

Researchers find polyploidy has occurred many times during the evolution of insects

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Assistant professor Mike Barker (right) and graduate student Zheng Li review data from their bioinformatic search. Credit: University of Arizona

University of Arizona biology researchers have made a discovery that helps resolve a conundrum that has puzzled scientists for more than a century.

The UA team, headed by Michael S. Barker, assistant professor and

director of bioinformatics in the UA Department of Ecology and Evolutionary Biology, has found that [polyploidy](#), the duplication of whole genomes, has occurred many times during the evolution of [insects](#), the most diverse group of animals.

Evolutionary biologists long have known that [genome](#) duplication was a common part of the evolution of plants, and Barker specializes in methods to detect the history of polyploidy in their genomes.

"We know that plants like kale, broccoli, cabbage, turnips, cauliflower, sunflower, soybeans, rice, corn, wheat—all those things that we eat and more—have all experienced polyploidy in their ancestry. We know these plants have done this a lot and we can see this in their genomes," Barker says.

Until now, there had been no evidence for this mechanism of genome evolution in insects, and scientists have been mystified as to why plants and animals have evolved so differently.

Scientists already were studying genetic mutations and chromosomes in the late 1800s. By the 1930s, it was clear that many plants had doubled sets of chromosomes, but this appeared to be very rare in animals.

The famous evolutionary biologist Theodosius Dobzhansky observed in 1937 that the biggest difference between the evolution of plants and animals may be polyploidy. The reasons for this difference have eluded biologists over the last century, but new analyses of genomes are revealing ancient duplications in places that Dobzhansky and his contemporaries could not see.

Barker and his team created their own bioinformatics program to measure and characterize [gene duplications](#) in the insects, just as they do in plants. They found evidence of 18 putative "whole [genome](#)

[duplications](#)" and at least six other "bursts" of gene duplication that occurred during the evolution of insects. The team includes three undergraduate students and a fifth-year graduate student, Zheng Li, who are co-authors on their paper, which has just been published in *Proceedings of the National Academy of Sciences*, a prestigious scientific publication.

"When Li first approached me about analyzing insect data, I thought, 'Sure, let's do it, but we probably won't find anything because sequenced insect genomes did not appear to have been duplicated, unlike the first [plant genomes](#),'" Barker says.

"Yet our analyses found the same genomic signatures of polyploidy in insects that we have observed in many plants. In the historical context of work on polyploidy, even from the plant perspective, this was shocking.

"We care about where novelty and innovation come from in organisms," he says. "Our results tell us that many of the models and hypotheses about novelty and polyploidy, developed from the study of [plants](#), fungi and other organisms, may now apply to insects."

Given that insects are one of the most successful and diverse groups of animals, it is exciting to have a new perspective to think about how that diversity may have evolved, Barker adds.

"And so now we need to figure out what are the consequences," he says. "What are these genes doing? How are they different from other kinds of (genetic) duplicates? And that is work that we are actively pursuing."

More information: Zheng Li et al. Multiple large-scale gene and genome duplications during the evolution of hexapods, *Proceedings of the National Academy of Sciences* (2018). [DOI: 10.1073/pnas.1710791115](https://doi.org/10.1073/pnas.1710791115)

Provided by University of Arizona

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