

New study unlocks mystery origin of iconic Aussie snakes

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Tiger Snake (*Notechis scutatus*). Credit: Max Tibby- Snake Catchers Adelaide

New research led by the University of Adelaide has found the first tangible evidence that the ancestors of some of Australia's most venomous snakes arrived by sea rather than by land—the dispersal route

of most other Australian reptiles.

In a paper published in *Genes*, the researchers analyzed the genomes of two Australian elapids (front fanged snakes), a tiger and a brown snake, and compared them to marine and semi-marine elapid sea snakes and Asian elapids.

They inferred that the ancestor of all Australian elapids had accumulated self-replicating and self-mobilizing [genes](#) (jumping genes) that were not present in their land relatives but came from another source altogether.

Corresponding author Professor David Adelson from the University of Adelaide's School of Biological Sciences says, "While we know all marine and semi-marine sea snakes descended from a common Australian land-based ancestor, the origin of Australian elapids has been debated for some time.

"Some believe their ancestors traveled by land, whereas others hold the more contentious view that a marine or semi-marine ancestor swam here.

"In our research we found a number of genes that were present in the ancestor of all Australian elapids but could not be traced to a snake ancestor; instead they could be traced to similar transposable gene sequences found in [marine life](#), including fish, sea squirts, sea urchins, bivalves and turtles.

"This indicates the [marine environment](#) transferred the new genetic material into the snakes and offers new support to the argument that the first Australian elapids swam to our shores. They must have previously acquired the new genetic material during an ancestral period when they were adapted to marine life."

The researchers identified 14 distinct transfer events of the new genetic

material from other [marine organisms](#), with eight genes uniquely present in the marine and semi-marine sea snake genomes. In the case of the semi-marine [snake](#) genome, the acquired genes accounted for as much as 8–12 percent of the total genome sequence.

"This meant that we could unambiguously determine the major genetic differences between land and marine/semi-marine snakes were a consequence of migration into a marine environment," said Professor Adelson.

"This is the first time that jumping genes have been used to confirm the evolutionary history of any animal species, and this research definitively proved that the common [ancestor](#) of all Australian elapids adapted to a marine environment.

"It may also have made it easier for the subsequent land to marine transition of sea snakes."

More information: James D. Galbraith et al, Horizontal Transposon Transfer and Its Implications for the Ancestral Ecology of Hydrophiine Snakes, *Genes* (2022). [DOI: 10.3390/genes13020217](https://doi.org/10.3390/genes13020217)

Provided by University of Adelaide

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