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Transcriptional responses in eastern honeybees (*Apis cerana*) infected with mites, *Varroa destructor*

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ABSTRACT. The *Varroa destructor* mite has become the greatest threat to *Apis mellifera* health worldwide, but rarely causes serious damage to its native host *Apis cerana*. Understanding the resistance mechanisms of eastern bees against *Varroa* mites will help researchers determine how to protect other species from this organism. The *A. cerana* genome has not been previously sequenced; hence, here we sequenced the *A. cerana* nurse workers transcriptome and monitored the differential gene expression of *A. cerana* bees challenged by *V. destructor*. Using *de novo* transcriptome assembly, we obtained 91,172 unigenes (transcripts) for *A. cerana*. Differences in gene expression levels between the unchallenged (Con) and challenged (Con2) samples were estimated, and a total of 36,691 transcripts showed a 2-fold difference (at least)

between the 2 libraries. A total of 272 differentially expressed genes showed differences greater than 15-fold, and 265 unigenes were present at higher levels in Con2 than in Con. Among the upregulated unigenes in the Con2 colony, genes related to skeletal muscle movement (troponin and calcium-transporting ATPase), olfactory sensitivity (odorant binding proteins, and Down syndrome cell adhesion molecule gene) and transcription factors (cyclic adenosine monophosphate-responsive element-binding protein and transcription factor mblk-1) appeared to be involved in *Varroa* resistance. Real-time polymerase chain reaction was performed to validate these differentially expressed genes screened by the sequencing approach, and sufficient consistency was observed between the two methods. These findings strongly support that hygienic and grooming behaviors play important roles in *Varroa* resistance.

Key words: *Apis cerana*; Gene expression; Transcriptome; *Varroa destructor*

