Applying "R-Osmos" To Quantify Hot-Moments in a High Mountain Watershed: Co-Development of Novel Methodology To Advance Terrestrial-Aquatic Interface Models

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Project Abstract: Watershed function is driven by habitat heterogeneity and microbial activity integrated over space and time. These habitats experience seasonal changes in redox zonation with water flow shifting biogeochemical cycles and perturbing the microbial communities that mediate biogeochemical processes. Features such as river meanders can create hot spots of biological activity, however they must be directly sampled to be understood. This newly funded project will quantify the impact of hot spots and moments on microbial rates, focusing on two critical processes: methane (CH_4) oxidation and nitrate (NO_3) reduction, at the DOE's East River Watershed Function Science Focus Area. We will deploy novel, continuous, time-integrating, *in-situ* microbial rate samplers to inform the magnitude and variation in biogeochemical processes across the terrestrial-aquatic interface, which upon completion, will be used to refine a reactive transport model for this area. To accomplish this goal, we will use uniquely configured osmotic samplers (OsmoSamplers) to continuously quantify the rate at which microbial communities transform methane and nitrate on either side of a meander. OsmoSamplers use a diffusion gradient to slowly pump water into tubes of such small diameter that sample mixing is negated. Multiple OsmoSamplers can be used together to continuously add solutes, preservatives, or collect samples for later analysis, providing a record of hot moments in long-term datasets. In this work, we will use rate-osmotic samplers (R-osmos) to acquire spatially explicit rate measurements by adding nitrate and methane (separately) to discern transformation of these critical compounds. Rates will be coupled with quantifications of natural solute composition (both NO_3 and CH_4) and quantitative gene abundance for the relevant processes (i.e., genes responsible for nitrate reductase and methane monooxygenase) allowing us to connect solute, rate, and microbiome characteristics. This project was recently initiated, with the majority of the work thus far being preparation for our planned year-long field deployment that will commence in summer 2022. In this presentation, we will cover the overall aims of the project, update progress to date, and highlight opportunities that this research framework may provide for collaboration with other SFA users.