

Title: ANALYSIS OF BACTERIAL DIVERSITY IN SOIL FROM DOURADOS-MS USING NEW GENERATION SEQUENCER.

Authors Rissi, D.V., Valensuela, S.S., da Silva, R.C., Júnior, R.B., Pereira, R.M.,

Institution UFGD - Federal University of Grande Dourados (Highway Dourados - Itahum, Km 12 - University Campus)

Summary:

The soil metagenomics is one of the main ways for detection, classification and identification of genes from organisms that are not cultivated in the laboratory. The objective of this study was to analyze the bacterial community in two soils: one under No-till and other under native forest. Soil samples were collected in Embrapa Agropecuaria Oeste in the city of Dourados-MS in a remnant of native forest and a no-till soil. The sequencer used was Hiseq of Illumina, which were sequenced samples of total DNA of soil (shotgun). The assembly of sequences was performed by IDBA-UD tool. The ORF's were identified using the FragGeneScan tool and the taxonomic classification realized through the web tool MG-RAST. Statistical analyzes were performed using the STAMP tool where was held the G and Fisher tests with 95% of confiability. On the soil of natural forest, the percentage of bacteria present was 94.5% - (53.65% Proteobacter, Actinobacter 18.11%, 6.15% Firmicutes, Acidobacter 5.65%), 4.1% Archeas, Eukaryotic 1%. In no-till soil, 97.7% were bacteria (52.53% Actinobacter, 36.41% Proteobacteria, 3.29% Firmicutes and Chloroflexi 1.92%), and Archeas 1.5% and Eukaryotic 0.6% . Among the bacteria, we found a large presence of Actinobacter in no-till soils. In the literature, the Actinobacter are closely related to the region of the rhizosphere of plants. In the soil of native forest, is most abundant the Proteobacter, which have a big contribution in the nitrogen, carbon and sulfur cycle in the soil. Next, were found, the Actinobacter, Firmicutes and Acidobacter. The Acidobacter usually occur in larger quantities in forest soils, and are hardly cultivable in laboratory however, those witch are knwon, have an important role in the carbon cycle. The collected soils from general, had the same groups of most common bacteria and the differences of abundance and dominance of each phylum are relatively linked to the type of the analyzed soil cover.

Keywords: Metagenomics, Native Forest, no-till

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