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A survey of the microbial communities from Amazonian anthrosols and their black carbon for sustainable agriculture and biotechnology

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Abstract

The processes of land conversion and agricultural intensification are a significant cause of biodiversity loss, with consequent negative effects both on the environment and the sustainability of food production. The anthrosols associated with pre-Colombian settlements in the Amazonian region are examples of how anthropogenic activities may sustain the native populations against harsh tropical environments for human establishment, even without a previous intentionality of anthropic soil formation. In a case study (Model I – Slash-and-Burn) the community structures detected by automated ribosomal intergenic spacer analysis (ARISA) revealed that soil archaeal, bacterial and fungal communities are heterogeneous and each capable of responding differently to environmental characteristics. ARISA data evidenced considerable difference in structure existed between microbial communities in forest and agricultural soils. Richness of archaeal operational taxonomic unit (OTU) was higher in primary forest soil (51.08) followed by lower OTU richness in pasture soil (42.33), secondary forest soil (42.16) and crops (40.25), consecutively. For soil bacterial communities the OTU richness in primary forest (23.08) was found similar to that of secondary forest (25.83). In this study, the fungal OTU richness was higher in primary forest soil (123.5) followed by lower OTU richness in secondary forest soil (73.92), pasture (71.0) and crops (58.0), respectively. In a second approach (Model II – Bacterial Diversity in Anthropogenic Soil), the bacterial community structures revealed by terminal restriction fragment length polymorphism (T-RFLP) differed among an Amazonian Dark Earth (ADE), black carbon (BC) and its adjacent non-anthropogenic oxisoil. The bacterial 16S rRNA gene (OTU) richness estimated by pyrosequencing was higher in ADE than BC.

The most abundant abundant bacterial phyla in ADE soils and BC were respectively, Proteobacteria – 24% ADE, 15% BC; Acidobacteria – 10% ADE, 21% BC; Actinobacteria – 7% ADE, 12% BC; Verrucomicrobia, 8% ADE; 9% BC; Firmicutes – 3% ADE, 8% BC. Overall, unclassified bacteria corresponded to 36% ADE, and 26% BC. Finally, in a third study (Model III – Functional Diversity in Anthropogenic Soil), bacterial aromatic hydrocarbons degraders communities from ADE and BC were examined by targeting the α-ARHD gene, with codes for alpha subunit of dioxygenases. Based on 123 ADE and 156 BC bacterial α-ARHD sequences, the richness estimates by Jackknife (34; 40), Chao1 (30.5; 36) and ACE (31.6; 38.4). The rarefaction curve approaches to a maximum for both libraries. Heterogeneity measures values were calculated using Shannon-Wiener Function and Simpson index (2.87; 3.05 and 0.07; 0.05, respectively). The richness estimates and heterogeneity measures indicated greater diversity in the BC library. Venn diagram showed twenty-four unique OTUs from BC, suggesting that specific microbial processes may be occurring in this environment. Considering the microbial complexity in highly fertile soils (ADE), we employed high throughput sequencing (pyrosequencing) to assess functional bacterial diversity. Regardless of current land uses, our data suggest that soil microbial community structures may be strongly influenced by the historical soil management and that anthrosols in Amazonia, of anthropogenic origins, in addition to their capacity of enhancing crop yields, may also improve microbial diversity, with the support of the black carbon, which may sustain a particular and unique habitat for the microbes.

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