

**TITLE:** BACTERIAL COMMUNITIES RELATED TO PLANT GROWTH-PROMOTION IN SWEET POTATO RHIZOSPHERE SHOW A GENOTYPE-DEPENDENT DISTRIBUTION

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**ABSTRACT:** Different factors such as plant developmental stage, plant species and genotypes can affect microbial communities in close contact with plant roots. Moreover, plant genotypes can also affect the accumulation of specific beneficial microorganisms in their rhizospheres by the secretion of root exudates. In a previous study, it was demonstrated that rhizosphere and endophytic bacterial communities associated with sweet potato plants were influenced by plant age and genotypes. The hypothesis that sweet potato genotypes can also influence the composition of the bacterial communities particularly related to phosphate solubilization and nitrogen fixation in sweet potato rhizosphere was tested here. Tuberos roots of field-grown sweet potato from genotypes IPB-149, IPB-052 and IPB-137 were sampled three and six months after planting. The total community DNA was extracted from the rhizosphere soil and analyzed by Polymerase Chain Reaction-Denaturing Gradient Gel Electrophoresis (PCR-DGGE) and quantitative real-time PCR (qPCR) based on *alp* gene (alkaline phosphatase coding gene) and on *nifH* gene (nitrogenase coding gene). The cluster analysis showed that plant age did not affect bacterial community related to nitrogen fixation. In agreement with cluster analysis and Principal Component Analysis (PCA), the statistical analysis of DGGE fingerprints (Permutation test,  $P < 0.05$ ) showed that nitrogen fixing bacterial community of IPB-052 statistically differed from genotypes IPB-149 and 137 after six months of planting. Five bands were extracted from *nifH* DGGE gel, sequenced and further identified as nitrogenase partial sequences of *Kosakonia oryzae* (identity of 99%), *Lusitaniella coriacea* (98% and 100%), *Bradyrhizobium* sp. (99%), *Azohydromonas australica* (97%). On the other hand, the DGGE statistical analysis showed that plant age slightly influenced bacterial community related to phosphate solubilization in the rhizosphere of IPB-137. The bacterial community of IPB-137 rhizosphere analyzed by *alp* gene also showed significant differences when compared to IPB-149 in both sampling times ( $P < 0.05$ ). PCA analysis confirmed the statistical results. In addition, *alp* gene copy numbers significantly increased in abundance in the rhizosphere of IPB-137 after six months of planting. These data suggest that the composition of bacterial communities associated with plant growth-promotion in sweet potato rhizosphere is clearly influenced by the plant genotype.

**Keywords:** bacterial communities, plant growth-promotion, rhizosphere, plant genotype, sweet potato.

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