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Antiviral defence mechanisms in honey bees infected with deformed wing virus

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Honey bees Apis mellifera are a eusocial insect species with ecological and economic importance. High colony losses indicate that the health and stability of bee populations are threatened by multiple pathogens. Due to their major impact on beekeeping and their role as one of the leading causes of colony losses, pathogenic viruses affecting honey bees are among the most intensively studied pathogens. Deformed wing virus (DWV) is a positive-sense single-stranded RNA virus transmitted by the ectoparasitic mite Varroa destructor. In infested colonies, V. destructor facilitates the rapid spread of DWV, leading to severe weakening or even colony collapse.

Honey bees detect and limit viral infections through the RNA interference (RNAi) pathway. One of the main components of RNAi is the enzyme Dicer, which cleaves viral double-stranded RNA into short RNA fragments, leading to the degradation of target mRNA and subsequent gene silencing. The RNAi mechanism regulates the expression of Vago gene, which increases in response to certain viral infections in honey bees. Additionally, bee antiviral protein 1 (Bap1) restricts viral infections through RNAi, while thioester containing protein 7 (Tep7) is involved in enhancing the immune response to infections, including viruses.

This study examines the antiviral defense in honey bees infected with DWV by measuring relative gene expression. RNA was isolated from the abdomens of infected bees and then converted into cDNA through reverse transcription. The expression of genes Dicer, Vago, Bap1 and Tep7 was quantified using quantitative PCR (qPCR). The results indicate significant changes in the expression of genes Dicer and Vago in DWV-infected bees. This suggests that honey bees are enhancing their antiviral defence mechanisms in an effort to limit viral replication and spread within the body.

These discoveries, along with a more comprehensive analysis of honey bee immunity, can enhance the understanding of protective mechanisms against viral infections. These insights could support selective breeding programs aimed at improving the resilience of honey bee colonies to viral diseases, ultimately helping beekeepers reduce colony losses and promote sustainable beekeeping practices.

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