

COUPLING METAPROTEOMICS WITH ORGANIC BIOMARKERS TO DETERMINE FUNCTIONAL RESPONSES OF NATIVE MICROBIOMES TO ORGANIC INPUTS IN THE WESTERN ARCTIC OCEAN

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How the functionality of marine microbial communities change over time and space are essential to understanding the ecology the regulation of elemental cycles in the oceans. We investigated the community metabolic response and degradation potential of two compositionally distinct marine microbiomes within the shallow shelf ecosystem of the Chukchi Sea following rapid fluctuations in algal organic matter availability. Novel bioinformatic tools were used with community proteomic (metaproteomic) techniques to characterize and quantify changes in bacterial community functioning and composition over time in parallel with changes in organic composition as lipid and amino acid biomarkers. Using a novel peptide-based enrichment analysis, significant changes in biological and molecular functions associated with carbon and nitrogen recycling were observed with microbiomes expressing increased peptides correlated to protein synthesis, carbohydrate degradation and cellular redox processes, while decreasing C1 metabolism. These findings argue that conditions which select for certain bacterial groups in the western Arctic Ocean may nevertheless show similar impacts on local chemical gradients. The information gained provides insight into the timing and characterization of *in situ* bacterial community responses to realistic environmental perturbations and how they influence changes in organic composition through selective degradation.