

Biologists map the family tree of all known snake and lizard groups

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The *Lyriocephalus scutatus*, pictured, is one of thousands of reptiles included in the phylogeny of squamates created by George Washington University Assistant Biology Professor Alex Pyron. Credit: George Washington University

(Phys.org) —A George Washington University biologist and a team of researchers have created the first large-scale evolutionary family tree for every snake and lizard around the globe.

The findings were recently published in the journal *BMC Evolutionary*

Biology. Alex Pyron, the Robert F. Griggs Assistant Professor of Biology in GW's Columbian College of Arts and Sciences, along with researchers from the City University of New York and Arizona State University, detail the cataloguing of 4,161 species of snakes and lizards, or squamates.

"Squamates include all lizards and snakes found throughout the globe, including around 9,500 species on every continent except Antarctica, and found in most oceans," said Dr. Pyron. "This is everything from cobras to garter snakes to tiny [geckos](#) to the [Komodo Dragon](#) to the Gila Monster. They range from tiny threadsnakes that can curl up on a dime to 10 feet monitor lizards and 30 foot pythons. They eat everything from ants to wildebeest."

The evolutionary [family tree](#), or phylogeny, includes all families and subfamilies and most genus and species groups, said Dr. Pyron. While there are gaps on some branches of the tree, the structure of the tree goes a long way toward fully mapping every genus and species group.

"It's like building an incomplete family tree for your family, but with half of the 'children' sampled. You're in it, but not your brother, one of your cousins is, but not another. However, because it's so complete, we know where the missing relatives go because there's no longer as much mystery as to how the missing species, or cousins, are related, with a few notable exceptions for some remaining species.

"This is also a community effort. We sequenced hundreds of these species ourselves but took thousands more from public databases, building on the work of others."

Understanding how various snakes and lizards are connected to each other fills a major gap in knowledge, said Dr. Pyron, because before this, there were no single reference for how all lizards and snakes were

related or what their classification was.

"A phylogeny and taxonomy is fundamental for all fields of biology that use lizards and snakes, to understand how to classify the species being studied, to interpret biological patterns in terms of relatedness, and even at a more basic level, to count how many species are in an area, for example, for conservation management purposes."

This project has been in the works since 2008 with the last five years being the most intense. It was funded by the National Science Foundation Postdoctoral Research Fellowship in Biological Informatics.

The researchers used DNA sequencing technology to genotype, or identify, the DNA of thousands of lizards and snakes.

"We have laid down the structure of squamate relationships and yet this is still the beginning," said Dr. Pyron. "As hundreds of new [species](#) are described every year from around the globe, this estimate of the squamate tree of life shows us what we do know, and more importantly, what we don't know, and will hopefully spur even more research on the amazing diversity of [lizards](#) and [snakes](#)."

More information:

www.biomedcentral.com/1471-2148/13/93/abstract

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