Proteomic analysis of Acropora cervicornis exposed to thermal acclimation

Samantha Shaw*¹, Anderson Mayfield², Cliff Ross¹, and Matthew Gilg¹

¹University of North Florida, Jacksonville, FL, 32224.

²National Museum of Marine Biology and Aquarium, Pingtung 944, Taiwan.

Abstract

Continuous warming of the oceans has led to increased bleaching events and higher levels of disease susceptibility. Current scientific efforts have predominately focused on utilizing transcriptomics to understand thermal stress responses. These efforts have shown that corals possess plasticity in their response to thermal stress, with certain genotypes responding well and surviving longer after an initial heat acclimation period. To better understand the mechanisms by which acclimation occurs, the proteomic response to thermal acclimation and heat stress of previously studied genotypes was analyzed. The three least and most plastic genotypes from a prior study were utilized. Fragments of each genotype were acclimated at 30°C for four days, returned to ambient temperatures (27°C) for five days, and then heat stressed at 32°C for 2 days. Samples for proteomic analysis were taken on day 0, before the experiment began, and then at each temperature transition. Data will be shown regarding proteomic changes throughout the acclimation process and subsequent heat stress. Comparisons among genotypes illustrate differences in thermal acclimation abilities.

*Email: <u>s.shaw@unf.edu</u>