

Woolly-mammoth genome decoded

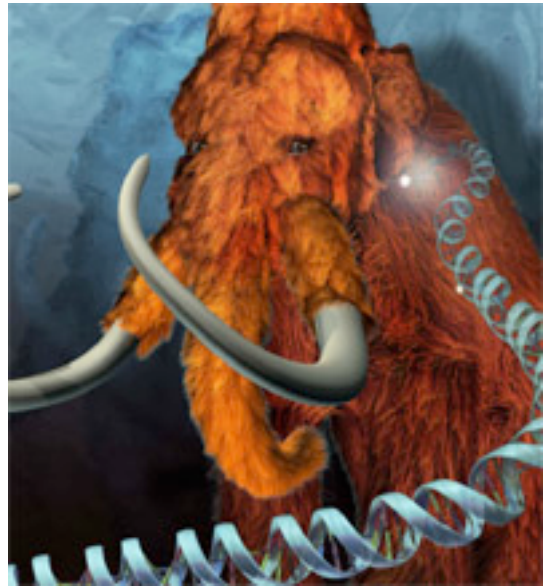
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Courtesy Penn State University and [World Science](#) staff

Biologists report that they have for the first time unraveled nearly the whole genetic code of an extinct animal: the woolly mammoth, the iconic giant elephant that roamed the cold northern hemisphere.

Past projects have decoded chunks of the DNA of ancient species, such as the cave bears, but not most of the genome, as the researchers in the new study claim to have done.

The researchers charted four billion bases, or “letters,” of code using cutting-edge DNA-sequencing instruments and a new high-efficiency approach, said Webb Miller of Penn State University, one of the project’s two leaders.



“Our data set is 100 times more extensive than any other published dataset for an extinct species, demonstrating that ancient DNA studies can be brought up to the same level as modern genome projects,” said Stephan C. Schuster, the project’s other leader and also at Penn State.

The researchers said the full woolly-mammoth genome probably consists of over four billion DNA bases, about the size of the modern-day African elephant’s genome. Although the study comprised more than four billion DNA bases, only 3.3 billion of them—a little over the size of the human genome—currently can be assigned to the mammoth genome, the investigators added.

Some of the remaining DNA bases may belong to the mammoth, they explained; others could belong to other organisms, like bacteria and fungi, from the surrounding environment that had contaminated the sample. The team used a draft version of the African elephant’s genome, which other scientists are working on, to distinguish those sequences of code that truly belong to the mammoth from possible contaminants.

“Only after the genome of the African elephant has been completed will we be able to make a final assessment about how much of the full woolly-mammoth genome we have sequenced,” said Miller. The team used DNA extracted from the hairs of a mammoth mummy buried in frozen Siberian ground for 20,000 years, and a second mammoth mummy estimated to be at least 60,000 years old.

By using hair, the scientists said they avoided problems that have bedeviled the sequencing, or decoding, of ancient genes from bones. That’s because DNA in the hair is more easily separated from contaminating DNA of bacteria and fungi. Also, hair components act as a biological plastic that encases and protects genetic material.

Genetic evidence indicates woolly mammoths evolved into two genetically distinct sub-populations starting around two million years ago, according to Schuster and Miller. One of these died out some 45,000 years ago; another lived on until after the last ice age, about 10,000 years ago.

The new research also shows woolly mammoths are more closely related to modern-day elephants than previously was believed, said Schuster and Miller.

“Our data suggest that mammoths and modern-day elephants separated around six-million years ago, about the same time that humans and chimpanzees separated,” said Miller. “However, unlike humans and chimpanzees, which relatively rapidly evolved into two distinct species, mammoths and elephants evolved at a more gradual pace.”

Also, “we discovered that individual woolly mammoths were so genetically similar to one another that they may have been especially susceptible to being wiped out by a disease, by a change in the climate, or by humans,” said Schuster.

Members of his group previously ruled out that humans might have killed off at least one of the Siberian sub-populations, which appears to have gone extinct when no humans lived in Siberia. But debate continues over the causes of extinction for mammoths that lived elsewhere, including North America.

Image; Woolly mammoth in an artist's image. (Courtesy Exhibit Ease LLC - Steven W. Marcus)