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Morphological Characterisation and Genetic Identification of Rhizobacteria in Cuban Agricultural Soils

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Abstract

The microbial activity in soil is one of the most important factors for maintaining sustainability in crop production. The ecology and diversity of microbes is the base to unravel the different process that take place in several ecosystems. This report aims the isolation and characterisation of microorganisms in cereal-legume intercropping system. Samples from common bean (*Phaseolus vulgaris* L.) nodules, soil and sorghum roots (*Sorghum bicolor* (L.) Moench) were analysed to determine the biodiversity of diazotrophic and rhizosphere bacteria in an agricultural Cuban system. The morphological analysis demonstrated several groups of isolates with differences in growth type, colour, polysaccharide production and border of the colonies. Genetic characterisation using 16S rDNA revealed 8 groups of bacteria belonging to the genera: *Agrobacterium*, *Rhizobium*, *Ochrobactrum*, *Sphingomonas*, *Stenotrophomonas*, *Bacillus*, *Brevibacillus* and *Paenibacillus*. 47% of the sequences matched for 100% sequences in the EMBL database, while 53% of the sequences scored above 99% of identity. In nodule samples 37.5% of the isolates were 100% similar to *Agrobacterium tumefaciens* or *Rhizobium* species. Two species of *Rhizobium* isolated (*R. etli* and *R. tropici*) were detected in nodule samples. In nodulation tests, *Agrobacterium* isolates were unable to nodulate the original host. No statistical difference was observed for nodulation between the *Rhizobium* isolates and the *R. etli* reference strain. The results presented in this study are of importance to determine the interspecies microbial relationships in the rhizosphere, possibly increasing our understanding on biotic factors interfering with the *Rhizobium*-legume symbiosis and as a source of inoculant strains for local environmental conditions.

Keywords: 16S rDNA, bacteria, diazotrophic, rhizosphere