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The effect of pathogens and pests on honey bee gene expression

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The effect of pathogens and pests on honey bee gene expression is a fascinating area of research in itself and can lead to new molecular tools for diagnostics and selection in beekeeping. In this framework, we first investigated *Varroa-bee* interactions by using a combination of nuclear and mitochondrial DNA markers of *Varroa destructor* to trace the parasite invasion of *Apis mellifera* since it shifted from *A. cerana.* The extremely low worldwide mite genetic diversity found on *A. mellifera* outside Asia contrasts with the variety of known bee phenotypes regarding their response to the parasite. This prompted us to further explore the response of bees to *Varroa,* by using a transcriptional study. We compared parasitized and non-parasitized full-sister pupae, from two different genetic stocks of bees: one susceptible and one resistant to*Varroa.* We used a honey bee cDNA microarray, which contained a total of ~ 6,778cDNAs representing ~ 5,500 different genes. We identified a set of genes that showed differential expression as a function of parasitization, another set that showed differential expression as a function of bee genotype, and a set of genes affected byboth factors. These patterns, and some of the genes that define them, are mostly involved in olfaction and sensitivity to stimuli. These results agree with the hypothesis that tolerance to *Varroa* is linked to a more efficient bee hygienic behaviour. In an ongoing work we further explore this hypothesis. Using q-PCR assays, we try to separate immunological and behavioral bee responses and also parasite effects from bee genotype effects.

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