

O11-05 : Comparative analysis of microbial diversities in volcanic soils under sulfate reducing conditions

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In this study we investigated the activity and diversity of sulfate reducing bacteria in various volcanic soils. Four volcanic soils, from different volcanic areas in Miyagi Prefecture, Japan: Zao, Aoso, Izumigatake and Nanatsumori were analysed. Cultivation experiments with modified Postgate 's medium showed that the sulfate reducing activities of these soils were different. Bacterial diversities in both the original soils and enrichment cultures were determined using clone library method based on 16S rDNA. Every original soil 's bacterial diversity consisted of mainly Proteobacteria and Acidobacter. The Zao soil was the most diverse. Phylogenetic analysis was performed on the 16S rDNA sequences likely to be related to sulfate reducing bacteria. In all the enrichment cultures clones belonging to the Firmicutes group were dominant. The Zao, Aoso and Izumigatake enrichment samples contained Desulfotomaculum clones, while the Aoso enrichment sample also had SRB clones belonging to the α -proteobacteria group. In the Nanatsumori enrichment sample clones of sulfate reducing bacteria were not detected. In the enrichment culture diversity of the dissimilatory sulfate reductase gene (dsrAB) was also analyzed. In the Zao enrichment culture 4 different dsrAB gene sequences were found, while in the Izumigatake enrichment sample only one dominant dsrAB sequence was detected.

keywords: microbial diversity, sulfate reducing bacteria, dissimilatory sulfate reductase, dsrAB gene, 16S rRNA