

## Study of microbial community from a mining environment

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### Abstract:

Mining industry has a broad importance in Brazilian economy. A critical issue in mining environments is the generation of acid mine drainage (AMD) that pollutes water and sediments with acids and metals. An alternative to conventional mining is biomining that use microbes to recover metals from minerals. In Brazil there are few studies focusing in mining environments. In this context, our aim is to assess the taxonomic diversity of microbial community in a mine area in Pará state. We collected AMD water; sediment and water from the surface and 15m depth of a tailings dam. The prokaryotic biomass from water samples was concentrated on filters with 0.22µm pores. Metagenomic DNA was isolated and the V3-V4 region of the 16S rDNA was amplified. Amplicon libraries were sequenced on Illumina Miseq. The sequences obtained were clustered into OTUs and taxonomic affiliated using the Brazilian Microbiome Project (BMP) pipeline. The rarefaction curves showed that the sampling and sequencing were significant to represent the main taxonomic groups of the environment. The PCoA of all the samples indicate a difference into microbial community of specific sites on the mining environment, since there were the formation of three distinct groups represented by sediment, water and AMD samples. Regarding the water samples, the PCoA also indicated that the seasonality might be modulating differences in the microbial community composition. The dominant phyla on water metagenomes were Actinobacteria followed by Betaproteobacteria and Bacteroidetes. The community from sediment showed difference in the proportion of each represented groups. In October the prevalent phyla were Firmicutes, Bacteroidetes, Betaproteobacteria and Delta/Epsilonproteobacteria. In April the groups Verrucomicrobia, Gammaproteobacteria, Betaproteobacteria, Acidobacteria and Planctomycetes were the most represented with similar proportion. The microbial community of AMD had a high representation of the domain *Archaea*. This fact may be explained by the extremely conditions of AMD (low pH, high concentration of sulfate and metals). Other observed phylum in AMD were Nitrospirae that were composed by genera that had important role in the biogeochemical cycle, as *Nitrospira* and *Leptospirillum*. Our data showed preliminaries results from the taxonomic profile of the microbial community from mining environment, however we also expect to analyze the functional potential of this community with shotgun sequencing.

**Palavras-chaves:** Mining environment, Biomining, Metagenomics

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