

Understanding Mechanisms of Temperature Adaptation Through Genome-scale Modeling and Transcriptomics

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The adaptation of marine microbes to diverse temperature conditions plays an important role in niche selection and could influence the composition and functional diversity of microbial communities. However, significant knowledge gaps remain in the potential mechanisms underlying the metabolic changes induced by temperature variations. Here, integrating genome-scale modeling with transcriptomics, we investigate the metabolic and functional variations of the deep-sea bacteria *Shewanella psychrophila* WP2 under different temperature regimes. Through the incorporation of temperature, reaction thermodynamics, and metabolite concentrations into the modeling of metabolic flux, our model revealed significant variability within the pathways of amino acids metabolism, nucleotide metabolism, and some parts of co-factor biosynthesis, under non-optimal temperatures.

The model-based prediction was overall corroborated with transcriptome samples taken from the early, mid, and late exponential phases for WP2 cultivated under the optimal (15°C), low (4°C), and high temperature (20°C) conditions. Specifically, the increased expression of various amino acid metabolism genes shows a potential role for this pathway in responding to changes in reactive oxygen stress and membrane fluidity. This study provides an example for future studies of key microbes in the Narragansett Bay. With future accumulation of GEMs for various cultivated organisms and environmental microbiomes, we will explore the metabolic dynamics and evolution of diverse microbial communities under changing temperature.