

New technique fills gaps in fossil record

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University of Pennsylvania evolutionary biologists have resolved a long-standing paleontological problem by reconciling the fossil record of species diversity with modern DNA samples.

Cataloging the [diversity of life](#) on earth is challenging enough, but when scientists attempt to draw a [phylogeny](#) — the branching family tree of a group of species over their evolutionary history — the challenge goes from merely difficult to potentially impossible. The [fossil record](#) is the only direct evidence scientists have about the history of [species diversity](#), but it can be full of holes or totally nonexistent, depending on the type of organisms. The only hope in such cases is to infer historical diversity from modern DNA sequences, but such techniques have a fatal flaw: the results they provide are demonstrably incorrect.

The Penn team has developed a new technique for analyzing phylogenies and shown that the results stand up against the known fossil history of whale species, a gold standard in terms of fossil records.

"We've put contemporary molecular approaches on equal footing with classical paleontological approaches," said Joshua B. Plotkin of the Department of Biology in Penn's School of Arts and Sciences and the Department of Computer and Information Science in the School of Engineering and Applied Science.

Plotkin conducted the research along with postdoctoral fellows Helene Morlon and Todd Parsons, both of Biology.

Their work will appear in the journal *Proceedings of the National Academy of Sciences*.

The limitations of the fossil record — and the lack of good alternatives — represent a longstanding problem in paleontology. Some species, due to the makeup of their bodies or the geology of the areas where they lived, don't leave fossils. If they leave any legacy to the present, it must be inferred from the DNA of their modern descendants, or from the descendants of their relatives.

For a few decades, scientists have compared the DNA of modern species, making mathematical inferences about the history of species diversity in a group going back to their most recent common ancestor. This reconstructive technique held much promise for the field, but a problem with the approach is now evident.

"When scientists use these phylogenetic techniques, they always infer patterns of increasing diversity. In whatever group of species they inspect, they see virtually no extinctions and a steadily increasing number of species over time," Plotkin said. "This molecular inference is problematic because it's known to be false. The fossil record clearly shows extinctions and long periods of diversity loss."

The cetaceans, a group of species that includes whales, dolphins and porpoises, are ideal for testing ideas about evolutionary diversification, as their fossil record is especially clear. Because they are large animals, and the sea floor is well suited to fossilization, paleontologists are confident that the cetaceans came into existence about 35 million years ago and reached a peak of diversity about 10 million years ago. The number of cetaceans then crashed from about 150 species to the 89 species in existence today.

"The problem with phylogenetic inferences is that you get the opposite

view when you apply it to the cetaceans. You would see the number of whale species increasing over time, so that the 89 species we have today is the apex. But we know that this is flat-out wrong because it's directly contradicted by the boom-then-bust pattern in the fossil record."

This realization was a major blow for the field; if molecular reconstructions can't be trusted, there would be no way for scientists to ever learn the history of species that don't have good fossil records. The only hope was that phylogenetic methods could be refined.

In their study, Plotkin and his colleagues added new variables to these methods. The flaw in existing techniques was the reliance on a static rate of diversification. Because that variable could never be negative, the number of species inferred necessarily increased over time.

"What we've done is a fairly modest extension of these techniques, but we allow for changing rates of speciation and extinction over time and among lineages," Plotkin said. "Most importantly, we allow for periods of time during which the extinction rate exceeds the speciation rate."

When applied to the DNA of the 89 whale species that survive today, Plotkin's molecular method closely matched the dynamics in the number of [whale species](#) during the last 35 million years as determined through traditional paleontological approaches.

"It's almost miraculous that we can inspect the DNA sequences of organisms living today and figure out how many such species were present millions of years ago," Plotkin said. "We're studying some of the largest [species](#) to have ever existed, and we are deciphering their evolutionary history based on information encoded in microscopic DNA molecules."

Provided by University of Pennsylvania

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