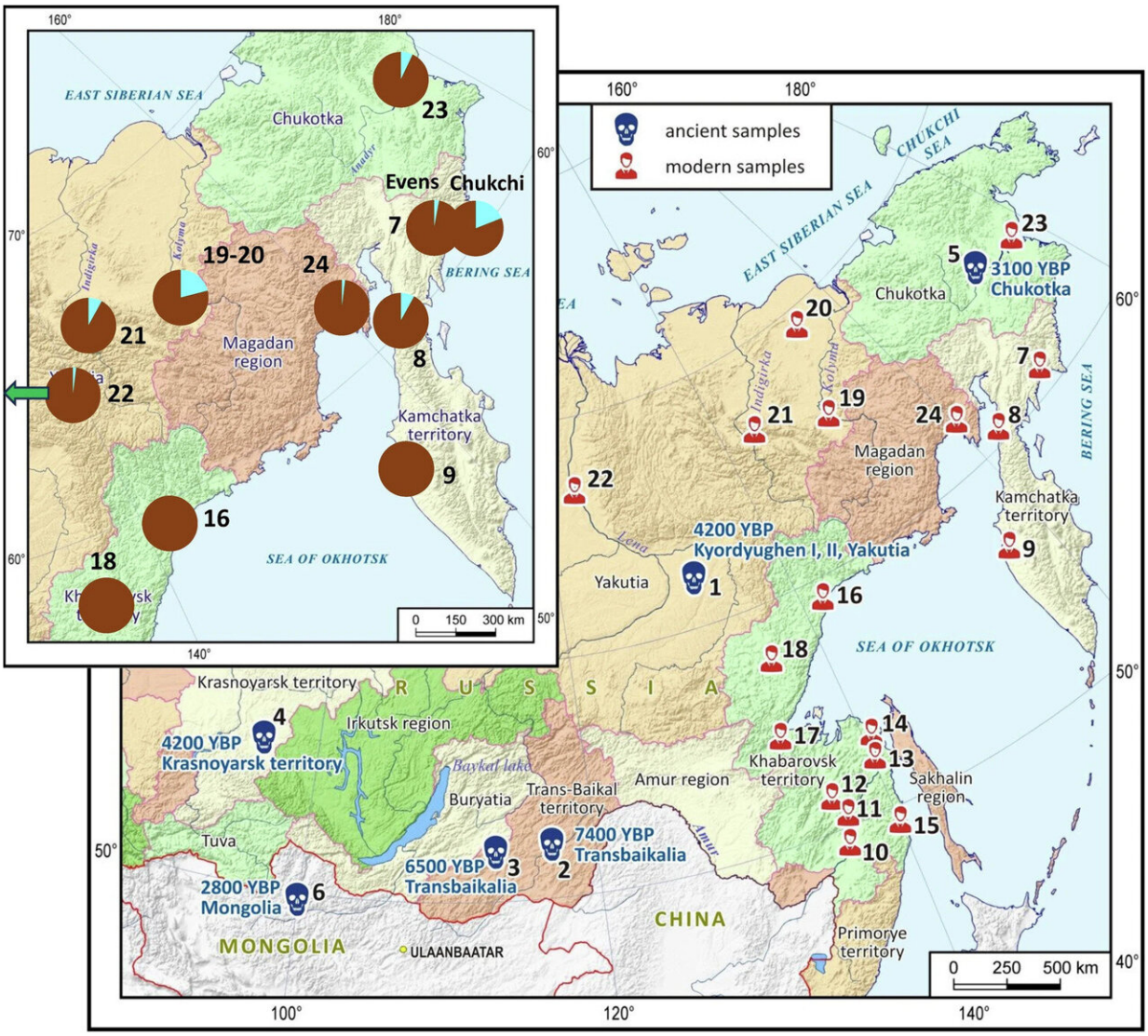
Who are his people? The 4,000-year hunt for a warrior's kin

May 4 2026, by Sayan Tribedi



Following the ancient paths: This map illustrates the widespread genetic footprint of the N-L708 haplogroup, showing the Kyordyughen warrior's origin

in Yakutia and the modern distribution of his descendants across Northeast Eurasia. Credit: Dmitry Adamov et al, Modern descendants of Kyordyughen warrior (Yakutia, 4200 years before present) in populations of Far East, *Journal of Human Genetics* (2026). DOI: 10.1038/s10038-026-01459-w

For 4,200 years, the Y chromosome of a Yakutian warrior has quietly echoed in Siberia's Arctic peoples. His extraordinary Stone Age grave was discovered in Russia's far northeast near Yakutsk in 2004 by scientists. The middle-aged hunter's skeleton was found on its back with arms at its side. Dozens of elk-bone plates were laid as a shield over the chest.

Analysis of the radiocarbon data hints that the person died nearly 4,000 years ago. The person is presumed to be from the Ymyyakhtakh cultural horizon. This cultural horizon contains the nomadic hunter-gatherers who used more sophisticated bone and antler weapons. This "Kyordyughen" warrior from Yakutia was richly equipped, but did any of his family line survive today?

Could a Stone Age warrior still have descendants?

To answer this question, the lead researcher of the new study, Dmitry Adamov, and his team performed a sequence analysis of the Y chromosome of this hunter, and then compared the findings with modern Siberian peoples' genomes.

The geneticists collected complete genome sequences from 256 men belonging to 11 native Russian groups hailing from the Far East region of Russia. Considering the Y chromosome lineage (transmitted only from father to son), researchers assigned the warrior to the haplogroup N-L708 lineage. The findings have been published in the *Journal of*

Human Genetics.

Surprisingly, that exact branch survives in people living today. The researchers found the warrior's Y-DNA signature in multiple modern Siberian groups. For example, about 19% of sampled Chukchi men in Kamchatka carry this haplogroup (versus 0% in, say, neighboring Eskimos).

In practical terms, roughly three out of the 256 individuals studied shared the warrior's ancient Y-line branch. Overall, Adamov's team reports that some one-quarter of the modern samples (67 of 256) "are, to various extents, genetically related to the Neolithic Yakutian individuals" (the ancient Kyordyughen samples). In short, a large slice of today's Far-Eastern men trace patrilineal ancestry back to these Neolithic Yakut hunters.

Where do his modern kin live?

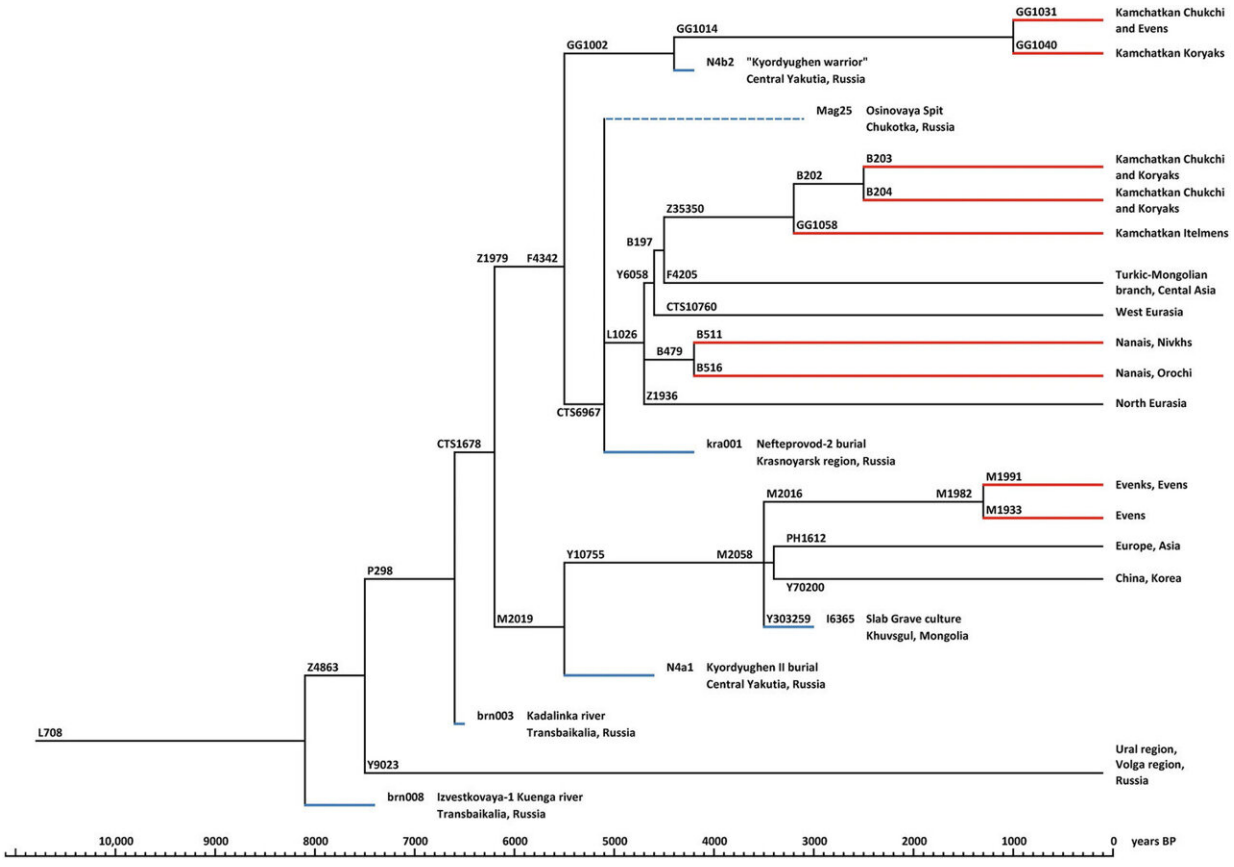
Tracing the branches of haplogroup N-L708 showed where the warrior's forebears migrated. Remarkably, the closest living relatives of this Yakutian warrior are not in his hometown but far to the east.

The study notes that "the most direct descendants of the famous Kyordyughen warrior (Kyordyughen I) are the indigenous peoples of Kamchatka and Chukotka"—specifically the Chukchi, Koryak and Even peoples of those regions. (These groups inhabit the tip of Siberia near the Bering Strait.) In other words, this Y chromosome lineage survived most strongly among Arctic populations on the Pacific coast, rather than in central Siberia.

The genetic divergence time also matches the archaeology. Based on mutation rates, the split between the warrior's lineage and the modern Chukchi men falls around 4,300 years before present—essentially the

same as the grave's age. This means the Chukchi and their kin likely share a great-great- … -great-grandfather with that Yakutian hunter. (Other related lineages of N-L708 appear in Evenks, Itelmens and other Far Eastern groups as well, painting a broad map of ancient movements.)

The big picture: this Neolithic Y chromosome thread runs across North Asia. As Adamov and colleagues write, their Y-chromosome tree "allows us to reconstruct the routes of ancient migrations of men with haplogroup N-L708 from their ancestral homeland—the territory of Transbaikalia."



The family tree of time: A simplified phylogenetic diagram showing the genetic relationships between the Kyordyughen warrior (highlighted) and his modern patrilineal relatives among indigenous Far Eastern populations, spanning

thousands of years. Credit: Dmitry Adamov et al, Modern descendants of Kyordyughen warrior (Yakutia, 4200 years before present) in populations of Far East, *Journal of Human Genetics* (2026). DOI: 10.1038/s10038-026-01459-w

Beyond the bones: The warrior's story continues

This study thus provides some insights into the missing puzzle of Siberian prehistory. For instance, there is a clear connection between the prehistoric individual under discussion and the present-day population. Moreover, the data obtained during the study supplements the archaeological evidence.

In other words, it has become possible to trace the genetic roots of the Ymyyakhtakh culture (4th millennium BC, Yakutia) by means of which only the remnants (such as bone shields) had been known until now.

At the same time, the authors note limitations. They focused only on the paternal Y-chromosome line, so this is just one branch of ancestry. Many other ancient lineages probably died out or weren't detected. And some ancient samples remain too fragmentary to analyze. Nonetheless, the study makes a compelling case that a Stone Age Yakutian is not entirely lost to time.

For indigenous communities, this work is especially meaningful. It provides a tangible connection to deep ancestry and migrations. By tracing the warrior's Y chromosome, researchers have shown that the proud men of Kamchatka and Chukotka carry a piece of a 4,000-year-old story in their genes.

This "genetic bridge" links the present to the past, enriching our understanding of how Siberian peoples moved and mixed over millennia.

As one geneticist put it, discovering these links "connects living people to a 4,200-year-old warrior, bridging ancient and modern worlds."

More information: Dmitry Adamov et al, Modern descendants of Kyordyughen warrior (Yakutia, 4200 years before present) in populations of Far East, *Journal of Human Genetics* (2026). DOI: 10.1038/s10038-026-01459-w

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