

High Throughput RNA Sequencing Reveals Temperature Tolerance Mechanisms in *Scylla serrata*

Ma. Carmen Ablan-Lagman¹ and Eli Meyer²

¹Biology Department, De La Salle University
2401 Taft Avenue Malate 1004, Manila
ma.carmen.lagman@dlsu.edu.ph

²Department of Systematic Biology, Oregon State University
Cordley Hall, Corvallis 93371 Oregon, USA

Abstract

The effects of increasing temperature from global climate change threaten the sustainability and production of mud crabs from farms and wild populations in mangroves. Adaptation of mud crab populations to temperature stress is difficult to evaluate until now, with the emergence of RNA-Seq, a method which evaluates total mRNA expression under different conditions. In this study, 10 individuals each of *S. serrata* from Buguey, Cagayan were exposed to 26 °C and 32 °C for two weeks and the mRNA profiles were compared based on 186 million high quality pair-end reads which were aligned to a *S. serrata* reference transcriptome assembled de novo from 24,350 contigs with an average N50 of 1564 bp. Temperature related differences in gene expression were not significantly detected between the control and treatment groups and this was mostly due to the highly expressed genes such as the low and high molecular weight heat shock proteins. However, variations were greater among genes involved in the process of cell cycle regulation, the dissimilation processes such as oxidative phosphorylation, reproduction and transport across membranes. Greater differences were observed between immature or mature males and females.