

Influence of the mitochondrial genome on patterns of gene expression in response to temperature stress in the European green crab (*Carcinus maenas*)
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(set of mutations in the mitochondrial DNA)

(Coyle et al. 2019). This was sequenced with a depth of 10 million reads each. To analyze this data, a reference

transcriptome was first assembled which used the raw data to compile a list of all RNA transcripts belonging to the green crab. This was accomplished with a series of programs including Trimmomatic (raw data filtering), Trinity (basic assembly) and BlastN (gene annotation) to yield a set of 70,000 transcripts. Then, using this, expression levels for each sequence were quantified and compared between samples/conditions using differential expression analysis (DEA). In doing so, only 9 differentially expressed genes were observed with a false discovery rate (FDR) under 5%, but many of these provided novel insights. Most notably, cytochrome C oxidase 1 (COI) and NADH dehydrogenase 1 (ND1), genes encoded by the mitochondria, were upregulated in the cold haplotypes at all temperatures. This indicates that mitochondrial haplotype influences its own expression, potentially altering ATP production during oxidative phosphorylation. Another interesting gene was AGPAT4 (Acylglycerophosphate acyltransferase 4) which was upregulated in warm haplotypes at 13.5°C as the most significant gene in any comparison (FDR < 0.0005%). It is involved with phospholipid biosynthesis and cell signaling, pointing towards a new potential pathway to explore.

The finding of constitutive upregulation of mitochondrial genes is especially notable, suggesting that thermal tolerance is not driven by stress response but instead a baseline expression profile. Furthermore, it indicates that other proteins must be regulating transcript persistence since transcription itself is equal across all mitochondrial genes (due to the genome's polycistronic nature) (Mercer et al. 2011). These results set the foundation for additional

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References:

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