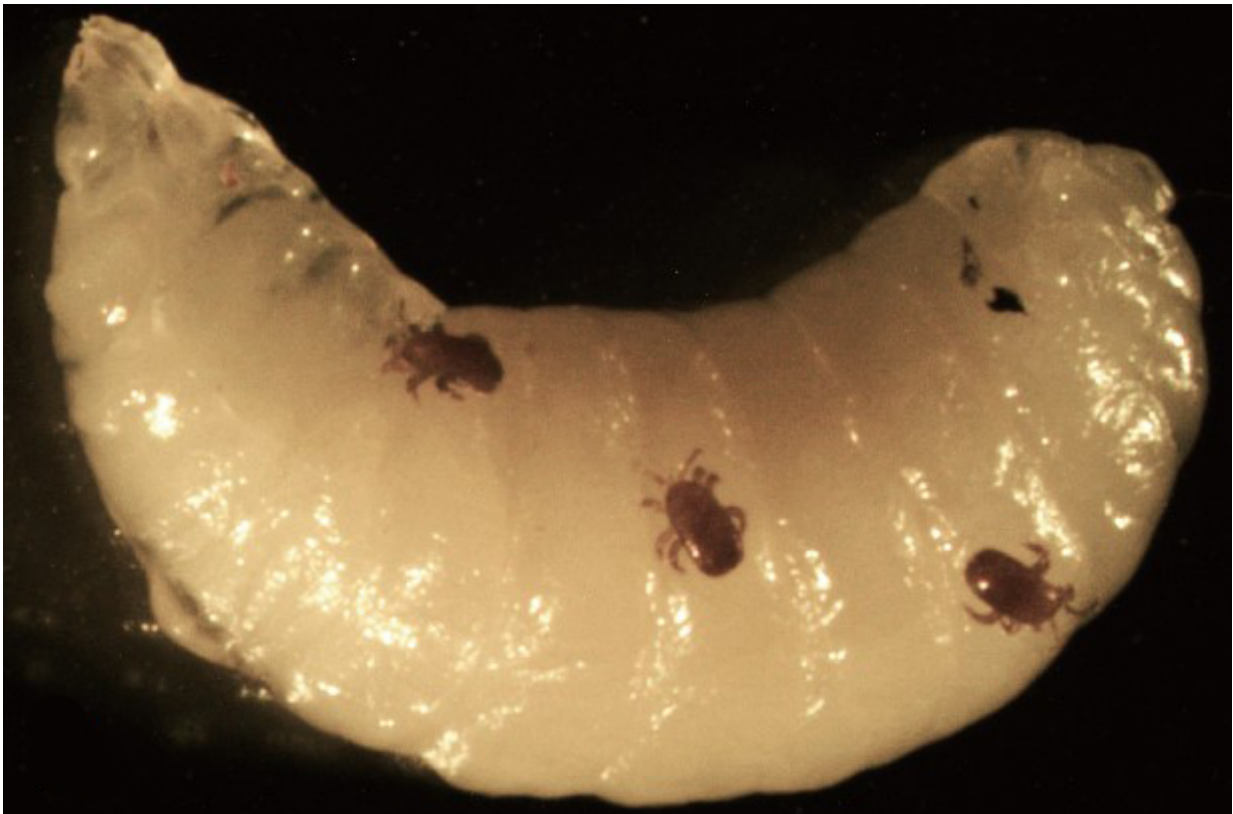


Honey bee parasite genome sequenced to aid in fight against bee colony destruction

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Three adult female *Tropilaelaps mercedesae* infesting the 5th instar honey bee larva. Credit: Dong et. al, Draft genome of the honey bee ectoparasitic mite, *Tropilaelaps mercedesae*, is shaped by the parasitic life history. *GigaScience* 2017

Published today in the open-access journal *GigaScience* is an article that

presents the genome of a parasitic mite, *Tropilaelaps mercedesae*, that infects bee colonies, which are facing wide-spread devastation across the entire world. The research was carried out by an international team of researchers at Jiaotong-Liverpool University and Liverpool University and focused on mites as they are one of the major threats to honey bee colonies. The work revealed that there were specific features in the *T. mercedesae* mite genome that had been shaped by their interaction with honey bees, and that current mechanisms to control mites are unlikely to be useful for *T. mercedesae*. The genome sequence and findings provide excellent resources for identifying gene-based mite control strategies and understanding mite biology.

Although there are many potential causes for the decline in honey [bee colonies](#), pathogens and parasites of the honey bee, particularly mites, are considered major threats to honey bee health and honey bee colonies. The bee [mite](#) *Tropilaelaps mercedesae* is honey bee parasite prevalent in most Asian countries, and has a similar impact on bee colonies that the globally present bee mite *Varroa destructor* has. More, *T. mercedesae* and *V. destructor* typically co-exist in Asian bee colonies and with the global trade of honey bees *T. mercedesae* is likely become established world-wide, as occurred with *V. destructor*.

Given the ongoing international devastation of bee colonies, the researchers sequenced the genome of *T. mercedesae*, to assess the interaction between the parasite and host as well as provide a resource for the ongoing battle to save honey bee populations.

The authors identified the genetic components in the genome and compared these to the genome of free-living mites. As opposed to the free-living mites, *T. mercedesae* has a very specialized life history and habitat that depends strictly on the honey bee inside a stable colony. Thus, comparison of the genome and transcriptome sequences with those of internal and free-living mites revealed the specific features of the *T.*

mercedesae genome and showed that they were shaped by interaction with the honey bee and colony environment.

Of particular interest, the authors found that the mite does not rely on sensing stimulatory chemicals to affect their behavior. The researchers noted that this discovery meant that, "control methods targeted to gustatory, olfactory, and ionotropic receptors are not effective." Instead, control measures will have to use other targets when trying to disrupt chemical communication. The authors further highlighted that, "there will be a need to identify targets for biological control."

The researchers indicated that there were additional difficulties for controlling the mites, saying "We found that *T. mercedesae* is enriched with detoxifying enzymes and pumps for the toxic xenobiotics and thus the mite quickly acquires miticide resistance. For developing chemical control methods, we need to search for compounds which may not be recognized by the above proteins."

Relevant to this, the researchers investigated the bacteria that infect the bee mite, as little is known about these bacteria. The scientists discovered that the symbiote *R. grylli*-like bacteria is commonly present in *T. mercedesae*, and they suggested that "Manipulating symbiotic *Rickettsiella grylli*-like bacteria, which is associated with *T. mercedesae*, may also help us to develop novel control strategies."

They further found that this bacteria was involved in horizontal gene transfer of *Wolbachia* genes into the mite genome. *Wolbachia* is a bacteria that commonly infects arthropods, but is not present in *T. mercedesae*. While the authors were not overly surprised at discovering the occurrence of horizontal gene transfer since it has been detected in about 33% of sequenced arthropod genomes, they did note that this "is the first example discovered in mites and ticks as far as we know", and that, since no *Wolbachia* were currently infecting the mite, this indicated

that Wolbachia was once a symbiont for *T. mercedesae* or its ancestor but it would have been replaced with *R. grylli*-like bacteria during evolution."

The extent of [honey bee](#) colony destruction remains a complex problem, but one that has an extensive impact crop productivity since honey bees are needed for pollination of a variety of plants. Indeed, in several places in China, farm workers have begun to carry out manual pollination to maintain high crop yield in orchards. Thus, research and resources to help combat this global threat are needed now. The findings, [genome](#), transcriptome, and proteome resources from *T. mercedesae* study add another weapon in the fight to save bee colonies.

More information: *GigaScience*, [DOI: 10.5524/100266](https://doi.org/10.5524/100266)

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