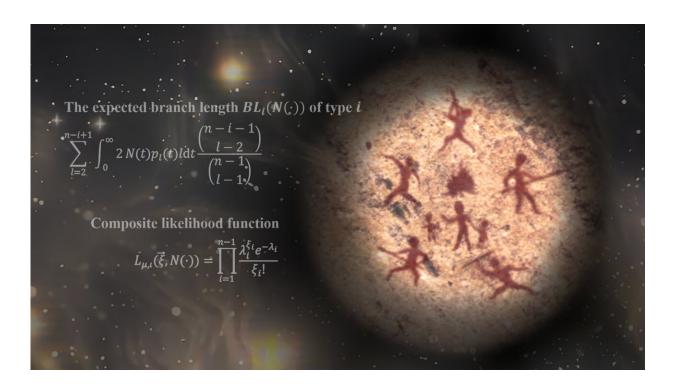


Early ancestral bottleneck could've spelled the end for modern humans

August 31 2023



The core formula of our new inference method is shown. The image depicts a cliff painting, illustrating the population of human ancestor pull together to survive the unknown danger in the darkness during the ancient severe bottleneck. Credit: Shanghai Institute of Nutrition and Health, CAS

How a new method of inferring ancient population size revealed a severe bottleneck in the human population which almost wiped out the chance for humanity as we know it today.



An unexplained gap in the African/Eurasian fossil record may now be explained thanks to a team of researchers from China, Italy and the United States.

Using a novel method called FitCoal (fast infinitesimal time coalescent process), the researchers were able to accurately determine demographic inferences by using modern-day human genomic sequences from 3,154 individuals. Researchers published their findings online in the journal *Science*.

These findings indicate that early human ancestors went through a prolonged, severe bottleneck in which approximately 1,280 breeding individuals were able to sustain a population for about 117,000 years. While this research has illuminated some aspects of early to middle Pleistocene ancestors, there are many more questions to be answered since uncovering this information.

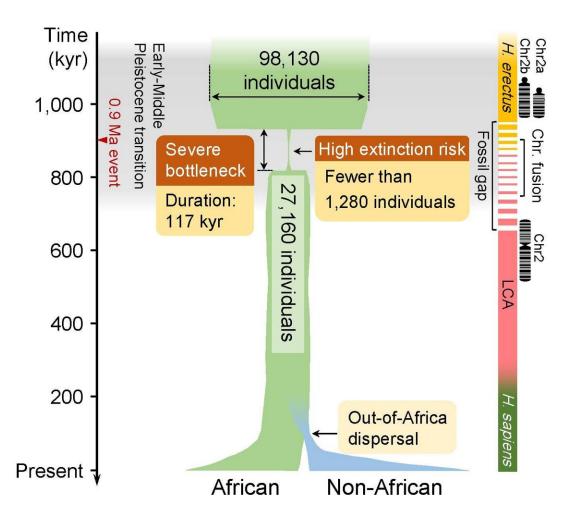
A large amount of genomic sequences were analyzed in this study. However, "the fact that FitCoal can detect the ancient severe bottleneck with even a few sequences represents a breakthrough," says senior author Yun-Xin Fu, a theoretical population geneticist at University of Texas Health Science Center at Houston.

The results determined using FitCoal to calculate the likelihood for present-day genome sequences found that <u>early human ancestors</u> experienced extreme loss of life and therefore, loss of genetic diversity.

"The gap in the African and Eurasian fossil records can be explained by this bottleneck in the Early Stone Age as chronologically. It coincides with this proposed time period of significant loss of fossil evidence," says senior author Giorgio Manzi, an anthropologist at Sapienza University of Rome.



Reasons suggested for this downturn in human ancestral population are mostly climatic: glaciation events around this time lead to changes in temperatures, severe droughts, and loss of other species, potentially used as food sources for ancestral humans.



The African hominin fossil gap and the estimated time period of chromosome fusion is shown on the right. Credit: *Science* (2023). DOI: 10.1126/science.abq7487



An estimated 65.85% of current genetic diversity may have been lost due to this bottleneck in the early to middle Pleistocene era, and the prolonged period of minimal numbers of breeding individuals threatened humanity as we know it today.

However, this bottleneck seems to have contributed to a speciation event where two ancestral chromosomes may have converged to form what is currently known as chromosome 2 in modern humans. With this information, the last common ancestor has potentially been uncovered for the Denisovans, Neanderthals, and modern humans (Homo sapiens).

We all know that once a question is answered, more questions arise.

"The novel finding opens a new field in human evolution because it evokes many questions, such as the places where these individuals lived, how they overcame the catastrophic climate changes, and whether natural selection during the bottleneck has accelerated the evolution of human brain," says senior author Yi-Hsuan Pan, an evolutionary and functional genomics at East China Normal University (ECNU).

Now that there is reason to believe an ancestral struggle occurred between 930,000 and 813,000 years ago, researchers can continue digging to find answers to these questions and reveal how such a small population persisted in assumably tricky and dangerous conditions. The control of fire, as well as the climate shifting to be more hospitable for human life, could have contributed to a later rapid population increase around 813,000 years ago.

"These findings are just the start. Future goals with this knowledge aim to paint a more complete picture of human.evolution during this Early to Middle Pleistocene transition period, which will in turn continue to unravel the mystery that is early human ancestry and evolution," says senior author LI Haipeng, a theoretical population geneticist and



computational biologist at Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences (SINH-CAS).

This research was jointly led by Li Haipeng at SINH-CAS and Yi-Hsuan Pan at ECNU. Their collaborators, Fabio Di Vincenzo at the University of Florence, Giogio Manzi at Sapienza University of Rome, and Yun-Xin Fu at the University of Texas Health Science Center at Houston, have made important contribution to the findings.

The research was first-authored by Hu Wangjie and Hao Ziqian who used to be students/interns at SINH-CAS and ECNU. They are currently affiliated with Icahn School of Medicine at Mount Sinai, and Shandong First Medical University & Shandong Academy of Medical Sciences, respectively. Du Pengyuan at SINH-CAS, and Cui Jialong at ECNU also contributed to this research.

More information: Wangjie Hu et al, Genomic inference of a severe human bottleneck during the Early to Middle Pleistocene transition, *Science* (2023). DOI: 10.1126/science.abq7487. www.science.org/doi/10.1126/science.abq7487

Nick Ashton et al, Did our ancestors nearly die out?, *Science* (2023). DOI: 10.1126/science.adj9484, www.science.org/doi/10.1126/science.adj9484

Provided by Chinese Academy of Sciences

Citation: Early ancestral bottleneck could've spelled the end for modern humans (2023, August 31) retrieved 27 April 2024 from https://phys.org/news/2023-08-early-ancestral-bottleneck-couldve-modern.html



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