

Mobile DNA elements in woolly mammoth genome give new clues to mammalian evolution

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The woolly mammoth died out several thousand years ago, but the genetic material they left behind is yielding new clues about the evolution of mammals. In a study published online in *Genome Research*, scientists have analyzed the mammoth genome looking for mobile DNA elements, revealing new insights into how some of these elements arose in mammals and shaped the genome of an animal headed for extinction.

Interspersed repeats, also known as transposable elements, are DNA sequences that can "jump" around the genome, causing mutations in the host and contributing to expansion of the genome. Interspersed repeats account for a significant fraction of mammalian genomes, and some of these elements are still actively mobile. In humans, interspersed repeats account for approximately 44% of the entire genome sequence. Even more extreme is the opossum genome, where more than half of the sequence is composed of repetitive elements.

Scientists recently sequenced the woolly mammoth genome, using [DNA samples](#) obtained from preserved specimens. Dr. Stephan Schuster and his research group at Penn State University, who were involved in the sequencing and analysis of the mammoth genome, are now looking deeper into the sequence for interspersed repeats. The mammoth genome is an excellent candidate for comparative analysis of interspersed repeats in mammals, as it had a remarkably large genome of approximately 4.7 billion bases, 1.5 times larger than the [human genome](#)

. Using the mammoth genome sequence and sequences of other mammals for comparison, Schuster's group found that the mammoth genome contained the largest proportion of interspersed repeats of any other mammal studied. In fact, a single class of elements, known as the BovB long interspersed repeat, accounted for nearly 12% of the mammoth genome alone.

Dr. Fangqing Zhao, a postdoctoral researcher in Schuster's group and primary author of the work, emphasized that the BovB family of repeats is particularly interesting, because while this family has been identified in other mammalian genomes, such as ruminants, snakes, opossum, and now the mammoth, its distribution in the mammalian lineage is inconsistent. Zhao explained that this finding in mammoth further supports the hypothesis that BovB may have been acquired "horizontally," meaning that vertebrate genomes attained the element from another organism, rather than inherited from ancestors.

Many species within the Afrotheria group of mammals, which includes the woolly mammoth, are at high risk for extinction or are already extinct. "Further analyses examining if the genomes of extinct and endangered Afrotherians contain more repetitive elements than non-endangered [mammals](#) may elucidate whether there is an interplay between repetitive elements and extinction," Zhao noted, underscoring the need to study genomes of species on the brink of extinction.

Source: Cold Spring Harbor Laboratory ([news](#) : [web](#))

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