

Molecular characterization of microbial communities in deep coal seam groundwater of Yubari area of northern Japan

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We investigated microbial methanogenesis and community structure based on 16S rRNA gene sequences from a coal seam aquifer located 843 to 907 m below ground level in Yubari; additionally, we studied the $\delta^{13}\text{C}$ and δD of coal-bed gases and other physicochemical parameters. Although isotopic analysis suggested a thermocatalytic origin for the gases, the microbial activity and community structure strongly implied the existence of methanogenic microbial communities *in situ*. Methane was generated in the enrichment cultures of the hydrogenotrophic and methylotrophic microorganisms obtained from coal seam groundwater. Methanogen clones dominated the archaeal 16S rRNA gene libraries and were mostly related to the hydrogenotrophic genus *Methanoculleus* and the methylotrophic genus *Methanolobus*. Bacterial 16S rRNA gene libraries were dominated by the clones related to the genera *Acetobacterium* and *Syntrophus* which have a symbiotic association with methanogens.

Reference

S. SHIMIZU, M. AKIYAMA, T. NAGANUMA, M. FUJIOKA, M. NAKO, and Y. ISHIJIMA, (2007) Molecular characterization of microbial communities in deep coal seam groundwater of northern Japan, *Geobiology*, **5**, 423-433.