Seasonal variation of bacterial key species maintaining an aquaculture environment

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In an aquaculture environment, as fishes are cultured in a high density, organic loads such as leftover feed and feces often exceed the environmental capacity and induce heavy organic pollutions. Among the various factors that determine the environmental capacity, bacterial biodegradation process would be one of the key factors. Therefore, it is important to understand well about the bacterial community in the aquaculture system. Seawater and sediment samples were collected bi-monthly at the coastal aquaculture site of Kinki University from May 2009 to March 2010. Bacterial cells were collected and subjected to bromodeoxyuridine (BrdU) and PCR-DGGE analysis. BrdU, halogenated nucleoside and thymidine analogue, has been used to monitor DNA-synthesizing or actively growing bacteria in natural environments. Both community structures of total and actively growing bacteria in the water and sediment samples showed seasonal variations; community structures of actively growing bacteria were distinguished from those of total bacteria. Interestingly, some bacteria were always present and growing actively throughout the year, even though bacterial community structures and environmental factors such as water temperature and chlorophyll a concentration changed seasonally. These bacteria which belonged to two uncultured alphaproteobacteria (Roseobacter group) or one uncultured gammaproteobacterium have been also found as actively growing bacteria from coastal environments, the Seto Inland Sea and Otsuchi Bay. They might be responsible for the environmental capacity in not only this aquaculture area but also ordinary coastal areas.

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Potential of subsurface microbes to produce natural gas

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Subsurface microbes anaerobically degrade organic matter in sediments and produce methane. Contribution of these microbial processes to natural gas resources worldwide is estimated to be at least 20 %. In particular, the origin of methane in water-dissolved natural gas and marine methane hydrate is mainly microbial. For efficient exploration and accurate assessment of such gas accumulations, we have been studying in situ activities of subsurface microbes producing methane in various fields, making the following findings to date.

Marine subsurface (areas of methane hydrate distribution): In the sediment cores from off Vancouver Island, we detected methanogenic activities using 13C-tracers. The rates through carbonate reduction are higher than through acetate fermentation, and the rates in deeper hydrate-zone sediments are higher than in near-surface. In the cores from Nankai Trough, we detected polar hydroxyarchaeols, with the concentrations highly correlated with those of total organic carbon.

Water-dissolved gas fields: In the formation water from Chiba and Niigata gas fields, we detected a wide range of methanogenic archaea with difference in substrate utilization, and successfully isolated a novel species of methanogenic archaea. High amounts of methane were produced from the cores slurried in the formation water and incubated at the subsurface temperature, implying that utilizable organic matter remains abundant in sedimentary rocks of geological ages.

Oilfields: In the formation water from Amamuru oilfield, we found hydrogenotrophic and methylotrophic methanogenic archaea, and detected their activities using 13C-tracers. In the water from Yabase oilfield, amended with crude oil plus 13C-tracers and incubated under the oil reservoir conditions, we found that syntrophic acetate oxidation coupled to hydrogenotrophic methanogenesis was the dominant pathway.

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