Institute for Universal Biology (IUB)
NASA Astrobiology Institute Seminar Lecture Series

Friday, May 2, 2014

12 noon – 1 pm

Lecture Hall 612

Institute for Genomic Biology

Directions: http://www.igb.illinois.edu/about/directions

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"Microbial Ecology of a methanogenic bioreactor degrading terephthalate as the sole carbon source"

Terephthalate is one of the top fifty chemical products in the world and produces a significant waste stream, which is predominantly treated by anaerobic biological processes. Different ecogenomics tools were used to characterize the microbial community of a hypermesophilic (~50°C) methanogenic bioreactor that has been operated for 8 years to treat terephthalate (TA)-containing wastewater. This community as characterized by 16S rRNA-based methods is dominated by three phylogenetic groups, *Pelotomaculum* (a member of the *Firmicutes* phylum that converts terephthalate to acetate and hydrogen), methanogens (archaea that convert hydrogen or acetate to methane and carbon dioxide), and a representative of candidate bacterial phylum OP5 (unknown function). We identified genes belonging to dominant *Pelotomaculum* species presumably involved in TA degradation through decarboxylation, dearomatization, and modified β-oxidation to H_2/CO_2 and acetate. These intermediates are converted to CH_4/CO_2 by methanogens. Our findings also predicted additional secondary syntrophic interactions in the community likely to safe guard the primary syntrophy. Overall, the findings provide unique insights into the ecophysiological features of the methanogenic community that carries out the anaerobic degradation of terephthalate.