Introduction

Corals are highly susceptible to environmental heat stress, as it can induce the expulsion of symbionts, referred to as coral bleaching. Understanding how elevated temperatures are affecting the genotype-specific transcriptional changes in coral is important for evaluating the response of coral reefs to rising global temperatures. However, many genes associated with the thermal stress response remain unannotated, termed “dark genes.” Reviewing gene expression networks can provide a framework for the annotation of dark genes that could enhance the understanding of the coral gene function.

The purpose of this study is to investigate how genotypic variation influences the differential expression of “dark” genes exposed to thermal stress and identify candidate “dark genes” that warrant further functional analysis.

Questions:
1. How does “dark gene” expression change between genotypes of coral under thermal stress?
2. What proportion of the differentially expressed genes are “dark” and how many “dark genes” are unique to each genotype?

Global Gene Expression Profile

Based on the normalization results of variance in the dataset, the PCA of time point 3 (TP3) showed the most variation in the treatment effect on each genotype.

Conclusions and Future Directions

1. “Dark gene” expression was significantly influenced by genotypic variation.
2. Four candidate “dark genes” with significant expression levels were identified that could be influential for the understanding of the bleaching response:
   - gfas1.m1.7037.m1
   - gfas1.m1.4504.m1
   - gfas1.m1.15168.m1
   - gfas1.m1.19938.m1
3. Characterizing these identified “dark genes” could enhance our understanding of both the genotype-specific nature of the thermal stress response and the thermal response in general.
4. Now that we have specific gene candidates, future directions should further characterize these genes through correlations with metabolomics, proteomics, and reverse genetics.

Acknowledgments and References

The work of this project would not have been possible without the invaluable help of Dr. Kevin Wong, Dr. Natalia Andrade Rodriguez, and Dr. Nikki Traylor-Knowles as well as the financial assistance of the Lou and Chosun Mastriani Undergraduate Research Award and the EDGE CMT NSF Grant: 2128071.

References