

# Taxonomic and functional investigation of a microbial community inhabiting a metal-rich tropical stream sediment

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The Iron Quadrangle (Minas Gerais, Brazil) is one of the world's largest mining regions, being historically exploited for over 300 years. Since then, many toxic metals and metalloids were released into the environment, leading to contamination of water bodies (Reis et al. 2013). Prokaryote species exhibit broad distribution, having been researched across a wide range of natural environments such as soil, marine, freshwater, plant, and animal, including human. Many have revealed to be important members for the health and/or ecological balance of various environments (Kasting and Siefert 2002).

Prokaryotic community was investigated since it influences the bioavailability of toxic metals and metalloids and is important in the ecological balance of various environments (Earth Microbiome Project). The study focused on the taxonomic and functional diversity in the microbiome from Mina Stream, historically metal-contaminated.

The sediment was collected from the Mina Stream located in the Iron Quadrangle (Brazil). Environmental DNA was extracted and was sequenced using next-generation platform. The data generated were submitted to bioinformatics analysis (Costa et al. 2015).

MSS microbiome resulted in 273,710 high quality reads with the average read length of 450

bp. Bacteria were by far the most abundant prokaryotic domain comprising 98.2% (30,738 OTUs), whereas archaeal reads showed a relative paucity (1.8%, 240 OTUs). Bacterial and archaeal phyla diversity are shown in Figure 1. A taxonomic profile that was obtained by comparison to the Greengenes database revealed a complex microbial community. A total of 30,738 OTUs were assigned to 52 known bacterial phyla. Nevertheless, most OTUs were affiliated with four phyla: Proteobacteria (45%), Bacteroidetes (18%) and an equal proportion (4%) of Acidobacteria and OD1. The group "other bacteria" comprised minor bacterial phyla such as Gemmatimonadetes, Cyanobacteria, OP3, OP11, Spirochaetes, TM7 among others, representing 8% of the OTUs. Furthermore, 2,157 OTUs were considered to be unclassified at the phylum level and thus may represent new bacterial taxa. Contigs were recruited by bacterial and archaeal genomes, especially *Candidatus Nitrospira defluvi* and *Nitrosopumilus maritimus*, and their presence suggests the process of N cycling in the Mina Stream sediment (MSS) (Costa et al. 2015).

The top species from CSS as well as the highest coverage of a reference genome were observed for neutrophilic iron-oxidizing bacteria, likely reflecting the elevated concentrations of iron (Fe) (21 g/Kg). A comparison between the

CSS and MSS microbiota revealed an overrepresentation of some genera, such as *Geobacter*, *Gallionella*, *Crenothrix* and *Mariprofundus* (Reis et al. data not published).

Twenty-eight functional subsystems characterized by biochemical pathways and gene clusters that work together or that are somehow related were identified in the MSS metagenome. Protein metabolism, clustering-based subsystems, miscellaneous, carbohydrates, and RNA metabolism presented the largest number of annotated contigs. Other subsystems were related to mobile elements (phages, transposons, integrons, plasmids, and pathogenicity islands, 4%) and stress response (3%), both responsible for the fast response and adaptation of the microbial community to changes in the environment. Functional reconstruction revealed a large, diverse set of genes for ammonium assimilation and

ammonification. These processes have been implicated in the maintenance of the N cycle and the health of the sediment. SEED subsystems functional annotation unveiled a high degree of diversity of metal resistance genes, suggesting that the prokaryotic community is adapted to metal contamination (Costa et al. 2015).

This study provides important insights into the structure of the prokaryotic community of a tropical freshwater sediment, indicating its possible role in the N and C cycles and in the transformation of Fe and As. Functional annotation unveiled a high diversity of several metal resistance genes, indicating that this microbial community is well adapted to metal contamination. Finally, the results reported herein may contribute to expand the current knowledge of the microbial taxonomic and functional composition of tropical metal-contaminated freshwater sediments.

## References

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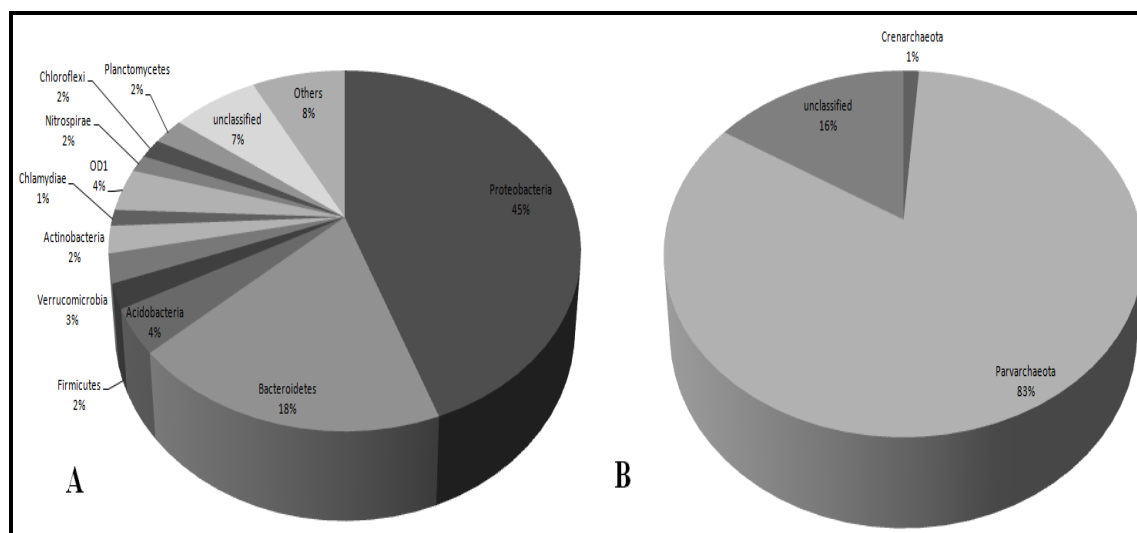


Figure 1 - Taxonomic composition of bacterial (A) and archaeal (B) taxa from MSS microbiome based on the Greengenes database. Other bacteria: Gemmatimonadetes, Cyanobacteria, OP3, OP11, Spirochaetes, TM7, Chlorobi, WS3, Elusimicrobia, GN04, TM6, GN02, Tenericutes, Armatimonadetes, BRC1, NC10, WPS-2, Fibrobacteres, Fusobacteria, H-178, FCPU426, Kazan-3B-28, WS5, NKB19, Thermi, AC1, TPD-58, WS6, Synergistetes, OP8, WS2, ZB3, SC4, OP1, SBR1093, SR1, Lentisphaerae, GAL15, PAUC34f, LCP-89 and MVS-104. (Reproduced from Costa et al. 2015)