Poster #190

Assessment of Microbial Community Responses Towards a Model Synthetic Community for Studying Multispecies Hg-methylation

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Neurotoxic methylmercury (MeHg) is produced by anaerobic bacteria possessing the genes *hgcAB*. The native *hgcAB* function is undetermined so it is unknown which if any carbon or electron sources may stimulate or hinder Hg-methylation. Several carbon sources were amended to East Fork Poplar Creek sediments and a background site to determine their effect on net Hg-methylation. Sediments were assessed for Hg and MeHg levels post-incubation as well as overall microbial diversity via 16S rRNA sequencing and Hg-methylating clade abundance via *hgcA* qPCR. Minimal increases in MeHg were observed with lactate, ethanol and methanol while a significant decrease (~70%) was observed with cellobiose in downstream EFPC. Sequencing revealed that unamended sediments consisted of Proteobacteria, Firmicutes, Bacteroidetes and Actinobacteria with *hgcAB*-containing Bacteria and Archaea identified across all sites. Cellobiose shifted the communities to ~90% non-*hgcAB* containing Firmicutes (mainly *Bacilli spp*. and *Clostridium spp*.) and were verified with *hgcA* clade-specific qPCR analysis. These results suggest that either expression of *hgcAB* is down-regulated or, more likely given the lack of 16S rRNA presence after cellobiose incubation, Hg-methylating organisms are largely incapable of surviving on cellobiose or its degradation products.

In an inter-task effort (see Brooks poster), we have been enriching sulfate- and Fe(III)- reducing bacteria as well as methanogens from East Fork Poplar Creek periphyton. These isolates will be used to construct a Hg-methylating model synthetic community to determine the effect of geochemical and other perturbations on net MeHg production.

We will take advantage of the carbon information and the effect on net MeHg production for use in our model communities. Finally, both in isolation and in the synthetic communities, we will utilize a new TNLEseq capability that will allow for determining the fitness of most genes in each community member species. This may also allow for the elucidation of the essential genes and biochemical pathways required for *hgcAB* functionality.