P-006

Metagenomics reveals metabolic capacity of methanogenic microbiota in a bioreactor treating soy sauce-processing wastewater

○Takashi Narihiro[1], Masaru K. Nobu[2], Kyohei Kuroda[3], Atsushi Tobo[4], Wen-Tso Liu[2], Masayoshi Yamada[4]

[1]Bioproduction Res. Inst., AIST, [2]Univ. Illinois at Urbana-Champaign, USA, [3]Natl. Inst. Technol., Kitakyushu College, Japan, [4]Natl. Inst. Technol., Kagoshima College, Japan

E-mail: t.narihiro@aist.go.jp

Metagenomic analysis of a methanogenic microbial community in an anaerobic bioreactor treating amino acid-containing soy sauce-processing wastewater revealed synergistic metabolic network of syntrophic substrate-oxidizing bacteria (syntrophs), methanogenic archaea (methanogens), and functionally unknown microorganisms. A laboratory-scale upflow anaerobic sludge blanket (UASB) reactor fed with wastewater discharged from soy sauce processing manufactory was operated at 20°C. 16S rRNA gene amplicon analysis has shown that the majority of microorganisms are assigned into the phyla *Euryarchaeota*, *Firmicutes*, *Synergistetes*, and *Bacteroidetes* (Tobo et al., presentation at 2016 JSME annual meeting). Metagenomic shotgun sequencing was performed by Illumina MiSeq sequencer. We successfully recovered metagenomic bins of dominant microbes in the reactor, including *Euryarchaeota* methanogens (*Methanosaeta*, *Methanosarcina*, *Methanospirillum*, and *Methanobacterium*), *Syntrophomonadaceae*- and *Pelotomaculum*- related syntrophs, and other bacterial members associated with the *Synergistetes* and *Bacteroidetes*. Metabolic reconstruction suggested that these organisms perform fermentative and syntrophic degradation of amino acids and catabolic by-products facilitated by various energy conservation systems. *Bacteroidetes* and *Synergistetes* organisms could ferment or syntrophically degrade amino acids. *Syntrophomonadaceae* and *Pelotomaculum* could utilize the by-products branched-chain and short-chain fatty acids presumably derived from the degradation of amino acids. Acetate and hydrogen were further converted to methane by aceticlastic and hydrogenotrophic methanogens. Thus, diverse anaerobic organisms may unite to form a metabolic network to perform complete degradation of amino acids in the methanogenic microbiota.