

Is the African ‘Eve’ Misconceived?

GREG J. BEASLEY

During the latter half of 1991 the Australian news media focussed much attention on the purported evolutionary origins of modern humans — in particular, the current debate between advocates of the so-called ‘**Multi-Regional**’ and ‘**African Eve**’ hypotheses.¹⁻³

The multi-regional hypothesis has been championed principally by Milford Wolpoff and Alan Thorne,⁴ whilst the case for an African Eve has been advocated by Rebecca Cann, Mark Stoneking and the late Allan Wilson.^{5,6} The two hypotheses approach the matter of human origins from two entirely different perspectives — that of the palaeoanthropologist and that of the biochemist. To date the two views have remained irreconcilable.⁷⁻⁹

THE ‘MULTI-REGIONAL’ HYPOTHESIS

The multi-regional hypothesis is founded on the belief that ‘modern’ humans emerged from several distinct ancestral streams — these lines being traceable to at least the *Homo erectus* phase of human evolution; that is to say, a hypothetical ‘common’ ancestor **preceded the emergence of regionally distinct variants of *Homo erectus***.¹⁰ The hypothesis does not preclude the possibility of **limited gene flow** between contemporaneous regional populations along the way to modern man, *Homo sapiens sapiens*. In fact, the unity of the modern species is attributed to such gene flow. However, according to the multi-regional model the common ancestor had to live some time before the appearance of *Homo erectus* (between 1.5 million and 700,000 years ago).

Evidence for the multi-regional hypothesis is **largely ‘fossil-based’** — confined almost exclusively to **observed morphological similarities (continuities) between successively developing (evolving) fossil types within a specific region**. For instance, the ancestors of Australoids (Australian aborigines) are traced to South-East Asian (Javanese) *H. erectus* fossils. East Asians, on the other hand, are traced to Asian *H. erectus* specimens such as Peking and Lantien Man, whilst modern Europeans are said to have their root stock in European *H. erectus* specimens, such as the Petralona hominid, and, more recently, the neanderthals (and presumably Cro-magnoids). Finally, modern Africans are traced back to *H. erectus* specimens such as Olduvai Gorge hominids,

OH 9 and 12.

Critics of the hypothesis point to difficulties in reconciling the **apparent recency** of divergence of the human species from a hypothetical ‘common ancestor’ (based on changes in nuclear and mitochondrial DNA) with the multi-regional hypothesis.^{11,12} Furthermore, the revised datings for proto-Cro-magnoids and neanderthals in the Levant would seem to indicate that the two groups **existed contemporaneously for at least 60,000 years**.¹³

THE ‘AFRICAN EVE’ (OR ‘OUT-OF-AFRICA’) HYPOTHESIS

The hypothesis of an African Eve incorporates the premise that **mitochondrial DNA (mtDNA)** mutates at a fairly **rapid and constant rate** — about ten times faster than that of nuclear DNA.¹⁴ As such, mtDNA makes an ideal **molecular ‘clock’** — facilitating the determination of the degree of variance in mtDNA sequences between living populations. It is then presumed that **the greater the number of acquired mutations in the mtDNA of a particular ethnic group, the older is its ancestry**.^{15,16}

The presence of mtDNA in every human cell and the relatively small amount of sequence divergence in the samples studied by Cann *et al.* (<0.6 percent in 147 individuals) indicated a **remarkably high degree of relatedness in the women sampled**. This suggested that **all living humans could have descended from a single (common) female ancestor in an earlier generation**.

Mitochondrial DNA was selected for several reasons. Firstly, it is **only inherited from the individual’s mother** — thereby averting the possibility of recombination between maternal and paternal genomes. The mutated mtDNA is **passed from mother to daughter over successive generations**, thereby affording molecular biologists the opportunity to establish relationships between individuals and various ethnic groups.¹⁷ Because mtDNA is inherited exclusively through the maternal line, comparative studies of selected ethnic populations can be interpreted as representing a genealogy, reflecting the maternal ancestry of these same individuals.¹⁸ Secondly, the mutations are **generally neutral** (rather than harmful) **and, therefore, more likely to accumulate with the passage of time**.¹⁹ Thirdly, the rapid mutation rate

(assumed to be between 2 and 4 percent per million years) renders it a suitable tool for assessing the antiquity of humanity²⁰ — which, evolutionists argue, has diverged from a hypothetical common ancestor with the African apes during the last 5 million years or so.²¹

Cann and her colleagues concluded in 1987 that the mother of all mankind (dubbed 'Eve') lived between 140,000 and 290,000 years ago, and most probably in Africa.²² Two earlier (and smaller) studies — by Johnson *et al.*²³ and Greenberg *et al.*²⁴ — have been cited by Stoneking and Cann²⁵ as being consistent with their own views. It should be pointed out that the data by Johnson *et al.* had to be reworked by Stoneking and Cann (using the midpoint rooting method) before it accorded with their notion of an African 'mother' for mankind.²⁶

Recent studies by Vigilant and Stoneking^{27,28} were said to reinforce the aforementioned conclusion; identifying the Khoisan bushmen of Southern Africa as having the greatest percentage of intrahuman mtDNA divergence.²⁹

Added support for the notion of a recent African origin for modern humans has come through the work of a team of geneticists from the College de France in Paris. The team, led by Gerard Lucotte, have been examining mutations in Y (male) chromosomes, seeking to discover the common paternal ancestor for humanity. They identified a number of characteristic chromosomal types and settled on one — haplotype XIII — as the basis for their comparative studies of various ethnic groups around the world. (A haploid chromosome is favoured because it is restricted to males.) Mutations were greatest in the haplotype XIII chromosomes of one particular group — the Aka pygmies of the Central African Republic. James Shreeve summarised the implications of the group's studies this way:

*'... molecular Eve has found her molecular Adam. He is about the same age as she, and his roots, like hers, are African.'*³⁰

The 'Out-of-Africa' hypothesis reduces fossil hominids such as the European, Asian and Javanese variants of *Homo erectus* as well as neanderthal man to unsuccessful evolutionary sidelines.

POSSIBLE WEAKNESSES IN THE 'AFRICAN EVE' HYPOTHESIS

Quite obviously, the notion that the ancestors of all modern humans lived in Africa as recently as 200,000 years ago has not gone down at all well with palaeoanthropologists such as Wolpoff and Thorne. They regard the notion of regional continuity as incontrovertible. Yet it is not only the physical anthropologists who have taken exception to the notion of a recent African Eve (and Adam). A number of molecular biologists and geneticists have also joined the ranks of those critical of the hypothesis. Their criticisms are worthy of our attention.

Wainscoat³¹ started the ball rolling in 1987 with his review of the original paper by Cann *et al.* He stated that: *'The recently identified common female ancestor should more correctly be recognized as our "mitochondrial Eve" as she has contributed little, if anything, to our nuclear DNA.'*

(Note that this claim by Wainscoat is founded on evolutionary assumptions; the biblical model would require the original woman, Eve, to contribute to both mitochondrial and nuclear DNA.) He then proceeded to add:

*'... But there is an alternative explanation for the data, which is that one ancestral mitochondrial DNA type has reached fixation by random genetic drift.'*³²

Whilst Wainscoat³³ described the dating of the African Eve as *'... obviously rather crude'*, other authorities have gone so far as to **question the very notion of a steady accumulation of mutations over evolutionary time.** (Of course, such an assumption merely reflects a commitment to the evolutionary principle of uniformitarianism.) Lewin,³⁴ for instance, notes that Morris Goodman, of Wayne State University, has argued for a **gradual slowdown of molecular clocks.** He has also correctly pointed out that, if the principle of the steady accumulation of mutations is found wanting, **then there is no molecular clock.**³⁵

Furthermore, the timing of the African Eve is **based upon curious reasoning.** Rates of mtDNA mutation have been determined for populations occupying three geographical regions — Papua-New Guinea, Australia and North America. These rates varied between 2.5 and 7.2 percent per million years, but were **presumed to be in general agreement with those for a wide variety of vertebrates — between 2 and 4 percent per million years.**^{36,37} However, the adopted rates presume that the elapsed time from first occupancy of a region is correct. For instance, in the case of Australia, occupancy is said to have occurred some 40,000 years ago; North America, only 12,000 years ago. If these dates, along with those presumed for vertebrates, were shown to be inflated, **then much higher divergence rates would need to be invoked.**

In attempting to rebut separate criticisms by Saitou and Omoto³⁸ and Darlu and Tassy,³⁹ Cann *et al.*⁴⁰ almost conceded the tenuous nature of their assumptions when they stated:

'Johnson et al. have made an ad hoc argument that the evolutionary rate may be higher on the primary branch leading exclusively to African mtDNAs . . . If this were so, the midpoint method would falsely put the root on the African side of the true root. Although current data do not rule out an African acceleration, we should be aware that this argument has a corollary, which is that the average rate of human mtDNA evolution would be higher than we estimated. As a consequence, our previous estimate of 200,000 years ago for the time when the common mitochondrial

mother lived would have to be revised toward an even more recent time.'

This is unthinkable for avowed evolutionists!

Darlu and Tassy⁴¹ have also raised a number of other factors that may influence relative rates of mutation, including **selective pressures**, admixture, **migration** and bottleneck effects.

Furthermore, many regions of the earth have produced contemporaneous 'archaic' and 'modern' types (including Africa). In such instances there is also an obvious conflict with the transformist's premise of a gradual transition from a 'robust' to 'gracile' skeletal morphology, as the multi-regional proposal would have it, though it could be argued that ancestral types could continue to live side-by-side with their descendants. In this regard Stringer^{42,43} has noted that:

'The Australian (fossil) evidence presents special problems for supporters of the Out of Africa model' because of the contemporaneity of robust and gracile types (one type was alleged to have rapidly replaced another without significant gene flow between the populations).

We also note that Saitou and Omoto,⁴⁴ using a different rooting technique (called the **neighbour joining method**), have produced two other phylogenetic trees — **both of which suggest that Papua-New Guineans diverged from the hypothetical common mtDNA ancestor about the same time as Africans.**

Perhaps the most savage blow to the hypothesis came recently with the admission by Hedges *et al.*⁴⁵ that the earlier statistical analyses of the data were no longer regarded valid because of **an inherent bias toward a common ancestor of African origin in the generated maximum parsimony trees.** Templeton⁴⁶ had independently come to the same conclusion. Nevertheless, Stoneking and other leading exponents of the African Eve hypothesis (including Chris Stringer) remain confident that the best interpretation of the mitochondrial and nuclear DNA data will eventually affirm an African origin for humanity.^{47,48} Furthermore, as Barinaga has noted:

*'... there is one piece of evidence from the Wilson group that remains unchallenged, says Harvard's Ruvolo. That is the fact that Africans have the greater diversity in their mitochondrial DNA than the inhabitants of any other continent. And that diversity, Ruvolo adds, is "the strongest piece of evidence for an African origin"—because it suggests that, to accumulate the largest number of mutations, humans must have lived longer in Africa than anywhere else.'*⁴⁹

POSSIBLE WEAKNESSES IN THE 'MULTI-REGIONAL' HYPOTHESIS

However, the 'multi-regional' hypothesis is not without its share of problems. For instance, the hypothesis

is based on all too few fossil remains⁵⁰ — many of which are poorly dated.^{51,52} Then, again, there is the problem of what to make of the molecular data.⁵³ On the other hand, if, as the advocates of an 'African Eve' suggest, the Asian mainland was colonised not by descendants of local variants of *Homo erectus*, but rather, migrating tribes from Africa, **can we be any less certain that these tribes didn't originate in the Near East?**

Whilst the comparative sequences of mtDNA point to a single, common ancestor for all women alive today, was she necessarily African? Can we depend on the assessment of the timing for divergence from the root stock of humanity? Is there a better explanation for our origins — one which embraces some of the better elements of the 'Multi-Regional' and 'Out-of-Africa' hypotheses?

A BIBLICAL PERSPECTIVE ON HUMAN ORIGINS

The biblical account of creation traces man's ancestry to some 6,000 years ago from a single pair of progenitors — Adam and Eve.⁵⁴ 1,656 years later, the descendants of Adam and Eve (excepting the patriarch Noah and his family) were wiped out in a global catastrophe.⁵⁵ Therefore, according to the biblical record of human history, all mankind owes its origins to the sons and daughters-in-law of Noah, who were preserved through the year-long Flood.⁵⁶ Although the ark of Noah landed in the mountains of Ararat⁵⁷ (in eastern Turkey), resettlement of the earth commenced from southern Mesopotamia some one hundred years later.⁵⁸

The 'Out-of-Africa' hypothesis postulates a comparatively recent and sub-Saharan origin for the immediate ancestors of modern man.⁵⁹ On the other hand, the 'Multi-Regional' hypothesis theorizes that modern man evolved simultaneously in at least four widely separated regions of the earth and over a much longer time-frame.^{60,61}

It is interesting to note that two recent attempts to trace the origins of Indo-European languages — the first by Renfrew⁶² and the second by Gamkrelidze and Ivanov⁶³ — have **converged on the areas of the Near East (Anatolia or Armenia).** These regions are less than 750 kilometres (450 miles) to the north of the biblical site of the 'confusion of tongues' (Babel).

More recently, Cavalli-Sforza⁶⁴ has suggested that: *'... the distribution of genes correlates surprisingly well with that of languages.'* However, this conclusion, which he draws from his comparative studies of the genetic and linguistic relationships between living human populations, is far from convincing.⁶⁵ For instance, Cavalli-Sforza's assertion of correlation is, to a large extent, **dependent on the validity of the Nostratic superfamily of languages including the Ethiopian and Berber/North African families of languages.**⁶⁶ Furthermore, the inferred relationship to selected Indo-European languages may

merely reflect contact with such groups at different times throughout history.

POST BABEL DISPERSION OF HUMANITY

The writings of the late Dr Arthur C. Custance provide many valuable insights into the dispersion of humanity after the Flood and Babel. In his book, **Noah's Three Sons**,⁶⁷ Custance examined the Table of Nations contained in the book of Genesis⁶⁸ and attempted to identify proto-nations arising from the listed patriarchs contained therein.

A long-held view of many older anthropologists saw humanity divided up into three distinct races; Caucasoids, Mongoloids and Negroids. These races were said to correspond broadly to the descendants of the three sons of Noah. (This overly simplistic view created many seemingly insoluble problems. For instance, not all races fitted readily into this tripartite pattern, for example, the Australian aborigines and many of the peoples from the Indian subcontinent.) Custance, however, **did not** equate all three of these races with the descendants of each of the three sons of Noah. Rather, he believed that there were good grounds for aligning the descendants of Shem with modern day Semitic cultures, and the combined mongoloid **and** negroid races with the descendants of Ham.⁶⁹ Finally, he identified the remaining Indo-European peoples as having been the descendants of Japheth.⁷⁰

Custance then postulated a dispersion of humanity from the Near East (Mesopotamia).⁷¹ Such a dispersion would necessarily have required some of the descendants of Ham to migrate southwards into the African continent and others in a north-easterly direction into Asia and the Americas. The descendants of Japheth migrated both in a north-westerly direction into Europe and westward into the Indian subcontinent and possibly Australia. The Semitic cultures, on the other hand, remained in the Near East and in parts of northern Africa.

Is it possible then to reappraise the mtDNA evidence in terms of the abovementioned migrations, remembering that there is **strong circumstantial evidence for an origin of Indo-European languages in, or immediately adjacent to, the Near East?**

AN ALTERNATIVE (BIBLE-BASED) MODEL

There may be a simple explanation for the variable divergence of mtDNA in modern human populations; one which isn't contingent upon the 'Out-of-Africa' hypothesis being correct.

Firstly, let's consider the descendants of Ham. According to Custance some migrated into the African continent shortly after the confusion of tongues. Their migration would have been into a continent largely shielded from the effects of a post-Flood Ice Age. Indeed, it would appear that much of Central and Eastern Africa was dense rainforest or woodland until comparatively recent times.

Therefore, the African descents of Ham migrated through or inhabited largely tropical, semi-tropical (hot and humid) or savanna zones — all of which would have been quite hot.

Contrast, then, the conditions experienced by the descendants of Japheth as they entered Europe. Europe was firmly in the grip of the Ice Age. **Therefore, the descendants of Ham and Japheth were subjected to opposing climatic extremes.**

Those migrating into warmer latitudes, such as Africa, would have been able to sustain a typically outdoors lifestyle, with minimal clothing requirements. On the other hand, proto-national tribes migrating into the generally higher and colder latitudes of eastern and western Europe would have been forced to 'rug-up' in order to survive a hostile Ice Age environment. Furthermore, they would have been forced to spend extended periods of time in caves or temporary rock shelters.

Now Ivanhoe⁷² has noted that a cline existed in late Pleistocene human skeletal morphology, '*. . . with the typical "neanderthal" traits decreasing towards the equator.*' He attributed this cline to two factors: firstly, variations in the amount of endogenous vitamin D (due to varying degrees of exposure to sunlight) and secondly, varying amounts of exogenous vitamin D (that is to say, differing amounts of dietary vitamin D as a result of climatic factors).

In a somewhat similar vein the number of mutations accumulated in the mitochondrial DNA of early post-Flood populations may have been influenced somewhat by the interplay of climatological, geophysical, migratory and sociological factors.

Now mutations have been induced experimentally by high-energy radiation, heat and certain toxic chemicals. In the natural realm, however, the primary causes (other than random copying mistakes) are exposure to **cosmic and solar radiation**. Barnes⁷³ has observed that:

'Most of the solar wind and some of the cosmic rays, both harmful forms of electrically charged radiation, are deflected away by the earth's magnetic field before it reaches the earth.'

The earth's magnetic field acts as a kind of shock front to solar radiation, deflecting much of the solar radiation away from the planet and along the magnetosheath. The field also exerts a force on cosmic rays — deflecting them away from the earth.

Now Barnes has also established that the earth's magnetic field is decaying naturally;⁷⁴ that is to say, exponentially. Therefore, we would anticipate the field strength to be significantly stronger in the recent past. For instance, at the time of the Biblical Flood — say 4350 years ago — the field strength would have been 11 times its present day value. Therefore, according to Barnes' model, radiation levels would have been considerably less at the time of the Flood.

If, however, this field had been disrupted (or even

weakened) for an extended period of time in the past, then the protective shielding afforded the earth would have been temporarily lost or reduced, **exposing all forms of life to a higher-than-usual dose of solar and cosmic radiation.** The recent work of Humphreys^{75,76} would appear to support just such a possibility.

Exposure to higher doses of radiation may have been the catalyst for many of the mutations in mitochondrial and nuclear DNA. Were such disruptions to the field to have coincided, in part, with the Ice Age, then it is possible that the incidence of mutation would be **greatest in individuals living in regions closest to the plane of the ecliptic** (solar radiation 'showers' being of **greater intensity** in such regions). Such regions would naturally tend to produce warmer climatic conditions. Therefore, individuals living in, or migrating through, these regions would be more likely to be exposed to these harmful forms of radiation than those caught up in the European Ice Age; **hence the higher number of mtDNA mutations in living populations of African ancestry.** Furthermore, the subtle differences in the mtDNA sequences of different populations from common climatological zones (for example, African pygmies, Papua-New Guinean highlanders and South American amerinds — all from different equatorial regions of the earth) may be due to the duration of their migration through regions of lesser solar radiation intensity.

The sudden 'switching-on' of radiation at the time of the Flood could also have been responsible, in part (at least), for the sudden decline in human longevity as documented in the book of Genesis.⁷⁷

Furthermore, if the population at the time of the initial dispersion was relatively small and inbreeding a relatively common practice for some time thereafter (due to enforced isolationism resulting from the confusion of tongues), then these factors would have tended to **accentuate the differences in the accumulated mutations in mtDNA between low and higher latitude populations.** Indeed, it may be this accentuation of genetic differences that is being interpreted by some authorities as an 'accelerated' accumulation of mutations in African (as well as Papua-New Guinean and Australoid) populations.

Given that the apparent divergence of mtDNA may be due, in part, to a combination of climatological, geophysical, migratory and sociological factors, it would appear unwise for creationists to give unconditional support to the 'Out-of-Africa' hypothesis, even if an African origin could somehow be reconciled with Scripture (for example, an early post-Babel migration or similar). The decidedly 'modern' appearance of many of the late Pleistocene hominids from East and South Africa (for example, the Omo and Border Cave skulls, respectively), together with the uncertainty surrounding their dating,⁷⁸ and the earlier dates for Levant hominid sites, raises the possibility that the inferred 'Out-of-Africa' migration **might be the very opposite of what actually happened!**

(It should be remembered that there are now a significant number of 'archaic' skulls from Africa that post-date the proto-Cro-magnoids from Qafzeh, for example, Jebel Ihroud, Broken Hill.)

CONCLUSIONS

Creationists would be remiss not to recognize the significance of genetic and morphological variance attested to by the African Eve and Multi-Regional hypotheses.⁷⁹ In fact, they would suggest that both models can be readily adapted to the biblical view of early human history. Firstly, the African Eve hypothesis invokes the notion of a single and, therefore, common female ancestor for all living humans (the biblical Eve⁸⁰). The variance in mtDNA sequencing need not infer an African nature and origin for this individual. Secondly, the African Eve hypothesis points to the comparative recency of this individual. Thirdly, the Multi-Regional (and to a somewhat lesser extent, the African Eve) hypothesis supports the notion of humanity dispersing across the face of the earth at some time in the past.⁸¹

It may well be that, in the final analysis, the observed variances in the molecular data (be they differing numbers of nuclear or mitochondrial DNA mutations) are merely pointing to the **greater susceptibility of nomadic/hunter-gatherer populations from low latitudes** (tropics and sub-tropics) **to naturally-induced mutations.** Accordingly, the subtle differences in divergence rates may be due to differing levels of exposure to harmful natural radiation and differing arrival times on the earth's continental land masses.

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Greg Beasley holds the position of Principal Analyst (Engineering) with City Rail's Planning Group in Sydney. He has a particular interest in palaeoanthropology and in the post-Flood fossil record of humans and primates. He has written previously for the **Ex Nihilo Technical Journal** (Volume 4) and currently resides in Prospect, New South Wales, Australia.