

Microbial methane production and denitrification in deep aquifer associated with the accretionary prisms

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To understand microbial potential of degradation of organic compounds, fermentation, methanogenesis, and denitrification in deep aquifer associated with the accretionary prism, the deep groundwater and natural gas samples were collected from 14 deep wells that were drilled to the aquifer. We performed a series of geochemical and microbiological analyses of the samples. Consequently, methane was the predominant component of the natural gas (51.4 to 99.4%). On the other hand, the natural gas samples containing N₂ (0.6 to 48.6%) were found in some samples. Stable carbon isotopic analysis suggested that the methane was derived from both biogenic processes and thermogenic reaction. Phylogenetic analysis targeting bacterial 16S rRNA genes indicated the dominance of H₂-producing fermentative bacteria in the groundwater. In addition to the fermentative bacteria, 16S rRNA genes related to denitrifying bacterium were identified at the sites where N₂ was detected from the natural gas. Phylogenetic analysis targeting archaeal 16S rRNA genes revealed the dominance of hydrogenotrophic methanogens in the groundwater. Anaerobic incubations using the groundwater amended with organic substrates indicated H₂ accumulation and rapid methane production. These results suggested that methane in the deep aquifer is produced by a syntrophic consortium of H₂-producing fermentative bacteria and hydrogenotrophic methanogens in a wide range of deep aquifer associated with the accretionary prism in Southwest Japan. In addition to methane production, microbial denitrification using methane or organic matters as electron donors seems to be present in the deep aquifer associated with the accretionary prisms.

Keywords: accretionary prisms, groundwater, subsurface microorganisms, methane production, denitrification