

**PROTEOMIC CHARACTERIZATION OF CENTRAL PACIFIC OXYGEN MINIMUM ZONE MICROBIAL COMMUNITIES.** Jaclyn K. Saunders<sup>1\*</sup>, Matthew McIlvin<sup>1</sup>, Dawn Moran<sup>1</sup>, Noelle Held<sup>1</sup>, Joe Futrelle<sup>1</sup>, Eric Webb<sup>2</sup>, Alyson Santoro<sup>3</sup>, Chris Dupont<sup>4</sup>, Mak Saito<sup>1\*</sup>. <sup>1</sup> Woods Hole Oceanographic Inst., <sup>2</sup> University of Southern California, <sup>3</sup> University of California, Santa Cruz, <sup>4</sup> J. Craig Venter Institute, \* Corresponding authors (jsaunders@whoi.edu & msaito@whoi.edu).

**Introduction:** Marine Oxygen Minimum Zones (OMZs) are regions of extremely low oxygen concentration which naturally occur and span about 1% of global ocean volume [1]. OMZs are extant models of ancient reducing oceans which prevailed during the Precambrian era. These oxygen deficient waters support chemosynthetic metabolisms that may be analogs for potential anoxygenic metabolisms supported on other oceanic exoplanets. In the absence of oxygen, nitrate is the next best electron acceptor for respiration therefore many microbes in OMZs make a living off of reducing nitrate to N<sub>2</sub> [2] resulting in 30-50% of global nitrogen loss occurring in OMZs [1]. The anoxic waters of OMZs support rare metabolisms including anammox, sulfate reduction, and methanogenesis amongst others [1].

The enzymes of these metabolisms are truly the engines driving biogeochemical cycles in the marine environment. In 2016, the ProteOMZ Expedition, a 6,000 kilometer transect across the Central Pacific Ocean, passed through the Eastern Tropical Pacific Oxygen Minimum Zone. Microbial metaproteomic samples throughout the pelagic water column, from the 0.2-3 µm size fraction, were analyzed providing a community profile of the microbial proteins present in these waters. The proteomic data, consisting of over 60,000 identified proteins from 103 samples, displayed strong relationships with physical and chemical oceanographic features, such as oxygen concentration. Nitrogen cycling enzymes were abundant within the most oxygen depleted waters, proteins associated with arsenic-related metabolisms were identified, and nutrient limitation patterns were evident within the cyanobacterial associated proteins.

Community proteomic profiling methods are ideal for surveying vast expanses in order to characterize the linkages between microbial communities and the biochemical transformations they mediate. Results from the ProteOMZ proteomic profiling transect in the Central Pacific demonstrate the capacity of this technique to identify and track the presence and distribution of key metabolic enzymes in marine pelagic ecosystems.

**References:** [1] Lam, P & Kuypers, M.M.M. (2011) *Ann Rev Mar Sci*, 3, 317-345. [2] Ulloa, O. *et al.* (2012) *PNAS*, 109, 15996-160003.