Males were saved by agriculture

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Around 12,000 years ago, settlers in the Fertile Crescent of West Asia domesticated a few wild plant and animal species. The emergence of agriculture is believed to have driven extensive human population growths, because food production by agriculture can support far higher population densities than hunting and foraging. Nevertheless, there is a "chicken or the egg" dispute between agriculture and initial population expansion in the Neolithic era.

Despite historical and archaeological efforts, previous genetic work—such as mitochondrial DNA analysis in worldwide populations—found that most major maternal lineage expansions began after the Last Glacial Maximum (LGM, about 15 kya) but before the first appearance of agriculture, and the increase of population was likely the driving force that led to the advent of agriculture. There are also numerous studies on population expansion using paternal Y chromosome single nucleotide polymorphism (SNPs) in the genealogical tree and rapidly mutating short tandem repeats (STRs), though lacking convincing results. This is due to the fact that nonrandom sampling of SNPs can result in an ascertainment bias, and whether to choose the evolutionary rate or the genealogical rate of STRs in Y chromosome dating is controversial, since the result can be almost three-fold difference.

As science and technology update rapidly, entirely sequenced Y chromosomes in numerous human individuals have only recently become available. With next-generation sequencing technology, the 1000 Genomes Project has sequenced whole Y chromosomes from more than

500 males, which provides a wonderful chance to estimate population sizes through time from a set of globally distributed populations without ascertainment bias.

To resolve the long dispute, researchers in Fudan University analyzed about 8.9 mega-base pairs on the unique regions of Y chromosomes and whole mitochondrial genomes of 526 male individuals from three African, five European, three Asian and three American populations sequenced in the 1000 Genome Project.

A maximum likelihood tree was constructed using Y chromosomal SNPs. Containing samples from haplogroup A, B, C, D, E, G, I, J, N, O, Q, R, and T, the tree is a good representation of geographical paternal lineages. To infer the expansion time, researchers calculated the date of each divergence event throughout the tree using Bayesian method with a constant mutation rate. The outcome demonstrates that most major paternal lineage expansions coalesced in Neolithic Time. In other words, these Neolithic expanding clades comprise a large proportion of current population.

Researchers then estimated effective population size through time via coalescent Bayesian Skyline plots to infer population size changes during the LGM and the advent of agriculture. Rapid, roughly exponential population growth in most European and Asian maternal lineages occurred right after the LGM (12-8 kya), followed by a long period of very slow growth (since 8-7 kya). However, on the paternal side, all the populations show the most pronounced expansion from 6.5 kya to 2 kya, with a 10- to 100-fold increase in population size. The fastest growth intervals for global male populations range from 1.5-3.3 kya, which are 1-3 ky later than the advent of agriculture.

The correspondence between the coalescence age of most paternal lineages and the population growing periods observed in skyline plots suggested that the initial male population expansion began within the Neolithic Time, probably due to the advent and spread of agriculture. "Agriculture has provided a much more stable food supply than hunting and foraging, leading to higher population fertility and infant survival rate, more importantly, as agriculture has kept male away from dangerous hunting, the reduction in hunting-related mortality of males might contribute most to this sex-biased Neolithic expansion," they propose.

More information: Agriculture Driving Male Expansion in Neolithic Time, *SCIENTIA SINICA Vitae* (2016). DOI: 10.1360/N052016-00126

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