

## Out of Africa 'assimilation' spells trouble for progressive creationists

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Creationists believe that God 'made of one blood all nations of men' (Acts 17:26). The Bible allows no room for any soulless 'prehumans' or 'apemen' predating humans, because 'from the beginning of the creation God made them male and female' (Mark 10:6). Hence, as humans were around from the beginning of time (the sixth day) then all fossil 'hominids' (creatures believed to be more closely related to humans than to chimpanzees) belong either to the genus *Homo*, and are descendants of Adam and Eve, or they belong to extinct australopithecine apes. However, progressive creationists propose that these soulless hominids roamed the earth before God created Adam and Eve (somewhere between 10 and 60 thousand years ago), and that the hominids eventually died out. They regard the descendants of Adam and Eve as the only truly human *Homo sapiens*. Progressive creationists accept the evolutionists' methods and assumptions, and have used evidence from morphology and mitochondrial DNA clock studies to exclude Neandertals from the human family. This view, already unbelievable for numerous reasons, faces a new challenge: a recent evolutionary analysis implies that all species of *Homo* were interbreeding back as far as 500,000 years ago!

### Competing evolutionary hypotheses

Human evolution is currently thought to have proceeded according to one of two competing models. The 'out of Africa' model proposes that modern humans evolved in Africa between 100,000 and 200,000 years

ago, and that all humans today can trace their maternal line of descent (through inherited mitochondrial DNA) back to a woman (mitochondrial Eve) who lived in Africa at this time.<sup>3</sup> An expansion of these modern humans from Africa is suggested as having occurred between 50,000 and 100,000 years ago,<sup>4</sup> and that in all continents they totally replaced the previous, more 'archaic' occupants, who were descendants from earlier expansions, including a *Homo erectus* exodus from Africa nearly 1.7 million years earlier.

The rival 'multiregional' model proposes that humans have evolved in parallel for about the last 2 million years, initially from *Homo erectus* populations that wandered out of Africa into other continents. Limited gene flow between regional populations is believed to have occurred. This would have kept continuity between them, ensuring that they evolved towards modernity as a single lineage, as opposed to evolving in total isolation, and hence at different rates and in divergent directions.

### Phylogeographic analysis

Alan Templeton, a geneticist at Washington University, and strong critic of the mitochondrial Eve concept,<sup>6</sup> has recently used 'nested clade phylogeographic analysis' to investigate models of human evolution.<sup>7</sup> Nested clade phylogeographic analysis is described as

'attempts to sort out the roles of recurrent forces (such as gene flow) from historical events (such as fragmentation or range expansion events) by overlaying the geographical distributions of haplotypes<sup>8</sup> and clades<sup>9</sup> of haplotypes upon the evolutionary tree of the haplotypes. By performing this geographical overlay upon an evolutionary tree, both space (geography) and time (the tree) are integrated into a single analysis.'<sup>10</sup>

Haplotype trees for different DNA regions were analyzed, including mitochondrial DNA, Y-chromosomal DNA, X-linked regions and autosomal regions.

From an evolutionary perspective (a creation perspective is given in the next section), results from the study indicate that there had been at least two major migrations of people out of Africa since the initial spread of *Homo erectus* about 1.7 million years ago. The time of the first 'out of Africa' expansion event (between 0.42 and 0.84 million years ago) was compatible with a substantial increase in brain capacity about 400,000 to 500,000 years ago. The most recent expansion out of Africa (between 0.08 and 0.15 million years ago) was compatible with the appearance of 'modern' cranial traits in Africa 130,000 years ago, and the subsequent movement out of Africa by these people more than 90,000 years ago. The analysis also indicated that 'African and Eurasian populations were linked by recurrent gene flow, certainly over the last half a million years, and probably longer'.<sup>11</sup> Also, the expansions out of Africa, particularly the most recent, were characterized by interbreeding, not replacement.

### A creation perspective

The method of analysis used by phylogeographers is highly theoretical, involving assumptions, speculations and large uncertainties. For example, in order to obtain absolute ages from the nested hierarchy of clades, as opposed to relative ages, the tree with its many branches has to be calibrated to some known event. In the Templeton paper, the time to the most recent common ancestral haplotype (TMRCA) is calculated from the assumption that humans and chimpanzees diverged from a common ancestor 6 million years ago. However, this 6-million-year calibration point was derived from dating of the fossils belonging to *Orrorin tugenensis* and *Ardipithecus ramidus kaddaba*,

neither of which makes a convincing case as an early hominid candidate.<sup>12</sup> In the past the human and chimpanzee calibration point (usually at 5 million years ago) has itself been determined by a molecular clock, the calibration point of which was the supposed branchpoint between Old World monkeys and apes 30 million years ago, as determined by conventional dating of fossils.<sup>13</sup> In either case, the absolute age of the calibration point comes down to radiometric dating, but radiometric dating is also based on unproven assumptions,<sup>14</sup> and so in the end the timescale of the molecular clock has no reliable correlation with absolute ages. In addition, the assumption that molecular clocks tick at constant rates is flawed.<sup>15,16</sup>



A Neanderthal skull replica

Interestingly, the TMRCA calculated for the different DNA regions varied remarkably, from 0.23 to 8.5 million years. Having alleles, such as the latter, more ancient than the speciation event (the alleged human and chimpanzee split 6 million years ago) does appear contradictory, but is suggested to be a ‘true biological possibility’. This phenomenon, dauntingly dubbed a ‘trans specific polymorphism’, is believed by evolutionists to be a characteristic result of ‘balancing selection’, which is the persistence in a population, through selection, of several genetic variants of a gene (different alleles at a locus). However, it is tempting to draw parallels with radiometric dating, where anomalous dates are conveniently discarded as contaminated samples. As indicated earlier, the data is fitted to an evolutionary tree, and so an evolutionary line of descent is assured *a priori*, even though specific details of within-tree interactions may not have been preprogrammed.

Because of the many uncertainties and ‘evolutionary’ assumptions in the study, the manoeuvring room in the analysis and the potential for error are large. Hence, it is no surprise that ‘refinement’ of the data leads to episodes, including the ‘out of Africa’ expansion events, coinciding at ballpark level with evolutionary events determined ‘independently’, such as the alleged appearance of ‘modern’ cranial traits in Africa 130,000 years ago or the expansion of cranial capacity in the mid-Pleistocene.

### Conclusion

Creationists reject the evolutionary timescale, but would agree with the evidence of interbreeding between ‘modern humans’ and ‘archaic’ humans (e.g. Neanderthals, *Homo heidelbergensis* and *Homo erectus*) because we believe they all belong to the one species. However, if this ‘hybrid model’ becomes the new evolutionary dogma, it will be quite a challenge to incorporate it into progressive creation theology. This is because the implications from the Templeton study are that ‘archaic’ human genes are mixed in with ‘modern’ human genes, inferring that if there was an Adam then he must have

lived, at the very least, 500,000 years ago. This would present progressive creationists with a choice of either an impossible biblical chronology or the (forbidden) interbreeding of soulless ‘prehumans’ with the descendants of Adam and Eve. The problem would disappear if they simply believed what the Bible says about our origins, rather than the latest evolutionary propaganda.

### References

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8. Haplotypes are linked alleles of different genes on a single chromosome, which are inherited as a unit.
9. A clade is a group of organisms that are believed to have evolved from a common ancestor.
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