FUNCTIONAL BIO-INDICATORS FOR SOIL QUALITY MONITORING FOR SUSTAINABLE MANAGEMENT OF SUGARCANE BIOMASS PRODUCTION (BIOSQ)

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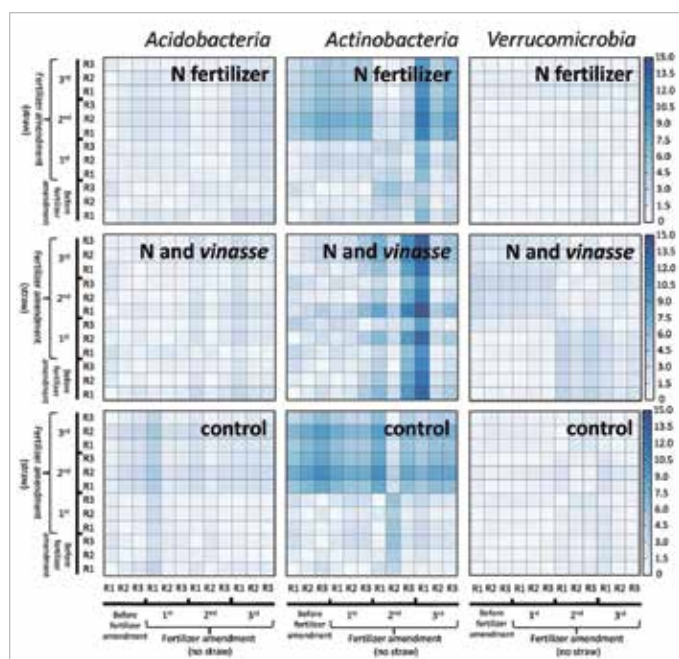FAPESP Process 2011/51749-6 | Term: Jul 2012 to Jun 2014

Figure 1. Taxonomical heatmap based on group-specific bacterial communities in sugarcane cultivated-soils. The actinobacterial community revealed a greater response to straw blankets compared with the response of acidobacterial and verrucomicrobial communities

Here, we propose to find bio-indicators that are responsive to sugarcane production under different sustainable management regimes (no-tillage, cover trash and diazotroph bacteria inoculation) as well as conventional managements. The aim is the identification of numerous taxa and genes that hold potential for use as bio-indicators of specific attributes of soil status, such as nutrient availability, level of disturbance and soil fertility, and provide proof-of-principle platform for soil quality assessment.

In order to achieve this aim, we propose to (1) determine the genes in key functions (nitrification, nitrogen fixation, denitrification, methane oxidation) most indicative of specific soil status; (2) determine functional bio-indicators involved in the emission/sequestration of greenhouse gasses (CO$_2$, CH$_4$ and N$_2$O); (3) develop high throughput platform (BIOSQ) to assess and monitor bio-indicators; (4) apply bioinformatics tools and appropriate basic and multivariate statistical analyses in order to integrate 'omics' data and soil physicochemical data for monitoring microbes and gene function under sugarcane biomass production; (5) test and validate the platform BIOSQ in different sites with sugarcane in São Paulo State.

SUMMARY OF RESULTS TO DATE AND PERSPECTIVES

The activities of the project have involved greenhouse and field experiments. A greenhouse mesocosm experiment monitored for gas emissions and chemical factors focused on the effects of organic and inorganic amendments and straw retention on the microbial biomass (MB) and taxonomic groups of bacteria in sugarcane-cultivated soils. Taken together, the results showed that MB carbon and MB nitrogen responded to changes in soil chemical factors and CO_2-C and N_2O-N emissions, especially for nitrogen (N) + vinasse (V)-amended soils. The results also indicated that several taxonomic groups of bacteria, such as *Acidobacteria*, *Actinobacteria* and *Verrucomicrobia*, and their subgroups acted as early-warning indicators of N+V amendments and straw retention in sugarcane-cultivated soils, which can alter the soil chemical factors.

In another study, disparate patterns were revealed for verrucomicrobial community in sugarcane rhizosphere sampled on optimal and deficient soil fertility for sugarcane. Verrucomicrobial community abundance in sugarcane rhizosphere was negatively correlated with soil fertility, accounting for 2 and 5 % of the total bacterial signal, under optimal and deficient soil fertility conditions for sugarcane, respectively. In nutrient-enriched soils, verrucomicrobial community structures were related to soil factors linked to soil fertility, such as total nitrogen, phosphorus, potassium and sum of bases, i.e., the sum of calcium, magnesium and potassium contents. This case study showed that community structure and abundance represent important ecological aspects in soil verrucomicrobial communities for tracking the changes in chemical factors linked to soil fertility under tropical environmental conditions, including management practices for sugarcane.

An ongoing study has applied GeoChip 5.0, a functional gene-array-based high-throughput environmental technology for microbial community analysis, in order to identify genes that hold potential for use as bioindicators of disturbance in sugarcane soils under zinc applications in sandy-textured soil with natural low fertility. Preliminary results have revealed that zinc applications at the doses of 10 and 20 kg ha^{-1} negatively affected the abundance of functional microbial genes associated to virulence. The abundance of specific genes associated to carbon, nitrogen, phosphorus cycling, zinc homeostasis, secondary metabolism and stress was also affected by zinc applications at the same doses (10 and 20 kg ha^{-1}) in comparison to 0 and 5 kg ha^{-1}.

MAIN PUBLICATIONS

Navarrete AA, Diniz TR, Braga LPP, Silva GGZ, Franchini JC, Rossetto R, Edwards, RA, Tsai SM. 2015. Multi-analytical approach reveals potential microbial indicators in soil for sugarcane model systems. *PloS ONE*. **10(6)**:e0129765.

Navarrete AA, Soares T, Rossetto R, van Veen JA, Tsai SM, Kuramae EE. 2015. Verrucomicrobial community structure and abundance as indicators for changes in chemical factors linked to soil fertility. *Antonie van Leeuwenhoek*. **108(3)**: 741-52.
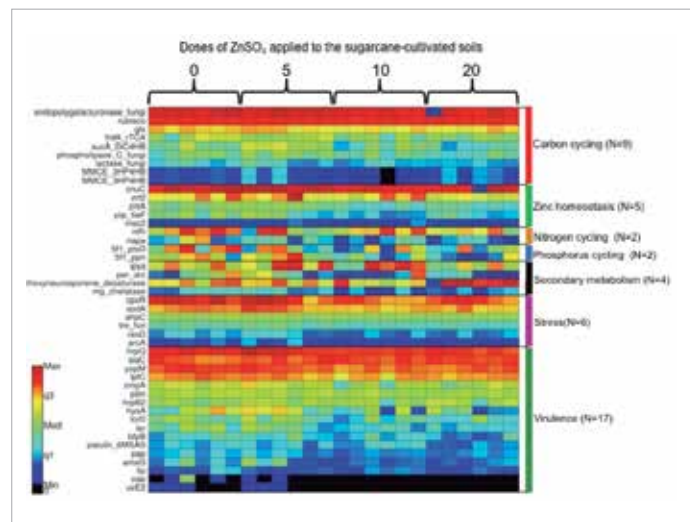
Figure 2. Functional heatmap based on GeoChip 5.0 data. Microbial functional genes associated to virulence decrease in abundance after applications of 10 and 20 kg ha-1 of ZnSO$_4$ to sugarcane-cultivated soils

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