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Ancient DNA reveals phylogeny of prehistoric armadillos

Before the last ice age, South America had an impressive array of megafauna including the megatherium, a sloth the size of an elephant, and a wide variety of glyptodonts, a group of imposing armored mammals. Glyptodonts have been traditionally considered to represent a phylogenetically distinct group close to the cingulates (armadillos). However, their exact affinities have remained an enigma until now. A research group led by the *Institut des sciences de l'évolution de Montpellier* (CNRS / Université de Montpellier / IRD / EPHE), the McMaster Ancient DNA Center in Canada¹, and also involving the *Centre de recherche sur la paléobiodiversité et les paléoenvironnements* in France (CNRS / MNHN Muséum national d'Histoire naturelle / UPMC) have answered this question by sequencing the whole mitochondrial genome of a 12,000-year-old specimen. The researchers managed to show that the glyptodonts are an extinct lineage of cingulates that experienced a spectacular increase in size following their appearance 35 million years ago. This research is published on 22nd February 2016 in the journal *Current Biology*.

Glyptodonts are classified in the Xenarthra superorder, together with armadillos, sloths and anteaters. Yet today's armadillos and glyptodonts differ from all other mammals by their carapace, made up of mobile bands, while that of their prehistoric cousins was in a single piece. Several morphological differences have led glyptodonts to be considered as a group in their own right, representing a sister group² to the armadillos within the Xenarthra. This traditional interpretation was recently called into question by a study on cranial and dental characters that classified the glyptodonts with the armadillos.

To investigate this issue, researchers studied the DNA from a fragment of carapace thought to be from a 12,000-year-old *Doedicurus*. This species was one of the largest glyptodonts, with a body mass of 1.5 metric tons and a characteristic spiny club-shaped tail. Sequencing of ancient DNA is difficult for a number of reasons, firstly because this DNA gets greatly fragmented by time and humid conditions. Furthermore, endogenous DNA strands need to be separated from any environmental contamination.

To do this, the researchers had to develop RNA probes capable of recognizing the genetic material of the target species, which is a challenging task when none of the genomes of closely related species are known. To overcome this obstacle, the group modeled plausible ancestral sequences using mitochondrial genomes from present-day Xenarthra (armadillos, anteaters and sloths). These bioinformatic sequences were then used to synthesize suitable RNA probes, which then made it possible to reconstruct the

¹ The Ancient DNA center at McMaster University in Hamilton (Ontario, Canada)

² For example, humans and chimpanzees belong to sister groups.



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mitochondrial genome of this extinct species almost completely. The phylogenetic analyses then clearly placed the glyptodonts within the cingulates, where they represent a distinct lineage. The last members of this lineage of giant cingulates, which dates back some 35 million years, died out only 10,000 years ago, at the end of the last ice age.

This study illustrates the potential of ancient DNA capture methods based on ancestral sequences reconstructed using bioinformatics, a technical approach used for the first time in this study.



Fossil *Doedicurus* specimen from the La Plata museum (Argentina)
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Bibliography

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