

## Biodegradation of Chlorinated Natural Organic Matter in Contaminated and Uncontaminated Sediment and Soil

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**Background/Objectives.** Organohalide respiring bacteria are able to degrade chlorinated chemicals and have traditionally been studied at contaminated sites; nevertheless, bioremediation at such sites has had varying levels of success, especially as the concentration of contaminant reaches relatively low concentrations. Many chlorinated chemicals are produced naturally, however, and exist at low concentrations in sediments and soils. Our previous research indicated that organohalide respiring bacteria are capable of respiring this chlorinated natural organic matter (CI-NOM). In this work, we studied the role of these bacteria in uncontaminated sediments and soils to better understand the bioremediation of low-concentration contaminants. This study analyzed the microbial communities and reductive dehalogenase (rdh) genes responsible for the dechlorination of CI-NOM, and how exposure to both PCBs and higher concentrations of CI-NOM impacted dehalogenation.

**Approach/Activities.** Sediment from two uncontaminated Midwestern lakes, one uncontaminated lake near the ocean, one PCB-contaminated river, and soil from another PCB-contaminated site were enriched with either CI-NOM or natural organic matter (NOM). All of these sediments were expected to vary in their past exposure to CI-NOM (higher near the ocean) and chlorinated pollutants. Degradation of CI-NOM was monitored by the release of chloride and the communities were analyzed via sequencing (Illumina) of the 16S rRNA genes present and qPCR quantification of target organisms. As rdh genes are extremely variable, a metagenomics approach (initial and after 150 days of enrichment) was used to determine which rdh genes were present.

**Results/Lessons Learned.** Degradation of CI-NOM was observed in all of the enrichment cultures; it was slower, however, in the PCB-contaminated samples and the near-ocean lake sediment, those samples with higher concentrations of chlorinated organics. The microbial communities in the Midwest samples may be less specialized, perhaps as a result of these communities being exposed to lower concentrations of a variety of compounds. This in turn aid in more rapid adaptation to the amended CI-NOM. Based on the 16S rRNA gene sequencing, bacteria other than *Dehalococcoides mccartyi* increased in abundance during incubation with the CI-NOM, including genera of *Anaerolineae* and other *Chloroflexi*, along with the known organohalide respiring bacteria *Desulfitobacterium* and *Desulfomonile*. These bacteria may play a larger role than *D. mccartyi* in the natural chlorine cycle, in which relatively low concentrations of chlorinated NOM are cycled. Additionally, initial analysis of the metagenomes indicated that even though reductive dehalogenation was occurring in the Midwest lakes, no rdh genes were present. Instead, several non-energy-generating dehalogenase genes were found. These genes may play an important role in the biodegradation of low concentration and perhaps less-chlorinated contaminants. These results imply that different bacteria containing different genes (dehalogenase, rather than rdh) may be needed to achieve bioremediation goals at sites with lower concentrations of contaminants.