Title: CONTRASTING SUGARCANE RHIZOSPHERE AND BULK SOIL MICROBIAL COMMUNITIES BASED ON TAXONOMIC AND FUNCTIONAL TRAITS

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Abstract:

Sugarcane is increasingly important to the Brazillian agriculture due to the high demand of renewable energy sources such as bioethanol for replacing the fossil fuels. The physical and chemical soil properties leading to productivity increase are well understood, but the biological fraction remains poorly known. The rhizosphere microbiome is responsible for many activities that promote plant growth and there is a need to understand its dynamics. This study hypothesized that the sugarcane rhizosphere microbiome is taxonomically and functionally modulated by selective pressures created by the roots. Twelve samples, 6 from rhizosphere (RZ) and 6 controls from bulk soil (BS) were collected randomly in a sugarcane crop field. Differences in bacterial community were assessed for both abundance (qPCR analysis targeting 16S rRNA gene) and diversity (Illumina sequencing of V4-16S rRNA genes). The functional divergence between the 2 environments was assessed by community level physiological profile (CLPP) and PICRUSt metagenome prediction. There were significant differences (P=0.007) between RZ and BS samples quantitation (average of $4.96 \cdot 10^9$ against $1.67 \cdot 10^9$ 16S rRNA gene copies soil g^{-1}), and a clear difference in bacterial community structure, revealed by NMDS and ANOSIM (P=0.002/r^2=1). The dominant phylum was Acidobacteria, followed by Proteobacteria. However, other phyla showed significant differences between the 2 locations, such as Nitrospirae, Verrucomicrobia (higher in RZ), Gemmatimonadetes and Actinobacteria (higher in BS); but lower taxonomic levels showed the strongest differences (e.g. Family). The CLPP analysis revealed 15 C-sources significantly different (P<0.05) between the two environments, 11 higher in RZ and 4 higher in BS. The most consumed C-source in RZ was D-galacturonic acid (P=0.001). The metagenome predictions categorized by KEGG pointed some functions significantly higher in RZ (carbohydrate metabolism/ cellular processes and signaling) and others in BS (environmental adaptation/ metabolism of terpenoids and polyketides). Considering the inferred genes, a remarkable pattern was observed for those codifying polygalacturonase (enzyme relative to D-galacturonic acid catabolism) and many proteins related to lateral gene transfer, both significantly higher (P<0.05) in RZ. These results show that sugarcane rhizosphere exerts a selection effect in bacterial taxa and functions, restructuring the community in order to fill its specific niches.

Keywords: Microbial ecology; metabolic profile; soil microbiology; natural selection; HGT.