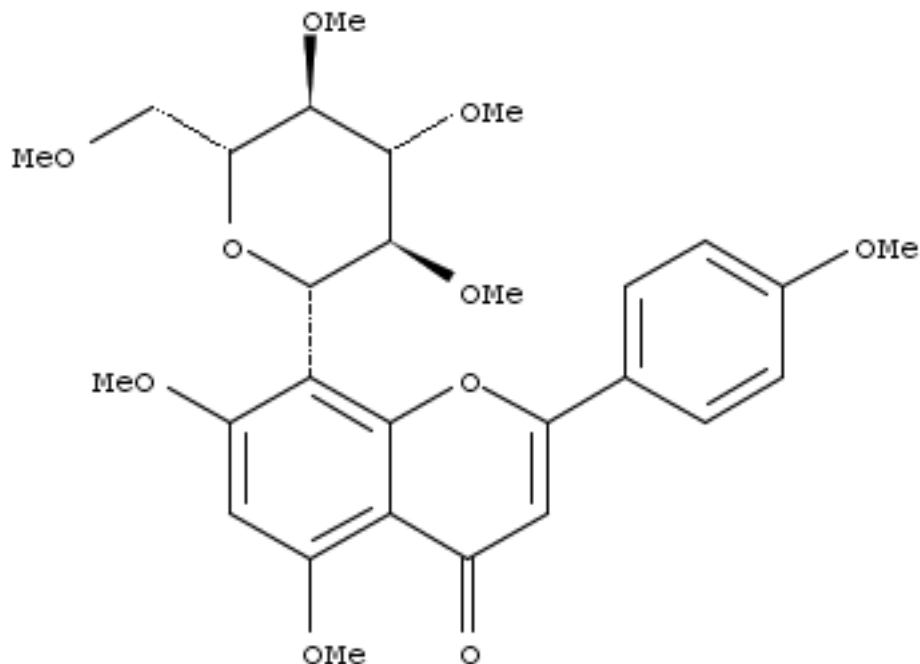
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151. A method of treatment with flavonoids for overcoming acquired or inherent resistance to chemotherapeutic compounds

By Roufogalis, Basil; Marks, Denese; Duke, Rujee

From *PCT Int. Appl.* (2007), WO 2007073583 A1 20070705, Language: English, Database: CAPLUS

The present invention provides a flavonoid compd. as well as analogs, homologs, derivs., mimetics and functional equiv. thereof including methylated forms thereof in substantially pure form, in a plant ext., in a chem. ext. or fraction and/or in combination with excipients, diluents, stabilizing mols., penetrants and/or one or more chemotherapeutic compds. The flavonoid of the present invention is useful overcoming acquired or inherent resistance to a chemotherapeutic agent. The preferred flavonoid is heptamethylapigenin-8-O-glycoside, also known as heptamethylvitexin, methylvitexin or R-substituted vitexin wherein the R group represents a single or multiple substitution of the hydroxy group on vitexin. Chemotherapeutic agents contemplated herein include agents used in the treatment or prophylaxis of cancer (including tumors), infection by pathogens (including potential or opportunistic pathogens) and/or the treatment or prophylaxis of a physiol. or clin. condition. The present invention further provides compns. including pharmaceutical compns. comprising a flavonoid capable of inhibiting or reducing a transport function of at least P-glycoprotein (Pgp) and optionally BCRP.



~1 Citing

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152. Ecology and molecular evolution of alfalfa nodulating Sinorhizobium *meliloti* strains analyzed in a long-term field experiment

By Puehler, Alfred; Keller, M.; Schlueter, A.; Selbitschka, W.; Stiens, M.

From *Biology of Plant-Microbe Interactions* (2006), 5, 300-305. Language: English, Database: CAPLUS

The ecol. behavior of bioluminescent Sinorhizobium *meliloti* 2011 derivs. L1 (RecA) and L33 (RecA+) differing in their RecA proficiency was tested in a long-term field release expt. After a period of seven years, it became obvious that the recA mutation did not influence the survival of *S. meliloti* in alfalfa field plots. However, it could be demonstrated that the released *S. meliloti* strains were out-competed by an indigenous *S. meliloti* population. Characterization of this population by PCR fingerprint methods showed that most of the indigenous *S. meliloti* strains could be classified into six dominant fingerprint groups indicating that a few dominant strain types had out-competed the released strains. Characteristic plasmids could be identified in the dominant *S. meliloti* subpopulations. One of these plasmids, termed pSmeSM11a, was selected for sequence anal. The annotated pSmeSM11a sequence turned out to be highly interesting. First of all, the plasmid contained a 42 kb region highly similar to the *S. meliloti* 1021 pSymA plasmid. In addn., several single base pair deletions which inactivated coding regions in the *S. meliloti* genome as well as in plasmid pSmeSM11a were obsd. suggesting the action of a specific mutational mechanism. The putative role of plasmid pSmeSM11a in the nodulation process was supported by the identification of genes predicted to be involved in the synthesis of the Nod factor and in the redn. of the plant hormone ethylene. Plasmid pSmeSM11a is characterized by a high percentage of insertion sequences indicating that these elements mediated acquisition of accessory plasmid modules. Evidently, the anal. of nodulating *S. meliloti* strains isolated during a long-term field expt. yielded insights into the ecol. and mol. evolution of this species.

~0 Citings

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153. Integrated weed management practices in garlic crop in Pakistan

By Mehmood, Tariq; Khokhar, Khalid Mahmood; Shakeel, Muhammad

From *Crop Protection* (2007), 26(7), 1031-1035. Language: English, Database: CAPLUS, DOI:10.1016/j.cropro.2006.09.013

Weed management studies in garlic crop were conducted during 2000-2001 and 2002-2003 at the National Agricultural Research Center, Islamabad Pakistan. During 1st yr, pendimethalin was sprayed at 0.80 l a.i. ha⁻¹ pre emergence 2 days after 1st irrigation in moist condition followed by different mech. weeding regimes. During 2nd yr, pendimethalin, oxadiazon, glyphosate, and metribuzin were sprayed at 0.80 L, 0.25 L, 0.6 L, and 0.45 kg a.i. ha⁻¹, resp., pre emergence 2 days after 1st irrigation in moist conditions followed by 1 hoeing at 80 days after herbicide application. Herbicide treatments were compared with weed free and weedy control. The most dominant weed species were *Phalaris minor*, *Coronopus didymus*, *Medicago denticulata*, and *Rumex dentatus*. All herbicide treatments followed by hoeing except metribuzin gave bulb yield at par with weed free treatment. Metribuzin resulted in min. bulb yield (0.59 t ha⁻¹) because of its extreme phytotoxicity to garlic crop, which resulted in the survival of a few plants. Pendimethalin in combination with manual hoeing gave the highest bulb yield and monetary returns.

~1 Citing

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154. Inefficient nodulation of chickpea (*Cicer arietinum* L.) in the arid and Saharan climates in Tunisia by *Sinorhizobium meliloti* biovar medicaginis

By Ben Romdhane, Samir; Elarbi Aouani, Mohamed; Mhamdi, Ridha
From *Annals of Microbiology (Milano, Italy)* (2007), 57(1), 15-19. Language: English, Database: CAPLUS

The aim of this work is to study the genetic diversity and the symbiotic effectiveness of the natural populations of rhizobia nodulating chickpea (*Cicer arietinum* L.) in six locations of South Tunisia, where chickpea had never been cultivated. Nodules were obsd. only in the two soil samples from Gafsa (0.8 nodules per plant) and Tataouine (2 nodules per plant). PCR-RFLP typing of 16S rRNA genes of 42 isolates indicated that all analyzed strains showed the same ribotype as the ref. strain *Sinorhizobium meliloti* RCR2011. These isolates induced ineffective nodules on chickpea and *Medicago sativa*; however nodules on *Medicago laciniata* were effective. Anal. of the symbiotic diversity by PCR-RFLP of the *nifDK* spacer suggested that all chickpea isolates from the South belong to the biovar medicaginis of *S. meliloti*. The present paper is, to our knowledge, the first report showing that chickpea is selectively nodulated under soil conditions by a specific biovar of *S. meliloti* showing specificity to *M. laciniata*. The specificity of this interaction as well the impact of this inefficient nodulation on chickpea cultivation needs to be investigated further.

~3 Citings

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155. Efficacy of metsulfuron and isoproturon alone and in combination against complex flora of weeds in wheat

By Yadav, Ashok; Malik, R. K.; Hasija, R. C.
From *Annals of Biology (Hisar, India)* (2006), 22(2), 153-159. Language: English, Database: CAPLUS

Based on the results of 3 field expts., it was found that metsulfuron+isoproturon at 4+750 or 4+1000 g ha⁻¹ being superior to their alone applications produced the grain yield of wheat statistically similar to weed-free plots by reducing the dry wt. of grassy and broadleaf weeds to the extent of 90-97 and 66-86%, resp. Combinations of 2,4-D Na at 500 g ha⁻¹ with isoproturon at 750 or 1000 g ha⁻¹ also resulted equally effective against complex flora of weeds but due to inclusion of 2,4-D Na sensitive wheat variety (WH 283), these treatments could not raise the grain yield to the level of plots kept weed-free. The performance of tank mix and ready mix applications of metsulfuron+isoproturon in the ratio of 1:250 each at 500, 750, and 1000 g ha⁻¹ against mixed flora of weeds was similar at resp. doses; however, these could produce grain yield statistically similar to weed-free treatment only at the highest dose (1000 g ha⁻¹). Metsulfuron at 4 g ha⁻¹ being superior to its lower doses and at par with higher doses was safe for the crop and reduced the d. and dry wt. of broadleaf weeds to the extent of 79-96% under different expts. But it was ineffective against grassy weeds. The weed control efficacy of 2,4-D Na at 500 g ha⁻¹ against broadleaf weeds was also similar to metsulfuron at 4 g ha⁻¹ and it was also not effective against grassy weeds. Crop phytotoxicity and malformation in wheat variety WH 283 was also noticed in the plots treated with 2,4-D Na at 500 g ha⁻¹ and above either used alone or as tank mix. Compared to metsulfuron alone 4 g ha⁻¹, there was no addnl. gain in weed control and grain yield of wheat with the use of either tank mix or ready mix of 2,4-D Na and metsulfuron particularly at higher doses. However, at lower doses, there was an improvement in their efficacy when used as tank mixed with each other and(or) in their efficacy when used as tank mixed with each other and(or) in combination with surfactant. Isoproturon 1000 g ha⁻¹ was significantly better than its lower doses (500 and 750 g ha⁻¹) and controlled grassy and broadleaf weeds in wheat to the extent of 77-84 and 61-70%, resp. Tralkoxydim proved ineffective against broadleaf weeds.

~0 Citings

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156. Phytoindicators of engineering-geological processes in urban setting

By Gusev, A. P.
From *Prirodnye Resursy* (2006), (3), 33-40. Language: Russian, Database: CAPLUS

Results of studying of sinantrophic vegetation as **indicator** of engineering geol. processes are considered in the article. Ecol.-floristic classification is applied to **indicate** the Braun-Blanquet approach. Syntaxons units of this classification well reflect conditions of a habitat and ecol. of communities, have high information loading. On the basis of researches in the urbanized landscapes of Polesye (Gomel, Retchitsa and others) the phytocoenotic structure of ruderal vegetation of the basic types of anthropogenic ecotops has been found out. It has been established, that engineering-geol. processes are reflected in phytocoenotic structure of vegetative cover of a city territory. Connection between prevalence of various assocns. and classes of conditions of the geol. environment detg. a degree of display of this or that engineering-geol. process has been established. A connection of phytocoenotic structure of vegetation with the depth of groundwaters has been considered. The communities as **indicators** of processes of flooding of city territory are singled out: assocn. Bidentietum tripartiti, community Stellaria media [Polygono-Chenopodion], assocn. Potentilletum anserinae, assocn. Phragmitetum communis, assocn. Urtico-Aegopodietum podagraria, assocn. Urtico-Calystegiето sepium. The work presents anal. of eroded resistance soils as factor of ecol. hazard. The method of estn. of deflationary hazard in anthropogenous landscapes is considered. The effective **indicator** of risk of a deflation is ruderal vegetation. The plant communities diagnosing sites, the subject deflation are revealed. Deflation dangerous sites display communities: assocn. **Melilotetum** albi-officinalis, assocn. Echio-**Melilotetum** albae, community Erigeron canadensis [Sisymbrietalia], assocn. Setario-Plantaginetum **indicae**, assocn. Bromo tectorum-Corispermetum leptopteri, community Oenothera biennis-Artemisia campestris [Dauco-**Melilotion**], assocn. Corynephorum canescentis Tx. 1928. Steady grounds and soils are diagnosed by communities: Galinsogo-Setarietum, Arctietum lappae, Lamio albi-Conietum maculati, Urtico-Aegopodietum podagraria and others. Communities which can represent themselves as **indicators** of water erosion of a soil cover are revealed. High degree destruction soil is diagnosed by communities: assocn. Digitalietum ischimi Tx. 1950, community Apera spica-venti-Matricaria chamomilla [Sisymbrietalia], community Oenothera- Artemisia campestris [Dauco-**Melilotion**], community Erigeron canadensis [Sisymbrietalia]. Actively developing ravines and gullies are to be diagnosed by communities of class Chenopodietea albi (Chenopodietum albi, Erigeronto-Lactucetum serriolae, Xanthietum strumari and others). In ravines, which ceased growing, domination of communities of classes Galio-Urticetea, Agropyretea repentis, Epilobietea angustifolii, Robinietea (Agropyretum repentis, Urtico-Aegopodietum podagraria, Urtico-Calystegiето sepium, Calamagrostietum epigeji and others) are marked.

~0 Citings

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157. Effect of sulfosulfuron, metsulfuron and 2,4-D alone and in combination against complex flora of weeds in wheat

By Yadav, Ashok; Malik, R. K.; Malik, R. S.; Hasija, R. C.

From [Environment and Ecology \(2006\), 24S\(Spl-3A\), 907-910](#). Language: English, Database: CAPLUS

A field expt. was conducted for two years (1996-97 and 1997-98) to evaluate sulfosulfuron, metsulfuron and 2,4-D Na alone and in combination against complex flora of weeds predominated by wild oat (*Avena ludoviciana*) and bathu (*Chenopodium album*) in wheat. Sulfosulfuron at 20, 25 and 30 g/ha being statistically at par with each other during both years, provided 80-96 and 75-86% control of grassy and broad leaf weeds, resp. Tank mixt. of metsulfuron and sulfosulfuron (1: 10) at 20, 25 and 30 g/ha being at par with alone applications of sulfosulfuron, also reduced the dry wt. of complex flora of weeds to the extent of 80-97% and all these treatments resulted into grain yield of wheat statistically similar to the plots kept weed free throughout the crop season. Combination of sulfosulfuron and 2,4-D Na (1: 10) at 400 and 600 g/ha being superior to its lower dose (200 g/ha) also significantly reduced the dry wt. of both grassy (91-98%) and broadleaf (89-100%) weeds but yielded significantly lower than weed free check in both years. Metsulfuron at 2 g + 0.2% surfactant, metsulfuron at 2.5 g/ha and 2,4-D Na at 400 g/ha being significantly better than 2,4-D Na at 200 g/ha, were equally effective against broadleaf weeds. But these were inferior to metsulfuron at 4 g/ha in both years of study. Metsulfuron and 2,4-D Na at all doses were ineffective against grassy weeds and produced grain yields significantly lower than weed free check. Weeds growing throughout the crop season caused 31-34% redn. in the grain yield of wheat.

~0 Citings

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158. Effect of dithiopyr alone and as tank mixture with other herbicides against weeds in wheat

By Yadav, Ashok; Malik, R. K.; Malik, R. S.; Hasija, R. C.

From [Environment and Ecology \(2006\), 24S\(Spl-3A\), 853-856](#). Language: English, Database: CAPLUS

Dithiopyr at 100, 120, 150, 180, 200 and 250 g/ha applied at 35 days after sowing (DAS) was ineffective against 2 grassy (*Avena ludoviciana* and *Phalaris minor*) and broadleaf weeds (*Rumex retroflexus* and *Melilotus indica*) in wheat. Chlorsulfuron at 20 or 30 g/ha and 2, 4-D Na at 500 g/ha resulted into 80-98% control of broadleaf weeds only. Sulfosulfuron at 20 and 25 g/ha provided 79-92% control of grassy weeds and ~50% control of broadleaf weeds. Tank mixt. of dithiopyr with 2,4-D Na at 100 + 250, 150 + 250, 200 + 250, and 250 + 250 g/ha reduced the dry wt. of grassy weeds <30% but resulted into 71, 76, 80 and 88% control of broadleaf weeds, resp. There was no addnl. grain of combined use of dithiopyr with sulfosulfuron or chlorsulfuron compared to solitary applications of sulfosulfuron and chlorsulfuron. Tralkoxydim at 300 g/ha was effective (88%) only against grassy weeds. Metribuzin at 200 g/ha alone or as tank mix with clodinafop (50 + 50 g/ha) caused >80 and ~60% redn. in the dry wt. of grassy and broadleaf weeds, resp. Tank mixt. of isoproturon and 2,4-D Na at 750 + 250 g/ha and isoproturon + tralkoxydim at 375 + 250 g/ha reduced the dry wt. of grassy and broadleaf weeds to the extent of 75-85 and 50-67%, resp. All the herbicidal treatments except dithiopyr at 100-180 g/ha raised the grain yield of wheat significantly more than weedy check during both years. However, none of the herbicidal treatments could produce grain yield of wheat statistically similar to the plots kept weed free throughout the crop season during both years. This might be due to either poor weed control or crop phytotoxicity or both. Weeds caused yield redns. to the extent of 37 and 20% in both expts. during 1997-98 and 1998-99, resp.

~0 Citings

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159. Performance of mon-48549 tank mixed with different herbicides, and sulfosulfuron with surfactants against weeds in wheat

By Yadav, Ashok; Malik, R. K.; Malik, R. S.; Hasija, R. C.

From [Environment and Ecology \(2006\), 24S\(Spl-3A\), 846-849](#). Language: English, Database: CAPLUS

Based on 2 expts. conducted during 1997-98 and 1998-99, it was found that 2,4-D Na at 200, 250, and 300 g/ha were at par with each other and superior to its lower doses (100 and 150 g/ha) provided 63-71% control of broadleaf weeds (*Rumex retroflexus*, *Melilotus indica*, *Coronopus didymus*, and *Chenopodium album*) in expt. 1. But it was ineffective against grassy weeds (*Avena ludoviciana* and *Phalaris minor*). Mon-48549 was ineffective against both grassy and broadleaf weeds during both years. Tank mixt. of mon-48549 at 5 g with different doses of 2,4-D Na each could increase its efficacy only ≤5-7% against broadleaf weeds. Metsulfuron at 4 g/ha and tralkoxydim at 350 g/ha provided 90 and 86% control of broadleaf and grassy weeds, resp. The treatments of 2,4-D Na at 100 g/ha and mon-48549 at all doses resulted into grain yield of wheat statistically similar to weedy check. In expt. 2, sulfosulfuron at 20 g/ha + 0.5% adjuvant (mon-0818), sulfosulfuron at 17.5 g/ha tank mixed with each of 2 dry surfactants (mon-59121 and mon-59123) at 500 and 1000 g/ha, and tank mixt. of mon-48549 at 5 and 10 g/ha each with clodinafop at 50 g and fenoxaprop at 100 g/ha being at par with each other, provided 78-82% control of grassy weeds and these were superior to all combinations of sulfosulfuron + mon-48549. However, sulfosulfuron + mon-48549 at 15+5 and 15+10 g/ha was better than their use at 10+5 or 10+10 g/ha against grassy weeds. All the treatments contg. sulfosulfuron as a component in mixt. (i. e. sulfosulfuron either with surfactants or mon-48549) being equally effective (35-70%) against broadleaf weeds were statistically better than tank mixt. of mon-48549 with clodinafop or fenoxaprop in this respect. Sulfosulfuron mixed with surfactants at all doses resulted into significantly more grain yield than all other herbicidal treatments.

~0 Citings

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160. Site-directed mutagenesis **indicates** an important role of cysteines 76 and 181 in the catalysis of hydantoin racemase from *Sinorhizobium meliloti*

By Martinez-Rodriguez, Sergio; Andujar-Sanchez, Montserrat; Neira, Jose L.; Clemente-Jimenez, Josefa M.; Jara-Perez, Vicente; Rodriguez-Vico, Felipe; Heras-Vazquez, Francisco J. Las

From [Protein Science \(2006\), 15\(12\), 2729-2738](#). Language: English, Database: CAPLUS, DOI:10.1110/ps.062452106

Hydantoin racemase enzyme plays a crucial role in the reaction cascade known as "hydantoinase process.". In conjunction with a stereoselective hydantoinase and a stereospecific carbamoylase, it allows the total conversion from D,L-5-monosubstituted hydantoins, with a low rate of racemization, to optically pure D- or L-amino acids. Residues Cys-76 and Cys-181 belonging to hydantoin racemase from *Sinorhizobium meliloti* (SmeHyaA) have been proved to be involved in catalysis. Here, we report biophys. data of SmeHyaA Cys-76 and Cys-181 to alanine mutants, which point toward a two-base mechanism for the racemization of 5-monosubstituted hydantoins. The secondary and the tertiary structure of the mutants were not significantly affected, as shown by CD. Calorimetric and fluorescence expts. have shown that Cys-76 is responsible for recognition and proton retrieval of D-isomers, while Cys-181 is responsible for L-isomer recognition and racemization. This recognition process is further supported by measurements of protein stability followed by chem. denaturation in the presence of the corresponding compd.

~5 Citings

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161. Evaluation of sulfosulfuron and metribuzin for weed control in irrigated wheat (*Triticum aestivum*)

By Pandey, A. K.; Gopinath, K. A.; Gupta, H. S.

From [Indian Journal of Agronomy](#) (2006), 51(2), 135-138. Language: English, Database: CAPLUS

A field expt. was carried out on sandy clay-loam soil in Northwestern Himalayas of India and the exptl. field had enough weed population. An av. decrease in grain yield by 29% was obsd. due to season-long weed-crop competition. The best weed-control efficiency (85.7-93.8%) was achieved with metribuzin compared to other herbicides, i.e. Sulfosulfuron, isoproturon, and 2,4-D (55.4-87.5%). Earlier timing of metribuzin application (40 days stage) provided excellent control of *Phalaris minor*, while control of *Polygonum plebeium* and *Melilotus indica* was better with application at 60 days stage. Sulfosulfuron showed high activity against all weed species except *P. plebeium* and at equiv. doses, control was greater at the earlier timing of application. Slight crop injury in terms of yellowing of leaves and stunted growth was obsd. in the plots treated with sulfosulfuron. It was more pronounced under delayed application of the herbicide. The injury, however, disappeared with the advancement of crop growth. All the treatments except 2,4-D application gave significantly higher grain yield compared to weeded check. The highest grain yield was recorded in manual weeding treatment. Lower doses of sulfosulfuron (20-25 g/ha) and metribuzin (230-245 g/ha) both applied at 40 days stage gave yields similar to manual weeding treatment.

~2 Citings

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162. Effect of defoliation stress on 2-hydroxy cinnamic acid content at different growth stages in *Melilotus* albus

By Nair, R. M.; Whittall, A.; Revell, D. K.; Dowling, K.; Hughes, S.; Craig, A. D.; Auricht, G. C.

From [Australian Journal of Experimental Agriculture](#) (2006), 46(12), 1601-1603. Language: English, Database: CAPLUS, DOI:10.1071/EA05284

Melilotus albus (Medik.) is a pasture legume with potential value in Australian farming systems, esp. in salt-affected areas. However, the use of this species has been limited because of concerns over high coumarin concns. The aim of this trial was to det. the effect of defoliation on the concn. of 2-hydroxy cinnamic acid, a coumarin precursor, at 3 stages of growth (vegetative, flowering and post-flowering) in 6 accessions. The concn. of 2-hydroxy cinnamic acid was detd. by high performance liq. chromatog. in leaves of plants grown in a glasshouse. Defoliation stress increased the 2-hydroxy cinnamic acid content in the leaves of all accessions studied by about 8%, from 0.89 to 0.96% of dry matter. The 2-hydroxy cinnamic acid concns. were not significantly different between vegetative and flowering stages in any of the accessions studied, but showed a significant increase post-flowering for 4 out of the 6 accessions studied. This study indicates that grazing may increase the coumarin or 2-hydroxy cinnamic acid concn. in *Melilotus* albus, but in screening for suitable accessions to progress to new cultivars, it is not necessary to subject plants to a defoliation stress to rank the accessions for 2-hydroxy cinnamic acid or coumarin concn.

~3 Citings

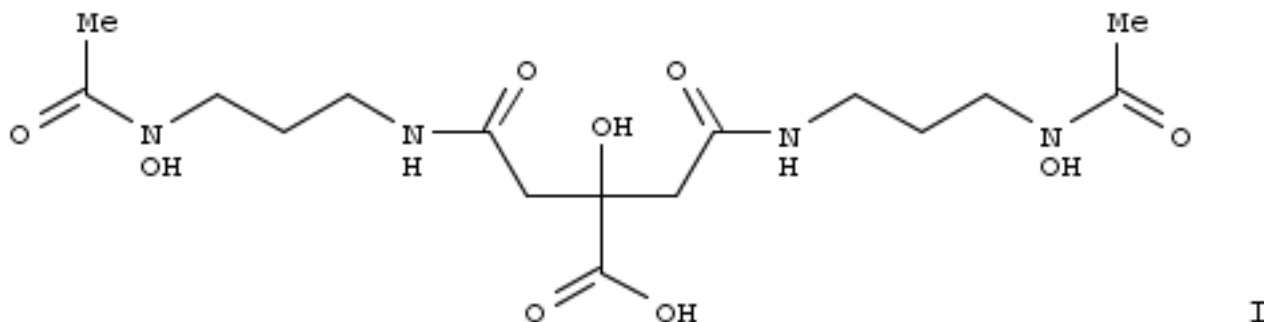
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163. Characterization of 'Schizokinen', a dihydroxamate-type siderophore produced by *Rhizobium leguminosarum* IARI 917

By Storey, E. P.; Boghozian, R.; Little, James L.; Lowman, Douglas W.; Chakraborty, R.

From [BioMetals](#) (2006), 19(6), 637-649. Language: English, Database: CAPLUS, DOI:10.1007/s10534-006-9001-7

The rhizobia comprise one of the most important groups of beneficial bacteria, which form nodules on the roots (rarely on the stems) of leguminous plants. They live within the nodules and reduce atm. nitrogen to ammonia, which is further assimilated by plants into required nitrogenous compds. The rhizobia in return obtain nutrition from the plant. Rhizobia are free-living soil bacteria and have to compete with other microorganisms for the limited available iron in the rhizosphere. In order to acquire iron, rhizobia have been shown to express siderophore-mediated iron transport systems. *Rhizobium leguminosarum* IARI 917 was investigated for its ability to produce siderophore. It was found to produce a dihydroxamate-type siderophore under iron restricted conditions. The siderophore was purified and chem. characterized. The ESMS, MS/MS and NMR anal. indicate the dihydroxamate siderophore to be 'Schizokinen' (I), a siderophore reported to be produced by *Bacillus megaterium* that shares a similar structure to 'rhizobactin 1021' produced by *Sinorhizobium meliloti* 1021. This is the first report of prodn. of 'Schizokinen' by a strain of *R. leguminosarum*. Therefore, it was carefully investigated to confirm that it is indeed 'Schizokinen' and not a degrdn. product of 'rhizobactin 1021'. Since ferric-siderophore complexes are transported across the outer membrane (OM) into the periplasm via an OM receptor protein, *R. leguminosarum* IARI 917 was investigated for the presence of an OM receptor for 'ferric-Schizokinen'. SDS PAGE anal. of whole cell pellet and extd. OM fractions indicate the presence of a possible iron-repressible OM receptor protein with the mol. wt. (MW) of approx. 74 kDa.



~8 Citings

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164. The pha2 gene cluster involved in Na⁺ resistance and adaption to alkaline pH in *Sinorhizobium fredii* RT19 encodes a monovalent cation/proton antiporter

By Yang, Lifu; Jiang, Juquan; Wei, Wei; Zhang, Bo; Wang, Lei; Yang, Susheng
 From [FEMS Microbiology Letters](#) (2006), 262(2), 172-177. Language: English, Database: CAPLUS,
 DOI:10.1111/j.1574-6968.2006.00385.x

Sinorhizobium fredii RT19 can tolerate up to 0.6 M NaCl, whereas all its pha2-disrupted mutants, constructed by Tn5 mutagenesis, failed to grow in even the presence of 0.1 M NaCl. No growth difference was detected in pha2 mutants at a pH < 7.5 in the presence or absence of K⁺, but growth redn. was obsd. in the presence of K⁺ when pH > 7.5. The pha2 gene cluster was able to completely restore the growth of the pha2 mutants of *S. fredii* RT19 in 0.6 M NaCl. Measurement of monovalent cation intracellular content suggested that pha2 was involved in both Na⁺ (Li⁺) and K⁺ efflux. The pha2 mutants exhibited K⁺/H⁺, but no apparent Na⁺(Li⁺)/H⁺ antiporter activity in everted membrane vesicles. Taken together, these results indicated that the pha2 cluster of *S. fredii* RT19 encodes a monovalent cation/proton antiporter involved in resistance to Na⁺ and adaptation to pH, which was very different from the pha1 cluster of *Sinorhizobium meliloti*, which encodes a K⁺/H⁺ antiporter.

~7 Citings

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165. Vodka scandinavia

By Gromov, V. K.
 From [Russ.](#) (2006), RU 2284352 C1 20060927, Language: Russian, Database: CAPLUS

FIELD: liqueur and vodka industry. SUBSTANCE: vodka comprises components in the following content per 1000 dal: peanut aqueous-alcoholic infusion of the 1-st blend, 1.8-2.4; 65.8% sugar syrup, 20.0-21.5 l; glycerol, 0.4-0.6 kg, and aqueous-alcoholic liquid, the balance, to provide the strength value 40%. Invention provides enhancing organoleptic indices of vodka and to confer to it aroma the light favorable tint of sweet clover flowers. The tasting score of vodka is 9.33. EFFECT: valuable properties of vodka. 4 ex.

~0 Citings

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166. Metabolite profiles of nodulated alfalfa plants indicate that distinct stages of nodule organogenesis are accompanied by global physiological adaptations

By Barsch, Aiko; Tellstroem, Verena; Patschkowski, Thomas; Kuester, Helge; Niehaus, Karsten
 From [Molecular Plant-Microbe Interactions](#) (2006), 19(9), 998-1013. Language: English, Database: CAPLUS,
 DOI:10.1094/MPMI-19-0998

An effective symbiosis between *Sinorhizobium meliloti* and its host plant *Medicago sativa* is dependent on a balanced physiol. interaction enabling the microsymbiont to fix atm. nitrogen. Maintenance of the symbiotic interaction is regulated by still poorly understood control mechanisms. A first step toward a better understanding of nodule metab. was the detn. of characteristic metabolites for alfalfa root nodules. Furthermore, nodules arrested at different developmental stages were analyzed in order to address metabolic changes induced during the progression of nodule formation. Metabolite profiles of bacteroid-free pseudonodule exts. indicated that early nodule developmental processes are accompanied by photosynthate translocation but no massive org. acid formation. To det. metabolic adaptations induced by the presence of non-fixing bacteroids, nodules induced by mutant *S. meliloti* strains lacking the nitrogenase protein were analyzed. The bacteroids are unable to provide ammonium to the host plant, which is metabolically reflected by reduced levels of characteristic amino acids involved in ammonium fixation. Elevated levels of starch and sugars in Fix⁻ nodules provide strong evidence that plant sanctions preventing a transformation from a symbiotic to a potentially parasitic interaction are not strictly realized via photosynthate supply. Instead, metabolic and gene expression data indicate that alfalfa plants react to nitrogen-fixation-deficient bacteroids with a decreased org. acid synthesis and an early induction of senescence. Non-effective symbiotic interactions resulting from plants nodulated by mutant rhizobia also are reflected in characteristic metabolic changes in leaves. These are typical for nitrogen deficiency, but also highlight metabolites potentially involved in sensing the N status.

~24 Citings

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167. Salinity-induced accumulation of poly- β -hydroxybutyrate in rhizobia indicating its role in cell protection

By Arora, N. K.; Singhal, V.; Maheshwari, D. K.

From [World Journal of Microbiology & Biotechnology](#) (2006), 22(6), 603-606. Language: English, Database: CAPLUS, DOI:10.1007/s11274-005-9077-1

Poly β -hydroxybutyrate (PHB) is an energy and carbon storage material accumulated in response to the limitation of an essential nutrient. The effect of different salt concns. on growth and PHB accumulation of four different *Sinorhizobium* strains was examd. Irresp. of the strain, a defined trend in the accumulation of PHB inside the cells was obsd. While min. PHB content was accumulated at low or zero salinity, max. was obsd. by the salt-tolerant strains at higher salt concns. This suggests a definite role for PHB in cell protection in saline conditions.

~3 Citings

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168. Temperate weeds in Russia: Sentinels for monitoring trace element pollution and possible application in phytoremediation

By Bashmakov, D. I.; Lukatkin, A. S.; Prasad, M. N. V.

Edited By: Prasad, M. N. V.; Sajwan, Kenneth S.; Naidu, Ravi

From [Trace Elements in the Environment](#) (2006), 439-450. Language: English, Database: CAPLUS, DOI:10.1201/9781420032048.ch23

Some weeds of the temperate zone of Russia were studied for their capacity to accumulate heavy metals and their possible application in phytoremediation. On the basis of the data obtained, the following propositions were made: for Cr-contaminated soils, detoxification is possible by cultivating *Artemisia absinthium*. For better biomass, it is necessary to apply the green manure to sagebrush before the flowering starts. Common garden snail feeding on *Taraxacum officinale* growing on metal-polluted soils has accumulated significant levels of toxic metals in its gastric system. Phytoremediation is one of the strategies to decontaminate toxic levels of metals in the environment and is an upcoming and novel technol. It was obsd. that some of these temperate weeds are natural hyperaccumulators of toxic metals. Metal accumulation has been investigated in plant roots and shoots of selected weeds: *Calamagrostis epigeios*, *Taraxacum officinale* (dandelion), *Artemisia absinthium* (absinthium), *Artemisia vulgaris*, *Amaranthus retroflexus*, *Chenopodium album*, and *Melilotus officinalis*. Heavy metal content phytoremediation in plant parts and soil samples was quantified following x-ray spectrometry. It was noted that *Calamagrostis epigeios* was a Pb, Zn, and Cu concentrator.

~1 Citing

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169. Desiccation responses and survival of *Sinorhizobium meliloti* USDA 1021 in relation to growth phase, temperature, chloride and sulfate availability

By Vriezen, J. A. C.; de Bruijn, F. J.; Nusslein, K.

From [Letters in Applied Microbiology](#) (2006), 42(2), 172-178. Language: English, Database: CAPLUS, DOI:10.1111/j.1472-765X.2005.01808.x

To identify phys. and physiol. conditions that affect the survival of *Sinorhizobium meliloti* USDA 1021 during desiccation. An assay was developed to study desiccation response of *S. meliloti* USDA 1021 over a range of environmental conditions. We detd. the survival during desiccation in relation to (i) matrixes and media, (ii) growth phase, (iii) temp., and (iv) chloride and sulfate availability. This study **indicates** that survival of *S. meliloti* USDA 1021 during desiccation is enhanced: (i) when cells were dried in the stationary phase, (ii) with increasing drying temp. at an optimum of 37°C, and (iii) during an increase of chloride and sulfate, but not sodium or potassium availability. In addn., we resolved that the best matrix to test survival was nitrocellulose filters. The identification of phys. and physiol. factors that det. the survival during desiccation of *S. meliloti* USDA 1021 may aid in (i) the strategic development of improved seed inocula, (ii) the isolation, and (iii) the development of rhizobial strains with improved ability to survive desiccation. Furthermore, this work may provide insights into the survival of rhizobia under drought conditions.

~14 Citings

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170. Repressor of phage 16-3 with altered binding specificity **indicates** spatial differences in repressor-operator complexes

By Ferenczi, Szilamer; Orosz, Laszlo; Papp, Peter P.

From [Journal of Bacteriology](#) (2006), 188(4), 1663-1666. Language: English, Database: CAPLUS,

DOI:10.1128/JB.188.4.1663-1666.2006

The C repressor protein of phage 16-3, which is required for establishing and maintaining lysogeny, recognizes structurally different operators which differ by 2 bp in the length of the spacer between the conserved palindromic sequences. A "rotationally flexible protein homodimers" model has been proposed in order to explain the conformational adaptivity of the 16-3 repressor. In this paper, we report on the isolation of a repressor mutant with altered binding specificity which was used to identify a residue-base pair contact and to monitor the spatial relationship of the recognition helix of C repressor to the contacting major groove of DNA within the two kinds of repressor-operator complexes. Our results **indicate** spatial differences at the interface which may reflect different docking arrangements in recognition of the structurally different operators by the 16-3 repressor.

~0 Citings

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171. A fodder from natural forage and its processing method

By Zhu, Chao

From [Faming Zhuanli Shenqing](#) (2005), CN 1618312 A 20050525, Language: Chinese, Database: CAPLUS

A fodder comprises forage, corn meal, stalk powder, bran cake meal, bone powder, shell powder and feed additive. The prepn. method comprises taking one or more of forage of Gramineae (such as ryegrass, DONGMU 70 *Lolium perenne*, Mexico corn, sugar grass, Sudan grass, awnless brome, orchard grass, hybrid *Herba Penniseti* or wheat grass), forage of Leguminosae (such as *Herba Medicaginis*, *Herba Astragali Melilotoidis*, RUZI, *Onobrychis viciaefolia*, *Trifolium Pratense* L., white clover leaf, flatstem milkvetch or crownvetch), or forage of other families (such as feeding amaranth 1, *Herba Pentanematis Indici*, Russian forage, tooth edge *Herba Ixeritis Denticulatae*, *Herba Amaranthi Viridis*, *Herba Amaranthi Tricoloris*, European *Herba Cichorii* or *Rumex*) as primary raw materials, making fresh raw materials into fresh pulp, mixing with corn meal, stalk powder, bran cake meal or bone powder, shell powder and feed additive, and instantly drying at 80-140°C with low consumption to make into powder or granule. Three kinds of high-quality fodder has different nutritional components and different planting seasons for their growth period, so as to be capable of satisfying demands of annual prodn. of fodder. The produced fodder can satisfy nutritional demands of different raising objects, such as pig, cattle, sheep, chicken, duck, rabbit, fish, shrimp, etc., and different growth and development stages, and has advantages of simple and rapid process, low prodn. cost, and high economic efficiency.

~0 Citings

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172. *Sinorhizobium fredii* HH103 mutants affected in capsular polysaccharide (KPS) are impaired for nodulation with soybean and *Cajanus cajan*

By Parada, Maribel; Vinardell, Jose M.; Ollero, Francisco J.; Hidalgo, Angeles; Gutierrez, Rocio; Buendia-Claveria, Ana M.; Lei, Wang; Margaret, Isabel; Lopez-Baena, Francisco J.; Gil-Serrano, Antonio M.; et al

From [Molecular Plant-Microbe Interactions](#) (2006), 19(1), 43-52. Language: English, Database: CAPLUS,

DOI:10.1094/MPMI-19-0043

The *Sinorhizobium fredii* HH103 rkp-1 region, which is involved in capsular polysaccharides (KPS) prodn., was isolated and sequenced. The organization of the *S. fredii* genes identified, rkpUAGHIJ and kpsF3, was identical to that described for *S. meliloti* 1021 but different from that of *S. meliloti* AK631. The long rkpA gene (7.5 kb) of *S. fredii* HH103 and *S. meliloti* 1021 appears as a fusion of six clustered AK631 genes, rkpABCDEF. *S. fredii* HH103-Rif mutants affected in rkpH or rkpG were constructed. An *exoA* mutant unable to produce exopolysaccharide (EPS) and a double mutant *exoA* rkpH also were obtained. Glycine max (soybean) and *Cajanus cajan* (pigeon pea) plants inoculated with the rkpH, rkpG, and rkpH *exoA* derivs. of *S. fredii* HH103 showed reduced nodulation and severe symptoms of nitrogen starvation. The symbiotic capacity of the *exoA* mutant was not significantly altered. All these results indicate that KPS, but not EPS, is of crucial importance for the symbiotic capacity of *S. fredii* HH103-Rif. *S. meliloti* strains that produce only EPS or KPS are still effective with alfalfa. In *S. fredii* HH103, however, EPS and KPS are not equiv., because mutants in rkp genes are symbiotically impaired regardless of whether or not EPS is produced.

~28 Citings

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173. Analyzing a *Sinorhizobium meliloti* 1021 orfeome in a functional genomic platform

By Schroeder, Brenda K.; House, Brent L.; Mortimer, Michael W.; Maloney, Scott C.; Taylor, Casey A.; Ward, Kristel L.; Ziemkiewicz, Hope T.; Clark, Scott; Bovitz, John J.; Jin, Hao; et al

From [Current Plant Science and Biotechnology in Agriculture \(2005\), 41\(Biological Nitrogen Fixation, Sustainable Agriculture and the Environment\), 127-128](#). Language: English, Database: CAPLUS

A review. The Gram neg. soil bacterium *Sinorhizobium meliloti* is a complex microorganism that can grow as part of the normal soil microflora or form a nitrogen-fixing symbiotic relationship with legumes such as alfalfa (*Medicago sativa*) and *Medicago truncatula*. The genome sequence of *S. meliloti* 1021 was detd. by an international collaboration. Sequence annotation of the chromosome and two megaplasmids, pSymA and pSymB (1.7 Mb), predicted that greater than 6200 ORFs were present. Anal. of these ORFs indicated that *S. meliloti* 1021 was genetically complex and metabolically diverse. The progress with a novel approach to experimentation on a genomic scale is presented.

~0 Citings

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174. Phosphate limitation induces catalase expression in *Sinorhizobium meliloti*, *Pseudomonas aeruginosa* and *Agrobacterium tumefaciens*

By Yuan, Ze-Chun; Zaheer, Rahat; Finan, Turlough M.

From [Molecular Microbiology \(2005\), 58\(3\), 877-894](#). Language: English, Database: CAPLUS, DOI:10.1111/j.1365-2958.2005.04874.x

Growth of *Sinorhizobium meliloti* under Pi-limiting conditions induced expression of the major H₂O₂-inducible catalase (HPII) gene (*kataA*) in this organism. This transcription required the PhoB transcriptional regulator and initiated from a promoter that was distinct from the OxyR-dependent promoter which activates *kataA* transcription in response to addn. of H₂O₂. In N₂-fixing root nodules, *kataA* was transcribed from the OxyR- and not the PhoB-dependent promoter. This is consistent with the accumulation of reactive oxygen species (ROS) in nodules and also indicates that bacteroids within nodules are not Pi-limited. Pi-limited growth also induced expression of catalase genes in *Agrobacterium tumefaciens* (HPI) and *Pseudomonas aeruginosa* (PA4236-HPI) suggesting that this may be a widespread phenomenon. The response is not a general stress response as in both *S. meliloti* and *P. aeruginosa* increased transcription is mediated by the phosphate responsive transcriptional activator PhoB. The phenotypic consequences of this response were demonstrated in *S. meliloti* by the dramatic increase in H₂O₂ resistance of wild type but not *phoB* mutant cells upon growth in Pi-limiting media. Our data indicate that in *S. meliloti*, *kataA* and other genes whose products are involved in protection from oxidative stress are induced upon Pi-limitation. These observations suggest that as part of the response to Pi-limitation, *S. meliloti*, *P. aeruginosa* and *A. tumefaciens* have evolved a capacity to increase their resistance to oxidative stress. Whether this capacity evolved because Pi-starved cells generate more ROS or whether the physiol. changes that occur in the cells in response to Pi-starvation render them more sensitive to ROS remains to be established.

~21 Citings

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175. Macrophage activators, and cosmetics and foods containing the macrophage activators and melanin production inhibitors

By Tanaka, Hiroshi

From [Jpn. Kokai Tokkyo Koho \(2005\), JP 2005281205 A 20051013](#), Language: Japanese, Database: CAPLUS

The invention relates to a macrophage activator characterized by contg. at least one component selected from a group consisting of Urtica root ext., Matricaria flower ext., Vitis leaf ext., Camellia leaf ext., Olea leaf ext., Salix bark ext., *Melilotus* ext., Ilex leaf ext., Malus pericarp ext., reduced glutathione, flavone, and rutin. A cosmetic or food compn. contg. the macrophage activator and a melanin prodn. inhibitor for prevention of skin stain is also disclosed.

~2 Citings

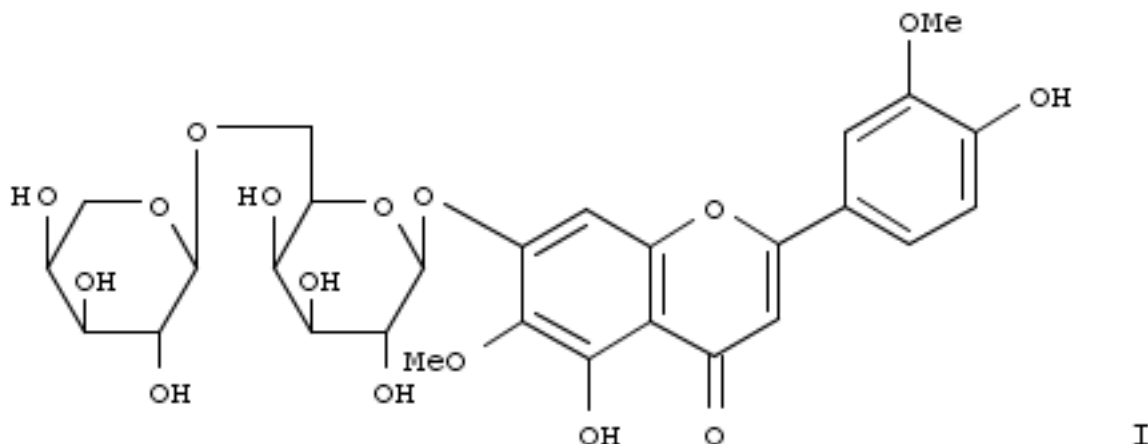
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176. A new bioactive flavone glycoside from the seeds of *Melilotus indica* All.

By Yadava, R. N.; Jain, S.

From *Journal of Asian Natural Products Research* (2005), 7(4), 595-599. Language: English, Database: CAPLUS, DOI:10.1080/10286020310001608949

Melilotus indica All. [Chopra, R. N., Nayar, S. L. and Chopra, I. C. (1956) Glossary Indian Med. Plants, 164 C.S.I.R. Publication New-Delhi; Kirtikar, K. R. and Basu, B. D. (1935) Indian Medicinal Plants, second Ed., Vol. I, pp. 703-704 Lalit Mohan Basuan Co. Allahabad. The Wealth of India (1962) A Dictionary of Raw Materials and Industrial Products, Vol. VI, pp. 329-331 (C.S.I.R. Publication: New-Delhi)] belongs to family Leguminosae, which is commonly known as 'Banmethi' in Hindi. It is found in North India, extending into S. Persia, S. Europe and the Tropical zone of India. The seeds are used as an anthelmintic, an antipyretic, for curing heart diseases, bronchitis, leprosy, bowel complaints and infantile diarrhea. The plant has also been used as a discutient, emollient, and as a fomentation. It is also useful in a plaster for swelling. It is considered astringent and narcotic. Earlier workers have reported the presence of C-glycosides [Sayed, E.L., Ishak, M.S. and Mabry, T.J. (1997) Asian J. Chem., 9, 551], methylene-dioxypterocarpan (MIS6) [Saxena, V.K. and Nigam, S. (1997) Fitoterapia, 68, 343-345], pterocarpane (MIS2) [Saxena, V.K. and Nigam, S. (1996) J. Institution Chem.68, 122-125] and prenylated pterocarpan [Saxena, V.K. and Nigam, S. (1997) Fitoterapia, 68, 403-407] from this plant. Here, we report the isolation of the new flavone glycoside 5,7,4'-trihydroxy-6,3'-dimethoxyflavone-7-O- α -L-arabinopyranosyl(1 \rightarrow 6)-O- β -D-galactopyranoside (I) from the seeds of this plant.



~3 Citings

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177. Positional analysis of a gene related to salt tolerance in *Sinorhizobium meliloti* by transposon rescue

By Li, Xiaohong; Du, Binghai; Zhang, Xiaoqing; Wang, Lei; Yang, Susheng

From *Yichuan Xuebao* (2004), 31(1), 91-96. Language: Chinese, Database: CAPLUS

Salt sensitive mutant 042BML-2 was obtained by mutating *Sinorhizobium meliloti* 042BM with transposon Tn5 carried on the plasmid pRL1063a. By transposon rescue, a 1.179 kb of DNA sequence of *S. meliloti* flanking the Tn5 insertion site was obtained. The sequence similarity anal. through BLAST anal. in GenBank revealed the transposon was inserted into a functionally unknown gene, which is 6,270 bp in length, of *S. meliloti*, and the gene was named *rtsC*. This study indicated that *rtsC* was assocd. with salt tolerance in *S. meliloti* 042BM. Hydrophobicity profile anal. of the putative amino acid sequence showed that two predicted transmembrane domains existed in N-terminal portion of *RtsC*. The significance of *RtsC* protein in the salt-tolerance in *S. meliloti* was discussed.

~1 Citing

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178. Grafting between model legumes demonstrates roles for roots and shoots in determining nodule type and host/rhizobia specificity

By Lohar, Dasharath P.; VandenBosch, Kathryn A.

From [Journal of Experimental Botany](#) (2005), 56(416), 1643-1650. Language: English, Database: CAPLUS, DOI:10.1093/jxb/eri160

Previous grafting expts. have demonstrated that legume shoots play a crit. role in symbiotic development of nitrogen-fixing root nodules by regulating nodule no. Here, reciprocal grafting expts. between the model legumes *Lotus japonicus* and *Medicago truncatula* were carried out to investigate the role of the shoot in the host-specificity of legume-rhizobia symbiosis and nodule type. *Lotus japonicus* is nodulated by *Mesorhizobium loti* and makes determinate nodules, whereas *M. truncatula* is nodulated by *Sinorhizobium meliloti* and makes indeterminate nodules. When inoculated with *M. loti*, *L. japonicus* roots grafted on *M. truncatula* shoots produced determinate nodules identical in appearance to those produced on *L. japonicus* self-grafted roots. Moreover, the hypernodulation phenotype of *L. japonicus* har1-1 roots grafted on wild-type *M. truncatula* shoots was restored to wild type when nodulated with *M. loti*. Thus, *L. japonicus* shoots appeared to be interchangeable with *M. truncatula* shoots in the *L. japonicus* root/*M. loti* symbiosis. However, *M. truncatula* roots grafted on *L. japonicus* shoots failed to induce nodules after inoculation with *S. meliloti* or a mixt. of *S. meliloti* and *M. loti*. Instead, only early responses to *S. meliloti* such as root hair tip swelling and deformation, plus induction of the early nodulation reporter gene MtENOD11:GUS were obsd. The results indicate that the *L. japonicus* shoot does not support normal symbiosis between the *M. truncatula* root and its microsymbiont *S. meliloti*, suggesting that an unidentified shoot-derived factor may be required for symbiotic progression in indeterminate nodules.

~15 Citings

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179. nifH promoter activity is regulated by DNA supercoiling in *Sinorhizobium meliloti*

By Liu, Yan-Jie; Hu, Biao; Zhu, Jia-Bi; Shen, Shan-Jiong; Yu, Guan-Qiao

From [Acta Biochimica et Biophysica Sinica](#) (2005), 37(4), 221-226. Language: English, Database: CAPLUS, DOI:10.1111/j.1745-7270.2005.00037.x

In prokaryotes, DNA supercoiling regulates the expression of many genes; for example, the expression of *Klebsiella pneumoniae* nifLA operon depends on DNA neg. supercoiling in anaerobically grown cells, which indicates that DNA supercoiling might play a role in gene regulation of the anaerobic response. Since the expression of the nifH promoter in *Sinorhizobium meliloti* is not repressed by oxygen, it is proposed that the status of DNA supercoiling may not affect the expression of the nifH promoter. Authors tested this hypothesis by analyzing nifH promoter activity in wild-type and gyr- *Escherichia coli* in the presence and absence of DNA gyrase inhibitors. These results show that gene expression driven by the *S. meliloti* nifH promoter requires the presence of active DNA gyrase. Because DNA gyrase increases the no. of neg. superhelical turns in DNA in the presence of ATP, these data indicate that neg. supercoiling is also important for nifH promoter activity. These study also shows that the DNA supercoiling-dependent *S. meliloti* nifH promoter activity is related to the trans-acting factors NtrC and NifA that activate it. DNA supercoiling appeared to have a stronger effect on NtrC-activated nifH promoter activity than on NifA-activated promoter activity. Collectively, these results from the *S. meliloti* nifH promoter model system seem to indicate that, in addn. to regulating gene expression during anaerobic signaling, DNA supercoiling may also provide a favorable topol. for trans-acting factor binding and promoter activation regardless of oxygen status.

~2 Citings

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180. Fatty acids composition of fifty-one plant species growing in Qatar

By Al-Easa, Hala S.

From [International Journal of Chemistry \(Calcutta, India\)](#) (2004), 14(4), 195-204. Language: English, Database: CAPLUS

The fatty acids compn. of the lipids extd. from 51 plant species belonging to 21 families growing in Qatar were detd. by gas chromatog. to evaluate these species for their nutritive values.

~0 Citings

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181. Glutathione plays a fundamental role in growth and symbiotic capacity of *Sinorhizobium meliloti*

By Harrison, Judith; Jamet, Alexandre; Muglia, Cecilia I.; Van de Sype, Ghislaine; Aguilar, O. Mario; Puppo, Alain; Frendo, Pierre

From [Journal of Bacteriology](#) (2005), 187(1), 168-174. Language: English, Database: CAPLUS, DOI:10.1128/JB.187.1.168-174.2005

Rhizobia form a symbiotic relationship with plants of the legume family to produce nitrogen-fixing root nodules under nitrogen-limiting conditions. We have examd. the importance of glutathione (GSH) during free-living growth and symbiosis of *Sinorhizobium meliloti*. An *S. meliloti* mutant strain (SmgshA) which is unable to synthesize GSH due to a gene disruption in *gshA*, encoding the enzyme for the first step in the biosynthesis of GSH, was unable to grow under nonstress conditions, precluding any nodulation. In contrast, an *S. meliloti* strain (SmgshB) with *gshB*, encoding the enzyme involved in the second step in GSH synthesis, deleted was able to grow, indicating that γ -glutamylcysteine, the dipeptide intermediate, can partially substitute for GSH. However, the SmgshB strain showed a delayed-nodulation phenotype coupled to a 75% redn. in the nitrogen fixation capacity. This phenotype was linked to abnormal nodule development. Both the SmgshA and SmgshB mutant strains exhibited higher catalase activity than the wild-type *S. meliloti* strain, suggesting that both mutant strains are under oxidative stress. Taken together, these results show that GSH plays a crit. role in the growth of *S. meliloti* and during its interaction with the plant partner.

~40 Citings

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182. Effectiveness of phytoremediation as a secondary treatment for polycyclic aromatic hydrocarbons (PAHs) in composted soil

By Parrish, Zakia D.; Banks, M. Katherine; Schwab, A. Paul

From *International Journal of Phytoremediation* (2004), 6(2), 119-137. Language: English, Database: CAPLUS, DOI:10.1080/16226510490454803

A greenhouse study was conducted over a 12-mo period to investigate the fate of polycyclic arom. hydrocarbons (PAHs) in soil using phytoremediation as a secondary treatment. The soil was pretreated by composting for 12 wk, then planted with tall fescue (*Festuca arundinacea*), annual ryegrass (*Lolium multiflorum*), and yellow sweet clover (*Melilotus officinalis*). Two sets of unvegetated controls also were evaluated, one fertilized and one unfertilized. Total PAH concns. decreased in the tall fescue, annual ryegrass, and yellow sweet clover treatments by 23.9, 15.3, and 9.1%, resp., whereas the control was reduced by <5%. The smaller 2- and most of the 3-ringed compds.-naphthalene, acenaphthylene, acenaphthene, fluorene, and anthracene-were not found in detectable concns. in any of the treatments. The most probable no. anal. for microbial PAH degraders did not show any statistically significant differences among treatments. There were significant differences among treatments ($p < 0.05$) for the residual concns. of 5 of the target PAHs. Root surface area measurements indicated that tall fescue and annual ryegrass both had significantly higher root surface area than yellow sweet clover, although the 2 species were not significantly different from each other. The tall fescue treatment resulted in the highest root and shoot biomass, followed by annual ryegrass and yellow sweet clover, and also had the highest percent of contaminant removal after 12 mo. These results imply a pos. relationship between plant biomass development and PAH biodegradn.

~34 Citings

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183. Residues of pendimethalin after weed control in cabbage crop (*Brassica oleracea* var L. Capitata)

By Arora, S.; Gopal, M.

From *Bulletin of Environmental Contamination and Toxicology* (2004), 73(1), 106-110. Language: English, Database: CAPLUS, DOI:10.1007/s00128-004-0400-6

Cabbage (*Brassica oleracea* L. Capitata) crop is one of the most important winter vegetables grown in India. It is attacked by no. of pests including weeds. While the losses caused by insect pests and diseases of cabbage crop are visible, there are various studies reported about them and they can be effectively controlled. The weed control has however not been studied that extensively. Major weeds of this crop are *Coronopus didymus* and *Melilotus indica* and minor weeds are *Parthenium hysterophorus*, *Rumex dentatus* etc. in and around Delhi. Expts. were carried out to record main weeds in this crop and quantitate the losses caused by these in realizing the potential yield of cabbage, besides recording the rate of dissipation of its residues in soil, under cabbage. Soil and cabbage samples were extd. with acetone and three methods, known for residue anal. of pendimethanlin [N-(1-ethylpropyl)-2,6-dinitro-3,4-xylidine] were evaluated to choose the best method by recovery expts. The method giving highest recovery was used for residue anal. of samples. The purpose of this study was to det. whether the herbicide and its metabolite translocated in the edible portion and for how long it remained in soil.

~7 Citings

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184. FixJ-regulated genes evolved through promoter duplication in *Sinorhizobium meliloti*

By Ferrieres, Lionel; Francez-Charlot, Anne; Gouzy, Jerome; Rouille, Stephane; Kahn, Daniel

From *Microbiology (Reading, United Kingdom)* (2004), 150(7), 2335-2345. Language: English, Database: CAPLUS, DOI:10.1099/mic.0.27081-0

The FixJ two-component system of *Sinorhizobium meliloti* is a global regulator, turning on nitrogen-fixation genes in microaerobiosis. Up to now, *nifA* and *fixK* were the only genes known to be directly regulated by FixJ. We used a genomic SELEX approach in order to isolate new FixJ targets in the genome. This led to the identification of 22 FixJ binding sites, including the known sites in the *fixK1* and *fixK2* promoters. FixJ binding sites are unevenly distributed among the three replicons constituting the *S. meliloti* genome: a majority are carried either by pSymA or by a short chromosomal region of non-chromosomal origin. Thus FixJ binding sites appear to be preferentially assocd. with the pSymA replicon, which carries the *fixJ* gene. Functional anal. of FixJ targets led to the discovery of two new FixJ-regulated genes, *smc03253* and *proB2*. This FixJ-dependent regulation appears to be mediated by a duplication of the whole *fixK* promoter region, including the beginning of the *fixK* gene. Similar duplications were previously reported for the *nifH* promoter. By systematic comparison of all promoter regions we found 17 such duplications throughout the genome, indicating that promoter duplication is a common mechanism for the evolution of regulatory pathways in *S. meliloti*.

~10 Citings

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185. Six nonnodulating plant mutants defective for Nod factor-induced transcriptional changes associated with the legume-rhizobia symbiosis

By Mitra, Raka M.; Shaw, Sidney L.; Long, Sharon R.

From [Proceedings of the National Academy of Sciences of the United States of America \(2004\)](#), 101(27), 10217-10222. Language: English, Database: CAPLUS, DOI:10.1073/pnas.0402186101

As the legume-rhizobia symbiosis is established, the plant recognizes bacterial-signaling molcs., Nod factors (NFs), and initiates transcriptional and developmental changes within the root to allow bacterial invasion and the construction of a novel organ, the nodule. Plant mutants defective in nodule initiation (Nod⁻) are thought to have defects in NF-signal transduction. However, it is unknown whether WT plants respond to NF-independent bacterial-derived signals or whether Nod⁻ plant mutants show defects in global symbiosis-assocd. gene expression. To characterize plant gene expression in the establishment of the symbiosis, we used an Affymetrix oligonucleotide microarray representing 9,935 *Medicago truncatula* expressed sequences. We identified 46 sequences that are differentially expressed in plants exposed for 24 h to WT *Sinorhizobium meliloti* or to the invasion defective *S. meliloti* mutant, *exoA*. Eight of these genes encode nucleolar proteins, which are implicated in ribosome biogenesis. We also identified differentially expressed transcription factors, signaling components, defense response proteins, stress response proteins, and several previously uncharacterized genes. NF appears both necessary and sufficient to induce most changes. Six of seven Nod⁻ *M. truncatula* mutants (*nfp*, *dmi1*, *dmi2*, *dmi3*, *nsp1*, and *nsp2*) showed no transcriptional response to *S. meliloti*, suggesting that the encoded proteins are required for initiating new transcription. The Nod⁻ mutant *hcl*, however, exhibits a reduced transcriptional response to *S. meliloti*, indicating that the machinery responsible for initiating new transcription is at least partially functional in this mutant.

~89 Citings

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186. *Sinorhizobium meliloti* sulfotransferase that modifies lipopolysaccharide

By Cronan, Glen E.; Keating, David H.

From [Journal of Bacteriology \(2004\)](#), 186(13), 4168-4176. Language: English, Database: CAPLUS, DOI:10.1128/JB.186.13.4168-4176.2004

Sinorhizobium meliloti is a gram-neg. soil bacterium found either in free-living form or as a nitrogen-fixing endosymbiont of a plant structure called the nodule. Symbiosis between *S. meliloti* and its plant host alfalfa is dependent on bacterial transcription of nod genes, which encode the enzymes responsible for synthesis of Nod factor. *S. meliloti* Nod factor is a lipochitooligosaccharide that undergoes a sulfate modification essential for its biol. activity. Sulfate also modifies the carbohydrate substituents of the bacterial cell surface, including lipopolysaccharide (LPS) and capsular polysaccharide (K-antigen) (R. A. Cedergren, J. Lee, K. L. Ross, and R. I. Hollingsworth, *Biochem.* 34:4467-4477, 1995). We utilized the genomic sequence of *S. meliloti* to identify an open reading frame, *SMc04267* (which we now propose to name *lpsS*), which encodes an LPS sulfotransferase activity. We expressed *lpsS* in *Escherichia coli* and demonstrated that the purified protein functions as an LPS sulfotransferase. Mutants lacking *lpsS* displayed an 89% redn. in LPS sulfotransferase activity in vitro. However, *lpsS* mutants retain approx. wild-type levels of sulfated LPS when assayed in vivo, indicating the presence of an addnl. LPS sulfotransferase activity(ies) in *S. meliloti* that can compensate for the loss of *lpsS*. The *lpsS* mutant did show reduced LPS sulfation, compared to that of the wild type, under conditions that promote nod gene expression, and it elicited a greater no. of nodules than did the wild type during symbiosis with alfalfa. These results suggest that sulfation of cell surface polysaccharides and Nod factor may compete for a limiting pool of intracellular sulfate and that *lpsS* is required for optimal LPS sulfation under these conditions.

~23 Citings

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187. Use of *Sinorhizobium meliloti* as an **indicator** for specific detection of long-chain N-acyl homoserine lactones

By Llamas, Inmaculada; Keshavan, Neela; Gonzalez, Juan E.

From [Applied and Environmental Microbiology](#) (2004), 70(6), 3715-3723. Language: English, Database: CAPLUS, DOI:10.1128/AEM.70.6.3715-3723.2004

Population-d.-dependent gene expression in gram-neg. bacteria involves the prodn. of signal mols. characterized as N-acyl homoserine lactones (AHLs). The synthesis of AHLs by numerous microorganisms has been identified by using biosensor strains based on the *Agrobacterium tumefaciens* and *Chromobacterium violaceum* quorum-sensing systems. The symbiotic N₂-fixing bacterium *S. meliloti* is rapidly becoming a model organism for the study of quorum sensing. This organism harbors ≥3 different quorum-sensing systems (Sin, Mel, and Tra), which play a role in its symbiotic relationship with its host plant, alfalfa. The Sin system is distinguished among them for the prodn. of long-chain AHLs, including C₁₈-HL, the longest AHL reported so far. In this work, we show that construction of a *sinI::lacZ* transcriptional fusion results in a strain that detects long-chain AHLs with exquisite sensitivity. Overexpression of the SinR regulator protein from a vector promoter increases its sensitivity without loss of specificity. We also show that the resulting **indicator** strain can recognize long-chain AHLs produced by unrelated bacteria such as *Paracoccus denitrificans* and *Rhodobacter capsulatus*. This *S. meliloti* **indicator** strain should serve as a tool for the specific detection of long-chain AHLs in new systems.

~36 Citings

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188. The expression of MaEXP1, a *Melilotus alba* expansin gene, is upregulated during the **sweetclover**-*Sinorhizobium meliloti* interaction

By Giordano, Walter; Hirsch, Ann M.

From [Molecular Plant-Microbe Interactions](#) (2004), 17(6), 613-622. Language: English, Database: CAPLUS, DOI:10.1094/MPMI.2004.17.6.613

Expansins are a highly conserved group of cell wall-localized proteins that appear to mediate changes in cell wall plasticity during cell expansion or differentiation. The accumulation of expansin protein or the mRNA for specific expansin gene family members has been correlated with the growth of various plant organs. Because expansin proteins are closely assocd. with plant cell wall expansion, and as part of a larger study to det. the role of different gene products in the legume-Rhizobium spp. symbiosis, we investigated whether a *Melilotus alba* (white **sweetclover**) expansin gene is expressed during nodule development. A cDNA fragment encoding an expansin gene (EXP) was isolated from *Sinorhizobium meliloti*-inoculated **sweetclover** root RNA by reverse-transcriptase polymerase chain reaction using degenerate primers, and a full-length **sweetclover** expansin sequence (MaEXP1) was obtained using 5' and 3' rapid amplification of cDNA end cloning. The predicted amino acid of the **sweetclover** expansin is highly conserved with the various α-expansins in the GenBank database. MaEXP1 contains a series of eight cysteines and four tryptophans that are conserved in the α-expansin protein family. Northern anal. and whole-mount in situ hybridization analyses **indicate** that MaEXP1 mRNA expression is enhanced in roots within hours after inoculation with *S. meliloti* and in nodules. Western and immunolocalization studies using a cucumber expansin antibody demonstrated that a cross-reacting protein accumulated in the expanding cells of the nodule.

~17 Citings

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189. Weed control in chickpea (*Cicer arietinum*) under late-sown condition

By Singh, R. V.; Sharma, A. K.; Tomar, R. K. S.

From [Indian Journal of Agronomy](#) (2003), 48(2), 114-116. Language: English, Database: CAPLUS

A field expt. was conducted during the winter season of 1993-94 to 1995-96 to study the effect of weed-management practices on chickpea (*Cicer arietinum*) under late-sown condition. Two hand-weedings at 30 and 45 days after sowing (DAS) (weed-free) completely controlled the weeds. Significantly lowest weed dry matter and highest weed-control efficiency were obsd. when 1 hand-weeding was done at 45 DAS. This treatment was followed by integration of 1 hand-weeding at 45 DAS with pre-emergence application of pendimethalin 0.75 kg/ha in reducing weed dry matter and in increasing the weed-control efficiency. Significantly higher grain yield (1,723 kg/ha) was recorded in weed-free plots. Among the weed-control treatments, pendimethalin 0.75 kg/ha coupled with 1 hand-weeding at 45 DAS recorded higher grain yield (1576 kg/ha).

~3 Citings

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190. The *typA* gene is required for stress adaptation as well as for symbiosis of *Sinorhizobium meliloti* 1021 with certain *Medicago truncatula* lines

By Kiss, Ernoe; Huguet, Thierry; Poinot, Verena; Batut, Jacques
From [Molecular Plant-Microbe Interactions](#) (2004), 17(3), 235-244. Language: English, Database: CAPLUS,
DOI:10.1094/MPMI.2004.17.3.235

In this article, we describe the *typA* gene of *Sinorhizobium meliloti*, the orthologue of *typA/bipA* genes found in a wide range of bacteria. We found that *typA* was required for survival of *S. meliloti* under certain stress conditions, such as growth at low temp. or low pH and in the presence of sodium dodecyl sulfate (SDS). The cold-sensitive phenotype of both *Escherichia coli bipA* and *S. meliloti typA* mutants were cross-complemented, indicating that the two genes are functionally equiv. *TypA* was indispensable for symbiosis on *Medicago truncatula* Jemalong and F83005.5 and contributes to the full efficiency of symbiosis on other host plant lines such as DZA315.16 or several cultivars of *M. sativa*. Hence, the symbiotic requirement for *typA* is host dependent. Interestingly, the symbiotic defect was different on Jemalong and F83005.5 plants, thus indicating that *typA* is required at a different stage of the symbiotic interaction.

~39 Citings

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191. A *Medicago sativa* haem oxygenase gene is preferentially expressed in root nodules

By Baudouin, Emmanuel; Frendo, Pierre; Le Gleuher, Marie; Puppo, Alain
From [Journal of Experimental Botany](#) (2004), 55(394), 43-47. Language: English, Database: CAPLUS,
DOI:10.1093/jxb/erh020

Haem oxygenases (HO) are ubiquitous enzymes catalyzing the oxidative degrdn. of heme into biliverdin, iron and carbon monoxide. Whereas animal HOs participate in multiple cellular functions including Hb catabolism, antioxidant defense and iron homeostasis, to date, plant HOs have so far only been involved in phytochrome metab. The expression of the HO1 gene was studied in *Medicago sativa*, esp. during the interaction with its symbiotic partner, *Sinorhizobium meliloti*. Transcript accumulation was higher in mature root nodules than in roots and leaves and was correlated to HO1 protein immunodetection. The anal. of HO1 expression following alfalfa root inoculation with *S. meliloti* indicates that transcripts do not accumulate during the early steps of symbiosis, but rather in the mature nodules. These results correlate with the expression of the *legHb* gene, which encodes the major heme-contg. protein present in the nodule. Contrary to its animal counterpart, alfalfa HO1 was not induced by pro-oxidant compds. including H₂O₂, paraquat and sodium nitroprusside, suggesting that it is not involved in the antioxidant defense. The results suggest that HO1 could play a role in the alfalfa mature nodule and its involvement in *legHb* metab. is hypothesized.

~35 Citings

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192. Isolation and symbiotic characterization of transposon Tn5-induced arginine auxotrophs of *Sinorhizobium meliloti*

By Kumar, Anvita; Vij, Neeraj; Randhawa, Gursharn S.
From [Indian Journal of Experimental Biology](#) (2003), 41(10), 1198-1204. Language: English, Database: CAPLUS

Seventeen arginine auxotrophic mutants of *Sinorhizobium meliloti* Rmd201 were isolated by random transposon Tn5 mutagenesis using Tn5 delivery vector pGS9. Based on intermediate feeding studies, these mutants were designated as *argA/argB/argC/argD/argE* (ornithine auxotrophs), *argF/argI*, *argG* and *argH* mutants. The ornithine auxotrophs induced ineffective nodules, whereas all other arginine auxotrophs induced fully effective nodules on alfalfa plants. In comparison to the parental strain induced nodule, only a few nodule cells infected with rhizobia were seen in the nitrogen fixation zone of the nodule induced by the ornithine auxotroph. TEM studies showed that the bacteroids in the nitrogen fixation zone of ornithine auxotroph induced nodule were mostly spherical or oval unlike the elongated bacteroids in the nitrogen fixation zone of the parental strain induced nodule. These results indicate that ornithine or an intermediate of ornithine biosynthesis, or a chem. factor derived from one of these compds. is required for the normal development of nitrogen fixation zone and transformation of rhizobial bacteria into bacteroids during symbiosis of *S. meliloti* with alfalfa plants.

~9 Citings

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193. Cell surface characteristics of two halotolerant strains of *Sinorhizobium meliloti*

By Bhattacharya, Indranil; Das, Hasi R.
From [Microbiological Research](#) (2003), 158(2), 187-194. Language: English, Database: CAPLUS, DOI:10.1078/0944-5013-00195

The halotolerant *Sinorhizobium meliloti* strain Rmd201 and its variant Rmd201 a were examd. for their cell surface properties. The variant strain formed rough colonies and was found to be more hydrophobic. Growth of the variant strain was not affected appreciably when NaCl concn. of the medium was increased from 2 mM to 700 mM. Exopolysaccharide (EPS) and the lipopolysaccharide (LPS) content of the variant strain was found to be 7- and 14-times less, resp., than the parent strain. However, enhanced synthesis of high mol. wt. LPS bands were obsd. in SDS-PAGE anal. in the variant strain when the NaCl concn. was raised from 2 mM to 700 mM. Ribose and glucosamine were present in the variant LPS only. Mannose appeared as a major LPS constituent of the variant when grown in high salt contg. medium. All these cell surface characteristics indicated that there were significant differences between the halotolerant strains of *S. meliloti*. The changes in the cell surface of the variant strain indicated the possible mutation in the gene(s) of cell surface polysaccharide biosynthesis.

~5 Citings

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194. Constituents of plants growing in Qatar. XXXIII. Proximate composition of thirty four food and feed plants growing in Qatar

By Al-Easa, Hala S.

From [International Journal of Chemistry \(Calcutta, India\) \(2003\), 13\(2\), 99-103](#). Language: English, Database: CAPLUS

Thirty four range plants belonging to fourteen families, growing in Qatar, were studied to evaluate their nutritive constituents and quantities. The plants were analyzed for moisture, lipid, carbohydrate, protein, crude fiber and ash content. The lipid content varied from 1.0 to 5.84% and protein content from 3.90 to 23.40%. The total carbohydrate varied from 15.35 to 42.59%, while the crude fiber from 9.84 to 46.70%.

~3 Citings

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195. Purification and characterization of homodimeric methylmalonyl-CoA mutase from *Sinorhizobium meliloti*

By Miyamoto, Emi; Watanabe, Fumio; Charles, Trevor C.; Yamaji, Ryoichi; Inui, Hiroshi; Nakano, Yoshihisa

From [Archives of Microbiology \(2003\), 180\(2\), 151-154](#). Language: English, Database: CAPLUS, DOI:10.1007/s00203-003-0570-3

High activity (>60 munit/mg protein) of 5'-deoxyadenosylcobalamin-dependent methylmalonyl-CoA mutase (EC 5.4.99.2) (I) was constantly found during growth of a strain of the root nodule-forming bacterium, *S. meliloti*, harboring an extra plasmid-encoded copy of the I-encoding bhhA gene. I was purified to homogeneity and characterized. Purified I was found to be a colorless apoenzyme. The apparent mol. wt. of I was calcd. to be 165 kDa by Superdex 200 HR gel filtration. SDS-PAGE of purified I resolved one protein band with an apparent mol. wt. of 80.0 kDa, indicating that *S. meliloti* I is composed of 2 identical subunits. The N-terminal sequence was identical to that predicted from the bhhA nucleotide sequence. Monovalent cations were required for enzyme activity.

~9 Citings

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196. The response of some common Egyptian plants to ozone and their use as biomonitors

By El-Khatib, A. A.

From [Environmental Pollution \(Oxford, United Kingdom\) \(2003\), 124\(3\), 419-428](#). Language: English, Database: CAPLUS, DOI:10.1016/S0269-7491(03)00045-9

Growth and physiol. response of plants was shown to be an effective tool for O₃ biomonitoring. The relative sensitivity of 5 common Egyptian plant species, namely, *Senecio vulgaris*, *Malva parviflora*, *Sonchus oleraceus*, *Medicago sativa*, and *Melilotus indicus* to elevated levels of ozone was studied. The plants were exposed to charcoal-filtered air (CFA) and different levels of O₃ (50 and 100 ppb) for 5 h per day. The studied parameters were recorded for 5 consecutive days after fumigation. The foliar injury varied significantly among species in a dose-dependent manner. Severe injury symptoms were recorded on the leaves of *M. sativa*. With the exception of *M. parviflora*, all species exhibited significant increases in the percentage redn. of the above-ground dry wt. as a result of redns. in both leaf and stem dry wts. *M. sativa* showed a marked redn. in its relative growth rate at elevated levels of O₃. The extent of chlorophyll a destruction was higher in both *M. sativa* and *S. oleraceus* than in the other species tested. No differences in the sensitivity of chlorophylls a+b and carotenoids to ozone levels were recorded in this work. The percentage redn. of ascorbic acid was higher in *M. sativa* and *S. oleraceus*, compared with the other species studied. With respect to relative percentages of proline, there was a significant difference in the responses of plants to ozone. According to the ozone resistance (R%), measured as relative growth rate, the test species were arranged in the descending order: *M. parviflora*>*M. Indicus*>*S. Vulgaris*>*S. Oleraceus*>*M. sativa*. In *M. sativa*, both determinant and correlation coeffs. are well reflected in the relationship between its physiol. response, its performance, and ozone levels, supporting its recommendation as a candidate for biomonitoring in Egypt.

~24 Citings

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197. Investigation on low doses of atrazine, metribuzin and pendimethalin on weeds and yield of wheat

By Pandey, J.; Gopinath, K. A.; Verma, A. K.

From *Acta Agronomica Hungarica* (2002), 50(4), 441-445. Language: English, Database: CAPLUS, DOI:10.1556/AAgr.50.2002.4.7

The results obtained showed that there was severe competition between wheat and the predominant weed species *Phalaris minor*, *Avena ludoviciana* and *Melilotus indica*. Competition by other weed species was normal. The max. redn. in grain and straw yields due to weed competition was 34.8% and 43.7%, resp. Weed control treatments lowered the weed population and weed biomass accumulation and boosted up the crop yield. A significant redn. in the weed population and weed dry wt. was obsd. with increasing doses of both atrazine and metribuzin. Metribuzin at 200 g ha⁻¹ killed all the plants of *M. indica* and gave excellent control of both *P. minor* (98%) and *A. ludoviciana* (89%). Atrazine at higher doses had an almost similar effect on *P. minor*, *A. ludoviciana* and *M. indica* with 83-87% control. Pendimethalin gave good control of *P. minor* and *M. indica* (75-83%) but poor control of *A. ludoviciana* (55%). The highest yield was recorded in hand weeding which was significantly superior to all other treatments. Metribuzin at 100 g ha⁻¹ was the next best treatment, and this rate was superior to the higher doses. Pendimethalin and atrazine also brought about a marked increase in the crop yield. Higher doses of atrazine and metribuzin had a phytotoxic effect on the crop, reducing the no. of productive tillers and finally lowering the crop yield, despite their excellent control of dominant weed species.

~1 Citing

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198. Evaluation of herbicides in peas (*Pisum sativum* L.) for seed under Tarai conditions of Uttaranchal

By Tripathi, S. S.; Singh, Govindra

From *Pestology* (2003), 27(2), 32-34. Language: English, Database: CAPLUS

Field expt. was conducted during winter 2000-2001 and 2001-2002 to evaluate the efficacy of herbicides against weeds in Peas grown for seed. The field was mainly infested with *Melilotus indica*, *Medicago denticulata*, *Fumaria parviflora*, *Chenopodium album*, *Anagallis arvensis*, *Phalaris minor* and *Cyperus rotundus* constituting more than 91% of the total weed population at 60 days after sowing. Other weeds having 9.3% d. were *Euphorbia hirta*, *Cynodon dactylon* and *Vicia sativa*. Uncontrolled weeds on an av. resulted in 69.8 per cent redn. in seed yield of peas as compared to weed-free treatment. Increasing dose of all the herbicides alone or in combination caused significant redn. in the d., dry matter prodn. by weeds and significant increase in seed yield as compared to weedy check. Chlorimuronethyl at 6 g ha⁻¹ being at par with pendimethalin 1000 g and mixt. of clomazone 250 g + pendimethalin 500 g ha⁻¹ produced significantly higher grain yield than rest of the herbicides and their combinations. Increasing dose of clomazone either alone or combined with pendimethalin did not increase seed yield significantly as compared within their increasing dose and their combinations. Chlorimuronethyl at 6 g, pendimethalin at 1.0 kg and prometryn at 750 g ha⁻¹ gave significantly higher grain yields than their lower doses.

~0 Citings

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199. Genetic identification and symbiotic efficiency of an indigenous *Sinorhizobium meliloti* field population

By Bradic, Mihaela; Sikora, Sanja; Redzepovic, Sulejman; Stafa, Zvonimir
From [Food Technology and Biotechnology \(2003\), 41\(1\), 69-75](#). Language: English, Database: CAPLUS

Soil bacteria *Sinorhizobium meliloti* are of enormous agricultural value, because of their ability to fix atm. nitrogen in symbiosis with an important forage crop legume - alfalfa. The main aim of this study was (i) to isolate indigenous *S. meliloti* strains from different field sites in Croatia, (ii) to assess genetic diversity and genetic relationships amongst strains of natural populations and (iii) to provide information about nodulation and symbiotic efficiency of indigenous *S. meliloti* strains. The nine strains isolated from alfalfa nodules collected from different field sites and three ref. strains were analyzed. Genetic characterization by PCR-RFLP of the 16S rDNA, rep-PCR and RAPD-PCR was applied to study the status of *Sinorhizobium meliloti* populations inhabiting nodules of alfalfa. The results of PCR-RFLP of the 16S rDNA revealed that all isolates belong to the *S. meliloti* species. Cluster anal. of rep-PCR and RAPD-PCR profiles showed significant differences among *S. meliloti* isolates. Both methods resulted in identical grouping of strains. Among indigenous strains two divergent groups could be detd. The biggest differences were detected among two ref. strains and all field isolates. Greenhouse studies were performed for evaluation of symbiotic efficiency and compatibility of *S. meliloti* strains with two alfalfa cultivars. Quant. expression of symbiotic efficiency was evaluated by measurement of nodule dry wt., content of proteins and total nitrogen in plants, dry matter and green mass yield of plants. All strains nodulated both alfalfa cultivars but with different efficiency. Significant differences in dry matter and green mass yield of alfalfa as well as protein content were detd. depending on the strain used. The results **indicate** that three indigenous *S. meliloti* strains can be characterized as the most efficient of all strains used in this study.

~11 Citings

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200. Colonization behaviour of *Pseudomonas fluorescens* and *Sinorhizobium meliloti* in the alfalfa (*Medicago sativa*) rhizosphere

By Villaceros, Marta; Power, Barry; Sanchez-Contreras, Maria; Lloret, Javier; Oruezabal, Roke I.; Martin, Marta; Fernandez-Pinas, Francisca; Bonilla, Ildefonso; Whelan, Clare; Dowling, David N.; et al
From [Plant and Soil \(2003\), 251\(1\), 47-54](#). Language: English, Database: CAPLUS

The colonization ability of *Pseudomonas fluorescens* F113rif in alfalfa rhizosphere and its interactions with the alfalfa microsymbiont *Sinorhizobium meliloti* EFB1 has been analyzed. Both strains efficiently colonize the alfalfa rhizosphere in gnotobiotic systems and soil microcosms. Colonization dynamics of F113rif on alfalfa were similar to other plant systems previously studied but it is displaced by *S. meliloti* EFB1, lowering its population by one order of magnitude in co-inoculation expts. GFP tagged strains used to study the colonization patterns by both strains **indicated** that *P. fluorescens* F113rif did not colonize root hairs while *S. meliloti* EFB1 extensively colonized this niche. Inoculation of F113rif had a deleterious effect on plants grown in gnotobiotic systems, possibly because of the prodn. of HCN and the high populations reached in these systems. This effect was reversed by co-inoculation. *Pseudomonas fluorescens* F113 derivs. with biocontrol and bioremediation abilities have been developed in recent years. The results obtained support the possibility of using this bacterium in conjunction with alfalfa for biocontrol or rhizoremediation technologies.

~38 Citings

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