

**TITLE:** MICROBIAL COMMUNITIES OF SOILS CROPPED WITH MAIZE UNDER DIFFERENT MANAGERMENTS: POTENTIAL BIOINDICATORS OF SOIL QUALITY

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## **ABSTRACT**

Improving soil quality is essential to achieve more sustainable agricultural systems. Conservation managements including no tillage, crop rotation and co-cultivation are promising strategies to this goal. The aim of this study is to investigate the soil microbiome of maize fields cropped with different management systems in order to identify microbial taxa correlated with higher levels of soil quality. We used an 8-year experiment located in N.S. Dores, Sergipe, containing five treatments randomly distributed in four blocks: conventional tillage of maize monoculture (CTM), no tillage of maize monoculture (NTM), no tillage of maize with annual rotation of soybean (NMT/S), no tillage of maize co-cultivated with *Brachiaria ruziziensis* and with annual rotation of soybean (NTMB/S), and fallow (F), where native vegetation grows since the beginning of the experiment. Composite soil samples were collected and submitted to physical, chemical, microbiological and molecular analyses, including mean weight diameter (MWD), water stability of soil aggregates (WSA), soil pH, soil organic matter (SOM), soil microbial respiration and microbial biomass-C (MB-C). Soil samples were also immediately stored at -80°C for DNA extraction. Partial results indicated that MWD, WSA and SOM increased in NTMB/S compared to the other agricultural managements, showing a positive effect in soil quality. Soils under F showed a lower MWD, but a higher WSA than agricultural soils. NTM/S showed the lowest values of SOM and WSA, suggesting that maize has a higher contribution than soybean for soil quality improvement. However, soil MB-C was higher in NTM/S than in the other agricultural managements, and comparable to F. Soil microbial respiration and qCO<sub>2</sub> showed lower values in NTMB/S, indicating a decreased loss of C in this treatment. Multivariate analyses showed that environmental variables (MWD, WSA and SOM) are positively correlated with NTMB/S and NTM/S, and negatively correlated with NTM/S and CTM. On the other hand, soil microbial respiration and qCO<sub>2</sub> are negatively correlated with SOM, which increases in NTMB/S samples. The next step is to submit the 16S rDNA amplicons of soil samples for next-generation sequencing using the Illumina MiSeq platform to assess changes in bacterial community structure between treatments and identify specific microbial taxa correlated with higher physico-chemical soil quality.

**Key-words:** soil microbiome; soil aggregation; microbial ecology; high-throughput sequencing

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