

Marine oxygen minimum zones (OMZs) support complex microbial assemblages with major roles in ocean biogeochemistry, including the cycling of climate active gases. Characterizing the structure and function of these communities is critical as low-oxygen waters are predicted to expand in frequency and extent under global climate change. The integration of sequence-intensive genomic analyses with coupled biogeochemical measurements is enhancing our understanding of OMZ microorganisms, revealing a richness of metabolic processes structured along the vertical redox gradient and previously unrecognized linkages between pelagic elemental cycles. For example, recent work by our lab has helped identify novel clades of OMZ bacteria mediating anaerobic methane and sulfide oxidation coupled to denitrification, as well as previously unrecognized adaptations to anaerobic metabolism by the world's most abundant bacterium. This talk highlights these and other OMZ metabolic processes in relationship to key environmental drivers, including water column nutrient and redox gradients and the microscale partitioning of communities between organic particle-associated and free-living microniches. Coupled genomic-biogeochemistry studies are necessary for understanding how oxygen concentration constrains pelagic microbial diversity and activity, and consequently for predicting how future de-oxygenation may affect elemental cycles and ecosystem structure.