

Christine Wang

**Carnegie Mellon University
Department of Biological Sciences, Pittsburgh, PA 15213**

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Abstract

Microbial anaerobic dechlorination renders polychlorinated biphenyls (PCBs) less toxic and more biodegradable. Microbial communities from two PCB contaminated sites, the Grasse River (NY) and the Hudson River (NY) sediments were studied to compare their dechlorination activities and other biogeochemical properties associated with reductive dechlorination of PCBs. To (1) test the hypothesis that changes in nutrient amendment may alter microbial dechlorination activities, and (2) characterize the phylogenetic properties and molecular diversity of dechlorinating microbial communities, 40-ppm 2,4,5-trichlorobiphenyl (BZ-29) spiked (nutrient amended) river sediment microcosms, and 16S rDNA clone libraries were prepared, respectively. These two sediments, though shared many properties, such as several nutrient contents and the population size of total aerobic heterotrophs, had distinct soil characteristics, gas production activities, and PCB dechlorination rate. In no nutrient amendment Grasse River sediment microcosms, the sediment of which being more clay, were active in both methane and carbon dioxide production, but the dechlorination did not occur until after a substantial amount of gas had been produced and accumulated in the head space (with seven to 12 weeks of anaerobic incubation). The granular and rocky Hudson River sediment no nutrient amendment microcosms, anaerobically dechlorinate PCBs at a relatively faster pace, within seven weeks of incubation, but no production of methane or any considerable amount of carbon dioxide was observed. All nutrient amendments resulted in an enhancement of dechlorination in Grasse River sediment microcosms. In Hudson River sediment microcosms, however, enhanced dechlorination was observed from organic phosphate (P), organic carbon (F), nitrogen plus organic carbon (NF), organic phosphate plus carbon (PF), and all three nutrient (NPF) amendments, while inhibitions in dechlorination were found in Hudson River sediment microcosms amended with nitrogen (N), or nitrogen plus phosphate (NP).

A lag period preceding dechlorination was observed in the Hudson River sediment microcosms inoculated with viable sediments that had been refrigerated and stored in the dark for nearly two years. Loss of extractable PCB mass over time was also seen in some nutrient amended Hudson River sediment enrichment microcosms.

Several known dehalogenators were present in fresh Grasse River and fresh Hudson River sediments, as well as in the enriched river sediment microcosms. Two dehalogenator groups, *Dehalococcoides* and *Desulfotobacterium* in both Grasse River sediment and Hudson River sediment enriched microcosms were further studied using PCR-based cloning approach. Phylogenetic analysis of the four libraries suggested that (1) in both Grasse River and Hudson River enriched sediment microcosms, the *Desulfotobacterium* communities had higher ecological diversity than the *Dehalococcoides* communities; (2) the enriched Hudson *Dehalococcoides* library had a higher (OTU) richness than the enriched Grasse *Dehalococcoides* library; and (3) in both cases of *Dehalococcoides* and *Desulfotobacterium*, the enriched Grasse and the enriched Hudson 16S rDNA libraries were statistically different.

Lastly, to understand whether the sequence information suggests the function and the substrate specificity of these recently arose dehalogenation enzymes, a phylogenetic analysis of currently known reductive dehalogenases was performed.