



Transcriptome sequencing and analysis of the coconut leaf beetle, *Brontispa longissima*

W. Yan^{1,2}, L. Liu¹, C.X. Li¹, S.C. Huang¹, Z.L. Ma³, W.Q. Qin¹ and Z.Q. Peng⁴

¹Coconut Research Institute, Chinese Academy of Tropical Agricultural Sciences, Hainan, China

²Key Laboratory for Silviculture and Conservation of Ministry of Education, Beijing Forestry University, Beijing, China

³Institute of Tropical Bioscience and Biotechnology, Chinese Academy of Tropical Agricultural Sciences, Hainan, China

⁴Environment and Plant Protection Institute, Chinese Academy of Tropical Agricultural Sciences, Hainan, China

Corresponding author: W.Q. Qin

E-mail: qwq268@126.com

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ABSTRACT. The coconut leaf beetle, *Brontispa longissima*, is a destructive pest of palm plants. Although its ecological and biological characteristics are well understood, its genetic information remains largely unknown. To advance our understanding of its molecular basis of biology and ecology, we sequenced and analyzed its whole transcriptome by using high-throughput Illumina paired-end sequencing technology. Approximately 8.08 Gb of clean reads were generated in a single run, which were assembled by using Trinity into 41,652 unigenes with an average length of 932 bp. By sequence similarity searches for known proteins, 23,077 (55.4%) unigenes were annotated by BLASTx searches against the NCBI non-redundant protein database. Of the unigenes assembled, 18,153 and 13,733 were assigned to Gene Ontology and Clusters of Orthologous Groups of proteins, respectively. In addition, 10,415 unigenes were mapped onto 247 pathways using the

Kyoto Encyclopedia of Genes and Genomes Pathway database. These transcriptomic resources will facilitate gene identification and elucidate the molecular mechanisms of biological and ecological aspects underlying this palm pest, in order to design a new control strategy.

Key words: *Brontispa longissima*; Transcriptome; Assembly