

**P-552 Plant growth promotion of *Echinocactus platyacanthus*, an endangered Cactaceae from Mexican highlands, by inoculation with isolates of methylotrophic bacteria**

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*Echinocactus platyacanthus* is distributed in arid areas of Mexico. Like other Cactaceae shows a very slow growth until the reproductive stage. Although it has a wide distribution, the human-dependent deterioration of its habitat, and the abuse for ornament and for traditional candy production, has put in danger its populations. Diverse taxonomic groups of bacteria, known as methylotrophs, are capable of metabolizing one-carbon sources. Different experiments have shown the potentiality of these bacteria as PGPRs in diverse plants, but not in cacti, to our knowledge. Tissue samples of *E. platyacanthus* and *Pseudonitzschia fulvipes* (Cactaceae) growing in arid areas of Puebla, Mexico, were used for isolation of aerenchyma- and endophytic bacteria in methanol-containing plates. Identification as methylotrophs was based on PCR amplification with primers intended for methanol dehydrogenase (*mxaF*) locus (McDonald and Murrell, 1997). ARDRA showed the presence of seven groups of methylotrophs. Four isolates and *Methylobacterium extorquens* JCM 2833T were inoculated in germinated seeds of *E. platyacanthus* growing in sterilized peat moss, as separate treatments. The plantlets were watered once a week with tap water. The growth was determined each month by measuring length of stem, dry weight of roots and stem, and number of ribs. Three strains induced growth in comparison with the non-inoculated controls until 6 month old plantlets. The inoculated strains were recovered from inoculated plants.

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McDonald, I, Murrell, J.C. 1997. The methanol dehydrogenase structural gene *mxaF* and its use as a functional gene probe for methanotrophs and methylotrophs. Appl. Environ. Microbiol. 63:3218-3224.

**P-1072 Does carbon flow from mycorrhizal fungi stimulate bacterial antibiotic production?**

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The presence of mycorrhizal-root associations markedly alters the quality of carbon flow from roots. We investigated how antibiotic production of the model *Pseudomonas fluorescens* strains were modulated by qualitative changes to C-flow. Specifically, we quantified the production of the antibiotic 2,4-diacetylphloroglucinol (DAPG), a known suppressant of root fungal pathogens. In the first experiment, wheat plants were grown for five weeks in sand inside split pots so that half of their root systems were colonised by arbuscular mycorrhizal fungi and half remained uncolonised. In the second experiment, wheat plants were grown without mycorrhizal fungi, with mycorrhizal fungi and with the root pathogen *Gaeumannomyces graminis* var. *tritici* (Ggt) and with both mycorrhizal fungi and Ggt. Roots were harvested and homogenate was used to challenge cultures of *P. fluorescens* strains. Each homogenate was balanced for molar C. To increase sample throughput and analytical efficiency, we used a 96-well plate Porvair Sciences Ltd Microlute® system containing a C-18 Solid Phase Extraction matrix. The analyte of interest (DAPG) in each cell in the growth plate was retained on the C-18 matrix until elution by methanol for HPLC analysis. We discuss how the presence of the arbuscular mycorrhizal fungi and Ggt affects the antibiotic production by root associated bacteria.

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**P-1064 Phosphate solubilizing microorganisms associated with maize rhizosphere in Brazilian acid savanna soils**

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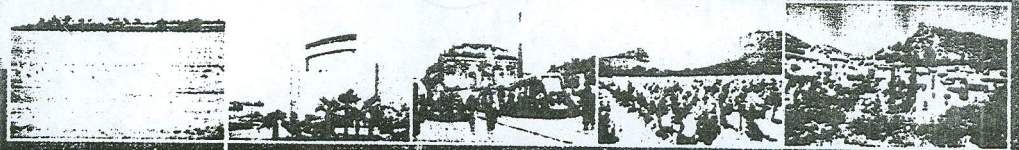
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Many soil microorganisms are able to transform insoluble forms of phosphorus to an accessible soluble form, contributing to plant nutrition as plant growth-promoting microorganisms (PGPM). The objective of this work was to isolate, screen and investigate the phosphate solubilizing activity of microorganisms in maize rhizosphere soil to manage soil microbial communities and to select potential microbial inoculants. Forty-five of the best isolates from 371 colonies isolated from rhizosphere soil of maize grown in an oxisol with P stress were selected based on the solubilization of inorganic and organic phosphates in a modified Pikovskaya's liquid medium culture containing sodium phytate (Phytic Acid), soybean lecithin,  $AlPO_4$ , and tricalcium phosphate ( $Ca_3(PO_4)_2$ ). The isolates were identified based on nucleotide sequence data from the 16S rDNA sequences for bacteria and actinomyces and ITS rDNA sequences for fungi. Bacteria produced the greatest solubilization in medium containing tricalcium phosphate. The strains B17 and B5, identified as *Bacillus* sp and *Burkholderia* sp, respectively, were the most effective, mobilizing 67% and 58.5% of the total P ( $Ca_3(PO_4)_2$ ) after 10 days, and were isolated from the rhizosphere of the P efficient maize genotype, L3 under P stress. These genera of bacteria have been reported in the literature as important PGPM. The fungal population was the most effective in solubilizing P in the aluminum, phytate, and lecithin forms of phosphorus. A greater diversity of P solubilizing microorganisms was observed in the rhizosphere of the P efficient maize genotypes in the no-till planting system. The P efficiency in these cultivars may be related to the potential to enhance microbial development interactions of P solubilizing microorganisms.

# Rhizosphere 2

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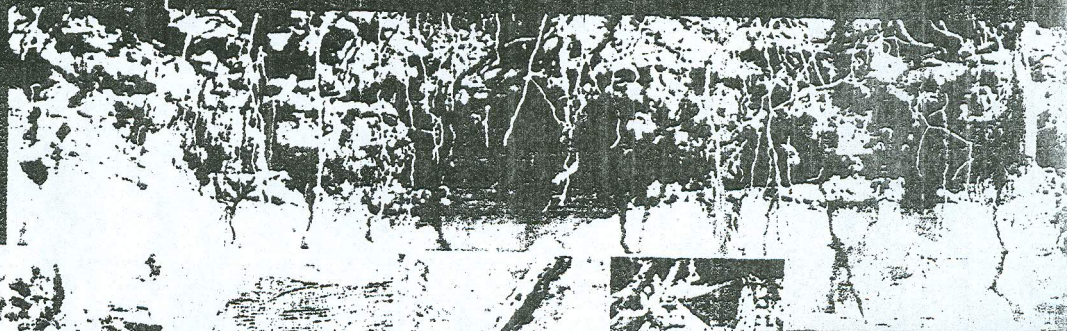


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