Everything You Wanted to Know about Honeybee Sex

There is an exquisite genetic control behind a honeybee's fate in the hive—from the lowly drone to the almighty queen—which literally represents the bee's knees for evolutionary scientists exploring how multiple mutations, or alleles, of a single gene called the complementary sex determiner (csd) can have a profound influence on honeybee society.

Unlike people, there are no X and Y sex chromosomes for bees. Rather, sex is determined by csd gene and its allelic composition and whether a queen bee chooses to fertilize her eggs. Female bees (queens or workers) come from fertilized eggs, always receiving two different (heterozygote) copies of csd. Fertile males always come from unfertilized eggs, receiving only one copy of csd. Two identical (homozygote) copies of csd in fertilized eggs is always lethal; these individuals are being killed at the early larval stage by worker bees as they would develop into diploid males which do not contribute to colony fitness.

Lechner et al. (2013) have now examined the exquisite molecular control behind the sex determination, finely identifying and tracing back a comprehensive number of csd alleles to create a richer understanding of the variability of the csd gene over evolutionary time. They looked at a data set of 244 csd sequences from queens, worker bees, and drones and showed that the total number of csd alleles found in bees ranges from at least 53 (locally) to 87 (worldwide), which is much higher than previously reported. Using an evolutionary model, they also extrapolated the presence of a total 116–145 csd alleles worldwide, a great example of the enormous sequence variability within csd. They were able to finely decipher the minimum number of mutations leading to heterozygous csd, identify faster evolving hot spots within the csd gene, and how these may contribute to variability.

“Comprehensive insights into the sequence variability of the sex determining gene csd in honeybees elucidate the evolutionary processes that lead to the enormous number of csd alleles found worldwide,” said Hasselmann.

Finally, they traced the data back over evolutionary time and found that a novel csd function affecting sex determination arises about every 400,000 years. The study provides one of the most comprehensive views of the enormous genetic diversity and the evolutionary forces shaping sex determination in bees, as well as how changes in csd affect honeybee colony fitness.

Reference


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Can Evolutionary Tools Reliably Tell Us about Dengue Virus’ Past Outbreaks?

The mosquito-borne dengue virus is most prevalent in southeastern Asia, with four common strains or “serotypes” of the virus infecting up to 10% of children in Vietnam annually. Dengue virus is a major challenge for evolutionary biologists because of its complex ecology and rapidly changing disease dynamics. But can evolutionary models become a reliable tool for epidemiologists studying infectious disease?

Coming up with a model to relate dengue’s genealogical history, or phylodynamics, with the epidemiology of the disease is challenging because of its complexity: seasonal infection rates, changes in mosquito population sizes, different viral strains, urban versus rural populations densities, and the widespread movement of people—where viruses can usurp geographic boundaries—are all contributing factors.

Now, Rasmussen et al. (2013) have looked at dengue virus serotype 1 (DENV-1) in southern Vietnam, the most dominant endemic strain of the virus, for which a large number of sequence samples (237) are available along with reliable data on dengue hospitalizations. They incorporated some of these additional ecological complexities to tweak different phylodynamic models and were able to reconstruct dengue’s past dynamics from genealogies that are consistent with the observed hospitalization data and also lead to new insights into factors shaping viral family histories.

Their best-fit models accounted for population variation in urban versus rural areas or the population dynamics of