

Complete Neandertal mitochondrial genome sequenced from 38,000-year-old bone

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A study reported in the August 8th issue of the journal *Cell*, a Cell Press publication, reveals the complete mitochondrial genome of a 38,000-year-old Neandertal. The findings open a window into the Neandertals' past and helps answer lingering questions about our relationship to them.

" For the first time, we've built a sequence from ancient DNA that is essentially without error," said Richard Green of Max-Planck Institute for Evolutionary Anthropology in Germany.

The key is that they sequenced the Neandertal mitochondria—powerhouses of the cell with their own DNA including 13 protein-coding genes—nearly 35 times over. That impressive coverage allowed them to sort out those differences between the Neandertal and human genomes resulting from damage to the degraded DNA extracted from ancient bone versus true evolutionary changes.

Although it is well established that Neandertals are the hominid form most closely related to present-day humans, their exact relationship to us remains uncertain, according to the researchers. The notion that Neandertals and humans may have "mixed" is still a matter of some controversy.

Analysis of the new sequence confirms that the mitochondria of Neandertal's falls outside the variation found in humans today, offering

no evidence of admixture between the two lineages although it remains a possibility. It also shows that the last common ancestor of Neandertals and humans lived about 660,000 years ago, give or take 140,000 years.

Of the 13 proteins encoded in the mitochondrial DNA, they found that one, known as subunit 2 of cytochrome c oxidase of the mitochondrial electron transport chain or COX2, had experienced a surprising number of amino acid substitutions in humans since the separation from Neandertals. While the finding is intriguing, Green said, it's not yet clear what it means.

" We also wanted to know about the history of the Neandertal's themselves," said Jeffrey Good, also of the Max-Planck Institute. For instance, the new sequence information revealed that the Neandertal's have fewer evolutionary changes overall, but a greater number that alter the amino acid building blocks of proteins. One straightforward interpretation of that finding is that the Neandertal's had a smaller population size than humans do, which makes natural selection less effective in removing mutations.

That notion is consistent with arguments made by other scientists based upon the geological record, said co-author Johannes Krause. "Most argue there were a few thousand Neandertals that roamed over Europe 40,000 years ago." That smaller population might have been the result of the smaller size of Europe compared to Africa. The Neandertals also would have had to deal with repeated glaciations, he noted.

" It's still an open question for the future whether this small group of Neandertals was a general feature, or was this caused by some bottleneck in their population size that happened late in the game?" Green said. Ultimately, they hope to get DNA sequence information for Neandertals that predated the Ice Age, to look for a signature that their populations had been larger in the past.

Technically, the Neandertal mitochondrial genome presented in the new study is a useful forerunner for the sequencing of the complete Neandertal nuclear genome, the researchers said, a feat that their team already has well underway.

Source: Cell Press

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