**PJ-07**

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

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Key word: fungal endobacteria, whole genome sequence

Our prior study gave microscopic and molecular evidence for the presence of endobacteria inside the mycelia of four out of twelve fungal isolates identified as Mortierella elongata. The 16S rRNA gene analyses revealed that they were related to Candidatus Glomeribacter gigasporum in the family Burkholderiaceae. 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 Nycodenz density-gradient centrifugation, treated with DNase to digest the host fungal DNA, 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 soft ware. 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 “replication, recombination and repair” and “amino acid transport and metabolism” in the 2,285 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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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 13 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 microbiomes did not (Hehemann 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 database (Qin J. et al, 2010) as a comparison, we have analyzed diversity and features of human gut microbiome genes. We’ll present the results obtained from these analysis.