

BIVALVES HEMOCYTE TRANSCRIPTOMES REVEAL A POWERFUL DIFFERENTIAL IMMUNE RESPONSE OF MEDITERRANEAN MUSSEL (*MYTILUS GALLOPROVINCIALIS*)

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ABSTRACT

Bivalves are one of the most successful animal groups on Earth and have been colonizing the interface between land and sea during the last 500 million of years. Like all invertebrates, they lack adaptive immune system; however, they are extraordinarily well adapted to adverse environmental conditions as high and low temperatures, desiccation, salinity variation and even pollution. The bivalve immune transcriptome was analyzed in mussels (*Mytilus galloprovincialis*, *Mytilus edulis*) and clams (*Ruditapes decussatus*, *Ruditapes philippinarum*) using 454 high-throughput sequencing of stimulated hemocytes.

Pyrosequencing resulted in more than 400,000 reads for all of the transcriptomes. The assembly process yielded a total of 14,158, 13,560, 7,318 and 37,093 selected sequences belonging to *M. galloprovincialis*, *M. edulis*, *R. decussatus* and *R. philippinarum* respectively. The percentage of sequences annotated was 49% in the case of mussels; this percentage decreases to about 30% in the case of clams.

Taking into account the whole 28,061 successfully annotated sequences of all the transcriptomes combined, these four bivalve species only share 785 common genes (2.80%). These common genes revealed a closer phylogenetic relation between mussels than that for clams, which show higher divergence.

After examining the immune-enriched transcriptomes of these bivalve species, we can conclude that mussels present an immune system that seems to be the opposite to what conventionally has characterized a simple and primitive innate immune response against invading pathogens. The enrichment analyses showed that *Mytilus* genus possess a significant higher number of sequences related to immune-processes or killing molecules than the *Ruditapes* genus. The same way *R. philippinarum* also showed a broader immune spectrum compared to *R. decussatus*.

The information found after functional comparison suggests that mussels have a higher transcriptomic repertoire after an immune challenge than clams. This could be related to the broader ecological niche of mussels and with little cases of mussel mass mortalities compared to clam mass mortalities.

KEYWORDS

Mytilus, Ruditapes, transcriptomics, hemocytes, innate immunity

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