

Transcriptomic signature of horseshoe crab *carcinoscorpius rotundicauda* hemocytes' response to lipopolysaccharides

ABSTRACT

Carcinoscorpius rotundicauda (*C. rotundicauda*) is one of the four species of horseshoe crabs (HSCs). The HSC hemocytes store defense molecules that are released upon encountering invading pathogens. The HSCs rely on this innate immunity to continue its existence as a living fossil for more than 480 million years. To gain insight into the innate mechanisms involved, transcriptomic analysis was performed on isolated *C. rotundicauda* hemocytes challenged with lipopolysaccharides (LPS), the main components of the outer cell membrane of gram-negative bacteria. RNA-sequencing with Illumina HiSeq platform resulted in 232,628,086 and 245,448,176 raw reads corresponding to 190,326,253 and 201,180,020 high-quality mappable reads from control and LPS-stimulated hemocytes, respectively. Following LPS-stimulation, 79 genes were significantly upregulated and 265 genes were downregulated. The differentially expressed genes (DEGs) were related to multiple immune functional categories and pathways such as those of the cytoskeleton, Toll and Imd, apoptosis, MAP kinase (MAPK), inositol phosphate metabolism, phagosome, leucocyte endothelial migration, and gram-negative bacterial infection, among others. This study provides important information about the mechanisms of response to LPS, which is relevant for the understanding the HSCs' immune response.