Hydro-Biogeochemical Process Dynamics in the Groundwater-Surface Water Interaction Zone: Macroscopic Processes

William Nelson (william.nelson@pnnl.gov) - PNNL, John Zachara (PI), James Stegen (Project Leader); Glenn Hammond; Eric Roden; Tim Johnson; Evan Arntzen; Xingyuan Chen; Chris Murray; Tim Scheibe; James Fredrickson; John Zachara (Co-PIs).

The subsurface zone into which surface water (e.g. river water) intrudes and mixes with groundwater (SIZ) is a major pathway for chemical transfer between terrestrial and aquatic systems. It is a more biogeochemically reactive domain than either groundwater or surface water because within the SIZ, superposition of limiting nutrients from different sources, including O2, C, and N, stimulates biological activity. It is a unique domain where microbial processes link biogeochemical transformation and sequestration of groundwater contaminants to mineralization of C and transformation of N from both groundwater and riverine sources. The Hanford Site 300 Area along the banks of the Columbia River is an excellent system in which to study these dynamics because of the detailed understanding of the hydrology and biogeochemistry of the aquifer.

A local (0.1-km2) section of the hyporheic corridor that represents a constrained transect from inland groundwater through the SIZ to discharge points in surface water will be monitored for microbial community structure, biogeochemical activity and hydrology during short- and long-duration surface water intrusion events. Novel ecological modeling techniques will be used to determine relationships between hydraulic conductivity of sediment deposits, biogeochemistry, contaminant transfer mechanisms and rates, and ecological processes shaping microbial communities.

Preliminary data indicates that organic carbon introduced to the SIZ from intruding river water stimulates microbial activity and, through a coupling with denitrification, yields inorganic carbon species. We hypothesize that within low hydraulic conductivity facies, this activity can result in anoxic conditions conducive to immobilization of U. Microbial communities will be analyzed in terms of operational taxonomic unit (OTU) composition via 16S rRNA gene sequencing (iTag analysis) and metabolic potential via shotgun metagenomic sequencing. Abundance of genes involved in C and N cycling and contaminant transport will be monitored and network analysis performed to assess relationships between environmental parameters, measured activity rates and microbial community composition functional potential.

The information generated by this project will be used to generate a predictive local-scale model of contaminant and C-cycling dynamics that will be generalizable to other groundwater-river water exchange systems.