

Title: THE INDIVIDUAL BEHAVIOR OF BACTERIA IN THE RHIZOSPHERE – USING SUGARCANE AS A MODEL

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Abstract

In the rhizosphere it occurs an intimate interaction between plants and soil-living microorganisms, in a relationship intermediated by root exudates. Although it is known to have several implication for plant life – as growth promotion and pathogen inhibition – little is known about the individual behavior of bacteria in this competitive niche. This study used sugarcane as a model to perform, based on cultivation approaches, an inference on individual responses of bacteria from the rhizosphere and the respective bulk soil. Samples of soil and rhizosphere of sugarcane were sowed in different media culture (TSB, MSSC, LAM, LGI and JNFb), originating 616 bacterial isolates (401 and 215 from rhizosphere and bulk soil, respectively). The enormous genetic diversity was evidence by the BOX-PCR patterns (95 patterns out of 280 isolates). The taxonomical affiliation indicated the prevalence of Proteobacteria in the collection (54% of the isolates), mainly affiliated to genera *Enterobacter*, *Burkholderia* and *Pseudomonas*. The phylogenetic similarities – promoted by the partial sequencing of the 16S rRNA gene sequencing - were also compared to the identity in metabolical parameters, as determined by BIOLOG®, where it was possible to verify that isolates highly correlated in the taxonomical analyses presented distinct capacities to use the carbon sources that were tested. A deeper view on bacterial singularities was achieved by pairwise comparisons – isolates from rhizosphere against isolates from soil -, where pairs of isolates with very similar 16 rRNA sequences, similar BOX-PCR patterns, but distinct BIOLOG® profiles were monitored for their multiplication, either in control conditions or in the presence of roots exudates. In general, isolated from rhizosphere were more efficient to multiply in the presence of roots exudates (valid for comparison of genera *Pseudomonas* and *Enterobacter*), with exception for the comparison of isolates belonging to the genus *Burkholderia*. These results indicate that, the individual variability within bacterial populations is an issue to be better targeted in future studies, and possibly, specific traits, that can be highly variable among cells within the same population, might trigger the rhizosphere benefits to plants.

Keywords: Bacterial cultivation; Exudates, Genetic diversity; metabolic diversity; DNA sequencing

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