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1159-1 IMPACTS OF SUCCESSIVE CULTIVATIONS IN MICROBIAL DIVERSITY OF AMAZONIAN DARK EARTHS

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Resumo:

Amazonian Dark Earths (ADEs) are small regions of high-fertility soil formations associated with human activities near Amazonian rivers, in contrast to the low-fertility soils prevalent in the Amazon region. This study aimed to investigate the microbial composition of ADEs in a secondary forest and an area cultivated for 40 years with Cassava, to understand how land use influences ADE microbial communities. Soil samples were collected from Caldeirão Experimental Research in Iranduba-AM, comprising six points (3 for Cassava crop in ADE and 3 for an adjacent Forest ADE) at two depths (10 and 20cm), with 3 subpoints each, totalizing 36 samples were analyzed. Chemical analysis was performed at EMBRAPA Amazônia Ocidental, while molecular analysis was conducted at the Laboratory of Cell and Molecular Biology from CENA/USP. DNA was extracted and metagenomes were sequenced using the shotgun technique on the Illumina NovaSeq 6000. The sequencing data were filtered, and genera were assigned using the software Kaiju in KBase. Frequency tables and chemical data were analyzed in R, considering non-normality. Kruskal-Wallis post hoc Dunn test was applied for differences. Alpha and beta diversity, network analysis, and ALDEx2 analysis were performed for metagenomic data. Results revealed that Cassava crop areas had lower nutrient levels ($p<0.05$ for P, Ca, and Na) than the Forest ADE, likely due to crop nutrient requirements and reduced organic matter cycling outside the forest. Cassava at 10 cm depth exhibited higher microbial diversity ($p<0.05$), potentially influenced by disturbances during crop harvesting and increased light exposure. Beta diversity analysis indicated distinct microbial community compositions between the two land uses ($R^2 = 0.42$, $p = 0.001$), independent of depth. Differential abundance analysis revealed higher quantities of *Rhodoplanes* and *Luteolibacter* in the Forest ADE, while *Sphingomonas*, *Mycobacterium*, and *Ktedonosporobacter* were more abundant in Cassava. Network analysis suggested that Cassava communities were more complex than Forests at 10 cm depth, but this relationship was reversed at 20 cm depth. These findings suggest that Cassava cultivation fosters a greater diversity of organisms associated with crops. At the same time, the Forest ADE exhibits a more stable microbial composition, particularly in deeper layers, with an abundance of bacteria involved in nitrogen cycling.

Palavras-chave:

Bacterial DNA, Bioinformatics, Culture-Independent Methods, Microbial Ecology, Soil Science