

Genealogy of scaly reptiles rewritten by new research

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The most comprehensive analysis ever performed of the genetic relationships among all the major groups of snakes, lizards and other scaly reptiles has resulted in a radical reorganization of the family tree of these animals, requiring new names for many of the tree's new branches. The research, reported in the current issue of the journal *C.R. Biologies*, was performed by two biologists working at Penn State: S. Blair Hedges, professor of biology, and Nicolas Vidal, a postdoctoral fellow in Hedges' research group at the time of the research who now is a curator at the National Museum in Paris.

Vidal and Hedges collected and analyzed the largest genetic data set ever assembled for the scaly reptiles known as squamates. The resulting family tree has revealed a number of surprising relationships. For example, "The overwhelming molecular-genetic evidence shows that the primitive-looking iguanian lizards are close relatives of two of the most advanced lineages, the snakes on the one hand and the monitor lizards and their relatives on the other," Vidal said.

"We gave this group the new name, 'Toxicofera' because of another discovery, reported in a related paper, that some lizard species thought to be harmless actually produce toxic venom, as do some snakes -- including some large monitor lizards in the same family as the giant Komodo Dragon and some large species of iguanians." Vidal, Hedges, and other researchers report this and other discoveries about the early evolution of the venom system in lizards and snakes in a paper led by Bryan G. Fry of the University of Melbourne in Australia, published in

the current issue of the journal *Nature*. "It's a really startling thing that so many supposedly harmless lizards actually are venomous," Vidal said, "but their sharing of this characteristic makes sense now that our genetic studies have shown how closely they are related."

The diversification of such a large group of animals, including 8,000 living species, into many ecological niches is a major pattern of biological evolution on Earth. "We used to think that venom evolved relatively recently, but this study shows that it evolved very early in the history of these species, about 200-million years ago, when dinosaurs were just getting started," Hedges explained. "We would like to understand what factors had major effects on biological evolution at that time in the Earth's history and why these species survived but the dinosaurs did not." This research also could help scientists find fossils of more species because it reveals new information about the age of the geological formations in which the fossils can be found. In a broader context, this work is part of astrobiology research, which seeks to understand general mechanisms of evolution that might apply to other worlds.

To increase the statistical confidence of their results, Vidal and Hedges included twice the amount of genetic information as was used in previous studies of these species. The team's data include nine nuclear-protein-coding genes from 19 species representing all major lineages -- mostly families -- of living snakes, lizards and a third related group of scaly reptiles, the amphisbaenians. The team analyzed these data using several statistical methods to determine how each species is related to the others. "Although these genes have the same functions in each species, there are small differences between the species -- mutations -- that have developed over time," Vidal explained. Comparisons of these evolutionary differences resulted in a family tree of squamates that Hedges says is almost completely different from the version that has appeared in textbooks for the past hundred years. The family tree in use

now is based primarily on comparisons of certain physical structures, known as morphological characters -- like the shape of a specific bone.

"The current textbook version of the family tree of reptiles places the iguanians, which is a huge group of 1,440 species of primitive-looking lizards, at the base of the tree -- but the iguanians now are near the top of our new tree in the new Toxicofera group, which we call the venom clade," Vidal explained. In addition to the new venom character, Vidal and Hedges discovered other physical traits whose importance in providing visible clues to the species' close genetic relationships had been overlooked before. For example, among the lizards and snakes that lay eggs, all the species above a certain point in the new tree have one egg tooth and all those below that point have two egg teeth. "In the old arrangement, using the number of egg teeth as an evaluating characteristic didn't make sense, but in the new arrangement it makes perfect sense," Vidal said. "If this new tree is correct, all the morphological characters that traditionally have been used to identify similarities between species will need to be re-evaluated to understand how these traits evolved."

According to Vidal and Hedges, the reason why the old and new family trees are so different is because they are based on different ways of gauging the relationships between species. The old tree is based primarily on morphology -- comparisons of certain characteristics of the animals' physical structure -- which can change considerably when a species adapts to changing conditions. For genealogy research this can be a problem if two unrelated species change in the same way, resulting in false evidence of relationships. The new tree is based exclusively on comparisons of the molecular structure of the animals' genes. "Although the molecular changes in the genes can occur quickly and slowly, and can change in response to the conditions in which the animal lives, those adaptive changes are limited to a small part of the gene. Most of the gene carries a genealogical signature which reveals the evolutionary history of

the species," Hedges explained.

Many of the groups on the existing, morphological, family tree were named for physical characteristics that no longer apply to the groups on the new tree. For example, as a result of the reorganization, a huge group of lizards -- the iguanians, which have soft tongues and number more than 1,400 species -- moved from near the bottom of the old tree into a grouping near the top of the new tree among squamates, which have hard tongues. As a result, Vidal explains, "We found we needed to replace many of the old names, like the one that referred to the texture of the tongue, because they no longer have any valid meaning in the new tree."

Among the new names are Bifurcata, which in Latin that means "split," for species with a split tongue; Toxicofera, which means "toxic animals," for species that have venom, Unidentata, which means "one tooth," for species with one egg tooth; Episquamata, which means "top squamates," for the iguanians and other species in this group near the top of the new tree; Laterata, which means "tile-like," for a group of lizards and legless reptiles whose scales are shaped like squarish tiles instead of the half-circle-shaped scales common to snakes and other lizard species.

"Because the current tree has been widely accepted for nearly a century, I think there is going to be a delay of maybe a few years before the general scientific community gets used to the new tree," Vidal said. "If other research groups working in this area find the same pattern with additional genes, then I believe the scientific community may accept these results more quickly."

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