

***Dehalococcoides* Social Networks in Chlorinated Solvent Environments**

Sebastien Cecillon (sebastien.cecillon@ec-lyon.fr) and Timothy M. Vogel (timothy.vogel@ec-lyon.fr) (Université de Lyon, Ecully, France)

Megan Altizer (Megan.Altizer@asu.edu), Anca G. Delgado (Anca.Delgado@asu.edu), Rosa Krajmalnik-Brown (Dr.Rosy@asu.edu) (Arizona State University, Tempe, AZ, USA)

Background/Objectives. The most commonly used bacteria for the bioremediation of chlorinated compounds, such as PCE and TCE, are *Dehalococcoides* strains. These bacteria are known to be “social” microbes. *Dehalococcoides*-containing microbial communities respond to the arrival of significant concentrations of chemical compounds, whether xenobiotic or not. The different microbial population responding include 1) those that use the compound(s) for energy and/or biomass (e.g., *Dehalococcoides*, other dechlorinators, fermenting bacteria), 2) those that benefit indirectly from the microorganisms that use the compound(s) directly, and 3) those that do not benefit (either by being outcompeted or inhibited, or completely independent). In addition, microorganisms might benefit from one compound and produce metabolites that help others benefit from other compounds. *Dehalococcoides* is thought to need other microorganisms, e.g., *Geobacter*, to provide metabolites and/or co-factors necessary for the degradation processes. These types of relationships can be described with ever increasing complexity and are usually critical for efficient chlorinated compound degradation. Understanding how *Dehalococcoides* interact with other microorganisms and identifying these other microorganisms could improve different bioremediation processes. In a contaminated environment insufficiently treated by *Dehalococcoides* bioaugmentation or biostimulation, identifying missing partners or functions could provide the basis for technology improvement. In metagenomics studies, this information is usually found in the middle of a forest of data. To circumvent the problem, we decided to use algorithms that are not unlike those used in the Panama Papers scandals and that are used daily to analyze social networks.

Approach/Activities. Our approach was to determine the covariance of microorganisms (16S rRNA gene sequencing or phylochips) and functions (high throughput sequencing of environmental DNA) in a range of soils or sediments that have undergone contamination by PCB or PCE, and in which *Dehalococcoides* has been identified as a player for chlorinated compound degradation. We have constructed community networks not unlike the social networks that try to determine who you know and who you might like. The robustness of this approach depends on the number of situations used in the calculations as well as the specificity of different relationships. We could, in this way, reconstruct the (social) network of *Dehalococcoides* and its potential functions and so highlight possible new degradation pathways and relationship with others, depending on the contaminant.

Results/Lessons Learned. When applied to the anaerobic degradation of chlorinated compounds, not only did *Dehalococcoides* reveal its “social” network, highlighting unexpected partners and metabolic pathway and cooperation, but other known dechlorinators and associated hydrogen and acetate producers were identified their social network page. In addition, these dechlorinators, including *Dehalococcoides* strains, had some specific electron transfer functions in their network pages. This approach may aid in deciphering the different microbial requirements for a healthy contaminant degrading subsurface.