Close correspondence between quantitative− and molecular−genetic divergence times for Neandertals and modern humans

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"The a" is as printed in the source.

Timothy Weaver, an anthropologist at the University of California at Davis and colleagues Charles Roseman and Chris Stringer created a model used prior information on how microsatellites, aka "junk DNA," can change, or drift, over time in The a species. Over time, those changes can accumulate enough for an entirely new species to evolve.

The researchers applied the model to 37 cranial measurements collected on 2,524 modern and 20 Neanderthal specimens. Their findings are published in this week's Proceedings of the National Academy of Sciences. Abstract below.

The Neanderthal−Human Split: (Very) Ancient History
Jennifer Viegas, Discovery News

March 17, 2008 −− Neanderthals and humans once shared a common ancestor, but we split from the stocky, hairy hominid group as long as 400,000 to 350,000 years ago, concludes a new study.

That estimate matches prior DNA studies, putting a date to the time when human beings first emerged on the planet. But would these first humans have been anatomically just like us? Probably not, suggests lead author Timothy Weaver, an anthropologist at the University of California at Davis.

"Early fossils along this lineage are quite different from later ones," he told Discovery News.

Fast evolution, in fact, probably drove the initial Neanderthal/human divergence, which likely began as genetic drift −− random changes in DNA. As the two groups parted ways, their changing environments likely drove more substantial changes in body shape and size, in response to differing needs.

Weaver and colleagues Charles Roseman and Chris Stringer created a model to determine how long it would have taken genetic drift to create the cranial differences observed between Neanderthal and modern human skeletons.

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Now that scientists have a better idea on when Neanderthals split from humans, they can zone in on which species might have been our common ancestor. They do this mostly by process of elimination. Fossils found long before 400,000 years ago, such as the 800,000−year−old Atapuerca humans from Spain, are simply too old to represent the common ancestor.

"I support the concept of a widespread ancestral species, Homo heidelbergensis," Stringer, a paleontologist at the Natural History Museum of London, told Discovery News.

Neanderthal features began to emerge from Homo heidelbergensis just before 500,000 years ago. "Heidelberg Man" was muscular and tall, had a relatively large brain, and usually grew to heights of 6 feet or more. Markings on bones suggest the burly hominid dined on enormous animals, such as mammoths, rhinos and elephants, some of which weighed over 1,500 pounds.

Stringer thinks that since Neanderthals and humans split relatively early, "we may need to designate the earlier part [on the human side] as 'Archaic sapiens.'" That would allow researchers to account for the different types of human fossils that fall between the divergence date and the appearance of more modern−looking people in Africa around 50,000 years ago.

Osbjorn Pearson, an associate professor of anthropology at the University of New Mexico, recently conducted similar research on Neanderthals and humans. He told Discovery News that he fully agrees with the new findings.

"From their, and other scientists' previous research, it has become clear that many of the physical differences between human skulls are due to random genetic changes that make populations diverge over time," Pearson said.

"It is gratifying −− and, for many anthropologists, perhaps unexpected −− that the bones and genes tell the same story."

"The results also reinforce the conclusion that it is unlikely that Neanderthals...contributed substantially to the modern human gene pool."

http://dsc.discovery.com/news/2008/03/17/human−neanderthal−split−print.html

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ANTHROPOLOGY

Close correspondence between quantitative− and molecular−genetic divergence times for Neandertals and modern humans

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Abstract

Recent research has shown that genetic drift may have produced many cranial differences between Neandertals and modern humans. If this is the case, then it should be possible to estimate population genetic parameters from Neandertal and modern human cranial measurements in a manner analogous to how estimates are made from DNA sequences. Building on previous work in evolutionary quantitative genetics and on microsatellites, we present a divergence time estimator for neutrally evolving morphological measurements. We then apply this estimator to 37 standard cranial measurements collected on 2,524 modern humans from 30 globally distributed populations and 20 Neandertal specimens. We calculate that the lineages leading to Neandertals and modern humans split {approx}311,000 (95% C.I.: 182,000 to 466,000) or 435,000 (95% C.I.: 308,000 to 592,000) years ago, depending on assumptions about changes in within−population variation. These dates are quite similar to those recently derived from ancient Neandertal and extant human DNA sequences. Close correspondence between cranial and DNA−sequence results implies that both datasets largely, although not necessarily exclusively, reflect neutral divergence, causing them to track population history or phylogeny rather than the action of diversifying natural selection. The cranial dataset covers only aspects of cranial anatomy that can be readily quantified with standard osteometric tools, so future research will be needed to determine whether these results are representative. Nonetheless, for the measurements we consider here, we find no conflict between molecules and morphology.

craniometrics | evolutionary quantitative genetics | microsatellites | population genetics | human evolution

Footnotes

Author contributions: T.D.W., C.C.R., and C.B.S. designed research; T.D.W. and C.C.R. performed research; C.B.S. contributed new reagents/analytic tools; and T.D.W., C.C.R., and C.B.S. wrote the paper.

The authors declare no conflict of interest.

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