**S12-1**

"Novel" iron-reducing thermophiles in marine hydrothermal environments  

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**Key word:** iron-reducer, thermophiles  
The speaker is a Ph.D. student in Kyoto University, studying thermophiles capable of using ferric iron as their terminal electron acceptor. Microbes are capable to use various electron acceptors, such as oxygen, nitrate, and sulfate. Ferric iron is also known to be used as an alternative electron acceptor by a wide phylogenetic diversity of microorganisms under anaerobic conditions. While ferric iron is one of the most energetically favorable electron acceptors when oxygen is not present, iron-reduction may be an important energy metabolism in anaerobic environments. However, information on the molecular mechanism of microbial iron-reduction is limited to some model organisms. Thus, it may be inappropriate to evaluate the diversity of iron-reducers in the environments only by culture-independent methods such as clone analysis based on 16S rRNA gene. In this symposium, I am going to talk about two “new” iron-reducers we have revealed using traditional culturing methods. One is a novel lineage of anaerobic, iron-reducing thermophile affiliated with a clone cluster of the phylum Chloroflexi, isolated from an iron-rich coastal hydrothermal field. Although the members of the phylum Chloroflexi are detected from a huge variety of environments, this is the first iron-reducer among them. The other is a hyperthermophilic archaeon Aeropyrum pernix formerly known as a strictly aerobe.

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**S12-2**

Isolation and cultivation of barely culturable soil bacteria  

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**Key word:** bacterial culture, barely culturable bacteria, oligotrophic bacteria  
I am a doctoral researcher in the lab of microbial ecology, Mokwon University, Korea. Ongoing research projects in our lab were biodiversity and ecocollections of soil bacteria, phylogenetic analysis and identification of novel oligotrophic soil bacteria by polyphasic classification. The number of colonies on diluted broth (DNB) plates increased with incubation time following double or triple colony formation curves (CFCs). The CFCs may be arbitrarily divided into three components (CFC I-III). To analyze the slow growing bacteria, 392 bacteria were isolated from the colonies found in CFC-III (696 to 1,200h). Eighty-seven isolates showed the capacity to grow on a 10⁻⁵NB, whereas their growth in 10⁻⁴NB was severely suppressed. These slow-growing DNB organisms were designated as "barely culturable bacteria". The class Alphaproteobacteria class comprised the largest portion of the 16S rRNA gene sequences (about 50% of the total isolates). The Rhizobiales were abundant members of barely culturable bacteria. Large proportions of these isolates were closely related to the Bradyrhizobium, Azospirillum, Nitrospira and Agromonas (BANA), composing dominant groups of barely culturable bacteria. They were successfully cultured using a diluted nutrient medium and a long-term culturing method.