

Elusive venomous mammal joins the genome club

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Photo Credit: Eladio Fernandez, Caribbean Nature Photography

Hispaniolan solenodon (*Solenodon paradoxus*) is one of the only extant venomous mammals. Its species separated from other insectivores at the time of the dinosaurs. Credit: Eladio Fernandez, Caribbean Nature Photography.

In the open-access journal *GigaScience*, scientists have presented a draft genome of a small shrew-like animal, the venomous Hispaniolan solenodon (*Solenodon paradoxus*). This species is unusual not only because it is one of the very few venomous mammals, it is also the sole remaining branch of mammals that split from other insectivores at the time of the dinosaurs. The genome sequencing and analysis of this endangered animal was carried out by an international team led by Dr. Taras K. Oleksyk from the University of Puerto Rico at Mayagüez. The availability of the solenodon genome sequence allowed the researchers to answer several evolutionary questions, in particular whether the solenodon species survived the meteor impact ended the dinosaurs.

As one of the only extant venomous mammals, the solenodon has modified salivary glands that secrete venomous saliva through grooves on the animal's sharp incisors ("solenodon" derives from the Greek for "grooved tooth"). They also have several other primitive and very unusual characteristics for a mammal—very large claws, a flexible snout with a ball-and-socket joint, and oddly positioned teats, which are on their rear. While the mammalian tree of life has been heavily researched, this is the most distantly related branch added to the "genome club." It has particular importance and implications for conservation because morphometric studies have suggested that southern and northern Hispaniolan solenodons may be subspecies rather than separate species.

Solenodon is genetically and geographically isolated. Highly endangered, they remain only in a few remote corners of the Caribbean islands of Cuba and Hispaniola. Its nocturnal lifestyle makes it even more elusive, and therefore less studied. Thus, it was crucial for the researchers to work with local experts at the Instituto Tecnológico de Santo Domingo and Universidad Autónoma de Santo Domingo and with local guides who helped them track and ambush passing solenodons at night.

One of the lead authors, Dr Juan Carlos Martinez-Cruzado, said, "Local

resources are absolutely necessary for this kind of work. Only they truly know their animal's behavior. This project may open doors to many others to come, and we always assumed this to be one of many projects that will help research, education and conservation efforts in the Dominican Republic."

The project entailed more than just the challenge of obtaining the organisms for blood samples; the solenodon genome proved particularly difficult to sequence. Carrying out genomics research in remote parts of the Caribbean provided a challenge, particularly in transporting high-quality DNA to the lab. Due to the constraints of poor-quality DNA as well as a limited budget, the commercial lab that conducted the sequencing turned out a very low coverage per individual.

Having already ventured into the jungle, the researchers embraced this new challenge by developing novel approaches to assemble the genome. First, the researchers reasoned that because the species has existed for tens of millions of years in isolation, it was extremely inbred and had a very homozygous genome. This lead to a potential workaround, because the five collected sets of genomic data could be pooled to increase the coverage. Despite initial doubts, this worked better than expected, especially when that strategy was combined with a string graph approach rather than the more standard de Bruijn graph assembly method. String graphs incorporate more of the sequencing data than de Bruijn graphs. Based on the results here, this new technique provides a low-budget alternative for [genome](#) assembly, particularly in the highly homozygous genomes of endangered species.

The first author of the paper, Kirill Grigorev, said, "For me, perhaps the most interesting part of this research was the challenge of delivering a de novo [genome assembly](#) that was suitable for comparative genomics, using an amount of sequencing data much smaller than in other similar projects."

After conducting their assembly, the researchers had data of sufficient quality for answering many scientific questions on solenodon evolution. With regard to conservation plans, the data supports the idea that there was a subspecies split within the Hispaniolan solenodon at least 300,000 years ago, meaning the northern and southern populations should be treated as two separate conservation units, and may therefore need independent breeding strategies.

These data also shed light on the initial speciation event for this branch, and showed that solenodons likely diverged from other extant mammals 73.6 million years ago. Dr. Oleksyk said, "We have confirmed the early speciation date for solenodons, weighing on the ongoing debate on whether the solenodons have indeed survived the demise of dinosaurs after the asteroid impact in the Caribbean."

More information: "Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered *Solenodon paradoxus* from the island of Hispaniola" [DOI: 10.5524/100422](https://doi.org/10.5524/100422)

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