50. Examining the post-transcriptional program governing the metabolic proteome of Micromonas pusilla

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Project Goals: To develop a systems biology approach to the study of the widespread marine alga *Micromonas* and use it to investigate gene function, pathways and consequences of environmental perturbations on primary production.

We are developing a model system for understanding land plant evolution and ecologically important marine primary producers. Thus far there are no such model systems for the Viridiplantae - the eukaryotic lineage containing all land plants and green algae. The primary drivers for developing our *Micromonas* system are: *i*) approximately half of global photosynthetic CO_2 uptake is performed by marine algae yet there is little understanding of the physiological consequences of current global change scenarios and *ii*) green algae provide insights to eukaryotic cellular processes and the ancestor of land plants.

Prasinophytes are a group of unicellular marine green algae that are evolutionarily distinct from the model green alga *Chlamydomonas*, but are related to both the latter and land plants. *Micromonas* is a widespread prasinophyte that is exceptional in its size (<2 micrometer diameter) and has a small genome (21 Mb). For our project, we focus upon the analysis of the metabolic proteome of *Micromonas pusilla*, a *Micromonas* strain that, notably, lacks known machinery for miRNA-based translational regulation. To examine this, we utilized a strategy that performed whole transcriptome and proteome profiling over the course of a triplicated diel experiment. Comparisons of the matched RNAseq and MS/LC proteomics samples indicated that considerable differences exist between dynamics of the transcriptomic and proteomics expression programs. Less than 10% of the genes considered for this analysis had correlated transcriptomic and proteomics expression profiles.

Despite these differences in the expression dynamics, transcriptomic and proteomic expression still exhibited considerable correlation between genes belonging to the same pathways. To examine these differences in the expression dynamics, we utilized an integrative regression framework which incorporated the matched RNAseq and MS/LC proteomics, along with other measures of various mechanisms of post-transcriptional control to generate several high- accuracy global models of protein expression. In addition, we also identified 22 co-expressed gene groups (modules) containing genes that share similar expression profiles in both the transcriptomic and proteomic data. Of these, we focused on three gene modules that are each enriched with genes in the oxygenic photosynthesis pathway. While all three gene clusters share similar mRNA expression profiles, they also exhibit highly dissimilar protein expression profiles. As a final step, we identify several potential mechanisms of post-transcriptional control which may explain the different proteomic expression programs of these gene modules.

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