

P-1050 On-station and on-farm field experiments to study yield, protein content and farmers' acceptance of common bean genotypes inoculated with *Rhizobium* and *Azospirillum* in the province of Piñar del Rio, Cuba

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Common bean forms part of two of the three daily meals in Cuba. It is a main source of protein and minerals. Nitrogen fixation contributes to the yield and protein content of the grain and offers farmers an alternative for nitrogen fertilizers. However, many factors, including P deficiency and soil acidity which characterize the soil in the Piñar del Rio province in Cuba, limit the impact of nitrogen fixation. Potential to select for bean genotypes with enhanced nitrogen fixation capacity under poor soil conditions exists. Further, plant growth promoting bacteria have shown potential to enhance nodulation and nitrogen fixation of common bean. In this study, four common bean genotypes were evaluated in combination with two inocula: a local *Rhizobium* strain 6bIII and a mixed inoculum of *Rhizobium* 6bIII and *Azospirillum brasilense* Sp245 and this on-station an on-farm, in collaboration with three farmers in Piñar del Rio. Plant parameters measured are nodulation, shoot and root dry weight at different growth stages, yield and protein content of the seeds. Further a survey on farmers' perception on bean varieties and microbial inoculation was performed. It was observed that *Azospirillum* provokes a differential plant and nodulation response among bean genotypes. Further, this differential plant and nodulation response to *Azospirillum* is dependent on P nutrition. Nodulation and yield of two out of the four genotypes is enhanced by *Azospirillum* under low P conditions, while a negative effect of *Azospirillum* is observed for the other genotypes under P deficiency. When P fertilizer is supplied, the four genotypes respond more similarly to *Azospirillum* co-inoculation. This study highlights the effect of the host genotype and the nutritional status of the soil in rhizosphere interactions.

P-852 The effect of *Zea mays* genotypes contrasting for phosphorus efficiency on mycorrhizal diversity analyzed by denaturing gradient gel electrophoresis (DGGE) and DNA cloning/sequencing

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Marginal soil fertility, soil acidity, aluminum toxicity, and a generalized low level of available nutrients, especially P, are some of the major limiting factors to crop production across the tropics. Plants have evolved several strategies to improve P acquisition, including symbiotic associations with arbuscular mycorrhizal (AM) fungi. Mycorrhizal population DNA fingerprints were generated from the roots and rhizosphere of maize genotypes contrasting for phosphorus efficiency, by denaturing gradient gel electrophoresis (DGGE) and DNA cloning/sequencing, to assess the variation in the AM fungi communities. Fragments of AM fungi rDNA were amplified using nested PCR with universal and specific fungal primers for Acaulosporaceae, Glomaceae and Gigasporaceae AM, Acaulosporaceae and Glomaceae specific primers and DGGE were efficient in differentiating the dynamics of mycorrhizal communities. Maize genotypes had a greater influence on the rhizosphere mycorrhizal community than the level of P in soil. DGGE profiles of maize roots revealed bands that were present only in P efficient genotypes, indicating that some mycorrhizal groups were favored by P efficient maize genotypes. Direct cloning of rDNA fragments amplified by AM fungi specific primers from root and rhizosphere DNAs of two of these contrasting genotypes indicated differences in the composition of root mycorrhizal communities. Genetic diversity in the microbial community of the root was reduced when compared to the rhizosphere, and there were some differences in the AM fungi species between the two genotypes. Sequencing analysis of cloned fragments revealed that, *Scutellospora* was the dominant genus found in efficient genotypes. Visualization of mycorrhizal colonization using stereomicroscope analysis demonstrated greater colonization in roots of the P efficient maize genotypes compared to P inefficient genotypes. The number of AM spores found in the rhizosphere was similar in both genotypes but significantly reduced in the roots of the P inefficient genotype. These results provide strong evidence that the maize genotype plays an important role in regulating microbial colonization of maize roots and influencing P acquisition.

