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TISSUE-SPECIFIC TRANSCRIPTOMES OF *Mytilus galloprovincialis* REVEAL NEW FUNCTIONS

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The Mediterranean mussel (*Mytilus galloprovincialis*) is a cosmopolitan, cultured bivalve with worldwide commercial and ecological importance. There is a need to increase our knowledge of the molecular mechanisms involved in *Mytilus* physiology from a qualitative and quantitative point of view. In order to start filling this gap we have used RNA-Seq to study the transcriptome of mantle, muscle and gills from naïve mussels and hemocytes exposed to distinct stimuli.

After the analysis of the complete mussel transcriptome, we confirmed that we have achieved a completeness of the transcriptome of 95.16%. As mussel and oyster are model species for bivalves, we compared them and found that the shared proteins with a sequence identity over 80% represent less than 10% of their transcriptomes. In the whole mussel transcriptome it is important to highlight that the response to infectious diseases and cancer were pathways highly represented. However, only 55% of the transcripts were shared across all tissues. Hemocyte and gill transcriptomes were most different, with 60% shared transcripts, while mantle and muscle transcriptomes were most similar, with 77% shared transcripts. The transcriptomes showed characteristic expression profiles in agreement with their structures and functions: stimulated hemocytes confirmed their immune function showing a high representation of defense and immune-related expressed genes; the gills presented many transcripts assigned to both structure and recognition of non-self patterns; the mantle showed an abundance of transcripts related to reproduction and shell formation and, finally, the muscle expressed many myofibril and calcium-related proteins.

However, we could find other complex and specialized functions of each tissue, not previously reported: gills and its probable osmotic and homeostatic function; muscle revealed unexpected defense functions; and in mantle additional and interesting antifungal and sensorial functions were discovered, but also hematopoiesis transcripts were exclusively expressed in mantle, confirming its possible role as the hematopoietic tissue in bivalves. This information will provide new insight to bivalves, and specially mussel, physiology.

Keywords: Mytilus galloprovincialis, transcriptome, NGS, RNA-Seq, NOISeq, KEGG, Gene Ontology, Blast2GO.

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