

Transcriptomic analysis of the Northern Krill (*Meganyctiphanes norvegica*)

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The Northern krill, *Meganyctiphanes norvegica*, is an abundant and widely distributed species in the North Atlantic that is an important prey item and can contribute significantly to carbon flux. Due to its extensive distribution and diel vertically migratory habits the species is naturally exposed to a wide range of temperatures, although populations show a very narrow physiological adaptation to local temperatures. To explore the gene patterns underlying this apparent ecophysiological sensitivity to variations in local thermal exposure, a RNAseq experiment was run using organisms collected with a MOCNESS from the Gulf of Maine in November of 2014. Healthy individuals were maintained in the laboratory at either 9° or 12° C for 3 days and provided food ad libitum. At the conclusion of the temperature exposure actively swimming individuals were preserved in RNAlater. The gender and cephalothorax size of each animal was documented and then RNA was extracted from equal middle sections of tail, randomly pooled in sets of five individuals per library, and sequenced on an Illumina HiSeq 2500 as a 125 bp PE project. Assembly and differential expression analyses were performed with the Trinity package and associated pipeline. Our de novo assembly of the transcriptome of these individuals provides initial insight into the gene expression and response of this keystone species to temperature fluctuations in the Gulf of Maine and provides sequences for further directed investigations.