

## THE EVE CONTROVERSY

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### ABSTRACT

The human race could not have descended from a single couple 200, 000 years ago as based on female mitochondria evidence. The genetics are too complicated by a wide margin. The reason humans seem to be so descended is because the mitochondrial DNA follows rules that are approximately similar to bacterial rules of descent.

**KEY WORDS** eve, mitochondria, human, descent, gene, Homo erectus

### INTRODUCTION

The paleoanthropologists who attempt to maintain that the people of the whole human race could not have had their mitochondria derived from a single woman 200,000 years ago [Thorne 1992] or 146,000 years ago [Horai, et al 1995] or possibly 400,000 years ago (assuming some paternal input) are not considering one possible circumstance. If a woman had a mutation among her mitochondria that gave her a significant advantage, that mitochondria would spread throughout her village. Furthermore, that mitochondria would eventually take over any surrounding village which acquired an "Eve" fertile woman. The gene could even conceivably have arrived originally from another primate that was able to have viable progeny with the human branch.

### DISCUSSION

If a gene arose, for instance, which enabled an "Eve" to average 10 babies in an average lifetime while all other non "eves" were averaging 9, that gene and its mitochondria associates would relentlessly supplant all others. The process would be slow and statistically uncertain at first, because an accident could remove a single individual or family. However, as the percentage of "eves" built up in the village, the continuance would become more certain and the speed of the takeover would increase. In a village maintained at 100 women, when the mathematically calculated number of "eves" passed 99 statistically there would be no "non eves", and the whole village would seem to be derived from a single couple from its mitochondria. In small populations, mitochondrial genes will either become 100% fixed or extinct. The smaller the population, the faster the result [Li].

The period when the new gene predominated in all the mitochondria of the cells would not be long either. It is possible for the percentage of the mitochondria in the cells to vary from 6% to 69% from the lung as opposed to the heart in the same individual, possibly because the mitochondria are taken preferentially [Meirelles], so a 100% takeover is theoretically possible in a couple of generations [Blok][Jenuth 1996,

1997]. There is even evidence that stem cells can insert mitochondria into other cells [Spees].

Even if a single woman was captured or seduced by a Neanderthal man in a local population of 10,000 Neanderthals, eventually "eve's" mitochondria would virtually exclude all others if it were not accidentally eliminated early on and much, much before 200,000 years. Even something as trivial as a one percent improvement in something like energy output would overwhelm the other mitochondria hosts well before such a time. Her nuclear genes, on the other hand, would likely be virtually undetectable only a few dozen generations later, and the Neanderthals would be virtually indistinguishable from their ancestors anatomically. The "Eve" gene would follow approximately the mathematical rules which bacterial genes are subject to (indeed mitochondria probably arose from a symbiosis of an ancient bacteria with eukaryote cells), not rules for nuclear genes, since mitochondria genes do not normally recombine (although they may do so occasionally [Wallis] ). This approximate bacterial rule would be especially close when all the mitochondria in an individual acquired the same advantageous gene. Bacteria have often been seen to have even trivially advantageous traits or deletions sweep through a population in a rather small number of generations.

The chance that all humans today are descended from a single couple only 200,000 years or less than 10,000 generations ago or so [Fitch p251] and still have the enormous nuclear diversity which they display today is completely impossible for hundreds of thousands of generations seem to be required [Wright p150] at least, so the above or something like it is essential. Mitochondrial DNA is poor at predicting the age of a genetic line. Low-diversity mitochondrial lineages, typically disregarded as important from a conservation standpoint, might sometimes correspond to recently selected, well-adapted haplotypes to be preserved [Bazin]. It has been estimated from analysis of the HLA immune genetic complex that human populations have never sunk down below a 50 or 100 thousand population [Ayala & Escalante, et al 1995, p205], let alone a single individual. Evidence from recessive disorders of the apolipoprotein C-II activator of lipoprotein lipase Japanese and Caucasian progenitors must have diverged two million years ago [Ayala & Escalante et al, p206]. We have seen one hundred human generations come and go with very little change in appearance, at least, judging from ancient portraits. To imprint a trivial nuclear genetic difference on a population requires large numbers of deaths or failures to reproduce. Humans have not had large numbers until recently, nor short life spans, nor have they ever had large numbers of progeny, say 100 or 200 to a woman. Trivial traits and mere differences in appearance take a long, long time to monopolize a population even when there is mild active sexual or other selection for them. Humans have a very large number of trivial differences in appearance and even a fair number of fundamental differences in organ design and enzyme systems. Humans reproduce largely by visual clues so that there is strong pressure to reject even small differences in appearance, especially in primitive societies. Humans have considerable individual and family choice in mate selection. Non gene sequences, which are subjected to zero selective pressure, show considerable per cent variation across the world [king]. In addition to all of the above, there is a definite tendency toward inbreeding within their villages and hierarchies, not from any obvious physiological bars, but only from cultural bars. Barring a drastic unknown difference in any of the above parameters in ancient times, it is safe to say that no single family

could possibly have been responsible for all the present day nuclear gene variety in only 200,000 years, or even 2,000,000 years. This all the more especially so since they were proposed to be confined to Africa the first 140,000 years or so [Macaulay]. Never mind variety, just splitting the races apart in such a time is impossible. It is thought to have taken over 12,000 years just to occupy the South American continent. Australian aborigines entered Australia 50,000 years ago [Bowler], and there is evidence that Australia was colonized by modern humans at least 50,000 or 60,000 years ago and these humans are more genetically different from Africans than any other groups are from each other. Obviously those aborigines split off from other humans then and thus left only 150,000 years or less to reach their diversity, given a single couple origin hypothesis. When human mitochondria swept across the world, but probably not from Africa (fossils show no sure evidence of modern humans in Africa [Thorne] ) and an out of Africa hypothesis is far from proven [Dennell], they would have had no problem picking up from or imparting traits to the "people" they met along the way, and surely must have. Fonda makes a persuasive case that humans arose in Eurasia and hybridized with *Homo erectus* and other hominids there, part of his argument being that Eurasians are more closely related to each other than to Africans, that artifacts showed up there first, and that Africans have more diversity than Eurasians and thus were presumably hybridized with resident populations. He has reviewed more recent genetic data [Fonda, Origins of humans].

The Mmacrohaplo groups, M and N, have been claimed to be of African origin, but the latest research shows that M is Asian (Indian). Further, the nuclear DNA affinities of Indians are to south east Asia, and the south east Asians are the most divergent from Africans of any people on earth. That is in accordance with Fonda's theory above, because Asian and African *erectus* were separated for nearly two million years, allowing much more divergence than the 50 or 60 thousand years that recent out of Africa populations would have had for diversity to arise and contradictory to the out of Africa hypothesis. There is a Eurasian-Hss component to both Africans and Australian DNA, and that is about the same, but the *Homo erectus* derived portions of the African and Australian DNA are very divergent, because the Asian and African *Homo erectus* components had 2 million years to diverge. Moreover, he notes that the fossil mtDNA inclusion on chromosome 11 of the nuclear DNA is very ancient, and its geographic distribution shows that it was of north east Asian origin. Since it is clearly antecedent to LM3 and all the other lineages of Australian mtDNA (except the Kow Swamp type that came in through New Guinea during the most recent ice age) belong to macro-N, he contends that N is also of archaic Asian provenance.

Fonda has presented a very elaborate analysis of Australian settlement and suggests that Australia was originally settled by central Asian migrants (Some of whose descendants later became Europeans), and then were supplanted by the current aborigines, who had been hybridized with southeast Asian *homo erectus* [Fonda, Australian ancestry].

Mishmar, et al, have found that there is a profound difference in sections of the mitochondrial genome from different sections of Asia, and that these differences seem to be related to climate primarily [Mishmar (you must zoom in to this PDF file)] . They conclude that natural selection is responsible for these fundamental differences, probably

having to do with energy production, and some of them at least partly responsible for the higher metabolism of northern people.

Begun proposes that *Dryopithecus* ape from Europe is the ancestor of the human line (hominin) [Begun]. I think that it is highly probable that all the hominids that arose after the Miocene could hybridize.

As for humans supplanting all humanoid primates, take note that they have not even supplanted non-humanoid chimpanzees or gorillas even today. Two hundred thousand years ago humans had no obvious technological advantage over their contemporaries, surely none, at least, which could not have been easily adopted by their contemporaries, especially those that hybridized.

Language diversity also denies evolution in only 200,000 years. Africa alone has 2000 language groups that represent nearly one third of the world's languages [Tishkoff]. There is no chance at all that that many different languages could appear from a single couple in only 200,000 years.

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