Phytoremediation to Degrade Airborne PCB Congeners from Soil and Groundwater Sources

The goal of Project 5 is to understand the mechanisms whereby plants and associated
rhizosphere bacteria may provide bioremediation of lower chlorinated PCBs from contaminated soils and sediments. This project works with all other projects and cores to provide a key element to the overall ISRP center investigating a public health strategy for intervention and reducing human exposure through research and understanding of bioremediation.

Aim 1: Identify plant metabolites of selected PCB congeners (PCB 11, 52, 77, 101, 126, 153) that are semi volatile, persistent, and toxic; and also the uptake/selectivity/metabolism of chiral compounds (PCB 91 and 95). In 2018 researchers showed that 4’-MeO-PCB 3 can be transformed to 4’-OH-PCB 3 by poplar. This is important because plant metabolites can be transferred through the food web, and OH-PCBs are often more toxic than their parent congeners -- they influence reproductive processes, the endocrine system and brain function in mammals. Researchers also investigated biotransformation by human liver microsomes (HLMs) of PCB 91 to OH-PCBs. Three metabolites and several atropisomers were found, as well as considerable variability in biotransformation among individual donor HLMs.

Aim 2: Elucidate the regulation of metabolism of PCBs by poplar plants at the epigenetic and transcriptional levels. In 2018, researchers conducted whole-genome expression analyses (Affymetrix) to compare the effects of 2,5-DCB and three of its OH-isomers, 2’-OH-, 3’-OH-, and 4’-OH-2,5-DCB (at 5 mg L-1), on Arabidopsis plants. The three OH-derivatives induced expression profiles similar to inhibitors of brassinosteroid synthesis resulting in severe iron deficiency in exposed plants. In agreement with these observations, 2’-OH-, 3’-OH-, and 4’-OH-2,5-DCB were shown to downregulate many genes involved in brassinosteroid synthesis and upregulate many genes involved in iron homeostasis.

Aim 3: Identify microorganisms and functional genes associated with PCB dechlorination in enrichment cultures derived from PCB-contaminated soil and in un-enriched PCB-contaminated sediment. Researchers identified potential PCB dechlorinators and gene sequences that may contribute to PCB dechlorination in unenriched contaminated field sediments. To determine if anaerobic natural attenuation could occur in the contaminated sediments and identify organisms and functional genes responsible, researchers established microcosms inoculated with the contaminated sediments. The microcosms contained contaminated sediment as inoculum and reduced anaerobic mineral media under a nitrogen headspace. They measured sediment PCBs, pore water PCBs, 16S sequence abundances of potential dechlorinators, and reductive dehalogenase sequence abundances over a 430 day incubation period. After 430 days, significant changes in the PCB congener concentrations occurred in microcosms with sediments from two locations.

Aim 4: Characterize PCB-induced changes by plants and their associated rhizosphere microorganisms at a contaminated site (Altavista, Virginia) and in contaminated sediments using gene sequencing and transcriptomic responses. To assess the PCB biodegradation capability of Burkholderia xenovorans strain LB400 from enrichment cultures in our lab, a biodegradation test was performed using Aroclor 1248 analytical standard, a mixture of PCB congeners. This Aroclor mixture was chosen because its profile most closely resembles the PCB profile detected at our field site, Altavista Virginia sediment. Relative to dead cell controls, live-cell treatments with and without biphenyl added as an inducing substrate, demonstrated 40% and 43% removal of total PCB concentration, respectively, over 48 hours. Furthermore, results from this biodegradation assay show that LB400 (alone) can degrade a wide spectrum of PCB congeners in the Aroclor 1248 mixture, spanning five homolog groups, up to hexachlorobiphenyls.

Recent Publications:


Datasets:

Datasets from Project 5 can be found on the NIEHS University of Iowa Superfund Research Program website [5].

Project Leader: Jerry L. Schnoor, PhD

Dr. Schnoor will manage the project and guide the research as the Principal Investigator (PI). He has managed over $25 million of research projects since 1980, and has considerable experience as the Editor-in-Chief of Environmental Science and Technology, and serves as the Chair of the EPA-ORD Board of Scientific Counselors. Dr. Schnoor is an international leader in the field of phytoremediation, co-editor of the book Phytoremediation - Transformation and Control of Contaminants (2003), and is the PI of the W.M. Keck PhytoTechnologies Laboratory [6] at the University of Iowa. In 2019 Schnoor received the American Chemical Society Award for Creative Advances in Environmental Science and Technology for pioneering the science and practice of phytoremediation.

Benoit Van Aken, PhD

Dr. Van Aken, George Mason University, leads our effort in the laboratory on molecular biological methods for analysis of catabolic enzymes and metabolic pathways of plants and microorganisms in phytoremediation. He has a background in environmental biotechnology and has published several key papers in the area of metabolite identification and enzymatic pathways. Dr. Van Aken led the discovery of a new endosymbiotic bacteria living inside hybrid poplar trees which mineralizes nitramine explosive compounds, Methylobacterium populi. This research was published in the International Journal of Systematics Evolutionary Microbiology [7] and Applied and Environmental Microbiology [8]

Timothy Mattes, PhD

Professor, Civil and Environmental Engineering, The University of Iowa. Tim's research interests include environmental biotechnology, oxidative biocatalysis, evolution of microbial biodegradation pathways, and the application of genomics and proteomics techniques in the study of environmentally relevant microbial communities.

Hans J. Lehmler, PhD

Professor, the University of Iowa College of Public Health. Dr. Lehmler leads the ISRP Synthesis Core [9].