

Genetic Studies: Do They Support Human Evolution?

By: Arnold C. Mendez, Sr.

The Battle Lines are Drawn

You would not know there is a war going on in evolutionary circles, but there is. This war is not the war that pits evolutionists against creationism and design. This war is being waged among the evolutionists themselves and the battle lines are clearly drawn. On one side of the battle lines are the traditionalists, those who use morphology, cranial shape, dentition, and skeletal clues to build evolutionary and phylogenetic trees. Squarely opposed to them and on the other side of the battlefield are the geneticists that say the best way to understand the evolutionary history of an organism is with genetic studies. These genetic studies involve mitochondrial DNA and other molecular molecules (1).

Many evolutionary scientists find themselves somewhere in the middle of this evolutionary battle. From an evolutionary point of view they find that both sides of the data provide useful information. What is interesting is that the adamant supporter of the opposing scenario feels that the other side is standing on very weak scientific grounds.

Before looking at the result of this battle let's go back a few decades. Back to a time before the genetic studies came to the forefront. Many scientists believed the fossil record revealed modern humans and the Neanderthals had evolved from *Homo erectus*. *Homo erectus* had descended from the Australopithecines and had moved out of Africa about 2 million years ago and had interbred with various regional hominids and gave rise to the diverse Homo branches. These branches included *Homo sapiens* or modern man, and *Homo neanderthalensis* or Neanderthal man. This was often called the "multiregional theory" since the erectus genes were scattered through many regions and all human ancestors, including modern humans and the Neanderthal, were more or less related. Many scientists felt and still feel very comfortable with the idea of the inter-relatedness of the various fossil men.

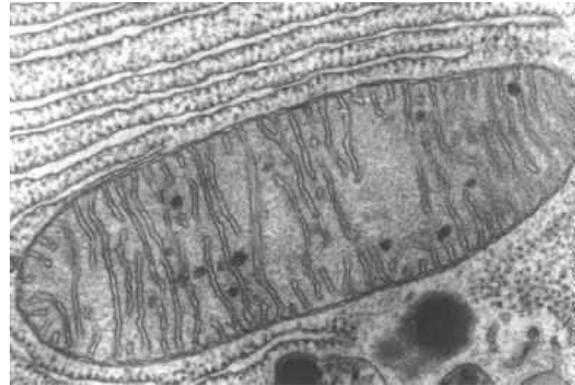


Figure 1. DNA removed from cellular mitochondria shown above is known as mtDNA.

Recently in about the last 10-15 years genetic studies have supposedly shown that the multiregional picture was not correct. In 1987 the research of Mark Stoneking, Rebecca Cann, and Allan Wilson (2) traced all modern humans to an evolutionary "Eve." This Eve's genes had migrated out of Africa about 200,000 years ago and had given rise to *Homo sapiens* with no interbreeding with various other hominids. This became known as the mitochondrial Eve theory, since the DNA material that was analyzed had been gathered from the fossil mitochondria (3) in the fossil substrate. This type of DNA is commonly called mtDNA (fig1).

This was the beginning of the "bones –vs.- genes" war. Since they are both based on different scientific approaches and they both lead to such divergent results there is no way that they could both be correct. Evolutionary trees drawn by geneticists and those drawn by traditionalists often do not look similar. Many fear that they will never agree!

Before examining the fallacies in these genetic studies it is important to review how these studies were undertaken. Also it is important to look at some of the assumptions that evolutionary scientists make which are pivotal to these hypotheses.

Out of Africa Eve

How exactly does the mitochondrial Eve theory work? Several assumptions are used in this hypothesis. The first is that only the maternal mtDNA material is studied since there is so much more of it in a typical cell. Mitochondria are the powerhouse of the cell. They convert biological compounds into energy. Each mitochondrion has a set of mitochondrial DNA (mtDNA) and each cell has many mitochondria. Therefore each cell has many more sets of mtDNA than nuclear DNA, which only exist in the nucleus. The mtDNA is passed from mother to daughter and is referred to as maternal DNA. This mtDNA is extracted and then amplified using polymerase chain reaction (PCR). The amplified DNA is then compared to a known modern standard DNA and the amount of differences is noted. These amounts of change in the two mtDNAs are caused by mutations. The known mutational rate for the mtDNA is then used to compute the amount of time that has transpired between the extracted fossil mtDNA and the modern mtDNA yielding a date. In the case of the mitochondrial Eve this date is approximately 200 kyr ago (kyr = thousand years ago).

Since the mtDNA is only passed through the maternal line, from mother to daughter, a woman is the ancestor of all the modern human descendants. She is the genetic Eve of all modern humans. This also means that all other maternal lines did not contribute to the current modern mtDNA gene pool. These other maternal genetic lines may or may not still exist. The mtDNA does not demand the extinction of the other maternal lines—It only says they are not contained in the genetic material that is being studied. By comparing the modern mtDNA sequences from many parts of the world and by genetic backtracking even the location can be ascertained—hence an "Out of Africa Eve" is postulated. In other words, according to the "Out of Africa Eve" theory about 200 kyr ago the genes for all modern humans spread out from Africa and these and only these genes are in the makeup of modern men and women. Since this genetic Eve is the ancestor of all humans this is often called the "African replacement model." This is in contrast to the "multi-regional evolution model."

Abstract—Mitochondrial DNAs from 147 people, drawn from five geographic populations have been analyzed by restriction mapping. All these mitochondrial DNAs stem from one woman who is postulated to have lived about 200,000 years ago, probably in Africa (2).

Once again we are engaged in a debate, this time over the latest phase of human evolution. The paleontologists say modern humans evolved from their archaic forebears around the world over the past million years. Conversely, our genetic comparisons convince us that all humans today can be traced along maternal lines of descent to a woman who lived about 200,000 years ago, probably in Africa. Modern humans arose in one place and spread elsewhere (4).

Assumptions

There are several assumptions that are used to arrive at the genetic endpoint of the African replacement model. The first assumption is the starting point of the genetic line. In other words what is the genetic code in the past that went through the various mutations—from what DNA do the evolutionists say humanity has evolved? The ending point is the present day human genetic code but the starting point is unknown. This is where the first evolutionary assumption comes in. Since evolution is considered to be a fact, evolutionists look for our closest living relative. According to the evolutionary philosophy this happens to be the chimpanzee. Therefore the starting point is chimpanzee DNA.

An estimate of the rate of sequence divergence of the hypervariable segments of the mtDNA control region was obtained by comparing the average amount of sequence difference between humans and chimpanzee...The apparent mtDNA sequence difference between chimpanzee and humans of 15.1% is adjusted in the following manner...(5)

Assigning the chimpanzee mtDNA as a starting point for the study is circular reasoning. Using as proof what you are trying to prove is unsound. Evolutionists assume something is true and then the assumption is used as a foundation. If evolution is not true then the chimpanzee assumption is fallacious and will lead to research errors.

The second assumption is the mutational rate. If the amount of genetic differences between chimpanzees and humans is known and the mutational rate is known then a time span can be computed.

In order to estimate the rate of mtDNA evolution, we need to know not only the amount of sequence divergence between chimpanzee and human mtDNA control regions, but also when human and chimpanzee mtDNAs diverged. The best estimate for the human-chimpanzee mtDNA divergence is about 4 to 6 million years ago. The rate of divergence of the hypervariable segments is thus roughly 11.5% to 17.3% per million years. This rate of divergence can be used to infer the time of existence of the most recent common ancestor of human mtDNA. The ancestor corresponds to the deepest node of the tree in Fig. 3 and is placed at 2.87% on the scale of accumulated sequence differences. Accordingly, the ancestor existed about 166,000 to 249,000 years ago...(5)

All of these evolutionary assumptions and many others are inherent in the mtDNA out of Africa theory. As with many of the assumptions made by evolutionists they can be shown to be false.

Original "Out of Africa" Study Flawed

One of the best-kept secrets in the original mtDNA Africa study is that it is flawed and was recognized as such by the scientific community! The original papers published in both *Nature* (2) and *Science* (5) have been reviewed in various scientific publications and many errors have been pointed out. Linda Vigilant of the University of Berkeley California, and her team of geneticists did the original study on the out of Africa mtDNA. Their paper as published in *Science* (5) was reviewed by Alan R. Templeton from the Department of Biology at Washington University he listed many computer and statistical errors. His paper critiquing the previously mentioned study appeared in the same journal at a later date (6). Notice what he says about the methodology of the original study.

Maddison's set of maximum parsimony trees contains cladograms with geographically mixed basal clades, thereby invalidating the original rationale for an African origin...The phylogenetic analysis of the mtDNA sequence data is similarly flawed. Apparently, a single heuristic run with simple, sequential addition was used for the analysis of the sequence data. Such an analysis is inadequate for a data set this large...However, the existence of this more parsimonious cladogram undercuts the validity of argument. This more parsimonious tree also invalidates the statistical analysis given in Vigilant *et al.* because that analysis is dependent on their "maximum parsimony" reference cladogram. Other serious flaws with their statistic include their estimation of the time of origin.

According to Templeton, the Vigilant team made several mistakes. The first mistake was that the data did not necessarily prove that the genetic Eve had come from Africa. She just a well could have been a non-African. Secondly, the data was entered into the computer incorrectly. If it had been entered in another order then the results would have been completely different, sometimes called in computer jargon, "Garbage in—Garbage out." Finally, the time of origin was based on faulty statistics.

A few pages later in the same article in *Science* the genetic scientists were allowed a rebuttal. This group of scientists includes Mark Stoneking, one of the original researchers in the Vigilant team. They admit that the data is flawed and that an African origin for "Eve" is not correct.

Thus, the two statistical tests made in the original analysis are not valid. Those tests cannot be performed on the trees present...because their branching order is not statistically resolved...the available sequence data are insufficient to statically resolve the geographic origin of human mitochondrial DNA (6).

In another article published in *Nature*, the author comments about the problems with the previously published study by Stoneking, Cann, and Wilson (2).

Four years ago, the late Allan Wilson and his colleagues at the University of California at Berkeley produced a family tree of human origins based on restriction enzymes maps of mitochondrial DNA (mtDNA) from more than 130 people of diverse racial type and dispersed geographical location. They concluded that all human mtDNA genomes now extant derive from a single ancestral mtDNA molecule in Sub-Saharan Africa about 200,000 years ago. Because mtDNA molecules are inherited maternally, the authors wrote that the ancestral mtDNA must have been present in "one woman," by implication the ancestor of all humanity...Inevitably, this form of words brought biblical imagery bubbling to the surface of the public consciousness. The popular evocation of Eve in her African Eden were such that one would have been forgiven for thinking that she had been interviewed in person for her comments on the *Nature* paper.

...the idea of an African genesis has suffered what may be a mortally venomous bite. In a letter in last week's *Science*, Alan Templeton from Washington University, St Louis, demolishes the concept in four curt paragraphs. In reply the survivors of the Berkeley group (now all at Pennsylvania State University) succumb: Eden in Africa is unproven...The answer may simply be that the researchers were using methods inappropriate for the job. As they say when the number of items (136 mtDNA sequences) exceeds the number of informative nucleotide positions (117), it is not surprising that the program outputs so much garbage. There are 10^{67} possible trees for the latest data set: the number of maximally parsimonious trees is unknown, but is certainly "much larger than 1 billion" (7).

The Out of Africa replacement model has been shown to be false. Other evolutionists who are totally committed to evolution published this critique. They cannot be accused of having a Biblical or creationist bias. When creationists disagree with the conclusions of the genetic studies they are often accused of being biased. How fair is it to allow the evolutionist to disagree with each other on scientific grounds but not allow the creationists the same benefit?

Disagreement With "Out of Africa" Conclusions

The popular press gives the impression that the mtDNA studies that supposedly show that we are the result of an out of Africa genetic migration are authoritative and final. The layman is bombarded with television shows, magazine, and newspaper articles, which imply that no respectable scientist disagrees with the previous conclusions and that there is total agreement among the scientific community. This is simply not correct. There are many published articles in anthropological and evolutionary science journals, which reveal that many scientists of impeccable scientific character are completely at odds with the mtDNA studies. Scientists that are evolutionists publish these contrasting studies. We have a unique situation in which evolutionary scientists are disagreeing among themselves and have come up with two different evolutionary explanations for the same outcome.

The Frayer study (8) published in the *American Anthropologist* journal is a good example of the difference of opinion that exists in the scientific community. This article sheds light on flaws in both the mtDNA studies showing an African replacement model and also the relationship between modern humans and Neanderthals.

While many previous and some current models about the later aspects of human evolution are riddled with untestable or non-excluding hypotheses, the difference between the "Eve" and the multiregional evolution models are so profound it is impossible for both to be correct...In spite of these points of agreement, multiregional evolution and the Eve theory are largely contradictory.

From our analyses of the East Asian material, we find undeniable evidence for the development of distinctive morphologies that are not only specific to the region, but that also persist over the long sequence of fossil to many recent and living Asians.

The case for continuity in Europe has the most contentious history, primarily because of the deep-seated opinion in Europe and the United States that Neanderthals could have had nothing to do with subsequent European Evolution... Some assume that no transitional fossils exist and that none of the Neanderthal features continue into the Upper Paleolithic, as the Eve theory requires...However, the rich skeletal record from the Middle and Upper Paleolithic of Europe rejects each of these contentions. ...the actual evidence provided by the extensive fossil record of late Pleistocene Europe show considerable continuity between Neanderthals and subsequent Europeans.

The persistence of a large number of features is improbable if Neanderthals were completely replaced or 'swamped out' by an invasion of people from Africa (or anywhere else).

In short while no one would argue that European Neanderthals are identical to the succeeding Upper Paleolithic people, the two groups share a number of cranial and postcranial nonmetric features signaling regional continuity. As with other geographic areas, the more modern inhabitants bear the morphological marks of their more archaic forerunners...Such evidence is incompatible with the predictions of the Eve total replacement theory.

In summary, the African fossil record offers little support of the Eve hypotheses...Nothing in the African fossil record supports this continent as a unique motherland.

Continued studies have supported the original interpretation...the Levant (Middle-East) sample as a whole cannot be clearly separated into "Neanderthaloid" and "modern" sets on either anatomical or behavioral (archeological) grounds. The total variation is less, often considerably less, than normally found in a modern city...although the Eve theory insists that these two sets of individuals must represent different species and that one is so superior to the other that a complete replacement occurred.

Because there are many equally parsimonious solutions to the mtDNA variation and because some of these coalesce to non-African ancestries, it is no longer statistically valid to define Africa as the ancestral place from the mtDNA data.

In short, with the continuing analysis of mtDNA and reconsideration of nuclear DNA variation it is becoming increasingly clear that the original prediction of recent African origin for all modern humans is without a genetic basis. . . From the paleontological analyses presented here, it is apparent that this model does not hold up under scrutiny and must be rejected.

Thorne Wolpoff is another evolutionist that is at scientific odds with the various genetic studies (9). He states that the mtDNA genetic record is not a very good predictor of the how evolution actually works.

What made the Eve theory revolutionary was not so much the idea of a single place of origin, but that modern humans (wherever they evolved) replaced, rather than mixed with, indigenous archaic humans. . . The Eve theory makes a number of predictions, which biologists can test by consulting the fossil record. According to the theory, Eve must have lived in Africa at the beginning of the Upper Pleistocene, between 100,000 and 200,000 years ago.

Crucially, there should be no continuity over time in the anatomical characteristics of humans living in any one region. By stark contrast, if modern people evolved locally in many different places, then each population ought to resemble its own antecedents. In this case regional continuity in the features of human fossils should be the norm.

In conflict with the Eve theory, our measurements show that modern Chinese, Australasians and Europeans each resemble their local predecessors much more than they resemble archaic Africans. But that is not all. In each region of the world, we have uncovered links that tie living populations to their own local antecedents, whose remains are preserved in the fossil record for the area.

So, if not in Africa, where did we originate? The fossils point to several places rather than just one. The era of the modern human began with a smooth transition rather than an abrupt invasion. Humans may be unique, but the signs are that we are not a new species.

mtDNA Neanderthal Studies

Although most Biblical scholars and creationists consider Neanderthal man and *Homo sapiens* to be related, the genetic scientists have kicked Neanderthal man out of the family tree. After steadily gaining ground and being accepted as a full-fledged member of the human family, Neanderthal man is now by some considered a genetic dead-end. The expulsion has been made possible by the Neanderthal genetic studies. The following quotes are from four published papers that deal with whether or not Neanderthals are in the human family tree. Notice that in these studies the mtDNA data seems to indicate that the Neanderthals are of a different species and are considered not to have contributed any genetic material to modern humans.

Abstract—DNA was extracted from the Neanderthal-type specimen found in 1856 in Western Germany. . . Sequence comparisons with human mtDNA sequences, as well as phylogenetic analyses, show that the Neanderthal sequence falls outside the variation of modern humans. . . This suggests that Neanderthals went extinct without contributing mtDNA to modern humans (10).

Taken together, the results support the concept that the Neandertal mtDNA evolved separately from that of modern humans for a substantial amount of time and lends no support to the idea that they contributed mtDNA to contemporary modern humans (11).

Phylogenetic analysis places the two Neanderthals from the Caucasus and western Germany together in a clade that is distinct from modern humans, suggesting that their mtDNA types have not contributed to the modern human mtDNA pool. Comparison with modern populations provides no evidence for the multiregional hypothesis of modern human evolution (12).

Although more extensive sampling of Neanderthals is obviously desirable, the current sequences indicate that the diversity of Neanderthals was restricted. Thus, it is highly unlikely that a Neandertal mtDNA lineage will be found that is sufficiently divergent to represent an ancestral lineage of modern European mtDNAs (13).

Humans and Neanderthals are Related

Other evolutionists hotly contest the idea of the genetic evolutionists that modern humans and Neanderthals are not related. They point to much scientific data that supports the idea that modern humans, Neanderthals, and *Homo erectus* are all interrelated. This would agree with the Biblical testimony that indicates that all three of these classes of people were related and descended from the Biblical Adam.

These traditional evolutionists reject the mtDNA studies that claim Neanderthals were an extinct side branch. The layman does not realize that many genetic studies have been done which show that Neanderthals are in the human ancestry. These studies reveal that *Homo sapiens* and Neanderthals were closely related. This genetic relationship also includes the *Homo erectus* fossils. As in the mtDNA out of Africa studies the public is only being told one side of the story.

Recently a very important paper was published that dealt with the overall subject of human genetics, evolution, and the ancient Australians. This paper is significant because it shows that a number of the foundational concepts of fossil genetic studies are incorrect. The following quotes are all from the paper published in the *Proceedings of the National Academy of Sciences* by Gregory J. Adcock (14).

Abstract—Our results indicate that anatomically modern humans were present in Australia before the complete fixation of the mtDNA lineage now found in all living people. Sequences from additional ancient humans may further challenge current concepts of modern human origins.

These findings were interpreted as strongly supporting the recent out of Africa model. However, this interpretation failed to recognize that the demographic history of a species cannot be inferred from the pattern of variation of a single nucleotide segment. Patterns of variation in different regions of the genome must be considered and interpreted in the context of paleontological and archeological evidence...and the idea that the pattern of human evolution can be deduced solely from the pattern of contemporary mitochondrial genome diversity is becoming increasingly untenable.

Techniques that recover mtDNA from fossil now permit analysis of sequence variation in ancient populations...The results have been widely argued as evidence that Neanderthals did not contribute genes to contemporary Europeans, thus supporting the recent out of Africa model. This interpretation may not be justified. mtDNA is a small component of the total genome, and the failure of a mitochondrial lineage to survive to the present does not imply a similar failure for the remainder of the genome. There is morphological evidence for the survival of Neandertal genes in Europe after the arrival of Cro-Magnon people.

These results show that, with the possible exception of KS8 and LM3, the ancient Aboriginal sequences, including those from individuals with both *robust* and *gracile* morphologies, are within a clade that includes the sequences of living Aboriginal Australians, and that they therefore diverged after the MRCA (most recent common ancestor) of contemporary Aboriginal sequences. mtDNA lineages fail to differentiate individuals with clearly distinct morphologies.

This finding does not imply that all living people originated in Australia, any more than previously described deep lineages in Africa demand a recent origin of humans on that continent. Deep lineages in Africa and our finding of an even deeper lineage in Australia are consistent with a number of possible models of the demographic and evolutionary history of our species.

Lack of association between the survival of nuclear and mtDNA lineages is expected because they have different transmission patterns between generations. This point is emphasized by the high frequency of the Insert on chromosome 11 in many human populations. Despite having the Insert, none of these populations have the LM3yInsert mtDNA lineage from which the Insert must originally have been transferred. There must have been genetic exchange between people with mtDNA genomes from the LM3yInsert lineage and those with the contemporary lineage. Similar exchanges between people with other Pleistocene mtDNA lineages, like that of the Feldhofer Neanderthal individual, may have occurred.

Our data present a serious challenge to interpretation of contemporary human mtDNA variation as supporting the recent out of Africa model. A separate mtDNA lineage in an individual whose morphology is within the contemporary range and who lived in Australia would imply both that anatomically modern humans were among those that were replaced and that part of the replacement occurred in Australia. An alternative explanation is that the LM3yInsert mtDNA lineage was replaced by a spread of the "contemporary" mtDNA lineage through late Pleistocene human populations under directional selection pressure.

Adcock raised some very important issues in this paper. First he states that the geographical origin of a species could not be ascertained by a study of a single nucleotide segment—mtDNA. Secondly he shows that the support for the recent out of Africa model may not be scientifically supportable. He also reasons that other DNA material may have survived in the descendants even though the mtDNA did not. This implies that if nuclear (in the nucleus of the cell) DNA was inherited then the out of Africa model, especially the dating of the African Eve, is not correct and also that all fossil men, including Neanderthal man and modern humans are related.

Adcock is also critical of the study by Stoneking *et al*, (10) where the mtDNA of the Feldhofer Neanderthal was examined. Adcock's reference to the Feldhofer Neanderthal is an indirect allusion to his disagreement with the conclusions that the Neanderthals are not in the human lineage. Finally he shows support for the multiregional evolutionary theory. Although the multiregional theory is incorrect, one of its basic underpinnings, the relatedness of all late human fossils is true.

The Adcock study if correct would be the death knell for the mtDNA studies and all that they purpose to show. Because of this some scientists have tried to reinterpret the geology of the Australia fossil on which Adcock based his studies, specifically the Mungo III human fossils. This reinterpretation would assign a younger age to the Mungo fossils and would invalidate the conclusions of the Adcock study. The prestigious science journal *Nature* is philosophically aligned with the mtDNA conclusion so it is not surprising that the following appeared in a recent issue.

Abstract—Mungo III, the source of the world's oldest human mitochondrial DNA, has been variously estimated at 30 thousand years (kyr) old, 42–45 kyr old and 62 ± 6 kyr old, while radiocarbon estimates placed the Mungo I cremation near 20–26 kyr ago. Here we report a new series of 25 optical ages showing that both burials occurred at 40 ± 2 kyr ago and that humans were present at Lake Mungo by 50–46 kyr ago, synchronously with, or soon after, initial occupation of northern and western Australia (15).

Adcock is not the only researcher to come to the conclusion that the mtDNA studies are incorrect. Many others also see the fallacious side of these studies.

Comparison of the Feldhofer sequence with living humans showed average differences less than found in 2 out of 3 comparisons of chimpanzee subspecies. Given this finding and the fact that the Neandertal-living human comparison spanned tens of thousands of years (thus generating more variation than expected at a single point in time), it seems possible that Neandertals were not a separate species, although they might be considered a different subspecies, as long suggested by a number of paleoanthropologists. In either case, the answer to the Neandertal question cannot be made based on regional comparisons of mitochondrial DNA across time, since both replacement and multiregional models can generate the same expected outcome. . . Therefore, the observed lack of regional affinity cannot prove one model of modern human origins to the exclusion of the other (16).

It will be interesting to see how the scientific community handles the two conflicting sides of this issue. As has been mentioned, they are both based on the latest scientific research, they both come to differing conclusions, and they will probably never be in agreement.

Cultural Similarities

Many other important studies support the idea that Neanderthals were related to and interbred with modern humans. Additional studies support the idea that Neanderthals were culturally advanced and had similar abilities as compared to modern man. If Neanderthals and *Homo sapiens* were culturally similar interbreeding would more likely take place. If they interbred then several things are obvious. The first is that the mtDNA Neanderthal studies are wrong. The second is that they are of the same species since only organisms of the same species can interbreed.

Were the Neanderthals culturally inferior or were they simply a variation of modern humans? Supplementary studies reinforce the latter conclusion. The following quotes are from the journal *Current Anthropology*, this article reveals that the Neanderthals were very much the intellectual and cultural equals of modern humans. This piece of writing reveals that they had developed and used many types of tools and ornaments including; awls for punching hides, needles for sewing and hair pinning, ivory and bone ornaments, and many different decorative and utilitarian type of articles made from bone. All these artifacts were of a technological design and manufacture that rivaled and in some cases surpassed those of *Homo sapiens*.

The presence of bone tools, personal ornaments, and apparently "modern" stone tools in European late Middle Paleolithic or pre-Aurignacian Paleolithic contexts is generally interpreted as the result of the acculturation of Neanderthal populations by anatomically modern humans. Analysis of the stratigraphic, and archaeological data from the key site of Grotte du Renne (Arcy-sur-Cure, France) shows that the notion of acculturation as commonly understood, is inconsistent with the evidence. It is argued here that this site is not an exceptional case and is best explained by models of independent development that are supported by a reevaluation of Chatelperronian technology and by the patterns of chronological and geographical distribution of Aurignacian, Chatelperronian, Uluzzian, and late Mousterian settlements.

Neanderthals may therefore have been the producers of all the pre-Aurignacian Upper Paleolithic technocomplexes of Western and Central Europe, as has been suggested by Hahn-1993 (17).

Archaic humans, often called Cro-Magnon, and Neanderthal interbreeding is supported by much scientific data. Scientists claim that many of the human fossils show a mix of Cro-Magnon and Neanderthal features. According to the mtDNA studies of the Neanderthals this interbreeding never took place.

Does the 25,000-year-old body of a child found in Portugal make it more likely that they are our Ancestors?...For the past few days newspapers the world over have been reporting the discovery in Portugal of the skeleton of a 4-year-old child, dead for 25,000 years. The discoverers, led by Portuguese archeologist João Zilhão, are making a ground-breaking claim, that the skeleton shows traces of both Neanderthal and modern human ancestry, evidence that modern humans did not simply extinguish the Neanderthals, as many researchers had come to think. Instead the two kinds of human were so alike that in Portugal, at least, they intermingled—and made love—for thousands of years.

Even more significant, he thinks, are the limb proportions. Trinkaus measured the shinbone and the thighbone and found that the ratio fell way over at the Neanderthal end of the curve. He compared the circumference of the bones with their length, and found that the child had leg bones strong enough to support a stocky Neanderthal body. The limb proportions along with the receding chin are enough, Trinkaus says, to prove the child had Neanderthal ancestors as well as Cro-Magnon ones. "It only takes one feature," he says. "We've got two."(18)

Another opponent of the various genetic studies is Alan Thorne, an Australian anthropologist. He is a former lecturer in the department of anatomy at the University of Sydney. He made the original studies of Mungo man and Mungo Lady, which were early human fossils excavated in Lake Mungo in southeastern Australia (fig. 2). He vehemently disagrees with the genetic separation that some scientists have placed among human ancestors. He was one of the coauthors of the paper (14) that used mtDNA studies to show that humans did not have a singular common fossil "Eve" ancestor. In effect his genetic studies came to the exact opposite conclusion of the genetic studies of the out of Africa proponents.

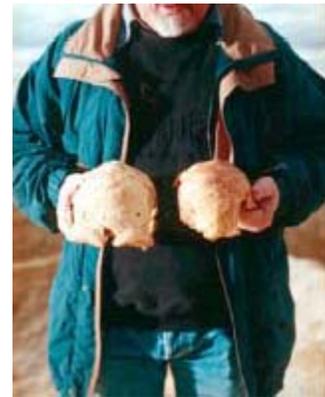


Figure 2. Alan Thorne holds the delicate skull on the right of Mungo man, which predates by tens of thousands of years the more massive thicker skull on the left. This unexpected reversal has challenged evolutionary theories.

Thorne preaches a revolutionary view called regional continuity. He believes that the species his opponents insist on calling *Homo erectus* was in fact *Homo sapiens*, and that they migrated out of Africa almost 2 million years ago and dispersed throughout Europe and Asia. As he sees it, there was no later migration and replacement: "Only one species of human has ever left Africa, and that is us."....

Why does this matter? Because if Thorne and his camp are right, much of what we think we know about human evolution is wrong. In the world according to Thorne, the human family tree is not divided into discrete species such as *Homo erectus*, *Homo antecessor*, *Homo heidelbergensis*, and *Homo neanderthalensis*. They are all *Homo sapiens*. Yes, Thorne agrees, from the outside all these hominids look different from each other, but so do humans today— a Korean, a Nigerian, and a Dane hardly resemble each other. Our ancestors displayed great variety, but they were similar in the only way that mattered: They were the same species, which meant they could have sex with each other and produce fertile offspring.

Those who believe in regional continuity tend to have a view of sexuality that is more generous and more inclusive than that of the out-of-Africa proponents. In the latter view, *Homo sapiens* led a kind of search-and-replace mission as they spread around the planet; these researchers believe that members of the new species would not have been able to successfully reproduce with members of earlier species, no matter how hard they tried. Thorne thinks that's nonsense. "European scientists have dominated this field for 150 years," he says. "And they've got a big problem in Europe. Namely, they've got to account for those Neanderthals. My opponents would say that Cro-Magnons"—humans identical to us who lived during the Ice Age— "simply 'replaced' Neanderthals with no intermingling. That's the part I object to. 'No intermingling.' Now, I ask you, does that sound like the human beings you know?" (19)

Analysis of the mtDNA Neanderthal Data

It is important to understand when looking at the genetic studies of Neanderthal man and the "Out of Africa Eve," that several conflicting issues are being dealt with. Some of these issues are accurate and some are inaccurate. Also bear in mind that none of the evolutionary issues are acceptable from a Biblical point of view.

The mtDNA studies reveal the following:

- Evolution as a general theory or philosophy is not correct.
- The dating of the mitochondrial Eve at 200,000 years is not correct.
- The idea that modern man and Neanderthal man are unrelated is not correct.
- The use of chimpanzee DNA as a genetic starting point is not correct and is circular reasoning.

On the other hand there are several issues that the genetic studies are correct about, although they are correct for reasons that have nothing to do with evolution. These include the following:

- The falsity of the multiregional theory of evolution is correct.
- The out of Africa scenario implies that there was once a population bottleneck and that we are all closely related to a single maternal set of genes, this is correct.
- The scientific findings that show that the Neanderthals and humans are similar morphologically and therefore interbred and are closely related are correct.

So do the genetic studies of early fossil humans agree with evolution or do they more likely agree with the scriptural account as outlined in the book of Genesis?

The Bible states that there have been two population bottlenecks. These bottlenecks occurred at creation when there were only two humans that supplied all the DNA material for all humanity. Also, later all humans except eight were destroyed in a great earth-wide flood. The survivors Noah, his three sons, and their wives were the providers of all extant DNA. Although the mtDNA out of Africa studies does not demand a population bottleneck in the past, the results of the studies would be expected if there had been a population bottleneck sometime in the past. The mtDNA studies do not prove the Bible but—and this is a very important distinction—they are consistent with the two Genesis bottleneck scenarios.

The Bible reveals that all men have descended from Adam. This would include *Homo neanderthalensis* (also *Homo erectus*). The fossil record and mtDNA studies of Neanderthals properly interpreted show that all fossil humans were closely related genetically and morphologically. In reality the Neanderthal people were simply a variation of the Adamic line.

Their slight distinct morphological features were the result of post and pre flood factors that affected them skeletally.

Many of the early humans have been found in graves buried in caves. Their burial practices coincided with the burial practices of the people in Genesis (see Genesis 23:17-20; 49:29). The fossil record reveals many burials where Neanderthals and humans were buried together. Even today only people of similar genetic background (relatives) are buried in the same grave or burial plot. This is further proof that the Neanderthals were related and simply a variation of *Homo sapiens*. The scientific community has greatly erred in assigning them a separate species status and in some cases even removing them from modern human lineage.

The Biblical record and the properly interpreted fossil record are in agreement. They reveal that humanity has descended from a small population bottleneck and that the various fossil men are related as proven by morphology and various genetic studies. This is what is to be expected since human have all descended from the original created pair, Adam and Eve, and later from a genetic perspective almost went extinct at the time of the great Earthwide flood.

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