Title: SOIL MICROBIOME FROM DIFFERENT LEVELS OF CONSERVATIVE AGRICULTURAL SYSTEMS

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Abstract

Land use changes associated with agriculture, as well as adopted farming practices, may promote severe alterations on physicochemical properties of the soil. In this way, they can alter the structures of soil microbial communities as the process for them performed. The adoption of conservationist soil management has been used to minimize the environmental impacts of agriculture, to preserve physical, chemical and biological characteristics, extending the resilience and raising the productivity. The purpose of this study is to assess soil communities structure and abundance of methanogens and methanotrophs – responsible for emission and consumption of CH_4, respectively – in different agricultural conservative tillage systems and reforestation area at Querencia-MT. For this study, soils were collected from 4 areas – crop-livestock integration (CLI), soybean-millet rotation system (SMR), reforesting (RF) and forest area (F) – with 5 samples each (composed by 5 subsamples). The microbial structure was evaluated by TRFLP (Terminal restriction fragment length polymorphism) and metagenomic analyses, while the abundance was verified by qPCR (quantitative PCR) of *Archaea*, *Bacteria*, methanogens (*mcrA*) and methanotrophs (*pmoA*). The TRFLP assessment report that the CLI has more stability than the SMR, due to the pasture root system that promotes higher protection to soil. Moreover, RF retains highest similarities with CLI at 85%; and 65% to forest area, which differed from other areas with rare OTUs (Operational taxonomic units). Furthermore, farming areas present strong influence of liming, which raises pH and concomitantly increase Ca and Mg contents. By metagenomic approach, Proteobacteria and Actinobacteria represent more than 50% of the communities in all areas with emphasis on Alphaproteobacteria and Gammaproteobacteria at forest in comparison with other areas and the reverse to Deltaproteobacteria. Furthermore, the methanotrophic community did not vary conforming to the methanogenic community in qPCR analyses.

Keywords: conservationist management, methane cycle, sequencing, qPCR, TRFLP

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