TITLE: MICROBIOME OF CAVES FROM SERRA DOS CARAJÁS – PA, BRAZIL

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ABSTRACT: Ferruginous caves are poorly explored environments in terms of biodiversity and community composition. Lack of photosynthesis and limited nutrient source makes the caves an extreme environment forcing the inhabitants to undertake diverse. The aim of this study was to characterize the community composition and functional profiles of microorganisms inhabiting ferruginous Caves at Serra dos Carajás - PA. Eleven soil samples were collected in three different cave areas: photic zone (FZ), semi-photic zone (SZ) and aphotic zone (AZ). Total DNA was extracted using PowerSoil DNA isolation kit (MoBio) and the Shotgun sequencing was performed by illumina MiSeq plataform. DNA sequences were analyzed and annotated using the EBI metagenomics pipeline (v.3). Additionally, taxonomic classification was improved using Kaiju, being more suitable for handling shotgun sequencing data. Analyses were performed using hit frequency to each individual taxa or subsystem normalized by dividing the total number of hits in order to remove bias of sequencing efforts. Taxonomic analysis revealed Proteobacteria as the most abundant bacteria phylum within samples. Bacteroidetes was the group presenting higher variance across samples, being more abundant in the FZ. Thaumarchaeota archeae phylum was the most abundant and Crenarchaeota the most variable among the zones, showing higher abundance in the AZ. Taxonomic composition showed to be significantly different for bacteria and archaea where the latter are more abundant in AZ. The most abundant taxonomic groups corroborate with previous studies of cave microbiomes. Several functional profiles were induced from Gene Ontology and InterPro. Multivariate analysis by PCA (2PCs ~ 70% total variance) was not able to separate all zones by functional profiles, only by the taxonomic profile. This may be due to the fact the more enriched functions are tightly linked to core functions, spreading evenly along zones. PCA over cellular component (GO) annotation was significantly enriched within the FZ. PCA over InterPro annotation was able to distinguish FZ sample over the other zones. Correlation analysis by the combination of both taxonomic and functional profiles (Person's Corr. > 80%) highlighted few taxonomic groups that might be acting as key clusters linked to the more enriched functions. Although the cave microbiomes were generally quite similar in, FZ samples were significantly different from AZ and SZ.

Keywords: Cave, Soil, Microbiome