

How reef corals respond to local heat stress: seasonal and experimental insights from *Leptoria phrygia*

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Coral resilience depends on the capacity to tolerate and respond to environmental variability under ongoing climate change. In southern Taiwan, corals inhabiting the nuclear power plant outlet (NPPOL) are chronically exposed to elevated and highly fluctuating seawater temperatures compared with nearby reefs at Wanlitong (WLT). To investigate the molecular basis of coral responses to contrasting thermal environments, we generated a high-quality reference genome for the reef-building coral *Leptoria phrygia* and integrated seasonal transcriptomic analyses from both field populations. Despite high connectivity and low genetic differentiation between sites, *L. phrygia* exhibited distinct seasonal transcriptional dynamics associated with local environmental conditions. Corals from NPPOL showed stronger seasonal shifts in gene expression than those from WLT. Differentially expressed genes were enriched in pathways related to metabolism, apoptosis, cytoskeletal remodeling, and tricarboxylic acid (TCA) cycle regulation during summer and winter periods. Additional enrichment analyses identified genes involved in translation, protein biosynthesis, and post-transcriptional regulation as important components of the seasonal response. Several stress-associated and regulatory genes, including vitellogenins and Ca²⁺-homeostasis genes, were consistently associated with environmental variation and may represent candidate markers of resilience. These findings suggest that coral responses to thermally variable environments are characterized by pronounced transcriptional reorganization rather than strong population-level genetic divergence. Our study provides an important genomic resource for *L. phrygia* and offers new insights into the molecular mechanisms underlying coral responses to localized thermal anomalies in reef ecosystems.