

DOI: 10.55278/OINO7677

Understanding how *Apis cerana* and *Apis mellifera* keep *Varroa destructor* away- a brief review

Salome Ruth Jimmy V.

Department of Biotechnology, Ramaiah Institute of Technology (MSRIT), Bangalore-560054,
Karnataka, India

Corresponding author: salomeruthj@gmail.com

Abstract

It is a well-known phenomenon in the field of apiology that honey bees have developed adaptive behaviours in displaying resistance against the *Varroa destructor* mite, since its widescale emergence and the host-jump displayed from *Apis cerana* to *Apis mellifera*, in the last few decades, allowing it to be found in almost every part of the world rearing honey bees. This brief review attempts to understand the mechanisms and general behaviours displayed by both species.

Introduction

Honey bees are one of the smartest of the class Insecta existing on the planet. Known as highly complicated superorganisms, honey bee colonies possess a variety of social immunity traits that can help shield them from dangers like disease and parasite infestations.

Honey bees are eusocial creatures. They work together to ensure the survival of the entire community, and not just their individual selves, and display characteristics such as social apoptosis. (Kate E Ihle, Lilia I de Guzman, Robert G Danka, 2022). With regard to this, as evolution has taken place, honey bees have shown to adapt at a rapid rate to protect themselves against threats, the biggest one being the *Varroa destructor*, a parasitic mite that attacks two species of honey bees namely *Apis cerana* and *Apis mellifera*. It is responsible for transmitting viral infections

that eventually lead to colony fatality if mite populations continue to grow without check. To combat this, honey bees display certain traits which have been studied for their gene expression and heritability such as allogrooming, brood cell recapping and hygienic behaviour.

Brood cell recapping

A study published (Gabel Martin et al., 2023) on heritability and genetic correlations for suppressed mite reproduction (SMR) and recapping (REC), in two populations namely Carnica and Buckfast of *Apis mellifera*, distinguishing between recapping of infested cells (RECinf) and all cells (RECall), found that both traits showed promise in further selection. They showed that the traits SMR, RECinf and RECall can be made greater by targeted selection and are also being adopted in few breeding generations. They concluded that

these traits alone do not guarantee complete resistance to the mite. During artificial selection it must be noted that, there must be, in addition to these desirable traits, other adaptive features to the respective environment as well. Another study (Melissa A.Y. Oddie *et al.*, 2021) compared surviving and susceptible colonies of *Apis mellifera* and demonstrated that there was higher recapping efficacy in surviving populations that had mite infestations.

Genetic mechanism behind grooming behaviour

Allogrooming is a common trait displayed by honeybees in resisting the parasite and it has been found that *Apis mellifera* shows lesser resistance than the host *Apis cerana* (Dorian J. Pritchard, 2016) in which it was first discovered. In relation to the paper by Gabel *et. al.*, another study (Nuria Morfin *et al.*, 2023) was published where the honeybees were bred for low *Varroa destructor* population growth (LVG) and high *Varroa destructor* population growth (HVG) and the 2 genotypes were classified as light and heavy groomers, thus giving a total of 4 groups that were evaluated (HVG light, HVG intense, LVG light, LVG intense). Approximately 20 mg of wheat flour was applied to the thorax with the help of a paintbrush. The flour acted as an irritant, and the self-grooming behaviour of the bees was observed for a span of 3 minutes each, to see how fast or slow the bees would be in removing the irritant off their thorax. The observer was not made aware of

the genotype of the bee. After this was completed, the brains of 50 randomly selected bees were taken and RNA was extracted. Analysis was done using a Pearson correlation test where the grooming of bees in different categories (LVG-intense, LVG-light, HVG-intense and HVG-light), viral abundance and transcript abundance were analysed. They found that there was a much greater number of intense to light groomers in both genotypes. They were able to identify 19 different pathways, odorant binding proteins and a gustatory receptor responsible. Given that both genotypes of bees had higher proportions of intense groomers than light groomers, this particular trait of intense grooming cannot prove to be the sole reliable way of distinguishing between LVG and HVG bees. This study however does provide valuable information by showing molecular mechanisms of behaviour traits of these honey bees. The study on viral levels enables scientists and breeders to understand the subsequent effect of pathogenicity and its role in behavioural immunity without human intervention. The results of this study give a great head-start to further delve into studying genomic assisted selection tools to improve breeding.

The switch between old hosts to new hosts

It is now common knowledge that this parasitic mite is found in both hosts viz. the Western (*Apis mellifera*) and the Eastern honey bee (*Apis cerana*). Wenfeng Li *et. al.* (2022) wanted to explore if the parasite *Varroa*

destructor had a cell preference between the old and new hosts. They demonstrated through cell invasion bioassays that there indeed was a preference for the new host- *Apis mellifera*. When analysed for levels of cuticular hydrocarbons (CHCs) a significant difference between the two species was shown. They found that methyl-alkane amounts were higher in *A.mellifera* and alkene amounts were higher in *A. cerana*. They then placed a dummy glass with larval CHCs of *A.mellifera* and found the mites favouring it. This study therefore indicated the role of these larval CHCs as one of the reasons for the parasite's preference. Another study (Zheng et. al., 2023) aimed to identify the genetic factors behind the reproduction of the mite if any, between those infesting the old and new hosts and separated them into two groups. They artificially infested both the hosts and performed transcriptome sequencing to find differentially expressed genes (DEGs). Firstly, they found that there was an upregulation in oogenesis of the mites in *A. mellifera* and the DEGs were associated with 9 genes partially responsible for oogenesis. Although the key mechanism still needs to be researched, they were able to determine the genes responsible in the reproductive process of these mites.

Discussion and Conclusion

Latest research and information obtained has opened exciting new avenues with respect to resistance against *V. destructor*, but there is significantly a greater amount of data available regarding the resistance

behaviours in *A. mellifera* to the parasite, in contrast to its counterpart *A. cerana*. Although genetic studies using high-throughput sequencing have become common in recent years, being also affordable, there are still a number of gaps in the research available, especially with respect to resistance in *A. cerana*. There is therefore a great need for researchers to study this as it may prove to be useful in selective breeding, and thereby assist beekeepers and breeders to combat the parasite. Resistance to the parasite is a sum of all factors such as environmental factors and not just the ones discussed in this review. Since variations continually take place in both the parasite and host populations, and breeding of new generations takes place at a rapid rate, attesting only a few known and discovered factors to resistance cannot be considered, although playing an absolutely crucial role in our understanding of this area.

References

- Dorian J. Pritchard 2016. Grooming by honey bees as a component of varroa resistant behavior, *Journal of Apicultural Research*, **55**:1, 38-48
- Gabel Martin, Hoppe Andreas, Scheiner Ricarda, Oberfell Jörg, Büchler Ralph. Heritability of *Apis mellifera* recapping behaviour and suppressed mite reproduction as resistance traits towards *Varroa destructor* 2023. *Frontiers in Insect Science*.**3**.

- Kate E Ihle, Lilia I de Guzman, Robert G Danka 2022. Social Apoptosis in Varroa Mite Resistant Western Honey Bees (*Apis mellifera*). *Journal of Insect Science*, **22**(1)
- Melissa A.Y. Oddie, Ashley Burke, Bjørn Dahle, Yves Le Conte, Fanny Mondet & Barbara Locke 2021. Reproductive success of the parasitic mite (*Varroa destructor*) is lower in honeybee colonies that target infested cells with recapping. *Sci Rep* **11**,9133.
- Nuria Morfin, Brock A. Harpur, Alvaro De la Mora, and Ernesto Guzman-Novoa 2023. Breeding honey bees (*Apis mellifera L.*) for low and high *Varroa destructor* population growth: Gene expression of bees performing grooming behaviour. *Frontiers in Insect Science*.**3**.
- Wenfeng Li, Yi Zhang, Hui Peng, Ruonan Zhang, Zhengwei Wang, Zachary Y. Huang, Yan Ping Chen, Richou Han 2022. The cell invasion preference of *Varroa destructor* between the original and new honeybee hosts. *International Journal for Parasitology*.**52**(2–3),125-134.
- Zheng, Shuai Wang, Yuqi Wu, Shengmei Zou, Vincent Dietemann, Peter Neumann, Yanping Chen, Hongmei Li-Byarlay, Christian Pirk , Jay Evans , Fuliang Hu, Ye Feng 2023. Genomic signatures underlying the oogenesis of the ectoparasitic mite *Varroa destructor* on its new host *Apis mellifera*. *Journal of Advanced Research*.**44**,1-11

MS Received 15 January 2023

MS Accepted 16 March 2023