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Metagenomic Analysis of Microbial Diversity in Acid Mine Drainage from the Syunik Region

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ABSTRACT

The oxidation of sulfide minerals under atmospheric conditions often results in the generation of acid mine drainage (AMD), which is characterized by low pH and elevated concentrations of dissolved metals, including heavy metals. In this study, a molecular biology-based approach was applied for the first time to analyze bacterial communities in AMD and tailing samples from the Syunik Region of Armenia. The microbial community analysis revealed that Proteobacteria was the dominant phylum across all three samples, followed by Actinobacteria and Bacteroidetes. The diversity at the genus level was found to correlate with the chemical composition of the samples. Metagenomic profiling identified a variety of metal resistance genes (MRGs), with the most abundant being related to resistance against copper (copA, copC, copF, copG, copR, ruvB), iron (acn), arsenic (arsC, arsT, pstB), silver (silA), and mercury (merA, merR1). A novel iron-oxidizing bacterium, designated Arm-12 (GenBank: PP389931), was isolated from AMD. It showed only 90% similarity to known Leptospirillum species, suggesting it may belong to a new genus. This strain is thermophilic, with optimal growth observed at 45°C and pH 1.8–2.0. Toxicity tests showed that its iron-oxidizing activity was inhibited in the presence of various metals, with the following order of toxicity: Mo > Cr > Co > Ni > Zn > Cu. Kinetic studies demonstrated Arm-12’s high potential for biogenic regeneration of ferric iron (Fe^{3+}), underscoring its applicability in bioleaching processes.

Keywords: acid mine drainage, metagenomic analysis, microbial biodiversity, metal resistance genes, copper recovery

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