Understanding Environmental Controls on the Composition, Function, and Cycling of Mercury within Fluvial Periphyton

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Project Abstract: Periphyton biofilms are complex assemblages that consist of algae, bacteria, fungi, detritus, extracellular polymers, invertebrates, and mineral particles. These complex biofilms play an integral role in stream ecohydrology as they are control points for ecosystem respiration, primary productivity, and organic matter cycling, while providing an important food source for higher trophic position organisms. Identifying the environmental physicochemical factors (e.g., disturbance regime, nutrient concentrations) that contribute to observed variability in fluvial biofilm community structure and function is needed for developing predictive models of stream biogeochemistry.

One poorly constrained biogeochemical function of fluvial biofilms is the production of monomethylmercury (MMHg) from inorganic mercury (Hg). Fluvial periphyton communities host the active anaerobic microbes capable of the microbially-catalyzed production of MMHg due to the steep geochemical gradients between fully oxic and anoxic conditions within these biofilms. Controlled laboratory experiments have demonstrated that actively photosynthesizing biofilms may generate a significant fraction of the MMHg flux in East Fork Poplar Creek (EFPC), a Hg contaminated creek in Oak Ridge, TN.

To better understand the relationship between environmental physicochemical factors and periphyton biofilm composition and function, we are conducting in-stream experiments within EFPC across multiple seasons to control for temporal variability. Utilizing a natural gradient of nutrient concentrations between two locations within EFPC, we can determine functional characteristics of biofilm colonized under relatively lower and higher nutrient concentrations, as well as assess the impacts of altering the nutrient regime to which an established periphyton community is exposed via physical translocation between locations. The resulting biofilms are then used in experiments to quantify measures of function (Hg methylation and MMHg demethylation kinetics, production of thiol-containing biomolecules) and community composition

(16s, 18s, ITS, and *hgcA* sequencing). Application of our transient availability model, developed for quantifying Hg methylation kinetics in biofilms, to biofilms grown under experimental treatments of varying length will allow us to quantify the impact of seasonally variable physicochemical factors on periphyton methylation rates. Sequencing data will be utilized to evaluate the relative impacts of community structure and interaction within the periphyton microbiome that drive variations in observed rates of Hg transformation. By providing insights into the environmental controls on the community composition and function of complex fluvial biofilms, this work aims to inform future research into the critical ecosystem processes in river corridors impacted by the activity of periphyton assemblages.