OR384

Differential seasonal honeybee immune genes expression exposed to deformed wing virus

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In temperate regions, honeybees, *Apis mellifera*, are characterized by physiologically distinct summer and winter bees. One feature of winter bees is their long life expectancy (~6-7 months), which may render them more prone to pathogen infections, especially in the close spatial proximity of winter clusters. Their immune system is characterized by cellular and humoral immune responses at individual level, and by defense mechanisms involving specific behaviors at the colony level. Most of the colony losses occur during the winter, suggesting that winter bees may have compromised immune function. Here, we evaluated whether the immune system differs between these two seasonal types of bees. We took advantage of natural infections with the ubiquitous deformed wing virus (DWV), which has been shown to interact with bee immunity and to contribute to a reduced longevity of winter bees. Individual workers were regularly collected during summer or winter and individually analyzed for DWV infections and gene expression of defensin-1, dorsal, eater, hymenoptaecin, juvenile hormone epoxidase (JHE), prophenoloxidase (PPO), prophenoloxidase activator (PPOa) and vitellogenin using qPCR. Our data show that summer and winter workers can display significant differences in gene expression patterns associated with DWV infection. Although higher DWV loads were found in winter, genes were actually downregulated in winter bees. In contrast, summer bees showed a significant positive correlation between DWV loads and immune gene expression. The results suggest that winter bees show a specific immune response, consistent with the hypothesis that downregulation is a mechanism to save energy even at the expense to increased risk of pathogen infection in the context of adult longevity. Sampling for future research on bee health should take into account the observed differences in immune responses.