

# UNDERSTANDING OF THE SHRIMP IMMUNE RESPONSE TO PATHOGENS FROM ITS TRANSCRIPTOME

Marcos De Donato\*, Carlos Fajardo, Hectorina Rodulfo, Acacia Alcivar-Warren, Ashutosh Sharma

Tecnológico de Monterrey, Escuela de Ingeniería y Ciencias, Querétaro, México  
mdedonate@tec.mx

According to GLOBEFISH, the global shrimp and prawn trade is estimated at USD 28 billion per year, representing one of the most important sectors in aquaculture industry, creating large number of jobs and being a key factor for economic development in tropical regions. The main challenge facing the sector is the incidence of viral and bacterial pathogens which has caused outbreaks throughout the world with large economic impact in production and profitability. Thus, there is the need to generate more knowledge that could be used to design strategies to prevent or treat infections that have been greatly affecting the shrimp industry. Genomic resources have been developed for *Penaeus vannamei*, *P. chinensis*, *P. japonicus* and *P. monodon*, with BUSCO completeness analysis higher than 93%, estimating the number of genes around 25-30 thousand. However, the high content of repetitive sequences found in shrimp genomes makes it difficult to build highly contiguous assemblies as well as to be able to annotate the genes to their full length. On the other hand, more than 1,500 RNA-Seq data sets have been published to date in the SRA database of NCBI. Most of the RNA-Seq experiments have used muscle, hemocytes, hepatopancreas and gills. Important processes related to the immune system have been identified in studies of penaeid shrimps when challenged by viral and bacterial pathogens, including those related to hemocytes function: autophagy, phagocytosis, antimicrobial peptides (AMPs) production, and the pro-phenoloxidase system. Specific components were identified, such as transglutaminase and lysozyme, alpha 2-macroglobulin, caspase, RAB7, chitinase, mucin, chitin deacetylase, Toll signaling pathway, anti-lipopolsaccharide factors (ALFs), penaeidins, astakine, catalase, peroxinectin, hemocyanin, glutathione peroxidase, glutathione-s-transferase, superoxide dismutase, lectins,  $\beta$ -glucan binding protein (LGBP), scavenger receptors (SRs), and Down syndrome cell adhesion molecule (DSCAM), among others.

This knowledge has shown that the innate immune responses in shrimp are activated through pattern recognition receptors (PRRs) by pathogen-associated molecular patterns (PAMPs), and are regulated by three major types of signal transduction pathways: Toll-like pathway, with a major function in controlling infections by both Gram-negative and Gram-positive bacteria, fungi and viruses; the immune deficiency (IMD) pathway, also with a major function in controlling infections but only by Gram-negative bacteria and viruses; and JAK/STAT pathway, mainly involved in antiviral defense responses (Fig. 1). However, there is a need to conform a collaborative and interdisciplinary project to generate a complete set of genes to allow us to understand and integrate all the mechanisms and elements involved in shrimp immune responses.

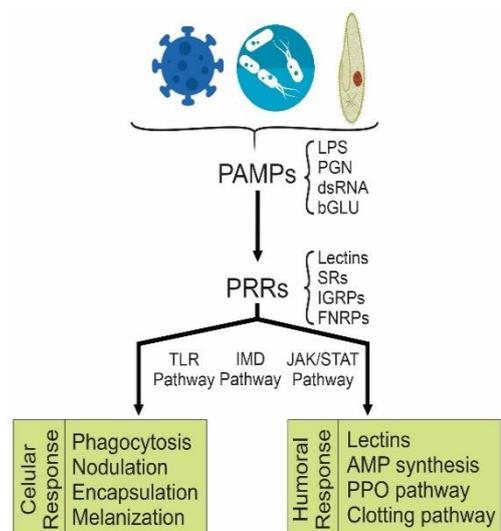


Fig. 1. Highlights of the shrimp immune response.