



The role of DNA methylation in environmental memory within and across generations in *Porites astreoides*



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Context

- Epigenetics mechanisms may facilitate intra- and cross-generational acclimatization, as marks can be influenced by environmental stimuli and inherited across generations¹
- Recent evidence has suggested that corals have the potential to rapidly acclimatize to stress events within and across generations outlining the potential resilience of these species to future climate change projections²
- One of the most studied epigenetic mechanisms is DNA methylation, which refers to the addition of a methyl group on cytosines primarily in a CpG context³
- In invertebrates, DNA methylation in gene bodies has been hypothesized to fine tune gene expression by reducing transcriptional noise and spurious transcription, or produce splice variants⁴

Objectives

- Determine if DNA methylation patterns differ due to long- or short-term thermal history.
- Determine if DNA methylation patterns differ due to life stages.

Major Findings

Global DNA methylation profiles differ by long term thermal history (Origin) and life stage

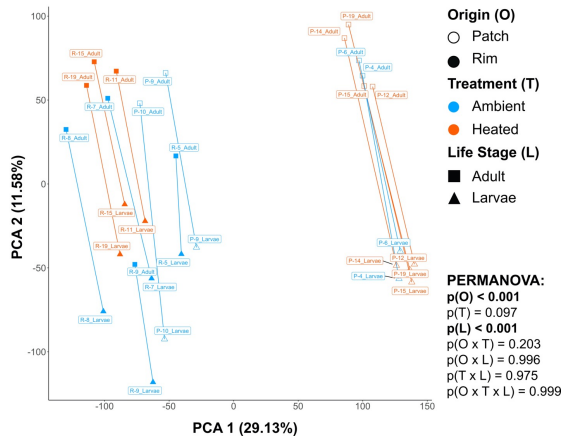


Figure 2. Principal component analysis of global DNA methylation profiles.

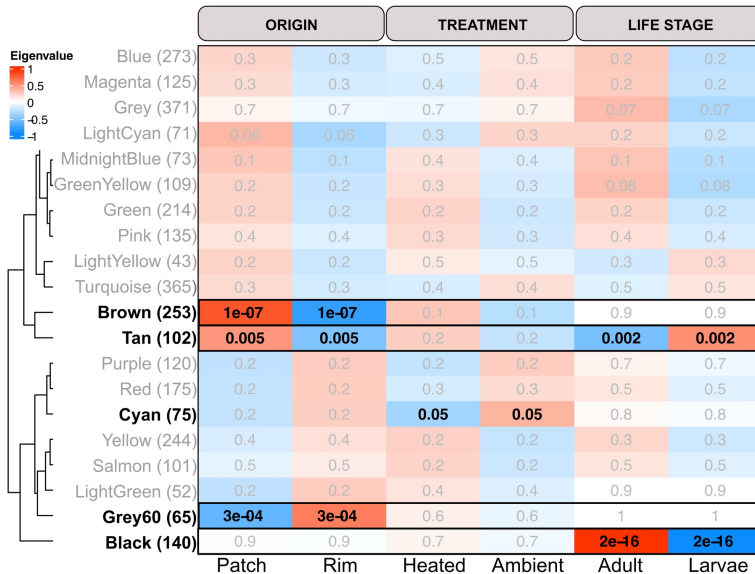


Figure 3. Weighted Gene Co-expression Network Analysis (WGCNA) module-trait correlations.

Methods

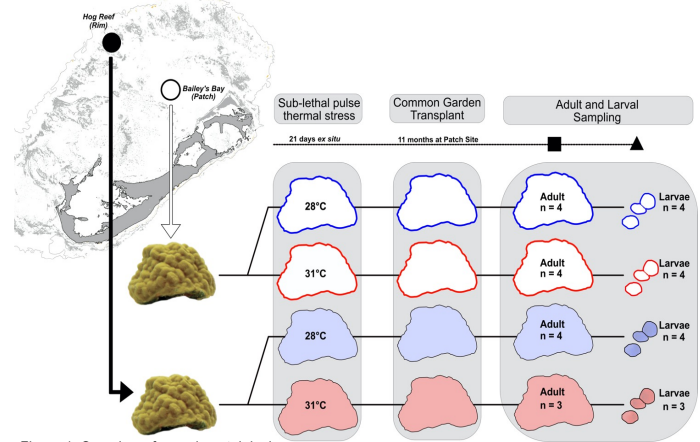
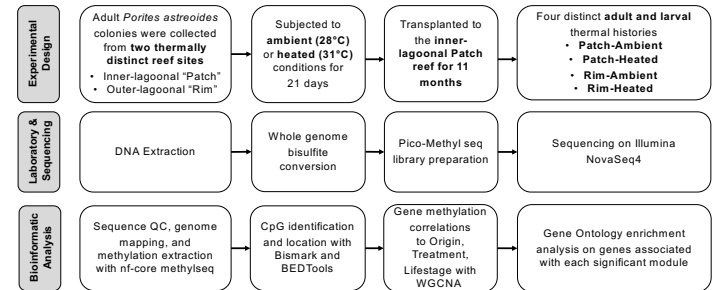


Figure 1. Overview of experimental design



Site of Origin GO Terms

- Increased methylation on wound regeneration (notch binding) and protein processing genes relating to more stressful environments (Patch)
- Increased methylation on genes relating to mitochondrial function and regulation of other epigenetic processes (histones) in the Patch samples

Life Stage GO Terms

- Adults had increased methylation on genes relating to mitochondrial function, possibly for increased metabolic demands
- Larvae had increased methylation on genes relating to microfilament motor activity and lipid utilization

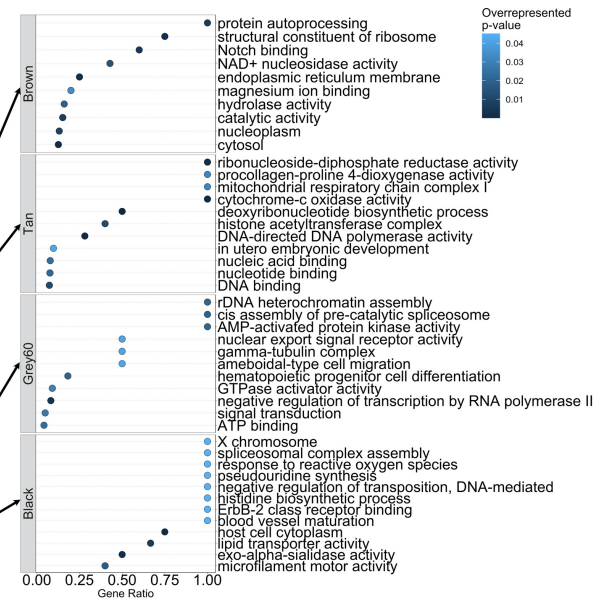


Figure 4. Significant gene ontology enrichment terms for each highlighted WGCNA module.