The Human Family Tree: 10 Adams and 18 Eves

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The book of Genesis mentions three of Adam and Eve’s children: Cain, Abel and Seth. But geneticists, by tracing the DNA patterns found in people throughout the world, have now identified lineages descended from 10 sons of a genetic Adam and 18 daughters of Eve.

The human genome is turning out to be a rich new archive for historians and prehistorians, one whose range extends from recent times to the dawn of human existence.

Delvers in the DNA archive have recently found evidence for a prehistoric human migration from Western Asia to North America; identified the people who seem closest to the ancestral human population; and given substantial weight to the whispers, long dismissed by historians, that Thomas Jefferson fathered a family with his slave Sally Hemings.

A new history of Britain and Ireland by Norman Davies, “The Isles,” (Oxford University Press) begins with an account of Cheddar man, an 8,980-year-old skeleton from which mitochondrial DNA was recently extracted. The DNA turned out to match that of Adrian Targett, a teacher in a Cheddar Village school, proving a genetic continuity that, despite numerous invasions, had endured through nine millennia.

Unlike the DNA test used in forensic cases, which is designed to identify individuals, DNA analysis that seeks to reach back in time usually focuses on lineages, not individuals. From patterns in the DNA data, biologists can often estimate the sizes of ancient populations and even the approximate dates when one group of people split from another.

Though DNA can bear on historical questions, often by acting as a long-range paternity test, its most spectacular use has been in prehistory, where it has added a new dimension to the bare framework provided by archaeology.

The most detailed human family tree so far available is one constructed over many years by Dr. Douglas C. Wallace and his colleagues at the Emory University School of Medicine in Atlanta. Dr. Wallace’s tree is based on mitochondrial DNA, tiny rings of genetic material that are bequeathed only by the egg cell and thus through the maternal line. A counterpart tree for men, based on analysis of the Y chromosome, has been prepared by Dr. Peter A. Underhill and Dr. Peter J. Oefner of Stanford University.

Population geneticists believe that the ancestral human population was very small -- a mere 2,000 breeding individuals, according to a calculation published last December. But the family tree based on human mitochondrial DNA does not trace back to the thousand women in this ancestral population. The tree is rooted in a single individual, the mitochondrial Eve, because all the other lineages fell extinct.

The same is true of the Y chromosome tree, a consequence of the fact that in each generation some men will have no children, or only daughters, so the number of different Y chromosomes may steadily diminish, even if the population stays the same size.
This ancestral human population lived somewhere in Africa, geneticists believe, and started to split up some time after 144,000 years ago, give or take 10,000 years, the inferred time at which both the mitochondrial and Y chromosome trees make their first branches.

Mitochondria, which live inside human cells but outside the nucleus, escape the shuffling of genes that occurs between generations and are passed unchanged from mother to children. In principle, all people should have the same string of DNA letters in their mitochondria. In practice, mitochondrial DNA has steadily accumulated changes over the centuries because of copying errors and radiation damage.

Because women were steadily spreading across the globe when many of these changes occurred, some changes are found only in particular regions and continents. Dr. Wallace discovered that almost all American Indians have mitochondria that belong to lineages he named A, B, C and D. Europeans belong to a different set of lineages, which he designated H through K and T through X. The split between the two main branches in the European tree suggests that modern humans reached Europe 39,000 to 51,000 years ago, Dr. Wallace calculates, a time that corresponds with the archaeological date of at least 35,000 years ago.

In Asia there is an ancestral lineage known as M, with descendant branches E, F and G as well as the A through D lineages also found in the Americas.

In Africa there is a single main lineage, known as L, which is divided into three branches. L3, the youngest branch, is common in East Africa and is believed to be the source of both the Asian and European lineages.

Dr. Wallace’s mitochondrial DNA lineages are known technically as “haplogroups” but more colloquially as “daughters of Eve,” because all are branches of the trunk that stems from the mitochondrial Eve.

The Y chromosome tree has not yet been published by the Stanford researchers, but in a book that came out in March, “Genes, People and Languages,” a colleague at the university, Dr. Luca Cavalli-Sforza, sketched a preview of the findings.

The tree is rooted in a single Y chromosomal Adam, and has 10 principal branches, Dr. Cavalli-Sforza reports. Of these sons of Adam, the first three (designated I, II and III) are found almost exclusively in Africa. Son III’s lineage migrated to Asia and begat sons IV-X, who spread through the rest of the world -- to the Sea of Japan (son IV), northern India (son V) and the South Caspian (sons VI and IX).

Dr. Cavalli-Sforza believes these Y chromosome lineages may be associated with the major language groups of the world. The South Caspian population, for example, may have spoken Eurasian, the ancestral tongue of Indo-European (to which English belongs) and most of the continent’s other major language families. But Dr. Wallace, asked if his mitochondrial DNA lineages also corresponded to the world’s major language groups, said he “tended to be more cautious than Luca.”

Dr. Wallace has recently been exploring the root of the mitochondrial tree. In an article published in March in The American Journal of Human Genetics, he and colleagues identify the Vasikela Kung of the northwestern Kalahari desert in southern Africa as the population
that lies nearest to the root of the human mitochondrial DNA tree. Another population that seems almost equally old is that of the Biaka pygmies of Central Africa. Both peoples live in isolated regions, which may be why their mitochondrial DNA seems little changed from that of the ancestral population. "We are looking at the beginning of what we would call Homo sapiens," Dr. Wallace said.

One of the most vexed issues in human prehistory is the timing and number of migrations into the Americas. Dr. Joseph Greenberg, a linguist at Stanford University, has proposed three migrations, corresponding to the three language groups of the Americas, known as Amerind, Na-Dene and Eskimo-Aleut. Dr. Wallace's mitochondrial DNA data broadly support this general thesis, though the arrival of the Amerind-speakers seems more complex than a single migration.

Of the A through D lineages found in American Indians, A, C and D also occur in Siberian peoples, suggesting that their ancestors were the principal source of the Amerind-speakers' migration. But the B lineage, though it is found elsewhere in Asia, has not turned up in Siberia, a hint that the B people may have taken a sea route to the Americas and then merged there with their A-, C- and D-carrying cousins.

In 1998, Dr. Wallace and his colleagues discovered the X pattern, a rare European lineage, among the northern Native Americans such as the Ojibwa and Sioux. At first they assumed it came from intermarriage with modern Europeans. But the American X lineage turned out to be pre-Columbian and its owners would have arrived in America either 15,000 or 30,000 years ago, depending on certain genetic assumptions.

The European X lineage seems to have originated in Western Asia around 40,000 years ago. Dr. Wallace suggests a part of this group may have made their way to America via Siberia, even though no traces of the X-lineage have yet turned up in eastern Asia. A trans-Atlantic route is a possible alternative.

When modern humans first started to leave Africa, about 50,000 years ago by present reckoning, they probably consisted of small groups of hunter-gatherers a few hundred strong. In their determined exploration of the world before them, they must have overcome, with the primitive means at their disposal, the extreme rigors of climate, terrain and perhaps the archaic human populations like the fearsome Neanderthals who had preceded them out of Africa.

The biologist Edward O. Wilson, in a recent interview with The Wall Street Journal, mused that a new basis for spiritual values might be found -- not in the usual religious sources but in what he sees as the inspiring story of human origins and history. "We need to create a new epic based on the origins of humanity," he said, adding: "Homo sapiens have had one hell of a history! And I am speaking both of deep history -- evolutionary, genetic history -- and then, added on to that and interacting with it, the cultural history recorded for the past 10,000 years or so."

Many of the biologists who are reconstructing the human past certainly believe their work has a value that transcends genetics. Although their lineage trees are based on genetic differences, most of these differences lie in the regions of DNA that do not code for genes and have no effect on the body. "We are all Africans at the Y chromosome level and we are really all brothers," Dr. Underhill said.

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Dr. Wallace remarked that since he started working on mitochondrial DNA in the late 1970’s: “What I have found astounding is that it clearly shows we are all one human family. The phylogeny in Africa goes back to the origins of our species, but the fingers of L3 are touching Europe and Asia, saying that we are all closely related.”

Whether or not genetic prehistory is suitable material for a modern origin myth, it is about to be made available to a wider public. Last month a company called Oxford Ancestors set up business with the offer to tell customers which of the seven daughters of Eve they are descended from. (Almost all Europeans belong to only seven of the nine mitochondrial lineages found in Europe). The test (see www.oxfordancestors.com) requires sending in a sample of cells brushed from the inside of the cheek. For a mere $180, anyone of European ancestry can establish the start of a genealogy far senior to Charlemagne’s.

The company’s founder is Dr. Bryan Sykes, a human geneticist at the University of Oxford in England. On the reasonable basis that the founders of Dr. Wallace’s mitochondrial DNA lineages were real women, Dr. Sykes gave them names and sketched in details of their likely dates and origin. Thus people found to belong to haplogroup U will be told they are descended from Ursula, who lived about 45,000 years ago in Northern Greece. Ancestor of the X’s is Xenia, who lived 25,000 years ago in the Caucasus mountains.

As if fulfilling Dr. Wilson’s suggestion, Dr. Sykes said he had “worked out a mythological framework for these seven women,” in respect of the arduous times in which they must have lived and the triumph of spreading their mitochondrial DNA to almost all the inhabitants of Europe.

He is now working on tests to identify other lineages around the world, including 14 in Africa, and 16 in Eurasia and the Americas. “I don’t think this stuff should be confined to academics,” he said.