

**Impact of Thermal Stress on Microbiome Composition and Diversity in the Mussel  
*Brachidontes pharaonis* (P. Fischer, 1870)**

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The rapid ocean warming associated with current climate change is a major stressor to marine organisms which can be direct, e.g., on the organism physiology, or indirect, for example, by impacting the associated microbiome. This latter aspect is so far much less studied. We tested the impact of warming on the rocky intertidal, tropical invader mussel *Brachidontes pharaonis*, now dominating many shores in the south and eastern Mediterranean Sea. However, *B. pharaonis* suffered mass mortality in the Summer of 2016, potentially due to a pathogenic response associated with heat stress. We hypothesized that elevated temperatures can disrupt physiological processes and alter the diversity of its microbiome. We exposed the mussels to both chronic (10 temperature steps) and acute heat stress (15°C and 30°C, as compared to 19°C Winter ambient). We assessed microbiome composition and diversity using amplicon sequencing of the 16S rRNA gene. We found that elevated temperature (30°C) significantly altered the mussel's microbiome, making it more diverse. There was an increase in the abundance of Firmicutes, Cyanobacteria, and Bacteroidota, at the expense of dominant Proteobacteria. Key microbial taxa, including *Endozoicomonas* and potentially pathogenic *Vibrio*, shifted significantly between control and treatment groups, highlighting the impact of temperature on microbiome composition. The response to chronic heat stress is currently being evaluated. This study provides initial insights into how rising temperatures affect the microbiome of *B. pharaonis*, indicating significant impacts on microbial community structure due to acute and chronic thermal stress.

**Key words:** *B. pharaonis*, thermal stress, gut microbiome, 16S rRNA gene, elevated temperature.