Hydrobiogeochemical Variability: Mechanisms Governing Reaction- to Basin-Scale Hydrobiogeochemical Regimes

Matt Kaufman[1*], Bob Hall[2], Jesus Gomez-Velez[3], and James Stegen[1]

[1]Pacific Northwest National Laboratory, Richland, WA; [2]University of Montana, Polson, MT; [3]Vanderbilt University, Nashville, TN

Contact: (matthew.kaufman@pnnl.gov)
Project Lead Principal Investigator (PI): Tim Scheibe
BER Program: SBR
Project: PNNL SBR SFA
Project Website: https://sbrsfa.pnnl.gov/

This element of the PNNL SFA seeks to 1) identify places/times across the Columbia River Basin (CRB) in which sediment-associated metabolism strongly influences active channel biogeochemistry, and 2) reveal drivers of underlying molecular properties. Sediment-associated organisms contribute from 3-96% of river corridor respiration. To represent these processes in predictive models, understanding how and why they vary in space and time is critical. Our team's recent work predicts spatial variation in sediment contributions to respiration (ERsed). To evaluate these predictions, we will use dissolved oxygen (DO) sensors across 1st-8th order streams in the Columbia River Basin (CRB). Sites will be in 4 sub-basins. At each location we will deploy two DO sensors: one open to channel water and one in a transiently open/closed chamber for 'dark bottle' incubations (DBIs). Results will be modeled to estimate total respiration for the integrated system (ERtot). Gross primary production (GPP) will be modeled by combining the DO data with stream morphology and flow. DBIs will be used to estimate respiration in the water column (ERwater). ERsed is found by difference: ERsed=ERtot- ERwater. Repeated DBIs will estimate dynamics of ERsed, which has never been quantified at the basin scale. Outcomes will be compared to NEXSS model predictions to guide additional mechanistic representation), enabling basin-scale ModEx.

At locations with large ERsed, we will study dissolved organic matter (DOM) chemistry and microbial gene expression. Field surveys across scales (expanded significantly by WHONDRS) indicate a diverse and variable molecular composition of DOM. Given the high reactivity of channel sediments, we expect DOM chemistry in both surface and pore waters will vary across reaches with large ERsed. Furthermore, microbes are key to translating variation in DOM chemistry to shifts in biogeochemical rates and solute dynamics. In turn, we expect reach-scale gradients in DOM chemistry, microbial gene expression, and nutrient concentrations. We will use surface water, pore water, and sediment samples distributed across reaches with large ERsed to test these hypotheses. DOM chemistry will be characterized using FTICR-MS, GC-MS, LC- MS, and NMR. Microbial gene expression will be quantified via metatranscriptomics, leveraging our active JGI project building a database of river corridor microbial genomes across >400 sites.