

A clearer picture of how assassin bugs evolved

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This photo shows a selection of different assassin bugs representing different evolutionary lineages. Credit: W. S. Hwang, Weinrauch Lab, UC Riverside.

Assassin bugs, so named because these insects lie in ambush for prey that they attack with speed and precision, are found all over the world. Nearly 140 species of these bugs are blood-sucking; because they can bite humans around the mouth, they are also called kissing bugs. All kissing bugs can spread *Chagas disease*, a neglected tropical disease that imposes an economic burden on society.

Surprising, then, that scientists' understanding of the evolutionary history of assassin bugs is riddled with difficulty. The data are incomplete. Fossils, which exist for only a few groups of assassin bugs, are young,

providing only patchy information on how these bugs evolved.

Now entomologists at the University of California, Riverside have produced a clearer snapshot of the entire evolutionary history of assassin bugs by integrating molecular, paleontological, behavioral and ecological data into their analyses. The result of their painstaking work is a new phylogeny—the representation of the evolutionary relationships between species—for assassin bugs. It includes the most number of assassin bugs to date and represents the most number of subfamilies.

"We can now zoom in on specific groups within the phylogeny to examine specific aspects of the evolution of that group," said Christiane Weirauch, an associate professor of [entomology](#) who reconstructed the assassin bug phylogeny with her Ph.D. graduate student Wei Song Hwang. "Our phylogeny significantly improves our knowledge about relationships within assassin bugs and will guide future research work in understanding how some of the interesting prey specialization behaviors and prey capture techniques have evolved."

Study results appeared last month in [PLoS ONE](#).

"One significant improvement is the addition of several assassin bug species from the [subfamily](#) Reduviinae, the second largest subfamily of assassin bugs," said Hwang, the first author of the research paper.

"Previous phylogenies have a very limited representation of Reduviinae, which means the overall interpretation of the phylogeny is of limited value."



This photo shows a representation of the diversity of blood-feeding kissing bug species in the world. Credit: W. S. Hwang, Weirauch Lab, UC Riverside.

Assassin bugs are estimated to have originated during the Middle Jurassic (~178 million years ago), making them a relatively old group of insects. They diversified significantly in the Late Cretaceous (~97 million years ago); indeed, nearly 90 percent of the existing species diversity we see today in assassin bugs started to diversify from this time onwards. The cause of this diversification remains unknown.

Blood-feeding kissing bugs

Weirauch and Hwang also determined that kissing bugs originated just 27-32 million years ago, the previous estimate being 107 million years ago. Mostly found in Central and South America, these bugs have evolved to feed on vertebrate blood—lizards, birds, opossums, armadillos, bats, etc., and humans—and can be found in diverse environments, from the Sonoran desert to the Amazon rainforest.

"The previous estimate of 107 million years ago linked the diversification of kissing bugs with the splitting of South America from Antarctica and provided a longer time-span for kissing bugs to speciate and spread across the continent and adapt," Hwang said. "Our research shows that this is not the case. By including more data and improving estimation methods, our younger estimate of 27-32 million years ago matches the time when the hosts, mainly mammals and birds, were diversifying at a rapid rate in South America."

The researchers caution that as natural environments get altered, more

kissing bugs may be seen adapting to new environments and hosts rather than going extinct.

"The colonization of human settlements by wild kissing bugs we are witnessing now is thus likely to increase in intensity as more natural environments are replaced by human activities," Hwang said.

With their comprehensive sampling of assassin bugs and large molecular dataset, Weirauch and Hwang also show that the blood-feeding kissing bugs either have a single origin or two separate but close origins. Until now, the possibility of two separate but close origins of kissing bugs had not been hypothesized nor demonstrated.

"The possibility that there are two separate lineages implies that there will be shared traits among the lineages, but also slight differences we need to be aware of when developing different preventative strategies," Hwang explained. "A single origin, on the other hand, means we can expect common traits shared among all [kissing bugs](#) that can be targeted for control or monitoring."

Building the Tree of Life

The current research is part of the scientific endeavor to reconstruct the entire Tree of Life—the biological concept that all living organisms are related and can be traced back to a single ancestor representing the origin of life on Earth.

"Reconstructing a [phylogeny](#), a framework from which we can infer the evolutionary history of any group of organisms, is thus the first step towards understanding how life evolved, how different species relate to one another, how specific traits evolved over time, and why biodiversity occurs the way it does today," Weirauch said.

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