

ポスター PE

Microbial community dynamics 微生物群集構造

PE-01

Characterization of subsurface prokaryotic communities in the Minami-Kanto gas field, Japan

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南関東ガス田における地下原核生物の特徴

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Key word : subsurface biosphere, natural gas field, 454 pyrosequencing, methanogenesis

After the disaster in Fukushima, alternatives to nuclear energy have become an important priority. Natural gas of dissolved-in-water type is clean energy fuel, due to the lack of toxic and polluting substances. This natural gas is of biogenic, i.e., derived from methanogenesis, as identified by the stable isotopic compositions of methane. Enhancing biogenic conversion of organic matters in subsurface, such as oil and coal, to methane by in situ microbial communities has being paid attention, but requires an understanding of their ecological traits. Previously, high methane production was detected in the culture of core sample from natural gas fields in Chiba, where approximately 90% of the natural gas in Japan is produced, indicating the possible methanogenesis *in situ*. To obtain insights into largely unknown microbial community including methanogens present in this field, integrated biogeochemical analyses were performed. Water samples were collected from commercial production wells at various locations, and subjected to chemical analysis, measurement of methane production rate by radiotracer and prokaryotic community structure analysis by tag-encoded 16S rRNA amplicon pyrosequencing. Here we show the bacterial and archaeal community profiles as well as the geochemical factors that may influence community structure and methanogenesis.

PE-03

Comprehensive analysis of bacteria communities in Kuruma shrimp farming pond by next-generation sequencer

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次世代シーケンサーを用いたクルマエビ養殖池の網羅的菌叢解析

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Key word : Bacterial community, 16S rRNA gene, Pyrosequencing, Aquaculture

In aquaculture, disease management is important for production efficiency. It is crucial to monitor farming conditions particularly the microbial community dynamics, because most diseases are caused by microbes. In this study, we investigated the bacterial community in a vibriosis-affected shrimp farming pond using next-generation sequencing technology. Periodic samples were collected from pond water, sediment, and shrimp intestinal contents, respectively. After DNA extraction, V1-2 regions of 16S rRNA gene were amplified using barcoded universal primers with modification and simultaneously analyzed using 454 GS FLX titanium platform. We obtained about 5,000 reads of 16S sequences per sample by filtering low quality reads out. OTU-based analysis revealed that many samples are composed of high proportion of unknown bacterial species having a low similarity of 16S sequences with those of known species. However, the analysis revealed lower microbial diversity of pond water than that of natural seawater and a dramatic time-dependent change of the bacterial community structure of pond water but much less for the sediment. We also found a significant correlation between bacteria community structure of pond water and several environmental data such as dissolved oxygen concentration, and several OTUs that showed strong correlation with mortality rate of shrimps.

PE-02

Methanogenic community structure and methane production potential of tropical dryland Indian paddy soils

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インド熱帯乾燥水田土壌中のメタン生成菌群集構造とメタン生成活性

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Key word : methane, paddy soil, community structure, methane production potential, India

Methane emission from rice fields is projected to intensify in future due to increase in the rice production in order to meet the food demand for the rapidly growing population. Therefore studies on methane production have become a matter of scientific concern. Five paddy field soils of tropical eczones having different hysic-chemical characteristics were studied for evaluating their methanogenic community structure as well as their potential for methane production. Pyrosequencing based metagenomics has been applied to analyse taxonomic and metabolic profiles of methanogens. Results reveal that the soils have representative genera of all five orders of methanogens. Members of *Methanosarcinales* were found to be dominant followed by *Methanomicrobiales*, *Methanobacteriales*, *Methanococcales* and *Methanopyrales*. Nineteen methanogenic species were detected in all soils with different abundance. Further, laboratory incubation experiments showed methane production potential of soils largest in Vertisol followed by Terai, Entisol, Inceptisol, Alfisol in this order. The results also indicate variation in the methanogenic community in terms of their diversity and abundance. The attributes like diversity, abundance and soil characteristics can be correlated to the methane production potential of the soils which varies across the soil types.

PE-04

Pyrosequencing analysis of bacterial community in aqua-farm sediment

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Key word : pyrosequencing, bacterial community, aquaculture, sediment

The bacterial diseases in aquaculture industry cause huge economic loss. However, only a few causative infectious bacteria were identified but larger bacterial community of aqua-farm sediment has not been examined so far. This study was focused on analyzing the bacterial community of aqua-farm sediments. Bacterial community from sediment of culture area was compared with that from non-culture area of aqua-farm by pyrosequencing of V3 region of 16S rRNA gene. Total 744,547 reads (average length: 380 bp) were obtained from the two sediment groups using pyrosequencing (GS-FLX titanium). From which, bioinformatic analysis resulted total 19,020 contigs from non-cultured region and 8,068 contigs from cultured region of aqua-farm sediment. All contigs obtained from pyrosequencing were analyzed through the database of Ribosomal Database Project (RDP, <http://rdp.cme.msu.edu/>). In the results, bacterial sequences consisted of 21 phyla and 1 unclassified in the cultured region, while 22 phyla and 2 unclassified in sediment of non-cultured region. *Proteobacteria* was the most abundant in non-cultured region sediments (53.1%), followed by *Chloroflexi* (4.9%), *Bacteroidetes* (4.6%) and unclassified bacteria (29.4%). Relatively, *Proteobacteria* was also the most abundant in sediments from cultured region (49.5%), *Chloroflexi* (6.6%), *Bacteroidetes* (4.8%) and unclassified bacteria (30.5%).