

Diversity of Biomining Microbes in Iran: A Mini Review



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Abstract

Due to the existence of various and large mines in Iran, the diversity of mining microorganisms is proportionally high. Very limited research has been done to study the biodiversity of biomining microbes, most of which have been limited to copper bioleaching. Large bioleaching projects such as the 50,000-ton copper cathode per year by the Iranian Babak Copper Company (IBCCO), and biomass heap bioleaching of low-grade chalcopyrite ore at the Sarcheshmeh copper complex are striking examples of the use of this large-scale microbial biodiversity in mineral industry. However, further development of such projects depends on extensive research work to identify through hybridization, 16S rRNA gene high-throughput sequencing, and to genetically engineer these microbes. Of course, further development of such designs depends on extensive research work to identify and genetically engineer these wild microbes and induce their mutation.

Keywords: Wild Microbes; Mines; Genetic and Metabolic Engineering; Scale-Up

Introduction

Although the identification of active mineral microorganisms is the first step in recognizing and developing microbial mining processes, the main step may be the genetic engineering of these microorganisms is to increase their efficiency in various processes from bioheap leaching to tank leaching. Despite the major challenges such as metabolic engineering of autotroph mining microbes for this idea remain, the development of genetic engineering in bioleaching will be a major step in the industrial development of biological mining. Although the possibility of genetic and metabolic engineering for heterotrophic microorganisms is well established and easily possible, this process requires further development for autotrophic bioleaching species. Industrial experiences of bioprocessing of recalcitrant chalcopyrite ores at Sarcheshmeh copper complex with genetically modified microorganisms have led to a significant increase of 60% copper recovery during the optimal 6-month operation. The missing link in the biomining chain is the accurate identification of these microorganisms that is currently underway at Sarcheshmeh Copper, Miduk, Sungun, Saghand, GolGohar, etc., Iran. In this short review, a brief reference is made to microbial activities in Iranian mines.

Discussion

Behrad-Vakylabad et al. have mainly dealt with the engineering aspects of the optimized copper bioleaching process in which only active microorganisms are isolated from the mineral environment (Sarcheshmeh copper mine) and used by adapting them to different conditions of smelter dust, concentrate, low-grade copper ore, and even relatively severe chloride conditions (bottom-up method). The microorganisms identified in this series of research works from Sarcheshmeh copper mine are: *Acidithiobacillus Ferrooxidans*_NC_011761, *Leptospirillum Ferrooxidans*_NC_017094, *Sulfolobus Metallicus*-NZBBBY01000167, *Leptospirillum Ferriphilum*NZJPGK01000018, *Acidithiobacillus Caldus*_NZ_LZYE01000319, *Acidithiobacillus Thiooxidans*-NZ-LWRY01000319, *Sulfolobus Thermotolerans*-CP019454, *Sulfolobus Thermotolerans*_CP019454-1, *Sulfolobus Acidophilus*-PXYV01000001[1-5] and *AT. Ferrooxidans* ATCC 23270 [6]. *Acidithiobacillus* sp. MR39 from other sulfur-containing springs. Of course, there is limited research on the metabolic engineering of wild microorganisms *Acidithiobacillus* sp. FJ2 in which they convert to induced mutants by the DES mutation method, which resulted in a significant increase in their oxidative activity for

uranium leaching [7-8]. Molybdenum (MoS₂) concentrate has been successfully biologically leached using two new thermophile species that have been isolated and purified from Sarcheshmeh mine. The culture medium of these microbes is 9K, and their optimum temperature is 70 °C. These highly acid-loving species belong to the family of chemolithotroph archaeobacteria, which have been identified by PCR amplification of the 16S rDNA. These two species *Acidianus ambivalens* and *Sulfolobus solfataricus* (accession numbers: KM555276.1 and KM555275.1, respectively) registered at NCBI, the USA have shown the ability to extract molybdenum and uranium [9]. A new species of *Acidithiobacillus ferrooxidans* has been isolated and identified from Aliabad copper mine, Yazd. This species of *Acidithiobacillus ferrooxidans* DSMZ 583 with an optimal pH of 1.5 and a temperature of 28 °C is a suitable species for acidic extraction of copper from mineral ores under dump leaching conditions [10]. From the same family of microorganisms *Acidithiobacillus* sp. Species *Acidithiobacillus* sp. SM-2, *Acidithiobacillus ferrooxidans* ATCC 23270, *Acidithiobacillus ferrooxidans* ATCC 53993 (accession numbers of deposits KP763724, KP779620 and KP779621, respectively), NCBI, the USA, have been isolated and identified from Ramsar (Iran) sulfur-bearing springs that have the ability to extract uranium with high efficiency [11]. Also, *Acidithiobacillus* sp. MR39 (accession number of KX817172). [12] is reported from sulfur hot spring, Fars, Iran. Salt-loving (halophile) microorganisms have been isolated and identified from Saghand uranium mine in Yazd, Iran. Phylogenetic analyzes have shown the arc species *Natrinema* and *Haloarcula* and the bacterial species *Halomonas*, *Bacillus*, *Staphylococcus* and *Gracilibacillus* with great biodiversity in different regions. Some of the long list of these bacteria microorganisms are: *Bacillus seohaeanensis* BH724(T), *Gracilibacillus saliphilus* YIM 91119(T), *Staphylococcus epidermidis* ATCC 14990(T), *Bacillus zhangzhouensis* DW5-4(T), *Staphylococcus warneri* ATCC 27836(T), *Staphylococcus warneri* ATCC 27836(T), *Halomonas gudaonensis* CGMCC 1.6133(T), *Halomonas koreensis* SS20(T), *Halomonas gudaonensis* CGMCC 1.6133(T), *Bacillus zhangzhouensis* DW5-4(T), *Gracilibacillus saliphilus* YIM 91119(T), *Halomonas koreensis* SS20(T), *Bacillus zhangzhouensis* DW5-4(T), *Bacillus paralicheniformis* KJ-16(T). Also, the isolated and identified archaea are: *Natrinema altunense* AJ2(T), *Natrinema altunense* AJ2(T), *Natrinema altunense* AJ2(T), *Haloarcula hispanica* ATCC 33960(T), *Haloarcula hispanica* ATCC 33960(T), *Haloarcula argentinensis* JCM 9737(T), *Natrinema altunense* AJ2(T), *Natrinema altunense* AJ2(T) [13].

Conclusion

The high biodiversity of inorganic microorganisms is an exceptional opportunity for the development of biomining. In this regard, the first step is isolating and accurately identifying these microbes, and forming their gene banks. Furthermore, the most important tool to engineer this opportunity is the genetic and metabolic engineering of these microorganisms to increase their

efficiency with the aim of industrial and economic development of metal extraction from precious minerals. Currently, the use of microorganisms in gold and copper mining is being implemented industrially in some fields. However, the development of biomining for various metals as well as their optimization requires special research work on wild microorganisms and their engineering into induced mutants.

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