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Effects of Salinity on Methylmercury Production and Microbial Community Composition in Everglades Coastal Mangroves

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Mercury (Hg) is an anthropogenic contaminant impacting aquatic food webs worldwide. In anoxic environments, such as wetland sediments, anaerobic microorganisms carrying the *hgcAB* gene pair convert inorganic Hg(II) to neurotoxic methylmercury (MeHg), a critical step in the bioaccumulation and biomagnification of MeHg in aquatic food webs. MeHg formation is governed by several biogeochemical factors, including (1) dissolved organic matter (DOM), (2) sulfate and sulfide, and (3) activity of *hgcAB*-carrying microorganisms. Although these controls are well-characterized in freshwater wetlands, saltwater intrusion poses a new threat to coastal wetlands by altering aqueous geochemistry and microbial dynamics, resulting in unknown consequences for Hg cycling. We hypothesize that inundation of coastal wetland soils will create hotspots of MeHg formation at oligohaline salinity regimes (0.5 – 5 parts per thousand (ppt)) due to the stimulation of *hgcAB*-carrying sulfate-reducing bacteria from marine sulfate inputs. To test our hypothesis, we sampled surface water, porewater, and sediments across a salinity gradient (ranging from < 0.5 ppt to > 30 ppt) within Everglades National Park over two years in wet and dry seasons. We measured Hg species, biogeochemical constituents that influence Hg speciation or reflect microbial activity (e.g., DOM, sulfate, sulfide, methane, small organic acids), and performed metagenomic sequencing on DNA from sediments. Porewater sulfide concentrations in oligohaline and mesohaline zones were elevated compared to freshwater and marine conditions, reflecting active sulfate-reduction under moderate marine sulfate inputs (*Figure 1A*). Porewaters between freshwater to mesohaline regions contained elevated concentrations of aromatic DOM (*Figure 1B*) and higher MeHg concentrations compared to marine endmembers (*Figure 1C*), reflecting enhanced Hg(II) bioavailability to methylating organisms. Seasonal comparisons showed that enhanced marine sulfate intrusion during the dry season shifted the location of MeHg formation along the salinity gradient, offering a window into future conditions that may alter MeHg production in coastal wetlands. Assembled metagenomes were used to examine the abundance and diversity of *hgcAB*-carrying microorganisms and to identify the microbial metabolic pathways facilitating MeHg formation across salinity gradients. Together, these microbial and geochemical findings provide insight into how saltwater intrusion may influence Hg cycling and MeHg production in coastal wetlands.

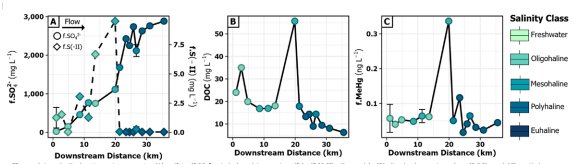

Figure 1. Longitudinal patterns in porewater (A) sulfate (f.SO_4^{2-}, circles) and inorganic sulfide (f.S(-II), diamonds), (B) dissolved organic carbon (DOC), and (C) methylmercury (f.MeHg) concentrations over a 35 km salinity gradient in Everglades National Park. Points represent individual sampling sites colored by salinity class, as determined by field conductivity at the time of sampling. Average concentrations are presented for field replicates with error bars presenting the minimum and maximum observed concentrations; some error bars are smaller than data symbols.