

## **Comparative transcriptome profiling of horseshoe crab *tachypleus gigas* hemocytes in response to lipopolysaccharides**

### **ABSTRACT**

Horseshoe crabs (HSCs) are living fossil species of marine arthropods with a long evolutionary history spanning approximately 500 million years. Their survival is helped by their innate immune system that comprises cellular and humoral immune components to protect them against invading pathogens. To help understand the genetic mechanisms involved, the present study utilised the Illumina HiSeq platform to perform transcriptomic analysis of hemocytes from the HSC, *Tachypleus gigas*, that were challenged with lipopolysaccharides (LPS). The highthroughput sequencing resulted in 352,077,208 and 386,749,136 raw reads corresponding to 282,490,910 and 305,709,830 high-quality mappable reads for the control and LPS-treated hemocyte samples, respectively. Based on the log-fold change of  $> 0.3$  or  $< -0.3$ , 1338 genes were significantly upregulated and 215 genes were significantly downregulated following LPS stimulation. The differentially expressed genes (DEGs) were further identified to be associated with multiple pathways such as those related to immune defence, stress response, cytoskeleton function and signal transduction. This study provides insights into the underlying molecular and regulatory mechanisms in hemocytes exposed to LPS, which has relevance for the study of the immune response of HSCs to infection.