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Methane and Nitrous Oxide Pore-Water Concentration and Flux at the Hyporheic Zone of a Large River

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Greenhouse gas (GHG) emissions from rivers are a critical missing component of current global GHG models. Their exclusion is mainly due to a lack of in-situ measurements and to a poor understanding of the spatiotemporal dynamics of GHG production and emissions which prevents optimal model parametrization. In this project, we are conducting data-driven field research on the hyporheic zone of a river shore section of the Columbia River. We aim to understand at an ecosite scale: (*i*) where and when are GHGs produced and if the production is impacted by river stage, (*ii*) what microbial processes control production and consumption of GHGs and, (*iii*) what is the effect of environmental conditions on GHG production at the Columbia River nearshore environment and what is the scale in which they operate and could be best modeled. We are using a multidisciplinary approach combining pore dialysis peepers to determine pore water concentration of GHGs, co-located GHG flux measurements with non-steady-state accumulation chambers, meta-omics of microbial communities in the sediment profile to identify microbial processes, and modeling to scale and interpret the observations. We have installed nine peepers in three transects covering shallow, intermediate and deep-water levels. Measurements of pore water concentration of methane (CH_4) and nitrous oxide (N_2O), and co-located flux measurements, were conducted during three different hydrological conditions (rising, falling and falling highly-regulated river stages). Overall, integrated CH_4 porewater concentrations along the sediment profile followed a pattern similar to that of CH_4 fluxes for the three water levels of the gradient during the hydrological conditions considered. However, hotspots in porewater concentrations occurred at different depths in the profile, indicating the influence of groundwater mixing in the patterns observed. In turn, N_2O porewater did not show discernible patterns for the hydrological conditions, and fluxes did not show statistical differences along the gradient of water levels. The next steps in our study are to link concentration and flux results with metagenomic and metatranscriptomic data to help explain the patterns observed (or lack thereof), and parametrize the biogeochemical model *ecosys* to represent individual microbial processes and evaluate their scaling across depths and spatially distinct sites. We expect that our findings help improve predictive understanding of how watersheds function as complex hydrobiogeochemical systems. We also envision that data and results generated in this project will benefit reactive transport models of microbial carbon cycling that can be integrated into the U.S. DOE ACME Land Model (ALM).