

Distribution and diversity of thermophilic sulfate-reducing bacteria within the Toyoha mine

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The distribution and diversity of thermophilic sulfate-reducing bacteria (SRB) at the Toyoha underground mine, Japan were investigated using PCR-denaturing gradient gel electrophoresis (DGGE) analysis based on 16S rRNA gene, and sequence analysis of dissimilatory sulfite reductase (DSR) gene. Hydrothermal waters from different boreholes penetrating the Cu-Pb-Zn sulfide veins were collected and concentrated with a sterile filter (pore size is 0.2 μ m) at sites-A (64 degrees), -B (71 degrees), and -C (48 degrees). Microbial mats developed at sites-A (53 degrees), -B (66 degrees), and -D (73 degrees) were harvested. The PCR-DGGE analysis showed 17 bacterial and 3 archaeal bands including two of sporeforming, gram-positive SRB, Desulfotomaculum-like 16S rDNA sequences from site-B. The phylogenetic analysis of α -subunits of DSR genes retrieved from the hydrothermal water and microbial mats revealed that Desulfotomaculum-like DSR sequences dominated in the groundwater at sites-A and -B, whereas Thermodesulfobacter-like sequences dominated within microbial mats at sites-B and -D. The distribution and diversity of DSR genes at the mine suggests the potential of in situ biological sulfide production through sulfate respiration by thermophilic SRB within the Toyoha Mine.