

Newly sequenced hornet genomes could help explain invasion success

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The genomes of two hornet species, the European hornet and the Asian hornet (or yellow-legged hornet) have been sequenced for the first time by a team led by UCL (University College London) scientists.

By comparing these decoded genomes with that of the giant northern hornet, which has recently been sequenced by another team, the researchers have revealed clues suggesting why hornets have been so successful as invasive species across the globe. Their work is published in *Scientific Reports*.

Hornets are the largest of the social wasps; they play important ecological roles as top predators of other insects. In their native regions, they are natural pest controllers, helping regulate the populations of insects such as flies, beetles, caterpillars and other types of wasps. These services are critical for healthy, functional ecosystems, as well as for agriculture.

But hornets also tend to be very successful as [invasive species](#). They can become established in areas to which they are not native, and cause potentially huge ecological and economic damage by hunting important pollinators, such as honey bees, wild bees and hoverflies.

To better understand how these species have so successfully expanded their ranges, the international team of scientists investigated the genomes of three types of hornets.

A [genome sequence](#) is the set of instructions—a [genetic code](#)—that makes a species. Comparing the genomes of different species can give insights into their biology: their behavior, evolution, and how they interact with the environment.

The researchers have newly sequenced the genomes of the native European hornet, *Vespa crabro*—an important top predator, which is protected in parts of Europe—and the invasive yellow-legged Asian hornet *Vespa velutina*, which has become established through much of Europe over the last 20 years threatening native ecosystems, and has occasionally been sighted in the UK. The research team compared these

with the [genome](#) of the giant northern hornet, *Vespa mandarinia*—a species known for its role as pest controller, pollinator and food provider in its native Asian range. It is a recent arrival in North America, where it may threaten native fauna.

By analyzing differences among the three [related species](#), the researchers were able to identify genes that have been rapidly evolving since the species differentiated themselves from other wasps and from one another, and found some noteworthy genes that are rapidly evolving, particularly relating to communication and olfaction (smell).

The study's first author, Dr. Emeline Favreau (UCL Centre for Biodiversity & Environment), said, "We were excited to find evidence of rapid genome evolution in these hornet genomes, compared to other social insects. Lots of genes have been duplicated or mutated; these included genes that are likely to be involved in communication and in sensing the environment."

Genome evolution allows organisms to adapt to their environment and make the most of their surroundings by developing new behaviors and physiology.

Co-author Dr. Alessandro Cini, who began the work at UCL before moving to the University of Pisa, said, "These findings are exciting, as they may help explain why hornets have been so successful in establishing new populations in non-native regions.

"Hornets are carried to different parts of the world accidentally by humans. All that is needed is a small number of mated queens to be transported, hidden in cargo perhaps. The genomes suggest that hornets have lots of genes involved in detecting and responding to chemical cues—these may make them especially good at adapting to hunt different types of prey in non-native regions."

Senior author Professor Seirian Sumner (UCL Centre for Biodiversity & Environment) said, "These hornet genomes are just the beginning. The genomes of more than 3,000 insect species have now been sequenced by efforts around the world, but wasps are under-represented among these.

"Genomes tell us about aspects of the ecology and evolution that other methods cannot. Evolution has equipped these insects with an incredible genetic toolbox with which to exploit their environment and hunt their prey."

Armed with these new genomes, the scientists hope to help improve the management of [hornet](#) populations, both for their ecosystem services as pest controllers in native zones, and as ecological threats in regions where they are invasive.

More information: Emeline Favreau et al, Putting hornets on the genomic map, *Scientific Reports* (2023). [DOI: 10.1038/s41598-023-31932-x](#)

Provided by University College London

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