

## MICROBIAL DIVERSITY IN SOILS CULTIVATED WITH SUGARCANE IN THE STATE OF SÃO PAULO: A BIOGEOGRAPHIC APPROACH

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FAPESP Process 2011/03487-2 | Term: Jun 2011 to May 2013

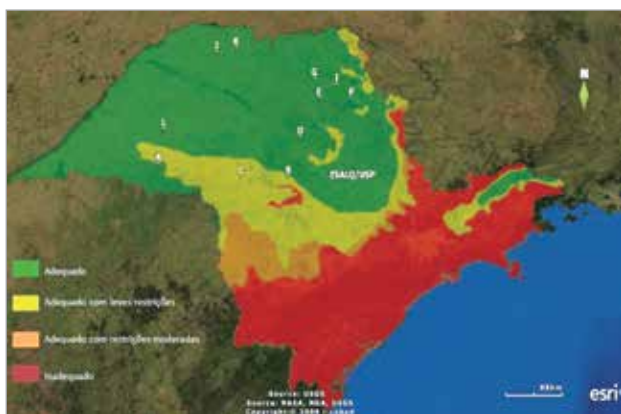


Figure 1. Location of the sugarcane fields (indicated by letters A to K) targeted along the sampling expeditions to compose the soil collection used in the present study

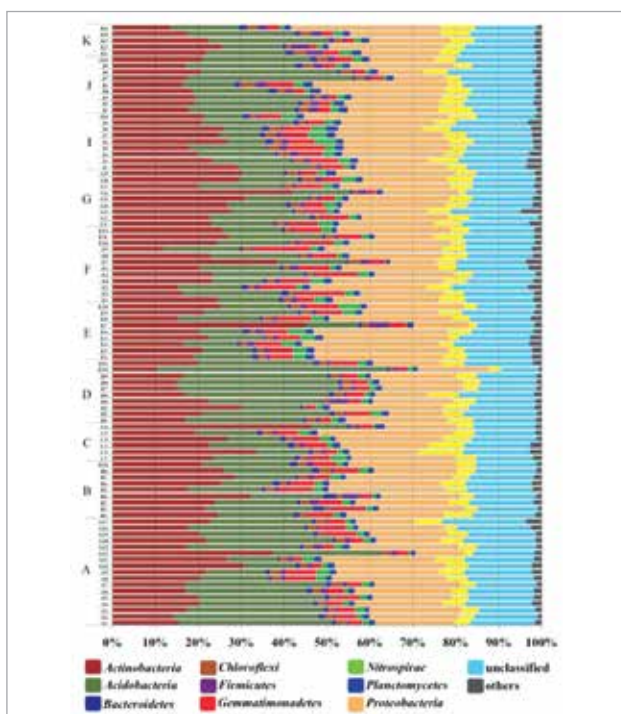


Figure 2. Bacterial diversity observed in 95 samples, by the analysis of the V6 region of the 16S rRNA gene (4,500 sequences per sample). Analyses were performed by affiliation of sequences into bacterial phyla

The sugarcane is the most important agricultural issue in the State of Sao Paulo, where the agro-climatic map describe the existence of two regions with distinct environmental conditions, where this crop can be cultivated, besides a new area, recently occupied by these plantations. However, with the expansion of the agriculture frontiers, a higher productivity and sustainability in the sugarcane production is highly desirable. In this context, among other factors, the role of the microbial community in the sugarcane field soils might be important, helping on the improvement of plant development, supplying it with nutrients or inhibiting the occurrence of diseases and pests. However, little is known about the microbial community residing in soils where sugarcane is cultivated. Then, this project has the aim to describe, in a biogeographic approach, the microbial diversity existing in soils used for sugarcane plantations in the State of Sao Paulo, encompassing the groups of archaea, bacteria and fungi. It is proposed to quantify these communities by quantitative real time PCR (qPCR), to analyze the structure of such communities by terminal restriction fragment length polymorphism (T-RFLP), and to determine the phylogeny of such organisms by pyrosequencing of phylogenetic genes found in targeted organisms. In this purpose, two types of samplings will be carried out aiming: i) to compare the variation on the microbial communities in macro-scale, among different areas describe in the agricultural map; ii) to obtain patterns in micro-scale of these communities, within each area demarked by the sugarcane cultivation map. At last, the microbiological data will be correlated with physico-chemical characteristics of the soils, resulting in a biogeographic approach of the analyzed soils, generating a microbiological map of the soils cultivated with sugarcane in the State of São Paulo.

## SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

Our data revealed a large variability in soils characteristics. For instance, soil pH varied from 3.7 and 6.6, organic matter contents varied from 4.0 and 37.0 g.dm<sup>-3</sup>, as well the proportion of sand, clay and silt in the soil mineralogy.

The taxonomical affiliation of bacterial 16S rRNA sequences was performed in 95 samples by high-throughput sequencing using the Ion Torrent platform. After trimming and rarefaction, 427,500 high quality sequences (4,500 sequences per sample). An average value of 15.3% of sequences from each sample could not be classified deeper than Bacteria, while others were majorly affiliated with the phyla Proteobacteria (23.1%), Acidobacteria (21.9%), Actinobacteria (19.6%) and Verrucomicrobia (5.1%).

Environmental characteristics (soil properties followed by agricultural practices) are prevalent over the geographical distance on the structuring of bacterial communities. The most explanatory variables within this group of variables were pH and soil granulometry. Among the evaluated management practices, the addition of vinasse, charcoal, filter cake, and the implementation of mechanical harvesting were found to have a determinant role on bacterial assemblages.

The T-RFLP-based profiling of fungal communities detected a total of 742 TRFs. Partial clustering of samples from the same production unit was observed, and the samples from distant locations were mostly segregated. Geographic distance and environmental distance interacted to explain 1.4%, indicating that environmental distance has only a weak correlation with geographic distance (*Figure S2*). Among the measured environmental variables, pH and clay content were the most significant. At larger spatial scales, geographic distance is likely to explain increasingly more of the variance in community composition, possibly due to dispersal limitation. We found a significant correlation between the fungal community similarity and geographic distance ( $\alpha = -3.3687$ ,  $p < 0.001$ ). Thus, the community structure showed a higher relatedness with the geographical distance than the environmental variables.

In combination, these results show that soil microbiomes might be managed, in order to generate better assemblages to improve plant growth and yields, what could lead to a better exploration of microbiomes for agricultural purposes.

## MAIN PUBLICATIONS

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- Gumiere T, Durrer A, Andrade PAM, Costa DP, Ferreira DA, Lima JE, Andreote FD. 2014. Microbial diversity in soils of sugarcane fields: a biogeographic approach. In: 15<sup>th</sup> International Symposium on Microbial Ecology, 2014, Seoul ISME15.

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