

IMPROVING *VARROA DESTRUCTOR* RESISTANCE IN HONEY BEES USING LARGE-SCALE METAGENOMICS ANALYSES

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Abstract

The ectoparasitic mite *Varroa destructor* remains the greatest biotic threat to managed honey bees in the Northern Hemisphere. Selecting for host resistance to this parasite is considered the most sustainable solution. However, breeding programs have shown limited success, partly due to the low heritability of *V. destructor* resistance traits. We hypothesized that failing to account for microbiome effects may bias and underestimate these heritability values. Indeed, the honey bee microbiome plays an important role in colony health, indirectly impacting the colony's ability to resist *V. destructor*. Moreover, specific pathogens or symbionts could directly affect the expression of resistance traits by modulating sensory perception, learning and memory, or immunity. Using large-scale publicly available metagenomic data, we characterized the microbiome (including prokaryotic and eukaryotic pathogens, gut microbiota, DNA viruses, and plant eDNA) of 1442 European colonies. After identifying microbiome taxa and principal components significantly associated with *V. destructor* load and resistance traits (recapping and decreased mite reproduction), we incorporated these factors as covariates to update genomic heritability estimates for *V. destructor* load and resistance traits. Both mite load and recapping were significantly associated with microbiome composition, albeit to a lesser extent than geography or sampling date. Numerous taxa showed significant associations with these traits. Notably, the core gut symbionts *Lactobacillaceae* and *Bifidobacteriaceae* were negatively associated with mite load, whereas non-core bacteria such as *Bartonellaceae* and pathogens including *Morganellaceae* and *Trypanosomatidae*, showed positive correlations. This suggests that *V. destructor* either disrupts the microbiome, or that the mite proliferates preferentially in colonies harbouring particular microbial communities. Finally, by including microbiome principal components and relevant taxa as covariates, we report increased genomic heritability estimates for *V. destructor* load and resistance traits. These findings indicate that integrating microbiome information into breeding frameworks could strengthen selection programs for *V. destructor* resistance and ultimately improve honey bee health.