PHYLOGENETIC HETEROGENEITY OF THE SPECIES
ACIDITHIOBACILLUS   FERROOXIDANS

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Thiobacillus thiooxidans was the first organism isolated from acidic bioleaching environments, and the bulk of subsequent microbiological research in this field has centered on elucidating the biochemistry, physiology, genetics, and ecology of this remarkable organism. Today, on the basis of the results of 16S rDNA sequence analysis, *Thiobacillus ferrooxidans, Thiobacillus thiooxidans* and *Thiobacillus caldus* were combined into a new genus, *Acidithiobacillus,* within the c-subclass of the Proteobacteria.

Considerable interest has been shown in *A. ferrooxidans* because of its use in industrial mineral processing and its unusual physiology. The major contribution of *A. ferrooxidans* to metal extraction is its ability to attack sulfide-containing minerals and convert the insoluble sulfides of metals such as copper, lead, zinc, or nickel to their soluble metal sulfates.

A. ferrooxidans is a gram-negative, rod-shaped bacterium that has a physiology which is well suited for growth in an inorganic mining environment. The bacterium is acidophilic with an optimum pH within the range pH 1.5 to 2.5. It obtains its carbon by fixing atmospheric carbon dioxide and is obligately autotrophic. Energy is obtained by the oxidation of either ferrous ions to ferric or reduced-sulfur compounds to sulfuric acid. The goal of our research was the phylogenetic reconstruction of the inter - and intraspecific genealogical relationships of the genus *Acidithiobacillus.* As object of research were selected partial sequences of 16S rRNA *A. ferrooxidans.* Search for homologous sequences in the NCBI database was carried out using the BLAST.

A 16S rRNA phylogeny of the genus A. ferrooxidans, should provide useful framework study of diversity and genetic differences of this microorganism, depending on the conditions of existence. The analyses presented here had several objectives. In addition to studying the phylogenetic proximity of selected homologues, we compared various methods used in constructing phylogenetic trees.

For the analysis package MATLAB was used. In our study we used one-parameter methods for estimating distances between sequences (Jukes-Cantor and the alignment score) and two-parameter methods (Tajima-Nei, Kimura, Tamura, Hasegawa Nei-Tamura).

The phylogenetic tree was built to analyze the 39 tested strains.

According to the results of this analysis, most of examined *A. ferrooxidans* strains, constituted a monophyletic cluster. However, within this cluster considerable strain heterogeneity was showed, despite the high degree their identity and homology, and strains fell into four phylogenetic groups.

All phylogenetic trees constructed using identical methods were roughly similar topologically.