World Academy of Science, Engineering and Technology
International Journal of Biological and Ecological Engineering
Vol:15, No:12, 2021

Transcriptome Analysis of Protestia brevitarsis seulensis with Focus On Wing Development and Metamorphosis in Developmental Stages

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Abstract : White-spotted flower chafers are widely distributed in Asian countries and traditionally used for the treatment of chronic fatigue, blood circulation, and paralysis in the oriental medicine field. The evolution and development of insect wings and metamorphosis remain under-discovered subjects in arthropod evolutionary researches. Gene expression abundance analyses along with developmental stages based on the large-scale RNA-seq data are also still rarely done. Here we report the de novo assembly of a Protestia brevitarsis seulensis transcriptome along four different developmental stages (egg, larva, pupa, and adult) to explore its development and evolution of wings and metamorphosis. The de novo transcriptome assembly consists of 23,551 high-quality transcripts and is approximately 96.7% complete. Out of 8,545 transcripts, 5,183 correspond to the possible orthologs with Drosophila melanogaster. As a result, we could found 265 genes related to wing development and 19 genes related to metamorphosis. The comparison of transcript expression abundance with different developmental stages revealed developmental stage-specific transcripts especially working at the stage of wing development and metamorphosis of P. b. seulensis. This transcriptome quantification along the developmental stages may provide some meaningful clues to elucidate the genetic modulation mechanism of wing development and metamorphosis obtained during the insect evolution.

Keywords : white-spotted flower chafers, transcriptomics, RNA-seq, network biology, wing development, metamorphosis
Conference Title : ICISB 2021 : International Conference on Insect Science and Bioregulation
Conference Location : Barcelona, Spain
Conference Dates : December 16-17, 2021

Open Science Index, Biological and Ecological Engineering Vol:15, No:12, 2021 publications.waset.org/abstracts/138739/pdf