Soils properties outpaces agricultural practices in the determination of bacterial community structure in sugarcane fields

Ademir Durrer*[1], Thiago Gumiere[2], Pedro Avelino Maia Andrade[2], Diogo Paes Costa[2], Rodrigo Taketani[3], Júlia Lima[2], Michele Pereira e Silva[2], Itamar Soares Melo[3], Fernando Dini Andreote[2]

[1] University of São Paulo, ESALQ, Brazil, [2]USP/ESALQ, Brazil, [3]EMBRAPA, Brazil

The sugarcane is the most important crop in Brazil, mainly produced to feed the sugar and ethanol growing markets. The increasing demand for these products is leading to the expansion of the sugarcane plantations to new areas. Considering this scenario, the search for sustainable alternatives is desirable, where one of the pillars would it be an exploration of the microbial communities present in such fields. This work aimed to deeply describe the structure of bacterial communities across 10 areas of sugarcane cultivation the São Paulo State (Southeast Brazil), where distinct agricultural practices are used, and soils differed in their properties and characteristics. In total, 95 samples were used, characterized in accordance with their physical (clay, silt and sand) and chemical (pH, Mg, Ca, K, P, organic Matter, H+Al and cation change capacity) features, while agricultural practices adopted in each area (application of vinasse, strategy of harvesting, mineral fertilization and filter cake addition) were recorded as dummy variables. The assessment of bacterial communities was promoted by high-throughput sequencing of the V6 region of the 16S rRNA gene. The resulting sequences (427,500 – rarified with 4,500 seqs per sample) revealed a total of 60,980 different operational taxonomic units at 3% of dissimilarity. The taxonomical prevalence was observed, in average, for sequences affiliated with Proteobacteria (23.1%), Acidobacteria (21.9%), Actinobacteria (19.9%), Verrucomicrobia (5.1%), Gemmatimonadetes (4.8%), Nitrospirae (2.1%), Chloroflexi (2.1%), Planctomycetes (1.5%), Firmicutes (1.3%), Bacteroidetes (1.0%) and others 27 phyla (1.9 %). Sequences recognized as bacteria-related but not classified represented 15.2%. Comparing the sampled area, shifts on these values were observed, with a seldom occurrence of Acidobateria and Actinobacteria over Proteobacteria. A network analyses, performed on the basis of an OTU table, revealed the negative correlation between groups of Actinobacteria, Acidobacteria and Proteobacteria. As determined by partitioning redundancy analysis (pRDA), the majority of variance was explained by soils characteristics, with a remarkable role of pH and clay contents, causing alteration on frequencies of Acidobacteria, Actinobacteria and Protebacteria. Still to be determined, is the role of geographical distance of samples, in a possible occurrence of biogeographical patterns in these soils. Therefore, these results constitute a first deep assessment of bacterial communities in sugarcane fields, describing physical and chemical characteristics of soils and dominant effectors over the agricultural practices on the structuring of such communities.