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Genome Study Provides a Census of Early Humans

By NICHOLAS WADE

From the composition of just two human genomes, geneticists have computed the size of the human population 1.2 million years ago from which everyone in the world is descended.

They put the number at 18,500 people, but this refers only to breeding individuals, the “effective” population. The actual population would have been about three times as large, or 55,500.

Comparable estimates for other primates then are 21,000 for chimpanzees and 25,000 for gorillas. In biological terms, it seems, humans were not a very successful species, and the strategy of investing in larger brains than those of their fellow apes had not yet produced any big payoff. Human population numbers did not reach high levels until after the advent of agriculture.

Geneticists have long known that the ancestors of modern humans numbered as few as 10,000 at some time in the last 100,000 years. The critically low number suggested that some catastrophe, like disease or climate change induced by a volcano, had brought humans close to the brink of extinction.

If the new estimate is correct, however, human population size has been small and fairly constant throughout most of the last million years, ruling out the need to look for a catastrophe.

The estimate, reported in the issue on Tuesday of The Proceedings of the National Academy of Sciences, was made by a team of population geneticists at the University of Utah led by Chad D. Huff and Lynn B. Jorde.

The human population a million years ago was represented by archaic species like *Homo ergaster* in Africa and *Homo erectus* in East Asia. The Utah team says its estimate of 18,500 implies “an unusually small population for a species spread across the entire Old World.”

But that estimate would apply to the worldwide population only if there were inbreeding between the humans on the different continents. If not, and if modern humans are descended from just one of these populations, like *Homo ergaster* in Africa, then the estimate would apply only to that.

Richard G. Klein, a paleoanthropologist at Stanford, said it was hard to believe the population from which modern humans are descended was as small as 18,500 “unless they were geographically restricted to Africa or a small part of it.”

There is no independent way of assessing a genetics-based estimate of population size at this period, Dr. Klein said, although archaeologists have developed ways of assessing ancient populations of more recent times.

The Utah team based its estimate on the genetic variation present in two complete human genomes, one prepared by the government's human genome project and the other by J. Craig Venter, the genome sequencing pioneer. The government decoded a single copy of a mosaic genome derived from a medley of people, apparently of European and Asian origin. Dr. Venter decoded both copies of his own genome, the one inherited from his father and the one from his mother.

The Utah team thus had three genomes to work with and looked at ancient elements known as Alu insertions, the youngest class of which appeared in the human genome around a million years ago. The amount of variation seen in the DNA immediately surrounding the Alu insertions gave a measure of the size of human population at that time.

Their estimate agrees almost exactly with an earlier one, also based on Alu insertions but with sparser data. The insertions tag ancient regions of the genome that are unaffected by the recent growth in population, Dr. Huff said.