



Transcriptomic identification of chemoreceptor genes in the red palm weevil *Rhynchophorus ferrugineus*

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ABSTRACT. Olfaction is crucial for insects' survival because it enables them to recognize various environmental information. It is primarily mediated by a large family of chemoreceptors, including olfactory receptors (ORs), gustatory receptors (GRs), and ionotropic receptors (IRs). Here, we assembled the transcriptome of the economically important pest of palms, *Rhynchophorus ferrugineus*, to reveal its chemoreceptor gene repertoire. About 8.08 Gbp data were generated using a HiSeq platform and their assembly led to a total of 24,439 unigenes. Among the transcripts, 12,523 (51.24%) showed significant similarity (E-value <10⁻⁵) to known proteins in the National Center for Biotechnology Information Nr database. From these sequences, 18 candidate genes of ORs were identified. Nine putative transcripts were homologous to GR genes, while 9 were similar to IR genes. The expression profiles of all identified chemoreceptor genes were

determined by quantitative real-time PCR in antenna, head, thorax, abdomen, and legs of both sexes. Most chemoreceptor genes were antenna-enriched. This study demonstrated a successful application of a transcriptome for discovering a large number of divergent chemoreceptor genes of a non-model organism. The findings provide a valuable sequence resource and gene tissue distribution information for systematic functional analysis of molecular mechanisms underlying chemoreception in this pest.

Key words: *Rhynchophorus ferrugineus*; Expression pattern; Transcriptome; Chemoreception