1A-1 (Japanese) D. 極限環境

沿岸熱水環境における通性好気性鉄還元菌

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Key Word : Thermophile, Iron reducer, Coastal hydrothermal field

Microbial dissimilatory iron-reduction is well recognized in several anaerobic environments, such as sediments and deep sea hydrothermal vents. Thus, most of the known iron-reducers are strictly anaerobes. In this study, we aimed to elucidate the diversity of thermophilic iron-reducers in an iron-rich coastal hydrothermal field, exhibit steep physico-chemical gradients such as oxygen concentration and temperature, by culture-dependent and -independent methods. Samples were collected from a coastal hydrothermal beach in Ibusuki, Kagoshima, Japan. Total DNA was extracted and molecular diversity of 16S rRNA gene was analyzed by clone library. Although 16S rRNA gene clone analysis revealed highly diverse bacterial and archaeal communities, none of known iron-reducers were detected. Quantitative culture-dependent method (MPN method) revealed the presence of hyperthermophilic archaeon *Aeropyrum pernix,* known as strictly aerobe, not only in the aerobic surface layer but also in the anaerobic bottom layer of the beach. In an attempt to examine whether *A. pernix* was able to grow under anaerobic conditions, N_2 was tested as gas phase in the presence of ferric iron as possible alternative electron acceptor. Under iron-reducing condition, weak growth of *A. pernix* was observed. Novel groups of Chloroflexi were isolated from both the surface and the bottom layer, under iron-reducing condition. Among the groups, representative strain 110S showed aerobic growth. It is assumed that capability of aerobic growth characterizes the iron-reducing thermophiles in the coastal hydrothermal field.

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1A-2 (Japanese) D. 極限環境

深部地下油層環境における原油分解とメタン生成

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Key Word : subsurface, methane, RI tracer, oil field

Microbial diversity and methanogenic potential of formation water derived from deep subsurface oil reservoir in Yamagata Prefecture were investigated by using 16S rRNA gene libraries and culture-based methods.

The depth and temperature at the center of the reservoir were 938m and 54° C, respectively. The predominance of isoprenoid over straight-chain alkanes in the crude oil indicated that the oil has partially been biodegraded. The ^{13}C enrichment of carbon dioxide in the associated gas suggested that methanogenesis proceeded during the oil biodegradation. The microbial population density of the samples estimated by the direct epifluorescence microscopic counts of the DAPI-stained cells was $3.2x10^5$ cells/ml. The number of culturable methanogens in the formation water was of the order of 10^3 cells/ml. The anaerobic incubation of formation water amended only with crude oil resulted in the methanogenesis that continued over 65 days. The incubation of formation water amended with specific substrates for methanogenesis, followed by the analysis of archaeal 16S rRNA genes revealed the occurrence of hydrogenotrophic and methylotrophic methanogens. The incubation of water amended with crude oil and a trace amount of specific substrate labeled with ^{14}C indicated the potential activity of methanogenesis from bicarbonate, acetate and methanol, with that from bicarbonate accounting for the majority. We also determined bacterial communities in the formation water based on 16S rRNA gene cloning analysis. Interestingly, most of these clones were not closely related to cultured species.

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