Investigation microbial community for gas-hydrate site off-Sakhalin Island

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Gas hydrates (GH) are widely spread in the sediments under the subsea floor and form at high pressure and low temperature. GH oriented gas were grouped to thermogenic and microbial gas according to composition carbohydrate gas and isotopic molecular weight of methane. The role of microbial communities in the GH sites have been already investigated by several research groups. Isotopic composition of gas hydrate is often use to determine gas derivation such as thermogenic or microbial gases. However, combination study both isotopic gas analysis and microbial diversity have not been performed at all. Recently we successfully obtained mix gas-derived GH core sediment in the western Sakhalin slope off Sakhalin Island by exploration using ultrasonic wave sonar and gravity coring, in SSGH 15 project by using Russian research vessel Akademik M. A. Lavrentyev. We will demonstrate that results of investigating molecular and isotropic composition of the sediment gas, sulfate and sodium compositions, and microbial composition of a GH-bearing sediment core obtained in SSGH15.

Molecular composition ratio C₁/C₂+C₃ below SMI were in the range between 116 and 225, while d¹³C and dD values of methane were in the range of -48.9 and -45.7 permil, and of -165 and -149 permil, respectively. These results indicated that the gas compose of large amount of thermogenic gas and small amount of microbial gas.

Forty two individual clones have successfully analyzed, until we submit this article. Three Aciduliprofundum related clones, and three Methanobrevibacter related clones were detected. These sequences were clustered into oceanic methanogen in the phylum Euriarcheota. This result implied that these archaeon generate microbial methane in the core, and may correspond to decrease isotopic ¹³C ratio of methane and increase the C₁/C₂+C₃ ratio. Slight amount of sequence in Crenarcheota, which may be involved anaerobic methane oxidation (annamox). Interestingly, heterotrophic bacteria in cluster of Dehalococcoidetes-related Chloroflexi, of Candidatus artibacteria (named as division J51/OP9), and of Planctomycetes were frequently widespread in the core. The phylum Chloroflexi is a lineage for which the class 'Dehalococcoidetes' was proposed to accommodate the tetrachloroethane respiring coccus Dehalococcoides (1). These bacteria may contribute to decomposition of difficultly degradable organic matters accumulated on deep sea floor. Planctomycetes have been often detected, and widespread in methane-seep (2), but the functional characters have been unknown. Recently, candidatus artibacteria have been revealed to play significant role as symbiotic scavenger in artificial methanogenic bioreactor, by using single cell genome analysis (3). According to the study, atribacteria may support methanogen and chloroflexi through the by-product generation such as acetate, butyrate, and H₂. These results implied that thermogenic and microbial mixed-derived gas composition may be formed by symbiotic metabolism of those species, but not simply generated from inorganic gases such as CO₂ and H₂ by methanogen.