The river-to-sea salinity gradient drives microbial diversity and functional patterns

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Abstract

Fresh water flows from rivers to estuaries and then to the sea, creating a salinity gradient as it meets the salt water of the ocean. While this salinity gradient is likely to have profound effects on the organisms that call these habitats home, its impact on microbial communities is far from clear. To fill this gap, researchers recently used genomic, transcriptomic, and geochemical data to examine microbial variation in both benthic and planktonic environments along a river-to-sea continuum. They observed a distinct increase in osmoregulation-related gene expression with increasing salinity and noted a prevalence of phosphate-acquisition activities among microorganisms inhabiting the freshwater zone, likely resulting from phosphate limitation, while carbon-, nitrogen-, and sulfur-cycling processes became dominant in brackish water, due to higher nutrient levels. In these brackish waters, photosynthesis was mainly conducted by cryptomonads in the water column and diatoms in the sediment. Interestingly, despite the predominance of bacteria across the whole continuum, ammonia oxidation was carried out mostly by archaea, while photosynthesis was mainly performed by microeukaryotes. These findings demonstrate the existence of clear ecosystem boundaries in an interconnected system, lending insight into the ecological roles of microbes in coastal environments as they become increasingly impacted by anthropogenic stressors.