Proteome Changes associated with Salinity Stress and DMSP Accumulation in *Fragilariopsis cylindrus*

Barbara R. Lyon[1,2,3], Peter A. Lee[2], Giacomo R. DiTullio[1,2] and Michael G. Janech[1,3,4]

[1] *Marine Biomedicine and Environmental Sciences Center, Medical University of South Carolina*
[2] *Hollings Marine Laboratory, College of Charleston*
[3] *Dept. of Medicine, Division of Nephrology, Medical University of South Carolina*
[4] *Ralph H. Johnson VA Medical Center, Charleston, SC*

Sea-ice diatoms comprise the greatest portion of biomass in fast and pack ice environments and have been identified as important contributors to global biogeochemical and climate cycles, in part through their production of dimethylsulfoniopropionate (DMSP). DMSP can be cleaved to form volatile dimethylsulfide (DMS), which affects both atmospheric chemistry and the earth's radiation budget. Therefore, understanding the impact of environmental parameters on the cellular biology associated with DMSP production is of critical importance to predicting interactions and effects of climate change and sea-ice loss. Ice-diatoms encounter extreme salinity gradients during seasonal environmental cycles. DMSP is a compatible solute that may serve osmoregulatory functions and act as an antioxidant during salinity acclimation. A previous experiment with *F. cylindrus* confirmed the hypotheses: (1) hypoosmotic conditions decrease intracellular DMSP with concomitant increase in the dissolved fraction (2) hyperosmotic conditions increase intracellular DMSP. The current experiment investigated global proteome changes associated with increases in intracellular DMSP under high salinity with the hypothesis that a subset of significantly up or down regulated proteins will be associated with osmotic stress and increased DMSP concentrations. Axenic log-phase cultures initially grown at salinity of 35 were gradually shifted over 24 hours to a treatment salinity of 70 or maintained at 35 control salinity (5 biological replicates per group). Cell density, DMSP, photosynthetic efficiency, pigment and protein changes were assessed at 48 hours. Two-dimensional gel electrophoresis was used to identify protein spots significantly increased or decreased in abundance (student's t-test, $p \leq 0.02$). These spots were selected for identification by tandem mass spectrometry. Results included decreases in light harvesting complex proteins, along with increases in general stress response, compatible solute synthesis, and S-adenosyl methionine (SAM) active methyl cycle proteins. This later group of proteins indicates the activated methyl cycle could be an important part of DMSP synthesis.

This work is supported by NSF-ANT-0739597 and NSF-ANT-0739446.