Bioremediation of Chlorinated Emerging Contaminants in Wastewater Digesters

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Background/Objectives: *Dehalococcoides*-containing microbial consortiums (SDC-9[™]) are commonly applied or bioaugmented for the anaerobic remediation of halogenated aliphatic groundwater pollutants, such as tetrachloroethylene (PCE) and trichloroethylene (TCE). However, it is not known whether the commonly applied dehalogenating consortia can effectively remediate chlorinated emerging contaminants such as triclosan (TCS) and triclocarban (TCC). Wastewater treatment plant (WWTP) anaerobic digesters are sites of limited bioaugmentation research, but systems that can concentrate chlorinated emerging contaminants in sludge before the final dewatered material is land-applied for crop production. In the 2001 EPA National Sewage Sludge Survey for pharmaceutical and personal care products in final WWTP biosolids, TCC and TCS were the most abundant analytes by mass. Our research seeks to investigate the microbial degradation of such emerging contaminants and bio-stimulation of anaerobic digester sludge with dechlorinating bacterium.

Approach/Activities: Genetic material from a large, urban WWTP anaerobic digester was surveyed for the phylogenetic diversity of dechlorinating (or associated) microorganisms already populating the anaerobic digesters. Methods included polymerase chain reaction (PCR), gel electrophoresis, and quantitative PCR. Anaerobic mesocosm experiments are being developed to test microbial culture treatments (SDC-9) with emerging contaminants TCC and TCS, by transitioning the dechlorinating organisms from aliphatic solvent TCE to aromatic compounds TCC and TCS as electron acceptors. Microbial abundance is quantified with qPCR and chemicals are quantified by GC-FID (TCE) and HPLC-MS/MS (TCC and TCS). Upcoming work also seeks to inoculate anaerobic digester sludge with the SDC-9 culture to assess the stability of the bioaugmented organisms in the anaerobic digester community at the mesocosm scale.

Results/Lessons Learned: The phylogenetic survey of anaerobic digester sludge revealed that the system contained obligate dechlorinating organisms *Dehalobium chlorocoercia*, *Dehalogenimonas*, and *Dehalobacter*, as well as facultative dechlorinating organisms *Desulfomonile*. These results suggest that dechlorinating organisms populate anaerobic digesters, and are therefore likely supported by chlorinated chemical present in the systems. While these organisms exist, they may not be at high enough concentrations to effectively remediate all emerging contaminants within the systems. For example, previous studies have shown consistent levels of both TCC and TCS leaving the final dewatered cake at the WWTP of study. The SDC-9 culture contains obligate organisms *Dehalococcoides Mccartyii*, *Dehalobium chlorocoercia*, as well *Dehalogenimonas*. *D. Mccartyii*, which was unique in the remediation culture, is suggested to dechlorinate both aliphatic and aromatic compounds, making it a good candidate for bioaugmentation of anaerobic digesters with SDC-9. Future work will focus on the activity of *D. Mccartyii* in the presence of chlorinated emerging contaminants in mesocosm experiments.