



Virus dynamics in naturally varroa-resistant honeybee populations

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Abstract

The ectoparasitic mite, *Varroa destructor*, together with its associated viruses is the most significant threat to honeybee (*Apis mellifera*) health world-wide. Since the introduction of varroa to the new host species, the European honey bee (*Apis mellifera*), it has been responsible for the near complete eradication of wild and feral honeybee populations in Europe and North America. However, a unique honeybee population on the Island of Gotland, Sweden, has acquired resistance to the mite through a natural selection process. A recent study also showed that Gotland mite-resistant population might have adapted tolerance and resistance to virus infections. This suggests that virus-host interactions may play a key role in the long-term survival of this population. The aim of this thesis was to investigate the role of the viral and bacterial microbiome in the enhanced survival of the mite-resistant (MR) honeybees on Gotland, to compare the role of virus tolerance and resistance in other naturally selected mite-resistant honeybee populations, similar to the Gotland population, and to unravel individual level virus-host interactions in honeybees.

First, by using a combination of high-throughput sequencing and different bioinformatics tools we found *Lake Sinai virus* and *Apis rhabdovirus-1*, including previously known honey bee viruses, in Swedish honey bees. Further molecular studies showed that Gotland MR bees have developed a colony-level resistance to these viruses, and tolerance to *Deformed Wing Virus* (DWV), the virus most commonly associated with mite infestation. Secondly, differences in the bacterial microbiome between MR and mite-susceptible (MS) bees were studied using the 16S rDNA, but the results indicated little differences between MR and MS bees throughout the season. Finally, individual level susceptibility of MR and MS honey bees to oral virus infection was tested for DWV virus and *Acute bee paralysis virus* (ABPV). The results demonstrate that DWV and ABPV infection dynamics were nearly identical in MR and MS bees, but that bees from the MR honeybee populations had significantly lower mortality rates than bees from the MS population.

In conclusion, the results of this thesis present strong evidence that naturally adapted mite-resistant honeybees have also adapted, through a natural selection process, tolerance and resistance to virus infections at both the colony and individual level. The bacterial microbiome did not appear to play a role in the enhanced survival of Swedish mite-resistant honeybees but more studies are required to investigate potential bacteria-virus interactions on honeybee health. Future work should aim to identify key genomic regions associated with virus resistance and tolerance that can be incorporated into honeybee breeding programs to improve honeybee health.

Keywords: *Apis mellifera*, *Varroa destructor*, viral metagenomics, deformed wing virus, acute bee paralysis virus, virus-host interactions

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