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Integrated crop-livestock-forest system presents a different soil microbial structure in comparison to other land uses

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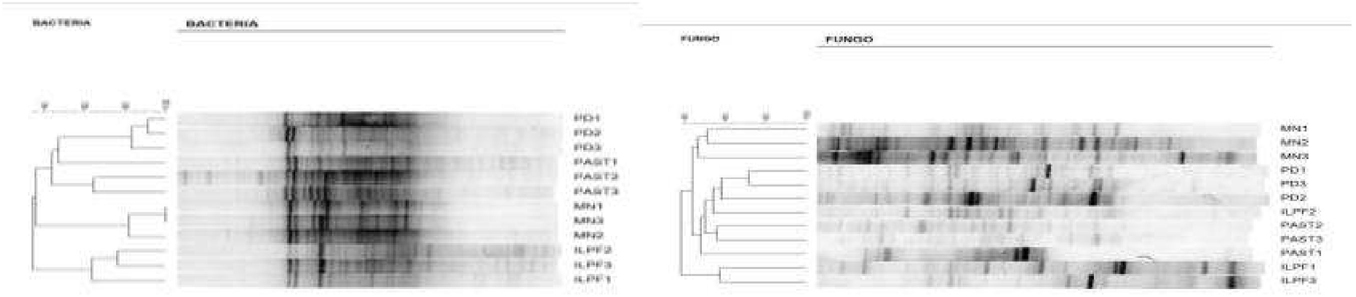
Introduction Soil organic matter (SOM) conservation is essential for environmental services maintenance, especially in tropical agroecosytems where this component is essential for soil fertility, structure and biological activity. Soil microorganisms are the main driver of nutrient cycling, since key processes, such as C and N mineralization, N immobilization, xenobiotics decomposition, denitrification and others are mediated by them. However when the agroecosystems are manipulated, these active components of soils are impacted, changing the carbon and nutrient dynamics. Therefore, the monitoring of the microbial communities is a good tool to indicate changes in soil dynamics. Our objective was to characterize the soil microbial communities under different land uses by using denaturing gradient gel electrophoresis.

Material and Methods

The study was carried out in the Municipality of São Raimundo das Mangabeiras (Cerrado Biome), Maranhão State. Treatments included (i) pasture of *Brachiaria brizantha* in monoculture, (ii) no-till cropping system (soybean-maize), both installed in 2005, (iii) integrated crop-livestok-forest system (*B. brizantha*, eucalyptus and soybean-maize) and a (iv) native vegetation. Soil samples were taken at 10 cm of depth for molecular analysis in 2013.

Results and Conclusions

Figure 1 shows the dendrograms of soil bacteria and fungi communities from different land uses (PD: no-till, PAST: pasture, ILPF: integrated crop-livestok-forest and MN: native vegetation).



The DGGE patterns clustered both bacterial and fungal community into three different groups: i. No-till and pasture, ii. Native and iii. integrated crop-livestok-forest (with exception of one sample of integrated crop-livestok-forest in fungal screening). Pastures and no-till system sampled tend to present similarity on their communities structures probably due the incorporation of grazing areas into the areas of PD. The distinct pattern present in the integrated crop-livestok-forest samples suggests that arboreal component plays an important role in structuring the microbial community. Additional studies should be done to confirm this hypothesis.

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