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Biology Professor Unlocks Method to Sequence DNA of Rare and Extinct Species

By Lawrence Lerner

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An RU-N Biology professor recently discovered a way to extract and sequence DNA from rare and extinct animals preserved in historic museum collections.

Assistant Professor Sara Ruane, along with Louisiana State University Professor Chris Austin, developed a protocol and tested a method for DNA sequencing several thousand genes from preserved snake specimens dating back to the early 1900s.

The breakthrough brings these once dormant specimens into the modern age of genomics, allowing scientists to start mapping the evolutionary relationships of various snake and other rare and extinct species, and furthering the study of the earth's ever-changing biodiversity.

"I had always thought it would be great if we could extract DNA from preserved specimens, especially those preserved in formalin," says Ruane. "Now that we have the computational power to handle short fragments of DNA for sequencing, it was just a matter of optimizing the extraction protocol."

Formalin, a variant of formaldehyde, preserves animal specimens and tissue samples for up to 500 years. But according to Ruane, it also locks up the DNA in these specimens, making it hard to extract. And DNA naturally degrades into tiny pieces over time, rendering it difficult to sequence using a conventional approach called the Sanger method, which requires large chunks of DNA.

“Putting millions of tiny pieces together and reading them over and over wasn’t computationally feasible until recently.”

Ruane and Austin found and tested a DNA extraction method that included heating the snake-specimen tissue to a very high temperature and letting it incubate for double the normal amount of time. The method had been used on human tissue preserved from pandemics but had not been tried on animal specimens. Ultimately it worked, making it easier to extract the DNA.

"We got loans of formalin-preserved tissues of 21 snakes from the Harvard Museum of Comparative Zoology and the California Academy of Sciences," says Ruane. "Of those, 13 emerged with noticeable amounts of extracted DNA after we tried this method."

The scientists sent the short DNA fragments from those 13 specimens to a company in Michigan to prep them for sequencing, then to another company in Oklahoma for the actual job. Ten of their extraction samples came back with DNA sequencing.

"Putting millions of tiny pieces together and reading them over and over wasn't computationally feasible until recently," says Ruane. "But the computing power behind DNA sequencing has advanced rapidly over the last decade, making what was once unthinkable possible."

The DNA sequences came back with thousands of genetic markers, enabling Ruane and Austin to integrate this data with modern samples to create a phylogeny, or genetic family tree, and map the evolutionary relationships of myriad snake species.

Ruane admits that she was a little surprised by their success.

"Folks have struggled to make this happen for so long that they stopped trying, but now the conditions were ripe for this to work," says Ruane. "It largely came down to timing and a willingness to give it a try. Fortunately, it worked out."



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