## The Naked Truth: The Fallacy of Genetic Adam and Eve

Greg Laden, Department of Anthropology, University of Minnesota

ince the mid 1980s, scientists have compared mitochondrial (mtDNA) from several different humans, reconstructing an ancestor of living human mitochondria about 100-200 thousand years ago, which probably lived in Africa (Cann, Stoneking and Wilson 1987). More recently, other researchers reported similar results from a study of human Y-chromosome DNA indicating a common ancestor of a large part of the human Y-chromosome at a similar or more recent time, also in Africa (Hammer, 1995; Hammer, Spurdle and others 1997; Gibbons, 1997). The studies of mtDNA immediately evoked the

Even if the historical now, the Y-chrorole of Adam and Eve is overstated. there is still reason for excitement about the mtDNA and Y-chromosome studies.

image of African "Eve", and mosome research has evoked a corresponding image African of an "Adam". The metaphorical association between genetic research and the Book of Genesis may have helped sell newspapers, but this metaphor involves a misunderstanding of the

meaning of these findings. In both the popular press and scientific journals, we see such statements as "All women/men can trace their ancestry back to a single female/male living in Africa X thousands of years ago." Such statements are misleading, and may obscure more interesting aspects of this important research (see side bar).

The genetic code includes units of information that are kept whole when they pass from generation to generation. Genes are passed on as whole units. The DNA in our mitochondria (cell organelles responsible for energy production) are also passed on as whole units, and a large part of the Y-chromosome is, similarly, passed on as a whole unit. Any stretch of genetic code so inherited necessarily has a single common ancestor-called a "coalescence point"-that existed in a particular individual. Furthermore, each of these units of DNA can, and probably does, have a different coalescence point. So, if there is a mitochondrial Eve and a Y-chromosome Adam, there is also a hair color Medusa and a melanin Midas.

Even if the historical role of Adam and Eve is overstated, there is still reason for excitement about the mtDNA and Y-chromosome studies. These bits of DNA are passed on in humans through only one parent. Mitochondria replicate asexually within cells. The ovum produced by a woman includes a small number of her mitochondria, which in turn reproduce to supply the mitochondria in all of the cells in her offspring's body. The non-recombining part of the Y-chromosome does not swap genetic material with the Xchromosome to which it is matched, so each human male gets all of these genes from his father. Therefore, it is possible to study genetic echoes that reflect different population histories for humans as a whole, females as a group, and males as a group.

Were we gibbons, who do not migrate far and who are very strictly monogamous, this would be less interesting; our mtDNA, non-recombinant Y, and other genes would show a similar pattern. However, humans are diverse and imaginative in their marriage and mating practices. At the very least, we practice serial monogamy. Polygyny happens. Hypergamy (unidirectional change of mates of one sex across a cultural boundary such as class), polyandry, and other varieties of marriage and mating practice are widespread in humans now and in

the past. Often, males and females differ in their patterns of residence after marriage (commonly, newlyweds move to a residence near the male's family). These factors shape separate histories for maternal and paternal lineages.

Coalescence is key to understanding this, so let's examine this concept more closely. Coalescence is a property of divergent systems, like genes, rumors, and chain letters. Chain letters come in different flavors—some asking for money others merely warning of bad luck. For each "species" of chain letter, there is a source to which all copies could be traced. As the letter is duplicated and passed from one person to others, it may be changed by accident or design, so over time there are many minor variants of the first document. A hard-working detective seeking the original version of a chain letter could work backwards through postal records to track down the very first copy written months, years, or decades earlier. A lazy detective might simply examine all of the available chain letters and reconstruct a document that must look much like the original (even if not exactly). Our lazy detective might even take a guess as to how many "generations" have passed since the initial letter was written, by noting the number of typos and alterations, assuming that more changes means more generations. In both cases, the first copy of that chain letter is a "coalescence" point. Our diligent detective has located the actual coalescence point, and our lazy detective has estimated or reconstructed

To reconstruct genetic coalescence points, scientists use the techniques of our lazy detective, not because they are lazy, but because genetic coalescence points are generally ancient and must be inferred from modern samples. "Mitochondrial Eve" and "Y-chromosome Adam"

SEPT/OCT 1997 REPORTS are not individuals, but estimates of coalescence points based on modern samples. New data added to the equation could move Adam or Eve (independently) back through time, or even to a new region of the earth.

Mathematical modeling of Y-chromosome and mtDNA data has revealed one or more "bottlenecks" in human population history. These bottlenecks are periods when our ancestors were reduced in number and confined to one or a few groups. Bottlenecks are detectable because they reduce the diversity of genetic material. We should not be surprised that our species has passed through these bottlenecks. Repeated severe "Ice Ages" of the last million years or so reduced the geographical range of many animals and plants, causing many species to go extinct (from the point of view of extinction, a bottleneck is a "near miss"). Eventually, genetic bottlenecks may be matched to these climate changes and to archaeological evidence from those times.

The bottleneck model for human history has led to further confusion about genetic Adam and Eve. Evolutionary change such as the rise of a new species is perhaps more likely when a population is broken up into small, isolated groups. Thus, a bottleneck is a good place to look for a speciation event. Also, the earliest modern *Homo sapiens* fossils date to about the same time as the mtDNA bottleneck. This has led to the idea that the genetic echo from this bottleneck marks the origin of modern *H. sapiens*.

It is important to remember, though, that coalescence points occur for all genetic units, whether there was a bottleneck or not, or a speciation event or not. The identification of a coalescence point is an inevitable outcome of comparing variants of a gene. Perhaps coalescence points will be found to cluster in time near important evolutionary events, but for now there is no evidence that this is the case. Perhaps the life and times of genetic Eve, Adam, Medusa and Midas were quite ordinary.

Not all bottlenecks are genetic; some are informational. The most recent Y-chromosome results are very interesting, and clearly deserving of news coverage. But there have been several studies of human Y-chromosome variability going back

several years which have not been as widely reported (see Gibbons and Dorozynski 1991; Shreeve 1991). Low variability in Y-chromosome DNA has been found in several populations. There is a Jewish Adam (Lucotte and David 1992; Lucotte, Smets and Ruffie 1993), a Finnish Adam (Sajantila, Salem and others 1996), and a Native American Adam (Karafet, Zegura and others 1997), for instance. If the geneticists have it right, and this variability is properly calibrated (the Ychromosome is a badly behaved genetic mess, perhaps not surprisingly), then it would appear that male population histories have more restrictions than do female histories. This accords with what we know about human reproductive patterns. Males vary more than females in their reproductive output. Some males have far more offspring than others, and many males have no offspring. Each female is likely to have a nearer to average number of offspring. This would cause apparent bottlenecks in the male lineage that would not appear in female-only DNA.

Stay tuned. Fifteen years ago, when this sort of research was just getting off the ground, it was difficult, time-consuming and expensive to analyze genetic data. The first studies of mtDNA required human placentas, which are not easy to come by. Now, geneticists extract, isolate, and sequence DNA from many different tissues, more cheaply and more quickly. Until recently, geneticists had all but given up on the Y-chromosome, which appeared to be poorly behaved as a genetic clock. Now somewhat redeemed, the Y-chromosome is starting to yield promising results. Although earlier work in human historical genetics was important, it is also true that the data are only now starting to roll in, and the next few years should be a very exciting time.

#### REFERENCES

Gibbons A, Dorozynski A. Looking for the father of us all: After finding the controversial "mitochondrial Eve," molecular biologists are hoping that the Y chromosome will lead them to the genetic Adam. *Science* 1991; 251(4992):378-80.

Gibbons A. Y chromosome shows that Adam was an African. *Science*. 1997; 278(5339):804-5.

Hammer MF, Spurdle AB, Karafet T, Bonner MR, Wood ET, Novelletto A,

# IN THE BEGINNING WAS THE WORD (ON ADAM AND EVE).

The following quotes are reproduced here to demonstrate a range of conceptions about mitochondrial and Y-chromosome historical genetics. They are taken from articles in the popular press, scientific journals, and web sites. The author has chosen to not provide citations for these phrases, in order to avoid pointing fingers at well meaning writers, and because many of these quotes are subtitles or pullouts that are probably the work of anonymous editors.

All men can trace their ancestry back to one man who lived 150 000 years ago and whose closest living relatives are a small tribe in South Africa, according to scientists who have spent a decade searching for the original Adam.

Scientists have "established "that all humans are descended from a single woman—a prebistoric Eve' born some 200 000 years ago in Africa. More recent studies of the male Y chromosome indicate that there was also a corresponding Adam from which all males are descended."

This source goes on to clarify (sort of)...

Any comparison to the Adam and Eve of Genesis would be mistaken, bowever, since the genetic Adam and Eve probably did not live on the same continent or during the same millennia.

One source reports that.

modern bumans descended from a common male ancestor who lived 188 000 years ugo. Although the new report does not say where that ancient man, whom some are calling "Adam," lived, bis age is close enough to Eve's for this kind of work.

To be fair, this source later adds:

Even though the studies refer to a single man or woman in the past, they do not imply that those people were a couple or even that they were the only parents of all humans.

Better. But the redemption is quickly mitigated by this follow-up:

Their (Adam and Eve's) primary significance is in pointing to the time when anatomically modern buman beings, Homo sapiens sapiens, evolved from a more primitive ancestor, generally thought to be an "archaic" form of Homo sapiens.

Oops.

A prestigious scientific journal reports that...

In the beginning, there was mitochondrial Evea woman who lived in Africa between 100 000 and 200 000 years ago and was ancestral to all living bumans...To test this view of buman origins, scientists have been searching ever since for Eve's genetic consort. Adam'... Now, after almost a decade of study, two international teams have found the genetic trail leading to Adam, and it points to the same time and place where mitochondrial Eve lived.



Malaspina P, Mitchell RJ, Horai S, Jenkins T, Zegura SL. The geographic distribution of human Y chromosome variation *Genetics* 1997; 145(3):787-95.

Hammer MEA recent common ancestry for human Y chromosomes. *Nature* 1995; 378(6555):376-9

Karafet T, Zegura SL, Vuturo-Brady J, Posukh O, Osipova, L, Wiebe, V, Romero F, Long JC, Harihara S, Jin F, Dashnyam B, Gerelsaikhan T, Omoto K, Hammer ME Y chromosome markers and trans-Bering Strait dispersals. *American Journal of Physical Anthropology* 1997; 102(3):301-16.

Lucotte G, David F. Ychromosome-specific haplotypes of Jews detected by probes 49f and 49a. *Human Biology* 1992; 64(5):757-61.

Lucotte G, Smets P, Ruffie J. Ychromosome-specific haplotype diversity in Ashkenazi and Sephardic Jews, *Human*  Biology 1993; 65(5):835-40.

Sajantila A, Salem A, Savolainen P, Bauer K, Gierig C, Paabo S. Paternal and maternal DNA lineages reveal a bottleneck in the founding of Finnish population. *Proceedings of the National Academy of Sciences of the United States* 1996; (93)21:12035-40.

Shreeve J. Madam, I'm Adam: Genetic ancestry of all humans may lead to a male African pygmy. *Discover* 1991; 12(6):24.

### NCSE Membership and College Admissions Tests

Richard A. Nisbett University of Oklahoma Health Sciences Center

Kevin M. Kelly The University of Iowa

n looking over the new 1997 membership directory, we were intrigued by the regional variation. As a first step toward some sort of explanation for this pattern, we decided to see if there were a correlation with state ACT scores. We calculated the number of NCSE members (listed in the directory) per 100 000 population for each state using current census figures. Then, we extracted the 1997 average composite score for each state as compiled by ACT and posted on the ACT website at <a href="http://www.act.org">http://www.act.org</a>.

We found the NCSE membership rate had a moderate but significant positive association with the mean ACT score (p < 0.0003; Kendall's Tau, B= 0.36126). In general, those states with the highest proportion of NCSE members had the highest ACT scores, while those with the lowest membership rate had the lowest scores. For the top 10 states in NCSE mem-

bership, all except one were above the national ACT average (21.0). For the bottom 10 states in membership, all except one were below the national ACT average. Examine these three similarly-sized states in the "Heartland" as examples.

We will resist the temptation to over-interpret our finding. However, we suggest that either: (1) a certain percentage of those members in states with NCSE memberships should move to states with low membership and disseminate their wisdom and lobbying energies; or (2) states with low scores should bus their children to schools in states with high membership. Alternatively, our NCSE colleagues in those states with low membership could encourage their peers to join NCSE in hopes that a successful membership drive will, ultimately, reach critical mass with a concomitant rise in state ACT scores.

State	NCSE Members per 100 000 Population	Mean ACT Scores
Colorado	4.29	21.5
Iowa	1.54	22.1
Oklahoma	0.60	20.6

#### Course 48: Creation, Evolution or Both? A Multiple Model Approach

Instructor: Craig E Nelson, Indiana University

Date: Apr 15-17, 1998 in Dayton, OH Registration fee: \$40

This course will provide updated content across the entire scope of the controversy and powerful options for classroom discussions. It will provide an overview of the central arguments of the "scientific creationists" and a summary of the current state of science in areas central to the controversy. Participants will examine a resources useful both in preparing for the classroom and for guiding students. The course will also review some recent developments in evolutionary theory with a major focus on the nature of science, decision theory, and modes of critical thinking. Both the overall sequence and the relative emphases will be adjusted in accord with the interests of the participants, though a major emphasis will be on developing selected topics so that participants may utilize them directly in their own teaching.

For college teachers of: all disciplines. Prerequisites: none.

To register or for more information contact George Minor, Physics Dept, University of Dayton,/ Dayton OH 45469-2314.

Phone 937-229-2327;

Email:<miner@neelix.udayton.edu>.

Applications will be accepted as long as any places are available.

Craig Nelson is an evolutionary ecologist who has won major awards for his teaching of evolution. He wrote "Creation, Evolution, or Both? A Multiple Model Approach," published by the American Association for the Advancement of Science in *Science and Creation*, edited by RW Hanson, in 1986.

SEPT/OCT 1997 REPORTS