

Bacterial community in copper sulfide ores inoculated and leached with solution from a commercial-scale copper leaching plant

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Most copper bioleaching plants operate with a high concentration of sulfate salts caused by the continuous addition of sulfuric acid and the recycling of the leaching solution. Since the bacteria involved in bioleaching have been generally isolated at low sulfate concentrations, the bacterial population in ores leached with the high-sulfate solution (1.25 M) employed in a copper production plant was investigated. The complexity of the original population was assessed by the length pattern of the spacer regions between the 16S and 23S rRNA genes, observed after PCR amplification of the DNA extracted from the leached ore. Six main spacers were distinguished by electrophoretic migration, but they could be further resolved into eight spacers by nucleotide sequence homology. The degree of homology was inferred from the electrophoretic migration of the heteroduplexes formed after hybridization. One of the spacers was indistinguishable from that found in *Thiobacillus thiooxidans*, four could b