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METAGENOMIC APPLIED TO MICROBIAL DIVERSITY STUDY IN A ZONE AFFECTED BY AN ACID MINE DRAINAGE: RELATION BETWEEN PHYSICOCHEMICAL PARAMETERS AND TAXONOMIC GROUPSJosé O Bonilla^{1,2}, Daniel G Kurth³, Raúl A Gil^{1,2}, Liliana B Villegas^{1,2}¹INQUISAL-CONICET. San Luis, Argentina.. ²Facultad de Química, Bioquímica y Farmacia, Universidad Nacional de San Luis. San Luis, Argentina. ³PROIMI-CONICET. Tucumán, Argentina.

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The most documented pollution associated with abandoned mining areas is the acidic water produced by the oxidation of sulfides ores exposed to surface. This acidic water is known as Acid Mine Drainage (AMD) and enhances the mobility of heavy metals from soil and sediments, what poses a threat to the environment. Likewise, AMD affected environments are low-complexity natural systems regarding to biodiversity. In San Luis-Argentina, the drainage that originates in a gold mine abandoned since 1894 is released to La Carolina stream and possesses AMD characteristics. In previous works, we reported the influence of the mine drainage on physicochemical parameters of La Carolina stream sediments. The aim of this study is to determinate the influence of these mine drainage on microbial diversity and to stablish specific relations between microbial taxonomic groups and physicochemical parameters of the affected zone. Twelve sediment samples from inside the mine (7) and from La Carolina stream (5), before and after receiving the mine drainage, were selected to total DNA isolation, which was performed using DNA soil kit, MOBIO. Metagenomic sequencing of PCR amplified products of 16S rRNA and 18S rRNA genes was carried out by MR DNA (www.mrdnalab.com, TX, USA) on MiSeq (Illumina) platform. Microbial diversity results were analyzed trough *Silva* NGS (<https://www.arb-silva.de/ngs>). In order to stablish specific relation between microbial taxonomic groups and physicochemical parameters of the zone, a Canonical Correspondence Analysis (CCA) was performed. CCA showed that prokaryotic diversity is affected majorly by pH values, favoring the presence of phyla *Actinobacteria* and *Gamma-proteobacteria* in samples characterized by low pH values (inside the mine). Phyla *Nitrospirae*, *Chloroflexi*, *Delta-proteobacteria*, *Thaumarchaeota* and *Euryarchaeota* are majorly abundant in samples that presented high concentrations of heavy metals. Likewise, *Alpha-proteobacteria* is abundant in samples that were taken in presence of sunlight (stream samples). Regarding to eukaryotic diversity, the greatest incidence is given by the sunlight presence. All samples taken inside the mine, in the absence of light, showed to fungi and protists members as the most abundant microorganisms. Those samples taken in the presence of light, presented to algae (green algae and diatoms) as the most abundant microorganisms. After receiving the AMD, the stream presents a decrease in diatoms abundance and green algae predominate, probably due to the acidification of the watercourse because of the incidence of the AMD in down-stream samples. It can be clearly observed that the AMD released to La Carolina stream influences on eukaryotic and prokaryotic diversity, favoring the presence of some microorganisms over others, depending of the physicochemical characteristics of the zone. This study shows the incidence of mining activities on natural sources, even long time after their closure.

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