

## Microbial diversity of bioleaching in continuous system

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The recovery of metals by applying microorganisms is now an established biotechnological technique. The predominant microorganisms in this process are extremely acidophilic bacteria. Due to the limited conditions of substrates available in bioleaching processes, would be expected that the microbial diversity was extremely poor, however, have reported a considerable number of species of prokaryotes in different processes of bioleaching. These identification has contributed to the consolidation of knowledge about the microbial ecology of these processes. Within this context, this work aimed to determine the microorganisms in the bioreactor of zinc sulfide in continuous system. The bacteria present in the bioreactor were collected by filtration for subsequent extraction of genomic DNA. The identification of microorganisms was performed using PCR and specific primers for conserved ribosomal regions. The amplified products were cloned, transformed and sequenced. The sequences obtained were aligned using ClustalX 2.0. Phylogenetic analysis was conducted by the program Mega 4.1 using the Neighbor Joining distance and bootstrap from 2000 replicates to obtain the consensus tree. The RFLP was used in the analysis of polymorphism of the fragments of rDNA digested with restriction enzymes. The results indicate the predominant presence of *Acidiphilium* sp. and *Acidithiobacillus ferrooxidans* in the bioreactor, suggesting a possible complementary role in the bioleaching of metals. Thus, our results suggest that the identification of diversity prokaryota in the process of bioleaching is an important step towards the understanding of the specific interest in industrial processes.

Keywords: Bioleaching, Acidophilic Bacteria, Molecular Characterization.

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