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Bacterial diversity in Biochar and Amazonian Dark Earth soil by pyrosequencing and T-RFLP

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Introduction

Soils called Amazonian Dark Earth (ADE) exhibit approximately three times more organic matter, nitrogen and phosphorus and 70 times more Biochar (BC) content when compared to their adjacent infertile soils (ADJ), without past history of anthropogenic activities by the Amazonian pre-Colombian native. The aim of this work was to study the structure and diversity of the bacterial communities in ADE, BC and ADJ using the T-RFLP (Terminal Restriction Length Polymorphism) and pyrosequencing technique. The soils were collected in the archaeological site Hatahara located in the Central Amazon, in the city of Iranduba-AM.

Results and Discussions

Bacterial fingerprints of the most dominant populations present in ADE and ADJ soil and BC were obtained by T-RFLP analysis. The principal component analysis (PCA) based on T-RFs of Bacterial communities indicated that the community structures were distinctly separated along the first and second axes from the graphic (Figure 1).

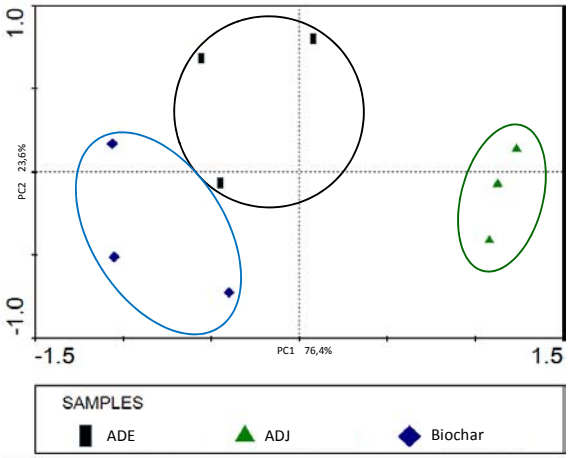

Figure 1. Principal components analysis (PCA) of bacterial communities using the software CANOCO v4.5.

Therefore, the T-RFLP technique in combination with the PCA ordination analysis is an important tool to reveal changes in the composition of microbial communities, and can contribute to further phylogenetic studies for the characterization of the soil microbial community structures. We observed higher richness on ADE soil (100) followed by Bichar (56.3) and the lower diversity was noted on ADJ (42.6). The pyrosequencing data indicate that the BC can host species of *Bacteria* in numbers not much lower than the ADE. Richness of bacterial Operational Taxonomic Units (OTU) was higher in ADE (1425) followed by lower richness in BC (1368) and ADJ (933). The most abundant bacterial phyla in ADE, ADJ soils and BC were *Proteobacteria* 49% ADE, 61% ADJ and 54% BC; *Acidobacteria* 32% ADE, 17% ADJ and 15% BC; *Actinobacteria* 5% ADE, 6% ADJ and 18% BC. The pyrosequencing data indicate that the BC can host species of *Bacteria* in numbers not much lower than the ADE; however, the latter had significantly greater OTU richness (Figure 2).

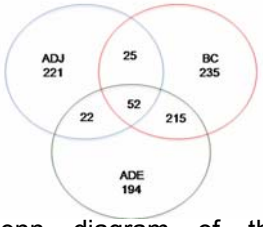

Figure 2. Venn diagram of the operational taxonomic units (OTUs) based on the sequencing by pyrosequencing.

Conclusions

Differences were noted in the bacterial community composition in ADE, ADJ soil and BC, and a higher bacterial diversity present in anthrosols was revealed by T-RFLP and pyrosequencing technique. The high fertility in the ADE associated with a higher soil bacterial diversity, even when under intensive cultivation by the native population.

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