

# Discovery of a preserved ancient Siberian moose with intact DNA

March 2 2016

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Scientists of the Tomsk State University have found preserved moose in Western Siberia with unique genetic features. This discovery will help determine the origin and path of moose movement in the last few tens of thousands of years and suggests that Siberia is a unique genetic repository. The research has been presented at the international conference "Theriofauna of Russia and adjacent territories," presented by the X Congress of the Russian Theriological Society.

Unique [moose](#) were found in the southeastern part of Western Siberia. Hunters of the Tomsk Region assisted in this discovery. Along with the license for opening the animals, they prepared for the capture of prototypes and a small profile.

After the genetic analysis of samples, the scientists codified data and compared it with data from GenBank, the international computer database. Zoologists have discovered previously unexplored genetic lines via this process, and the Tomsk researchers were similarly able to draw a conclusion about the existence of a new West Siberian haplogroup of moose similar in DNA structure. It is assumed that these genetic lines were widespread 30 to 40 thousand years ago, but disappeared during the last glacial maximum about 18 to 24 thousand years ago.

Molecular studies of animals in Western Siberia are still rare, says Olga Nemoykina, an employee of the Laboratory of Biodiversity Monitoring of Institute of Biology TSU. "This discovery confirms the existence of a refugium—places with favorable conditions in the south of the region,

where groups of forest species might be saved during global cooling."

According to Nemoykina, mitochondrial DNA, which is not subject to recombination, was used for analysis. For the entire span of time from ancient moose to their present day descendants, the mitochondria express only mutation changes. At the same time, according to the molecular clock hypothesis, the mutation process occurs a certain speed: about 3,000 years elapsed for the emergence and consolidation of one mutation in the DNA fragment used by scientists.

Nemoykina emphasizes that moose of Western Siberia are characterized by a high level of [genetic diversity](#), for moose.

"It allows us to assume that we also have the chance to find an unusually high genetic diversity of other [forest species](#) of our region," she says.

"Due to the fact that the high genetic diversity of populations increases the likelihood of their survival when environmental conditions change, wildlife in Western Siberia can be a repository of such diversity for those species that are well represented here." The zoologists' next step will be identifying patterns between the genotype and the appearance of new species of moose.

Provided by Tomsk State University

Citation: Discovery of a preserved ancient Siberian moose with intact DNA (2016, March 2) retrieved 20 April 2024 from

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