

# Student publishes case for faster, less expensive DNA analysis

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A Washington State University student's undergraduate research is challenging a widely held assumption on the best way to analyze old DNA in anthropological and forensic investigations.

Sarah "Misa" Runnells' claim is weighty enough to be published this week in the peer-reviewed, online journal [PLoS ONE](#).

At issue is the best way to sequence "ancient" DNA, bits of [genetic code](#) pulled from remains up to 800,000 years old. Such remains tend to be chemically degraded, making it difficult to draw accurate connections between, say a woolly mammoth and modern animals, or [Neanderthals](#) and humans.

The techniques are also an issue in forensic investigations where remains, while relatively new, can still be severely compromised.

In 2000, researchers writing in the journal Science recommended a set of standards that emphasized cloning bits of [ancient DNA](#) to detect errors and contamination from modern DNA.

"Those rules became gospel," says Brian Kemp, a WSU [anthropologist](#) and [molecular biologist](#). In fact, they became so widely adopted that his preferred technique—direct sequencing—is often dismissed by journal reviewers.

"I've had papers outright rejected because they said, 'You did not

clone," says Kemp.

Kemp wanted to demonstrate that direct sequencing worked just as well by directly comparing it to cloning, but he had a problem: He didn't have experience with cloning.

Then he met Runnells, who had learned to clone while majoring in biotechnology as a WSU undergraduate. The two used both methods to analyze 3,500-year-old northern fur seal bones.

"After five samples with both cloning and direct sequencing, we got the same answer from both methods," says Runnells, who has published under her soon-to-be married name of Winters.

Their findings even held up with one particularly degraded sample. Cloning gave conflicting DNA sequences in the sample, while direct sequencing showed gaps in the code.

"In no case did the results of one method conflict with another," says Kemp.

The *PLoS ONE* paper is the first published on a \$595,000 grant Kemp received from the U.S. Department of Justice. One goal of the grant is to find more cost-effective ways of analyzing degraded DNA.

Direct sequencing can cost a fraction of cloning and be done in less time, says Kemp.

"That's really applicable to the justice system, where you want to save money and time," says Runnells, who is now a second-year Master's student in zoology.

"Everybody wants to save money and time," adds Kemp. "There are

more forensic cases than they can work on. There's a backlog of forensic cases."

Direct sequencing can also be increasingly helpful to academic researchers in a time of shrinking budgets, says Kemp.

"If you have an infinite amount of resources and funding, you can do anything," he says. "You can clone everything a thousand times. It doesn't matter. But for the assistant professor at WSU who has a limited budget, we need to make smart choices."

**More information:** "To clone or not to clone: Method analysis for retrieving consensus sequences in ancient DNA samples":

[dx.plos.org/10.1371/journal.pone.0021247](https://doi.org/10.1371/journal.pone.0021247)

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