



## Comparative proteomic analysis reveals mite (*Varroa destructor*) resistance-related proteins in Eastern honeybees (*Apis cerana*)

T. Ji<sup>1</sup>, F. Shen<sup>1</sup>, Z. Liu<sup>2</sup>, L. Yin<sup>3</sup>, J. Shen<sup>1</sup>, Q. Liang<sup>4</sup> and Y.X. Luo<sup>5</sup>

<sup>1</sup>College of Animal Science and Technology, Yangzhou University, Yangzhou, China

<sup>2</sup>Shandong Agricultural University, Shandong, China

<sup>3</sup>Institute of Food Science and Technology, Jiangsu Agri-Animal Husbandry Vocational College, Taizhou, China

<sup>4</sup>College of Bee Science, Fujian Agriculture and Forestry University, Fuzhou, China

<sup>5</sup>Guangdong Entomological Institute, Guangzhou, China

Corresponding author: T. Ji

E-mail: [tji@yzu.edu.cn](mailto:tji@yzu.edu.cn)

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**ABSTRACT.** The mite (*Varroa destructor*) has become the greatest threat to apiculture worldwide. As the original host of the mite, *Apis cerana* can effectively resist the mite. An increased understanding of the resistance mechanisms of Eastern honeybees against *V. destructor* may help researchers to protect other species against these parasites. In this study, the proteomes of 4 *Apis cerana* colonies were analyzed using an isobaric tag for relative and absolute quantitation technology. We determined the differences in gene and protein expression between susceptible and resistant colonies that were either unchallenged or challenged by *V. destructor*. The results showed that a total of 1532 proteins were identified. Gene Ontology enrichment analysis suggested that the transcription factors and basic metabolic and respiratory

processes were efficient and feasible factors controlling this resistance, and 12 differentially expressed proteins were identified in Venn analysis. The results were validated by quantitative polymerase chain reaction. This study may provide insight into the genetic mechanisms underlying the resistance of honeybee to mites.

**Key words:** *Apis cerana*; Differential expression; Proteome; *Varroa destructor*