**PJ-07**

**Genome sequence of the endobacterium localized inside the mycelium of the fungus Mortierella elongata**

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**Key words**: fungal endobacterium, whole genome sequence

Our prior study gave microscopic and molecular evidence for the presence of endobacteriae inside the mycelia of four to twelve fungal isolates identified as *Mortierella elongata*. The 16S rDNA genes analyzed revealed that they were related to Candidatus Glomeribacter gigasporum in the family *Barkholideria*. Here we present the genome sequence of the endobacterium recovered from M. elongata FMR23-6 B1. Endobacterial cells were separated from the fungal cell homogenate by Nycoplas density-gradient centrifugation, treated with DNase to digest the host fungal DNA, and then subjected to the extraction of the genomic DNA. The genome sequence was obtained by a whole-genome shotgun strategy using Roche 454-pyrosequencing and the shotgun reads were assembled by Newbler software. The endobacterial draft genome sequence has a total of 2,796,381 bp distributed in 12 scaffolds and a GC content about 49%. The gene categories analysis using COG database showed higher proportions of genes for "expansion, recombination and repair" and "amino acid transport and metabolism" in the 2,265 predicted genes. The genes of type II, III, IV and VI secretion systems were predicted in the largest scaffold by BLAST analysis using KEGG database. The genome annotation is now in progress to give a better understanding of the fungus-endobacterium interaction.

**PJ-08**

**Feature elucidation of Japanese gut microbiome**

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**Key words**: metagenomics, human microbiome, next-generation sequencer, gut, diversity

Large numbers of bacteria colonize human intestines. The total number of those bacteria cells is greater than that of human cells, and have great influence on human physiology. However, since the majority of them are likely unculturable, it is not easy to elucidate the whole structure and function of gut microbiome (collective genome of microbes). Previously, we conducted metagenomics of 15 Japanese gut microbiomes, and identified and characterized about 660,000 genes in gut (Kurokawa K et al. 2007). In 2010, it was reported that the Japanese gut microbiomes have a degrading enzyme of polysaccharides of aquatic plants such as Wakame or Nori, but the American gut microbiome did not (Heinemann JH et al. 2010). This strongly suggested that traditional food culture largely influences the shaping of gut microbiome. From these backgrounds, we have considered that by comparing Japanese gut microbiome and that of non-Japanese or other ethnic's, we could find genes unique or significantly high frequent in the ethnic population. We have so far collected metagenomic sequences by 454 pyrosequencing of over 90 Japanese fecal samples and identified about 4 million non-redundant genes. Using large European microbiome dataset (Qin J et al. 2010) as a comparison, we have analyzed diversity and features of human gut microbiome genes. We will present the results obtained from these analysis.

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**PK-01**

**Occurrence of endosymbiotic bacteria in a vestimentiferan tube worm, Lamellibrachia satsuma**

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**Key words**: Lamellibrachia satsuma is the tube worm which is living at cold seeps where reduced gases are leaking out from the seafloor. The tube worm is entirely reliant on internal, sulfide-oxidizing bacterial symbionts for its nutrition. The tube worm provides the bacteria with hydrogen sulfide and oxygen by taking them up from the environment and binding them to a sulphurized hemoglobin molecule, which transports these ingredients to a region called trophosome. The symbionts inside of trophosome convert these ingredients to organic carbon which nourishes the tube worm. Whole species of vestimentiferan tube worms live in deep waters below the photic zone, L. satsuma was discovered in Kagojima Bay, at a depth of 80-110 m. The shallows in the depth record for a vestimentiferan. The purpose of this study is to determine the complexity of the microforms associated with the trophosome content of a vestimentiferan tube worm, L. satsuma, and also their specific occurrence within trophosome body. The identification of bacterial endosymbionts have been done based on the analysis of 16S rRNA sequences and the evolutionary trees were constructed using the neighbor-joining method. Several operational taxonomic units (OTUs) were detected from the trophosome of L. satsuma. The major OTUs were closely related to a Proteobacteria which is most abundant in the Vestimentiferan of Shinkoiwa, a-Proteobacteria (Rhodobacterales) and ε-Proteobacteria which is closely related to the coryneform of R incurvisulca. On the basis of the 16S rDNA, species-specific oligonucleotide probes have been designed and labeled with fluorochrome to find the occurrence within the trophosome by fluorescence in situ hybridization (FISH). The FISH experiment shows the distribution of the endosymbiotic microorganisms in the trophosome of tube worm and it will be discussed what the major player in the tubeworm is.

**PK-02**

**Population genetic analysis of deep-sea hydrothermal vent gastropod Alviniconcha and their bacterial endosymbionts**

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**Key words**: co-evolution, deep-sea hydrothermal vent, endosymbionts

Most deep-sea hydrothermal vent invertebrates depend on chemosynthetic bacteria for their nutrition. The hydrothermal vent gastropod *Alviniconcha* is no exception. The interdependent relationships between host and symbiont could cause co-evolution. However, there is a few knowledge of co-evolution in deep-sea hydrothermal fields. Therefore, we focus on the host-symbiont relationships in one of the dominant gastropods, *Alviniconcha*. Previous studies revealed that *Alviniconcha* had endosymbionts from the Mariana Trough harbored **Gammamproteobacteria** and *Alviniconcha* sp. from Indian Ocean harbored **Epsilonproteobacteria**. In our previous study, host-symbiont genetic relationships in *Alviniconcha* sp. from Central Indian Ridge was analyzed using multi locus sequence analysis (MLSA). However, no clear evidence of co-evolution was obtained. In this study, we analyzed host-symbiont genetic relationships between *A. hassleri* and **Gamma** and **Epsilon** proteobacterial endosymbionts from the South Mariana Trough. We intend to report the results of analysis, mentioning comparison with Central Indian Ridge and discuss co-evolution in deep-sea hydrothermal fields from the point of view of population genetics.