DEEP METHAGENESIS AND IODINE-RICH AQUIFER: INSIGHT FROM ORGANIC GEOCHEMICAL APPROACH

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Introduction. Biological methanogenesis in subsurface environments has been explored from the view of global carbon cycle and biogeochemical processes. Subsurface biogenic methane is produced by methanogenic archaea (methanogens) up to 600 Tg CH4 y−1 in shallow terrestrial and marine environment (e.g., Conrad, 2009), also in deep subsurface environment (e.g., down to ~2.5 km below seafloor: Inagaki et al., 2015). To define the potential of ongoing archael methanogenesis, Kaneko et al. (2014) estimated the cell number of methanogen using the key coenzyme of factor 430 molecules.

Minami-Kanto gas field located at Chiba pref., Japan on terrestrial environment is known as one of the largest domestic natural gas fields (purity of methane > 99%) and the largest iodine deposits in the world; the ancient brine contains high concentrations of iodine (<1.2 mM; e.g., Amachi et al., 2005) and humic-rich dissolved organic matter (DOM). Assessing the microbial habitat in the deep subsurface, Mochimaru et al. (2007) described modern methanogen community in the brine-rich groundwater.

Scientific objectives. To date, organic geochemical aspects are still enigmatic from the scope of prokaryotic ecology and deep iodine interactions. For further elucidation of those unseen points, we firstly conducted lipid-based analysis together with small subunit (SSU) rRNA gene sequence analysis to verify the microbial community using the sample of deep aquifer, bubbled scum (i.e., floating on the surface of the water), and headspace gas collected from the well (Fig.1). We determined the living signature of biomass and prokaryotic ratio (i.e., bacteria/archaea) in the deep aquifer. Secondly, we performed methane-specific radio carbon isotope analysis (Δ14Cmethane) using the accelerator mass spectrometry (Yokoyama et al., 2010) to assess the origin of deep carbon.

Results and Discussion. Lipid-based biomarker analysis showed that domain archaea was approximately less than 10% overall, implying the dominance of bacterial community (Fig. 1). SSU rRNA gene sequence analysis supported the lipid-based estimation and also revealed the unique archaeal community including the predominant Woesearchaeota (Castelle et al., 2015) and Euryarchaeota (e.g., Methanosarcinales). Here, we note the distinct molecular signature of iodine-oxidizing bacteria (IOB), which oxidize iodide (I−) to molecular iodine (I2), i.e., Iodidimonadales of the class Alphaproteobacteria.

Carbon isotopic composition of methane showed typical biogenic origin (δ13Cmethane, -71.6 ± 1.9 ‰, vs. VPDB; cf. δ13Csum showed -18.7 ‰ (n=2, ave.); δ15N, +2.5 ‰, vs. Air; whereas C/N ratio, 21.5). The Δ14Cmethane (-997.4 ± 0.3 ‰) indicated that carbon in the deep aquifer has been isolated from modern atmospheric carbon and ambient seawater. We will discuss the process of deep methanogenesis and further perspectives for biogeochemical cycles of iodine in the brine-rich aquifer.

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Figure 1 (A) The photograph of the deep brine, bubbled scum and headspace gas, (B) Vent and iodine-rich chimney deposit. (i) Lipid-based prokaryotic ratio of Bacteria (blue) / Archaea (red) in the brine-rich groundwater (a, d), scum (b, e) and chimney (c, f) (method after cf. Takano et al., 2018). Fig. a, b, c are based on archaeal isoprenoid and fatty acids (n-C16 & C18) analysis, (ii) Fig. d, e, f are based on UUS rRNA gene sequence analysis (method after Imachi et al., 2019).

References
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