S08-3
Metabolic pathway analysis of genome-wide study in *Rhodococcus* strain highlights aromatic hydrocarbon-degrading genes for bioremediation
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**Key word**: bioremediation, aromatic hydrocarbon, *Rhodococcus*, genome analysis

*Rhodococcus* strains, metabolically versatile bacteria found in the environments, are recognized as a significant, and several public and private genomic analysis projects involving *Rhodococcus* strains are now in progress to promote future application for bioremediation. *Rhodococcus opacus* strain SAO101, which was isolated from forest soil by enrichment of a medium containing dibenzofuran as a sole carbon and energy source, has ability to degrade aromatic hydrocarbons, such as dibenzofuran, dibenzo-p-dioxin, and naphthalene as well as nitroaromatic compounds. To elucidate the physiological and evolutional aspects of this strain, genome analysis of strain SAO101 has been performed by next-generate sequencing technologies. From the genomic sequencing analysis, putative CDSs (coding sequences) was assigned to the 20 aromatic hydrocarbon biodegradation pathways for a quarter of the total number of the putative CDSs. Interestingly, the genome structure of strain SAO101 is unique that a part of putative CDSs assigned to the aromatic hydrocarbon biodegradation pathways in strain SAO101 were not annotated in the other *Rhodococcus opacus* strain genomes. Genomic sequencing revealed that strain SAO101 contains a multiplicity of catalytic genes, and exchange and reshuffling of genetic modules, as well as transfer of plasmids, may have occurred in the evolution of *Rhodococcus* strains.

S08-4
Microbial community design for environmental purification using systematic methodology
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**Key word**: mathematical model, microbial community design, microbial granule, wastewater treatment

The aim of this study is to establish systematic methodology, in which predictions made by mathematical models are used for designing microbial community that optimizes performance of environmental biotechnology processes. As a model case applicable of this approach, simultaneous nitrogen and phosphorus removal process using microbial granular sludge in a wastewater treatment plant is considered. In this process, nitrogen and phosphorus are removed simultaneously in a single reactor because nitrifying bacteria and denitrifying polyphosphate-accumulating organisms can coexist within the granular sludge. Because of this complexity, constructing a mathematical model for this process by considering interactions between solute and particulate species is essential to predict microbial community structure and/or to optimize the treatment performance. By connecting macroscopic and microscopic models, a unified computational model was developed for the growth process of microbial granules in a sequencing-batch reactor. Simulation results using this unified model were in good agreement with the experimental data such as spatial distributions of bacterial species in the granule and nutrient concentration in the effluent. These results implies the validity and usefulness of the computational model developed in this study.