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Human mitochondrial DNA diversity is compatible with the multiregional continuity theory of the origin of *Homo sapiens*

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ABSTRACT: Confidence intervals for estimates of human mtDNA sequence diversity, chimpanzee-human mtDNA sequence divergence, and the time of splitting of the pongid-hominid lineages are presented. Consistent with all the data used in estimating the coalescence time for human mitochondrial lineages to a common ancestral mitochondrion is a range of dates from less than 79,000 years ago to more than 1,139,000 years ago. Consequently, the hypothesis that a migration of modern humans (*Homo sapiens*) out of Africa in the range of 140,000 to 280,000 years ago resulted in the complete replacement, without genetic interchange, of earlier Eurasian hominid populations (*Homo erectus*) is but one of several possible interpretations of the mtDNA data. The data are also compatible with the hypothesis, suggested earlier and supported by fossil evidence, of a single, more ancient expansion of the range of *Homo erectus* from Africa, followed by a gradual transition to *Homo sapiens* in Europe, Asia, and Africa.

KEY WORDS: mitochondrial DNA; mtDNA coalescence time; pongid-hominid divergence; multiregional evolution; *Homo erectus; Homo sapiens*

Historical perspective

The mtEve story has at its core some necessary evolutionary events that extend back to a phyletic origin, not of a Biblical woman, Eve, but rather of a genomic unit, the mitochondrion. However, all but lost in the initial excitement about the possibility of being able to trace events in human ancestry by using molecules rather than bones are a few essential elements – essential for real science, that is, though not for the now omnipresent journalistic phagocytosis (growth by engulfing and feeding upon some tempting subject matter) that for several decades has been a surrogate for genuine knowledge. What are the es-

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sential elements for understanding the genuine science behind what became the propagandized mtEve tale?

First, there is awareness that the phylogenetic trees being reconstructed concern genes rather than people: Gene lineages can and commonly do cross species boundaries (Eckhardt 2003; Eckhardt, Protsch 1995), singly or as sets of alleles, the insufficiently appreciated phenomenon of trans-species polymorphism, documented in hominoid Primates (Eckhardt 1994). Mitochondrial lineages antedate not only Eve but all vertebrates, giving deep meaning to the upended metaphor of "old wine in new bottles."

Second, as is done of necessity briefly in this introductory historical framing section, the preferable approach in reconstruction of evolution is not through using molecules *rather than* fossils, but instead by using both sources of evidence in combination. As an aside, it is easy to understand why, in an age of academic super-specialization, nearly all evolutionary biologists use either one body of evidence or the other, bones or molecules: Nearly all have learned only one discipline to some degree. In contrast, from early on in my own career I have worked with both genetics and morphology. As an undergraduate I originally planned to become an applied scientist of sorts (a veterinarian). In my first three years at Rutgers University, I did enough comparative anatomy (dealing with small-scale constitutive details in multiple non-mammalian species) to provide a foundation for later extensive research and teaching in comparative primate and human anatomy and then subsequently more concentrated work in morphology (extending anatomy to larger-scale matters of form and structure) and paleontology. In my first three years at Rutgers, I also took all of the genetics on offer to undergraduates, and managed in my senior year, just a decade after discovery of the DNA double helix, to talk my way into a fustily-named course in Physiological Genetics taught by Professor Charlotte Avers of Douglass College. Later, in graduate school at the University of Michigan I pursued a Joint Program in Anthropology and Human Genetics. To my knowledge I am the only one to have completed that joint program there in over 50 years, not surprising since the joint degree then required approximately two-thirds of the content for each independent graduate program. Along the way I also included an M.S. in Human Genetics and an M.A. in Anthropology. In contrast, it is a matter of fact that none of the three authors of "Mitochondrial DNA and human evolution" published by *Nature* in 1987 had any detailed substantive knowledge of the human fossil record. Part of the attraction for them, and perhaps for others, was that the concept of total "replacement" by whatever means, however fanciful, of all pre-existing populations of humans in Eurasia and elsewhere as postulated, obviated all such knowledge of fossil morphology as effectively superfluous.

Third, and a major focus of this introductory material, is that the mitochondrial phylogenies have been represented as coalescing on an ancestor at a depth in time that is far, far less constrained than was represented not only in the original paper by Cann, et al. (1987), but rather consistently since then. Error terms have been prodigiously under-estimated by most (but not all) molecular geneticists. As documented in detail in this brief critique, the convergence of all humans to a female ancestor who reportedly lived

between 140,000 and 280,000 years before the present time simply ignored the inherent uncertainties in the several separate components of error that influence estimated convergence time.

In contemplating all of the above three problems, but particularly the effect that the widespread, uncritical acceptance of a relatively recent convergence has had on the reconstruction of human evolution *for more than thirty years* I find myself remembering a key lesson from Barry Marshall's (2005) Nobel Prize Lecture, "Helicobacter Connections." In his second paragraph he refers to the line by the historian Daniel Boorstin (and evidently used by many others): "The greatest obstacle to knowledge is not ignorance; it is the illusion of knowledge." Just as the belief that peptic ulcers were caused by stress long prevented discovery of the causal role played by *Helicobcter pylori* infection, acceptance of the supposed reality of "mtEve" fostered the illusion that the mitochondrial DNA data necessarily *required* replacement of pre-existing archaic hominins by a second, relatively recent, human wave out of Africa. It did not. It does not still, though that point now is being conceded grudgingly and without widespread realization of the broad implications for human evolution.

This is not the place for a review of the staggeringly extensive literature on human phylogeny published over more than the last three decades. More than a little of it, even before the "mt Eve" era *per se*, has manifested a hubristic assurance that molecular perspectives are so compelling that, even when attempts are made to compare them with some cursorily considered fossil evidence, then the most arresting scientific conundrums or nonce resolutions (possible, perhaps, but scarcely indisputable) are worth publishing. One of my (least) favorite examples is the earlier paper by Hasegawa and colleagues (1985), who used mitochondrial data to estimate a divergence time of humans from apes of 2.7±0.6 million years ago, and then remarked (with dauntingly insouciant understatement) that "…although there is some uncertainty in the clock...this dating may pose a problem for the widely believed hypothesis that the bipedal creature, *Australopithecus afarensis*, which lived some 3.7 million years ago,…was ancestral to man and evolved after the human-ape splitting... Another likelier possibility is that mtDNA was transferred through hybridization between a proto-human and a proto-chimpanzee after the former had developed bipedalism…." From this estimation of the relative "likelihood" of hypotheses it can be seen that in 1987, Cann, et al., were not alone in the blithe assurance that they had in using molecularly based estimates to contradict inferences from fossil evidence, or the extent to which they grossly underestimated sources and extents of error in the mitochondrial data. Well before the beguiling speculations of Hasegawa, et al., in 1971 and 1972 I had combined molecular and fossil evidence to give what then was a crude – and widely criticized – estimate of an ape-human split in the range of 6 to 8 million years ago. That estimate was not confirmed until our paper in 2004 used morphological evidence to document that the Kenyan hominoid "Orrorin tugenensis" walked bipedally six million years ago (Galik et al. 2004). In this context it should be noted that decades after the dubious work by Hasegawa, Cann, and many others, in contrast Alan Templeton (2002 in particular, but see also 1993, 2010, 2018) has done much

to show that the preference for narrowly interpreted molecular data is a matter of personal choice by many writers and never was inherent in the primary evidence, molecular or morphological.

The very old manuscript that follows should be seen not as a current scientific publication to be judged out of its long-ago temporal context, but rather as a historical document of sorts (with some notably different dates for earlier human populations that were based on far fewer data than now available, and with different notations for units such as mya for Ma, as well as shifts in notation such as "hominin" for "hominid" that nonetheless are understandable in context). In a great many ways, the document is a product of its own time, although careful reading will show just how much the ideas it expressed were conceptually before their temporal era. The manuscript had been thought about and discussed for several years after 1987, then written in a great many drafts over the course of several months, a period that ended in early 1992. The paper as reproduced here has been retyped from a hard copy dated 4/10/1992; since about that time I have moved offices and labs six times, with understandable loss of computer and other files.

The work as published here bears my name alone as an author, but it represents effort contributed by two others (Professor Robert K. Selander and Terry W. Melton, then a graduate student in the Graduate Program in Genetics). The original plan was to have the paper submitted jointly by the three of us in the form of a Contributed Paper to *Proceedings of the National Academy of Sciences* by Robert K. Selander, an Academy member. In the end, Selander chose not to follow that plan. At the time not all of his reasons were clear, but a major factor was our disagreement over the relative importance of what might be referred to as "consensus views" in the field. Paramount among these was widespread belief then in a relatively shallow ape-human divergence time, in the range of 3 to 5 million years ago, while my much surer knowledge of the fossil record had led me to favor a temporally deeper split (later confirmed to about 6 million years ago as already noted above). After submissions without Selander to (as I recall) *Nature* and *Science* were rejected swiftly *pro forma* (along the lines of the paper not representing the prevailing views in the field – no little surprise there), the graduate student decided to withdraw from the project and shift both focus and mentorship (pragmatically in the event, as she eventually completed a routine Ph.D. degree). Results in the paper were reported by me at several international meetings and were well received. However, shortly afterward, my major academic shift between Departments and Colleges at Penn State gave rise to much new work, research opportunities, and graduate students with different foci, so the paper languished until the revolution in human evolutionary frameworks (Bednarik 2015) that has helped to provide a framework for questioning intensely the validity of some previously accepted hominin taxa (Eckhardt and Henneberg 2021), with this skepticism increasingly being confirmed, as by recent fossil finds in the 300,000 year bp range (Wu et al. 2019) that now make the original relatively recent "Out of Africa" replacement as clearly naïve to some others now as it was to me then.

One last unorthodox point: The references for the brief historical perspective at the beginning of this paper follow

the standard *Anthropological Review* format. Since the body of the paper itself originally was written for submission to *Proceedings of the National Academy of Sciences, USA*, the references for that portion might have have been left in their original highly abbreviated 1992 form in an attempt to reproduce as faithfully as possible what would have been available for readers in 1992, no less and no more. However, the Editors of *Anthropological Review* felt that readers would be served best by also providing the earlier references in standard *Anthropological Review* format, which has been done here.

Introduction

Measurements of mtDNA sequence variation in populations of humans and the common chimpanzee (*Pan troglodytes*) were used in 1987 to erect a hypothesis placing "the common ancestor of all human mtDNA diversity in Africa 140,000–280,000 years ago (Cann et al. 1987). More recently, additional mtDNA sequence data have been interpreted as evidence that the "ancestral [mtDNA] type links types that have diverged by an average of 2.00% and therefore existed about 280,000 years ago" (Vigilant et al. 1989) and that "the age of the common human mtDNA ancestor is placed between 166,000and 249,000 years ago" (Vigilant et al. 1991). Yet in the same series of studies, the estimated amount of human mtDNA sequence differentiation used to derive mtDNA coalescence times increased from 2.00% in 1989 (Vigilant et al. 1989) to 2.87% in 1991 (Vigilant et al. 1991). Other things being equal, a 43% increase in the amount of diversity should have resulted in a concomitant increase in the estimated time of coalescence to a common ancestral sequence, but the dates have remained within the originally announced range of 140,000 to 280,000 years ago. Although never mentioned, a comparison of the reports above shows that in the same series of studies, the estimated rate of mtDNA evolution (expressed as change per million years) increased from 2–4% per million years, based on restriction mapping of the whole mtDNA molecule (Cann et al. 1987), 8.4% per million years, based on sequencing of the mtDNA hypervariable region (Vigilant et al.1989), to 11.5–17.3% (Vigilant et al. 1991). Thus, as mtDNA diversity increased, the rate of estimated sequence divergence increased as well.

Dates for mtDNA lineage coalescence have been used as the basis for a scenario of human evolution that contradicts reconstructions derived from fossil evidence. Thus, mitochondrial DNA phylogenies have been used to support the proposition that widespread ancient hominid populations (*H. erectus*) that had existed in Eurasia since about 800,000 years ago were totally replaced, without genetic interchange, following a migration of anatomically modern human populations (*H. sapiens*) from Africa sometime in the 140,000 to 280,000 year range.

A recent technical comment (Templeton et al. 1992) questioned the idea that the maximum parsimony method of phylogenetic reconstruction supports an African origin for human mitochondrial DNA and showed that the phylogenetic analysis of the mtDNA data is flawed. This point was made previously (Krüger and Vogel 1989; Maddison 1990; Saitou and Omoto 1987) and responded to (Wilson et al. 1991) but not resolved, since neither a maximum parsimony (Templeton et al. 1992) nor

a neighbor-joining approach (Hedges et al. 1991) provides statistical support for an African geographic origin of human mitochondrial DNA. While technically correct, these considerations deflect attention from a more central problem posed by a high level of indeterminacy in the estimated age for the time of existence of the most recent common human mtDNA ancestor.

Here we examine the relationship between an estimate of the age of a common ancestor of all mtDNA types in extant humans that is held to have remained constant and studies of human mtDNA diversity and molecular evolutionary rates that appear to be increasing steadily. We also consider the question of whether or not the mtDNA evidence requires a replacement of Eurasian *H. erectus* by modern migrants from Africa.

In this investigation, as well as in previous attempts by others (Cann et al. 1987; Vigilant et al. 1989; Vigilant et al. 1991) to estimate an age for the existence of a common mtDNA ancestor of living humans, several variables enter into the calculations: the extent of observed within-human population sequence diversity; the degree of mtDNA sequence differences between humans and another hominoid primate, the common chimpanzee; an adjustment factor for the transition-transversion ratio that takes into account loss of information about the frequency of mutation due to multiple hits that occur at certain sites; and estimates for the time of the chimpanzee-human divergence. We introduce here measures of the error terms associated with these variables and evaluate their influence on the resultant variation in age estimates for the common ancestor of mtDNA sequences now found in human populations.

Materials and Methods

Human mtDNA variation and human-chimpanzee mtDNA differences

Our analysis is based on mtDNA sequences studied previously (Foran et al. 1988; Kocher and Wilson 1991; Vigilant et al. 1991) and reanalyzed here. Included in this sample were 189 individuals representing 135 distinct mitochondrial types, including 121 Africans, 8 African Americans, 20 natives of Papua New Guinea, 1 native Australian, 15 subjects of European ancestry, and 24 Asians. On average, for any given individual in the human sample (Vigilant et al. 1991), 610 bases are represented out of a maximum possible total of 692 bases from two hypervariable segments of the mitochondrial DNA D-loop.

Three common chimpanzee sequences as well as those of 14 humans (Kocher and Wilson 1991) were used in calculating diversity within the three chimps, diversity within 14 humans and the mean pairwise sequence difference between the species d_{xy}, the average number of nucleotide substitutions per site between the two groups, chimpanzee and human, respectively), with estimations of standard errors. The sample of 14 humans included eight of African origin, four Asian, one Australian, one European; all but the European were part of the larger group of 189 (Vigilant et al. 1991). Using a phylogenetic tree (not shown here) that places the deepest node for a common human ancestor between a group of six Africans and the remaining 129 individuals as in a previous study (Vigilant et al. 1991), and without changing placement of this node, diversity within the groups of six and 129 sequences and d_{xy} between these

two groups were calculated, with standard errors.

In order to derive error terms for within-species diversity and between-species divergences, the following methods were used: Pairwise distances between sequences were found by both the Jukes-Cantor method (Jukes and Cantor 1969) and by calculating proportions of nucleotide differences with standard statistical packages. Jukes-Cantor distances can be considered close to proportions of nucleotide differences when distances are small ($d < 0.1$), but the Jukes-Cantor method takes into account the probability of multiple hits. Pairwise distance matrices were created for humans alone (135 sequences) and then for the smaller groups of humans and chimps together (17 sequences). These matrices were then used in a modified program designed to compute standard errors of nucleotide diversity within populations and nucleotide divergence between populations (Jin 1988). Results include matrices of patristic distances based on either UPGMA (Sneath and Sokal 1973) or neighbor-joining (Saitou and Nei 1987) tree-making methods, and the within-species diversity and between-species divergence values, with associated estimates of standard error. Variances of nucleotide diversity and d_{xy} are those due to estimation errors of nucleotide substitution. The formulas for calculation of variances of the average number of nucleotide substitutions within and between populations are given by Nei and Jin (1985).

Results

Estimates of sequence divergence in humans and chimpanzees

Table 1 shows our estimates of sequence differences and their standard errors in the 692 base hypervariable region of mtDNA. Among 135 humans the Jukes-Cantor/UPGMA and proportion of nucleotide difference/neighbor-joining methods gave virtually identical estimates ($2.91 \pm 0.46\%$ and $2.91 \pm 0.47\%$, respectively); only the results derived from the latter approach are reported here for other variables. Based on our analysis, the 95% confidence interval for sequence variation in the human mtDNA D-loop hypervariable region is 1.97% to 3.85%. Our estimate of $2.91 \pm 2(0.47)\%$ is only slightly different from the value of 2.87% reported previously without any estimate of an error term (Vigilant et al. 1991). These values, both of which derived from

Table 1. Estimates of sequence differences and their standard errors in 692 base hypervariable region of mtDNA for 135 humans and 3 common chimpanzees

135 human mtDNAs				3 chimp-14 human mtDNAs		
diversity within human total	diversity African group of 6 (PAUP) *	diversity 129 other humans (PAUP) *	d_{xy} 2 popns. of 6 and 129 humans	diversity within 14 humans (subset)	diversity within 3 chimps	d_{xy} chimp-human
2.14 ± 0.19	0.91 ± 0.23	2.07 ± 0.19	2.91 ± 0.47	2.66 ± 0.31	8.63 ± 0.94	15.40 ± 1.36

Diversity, the average number of nucleotide substitutions per site over all pairwise comparisons, is shown for different groups, as well as dxy, the average number of nucleotide substitutions between two populations. All values are expressed as percent. Values obtained using Jukes-Cantor with NJ r UPGMA and proportion of nucleotide differences with UPGMA are not shown, but were virtually identical.

* PAUP tree groups as derived in (3).

a sample of 189 individuals exhibiting 135 different mitochondrial types, differ substantially from an earlier estimate of 2.00% within-human difference, based on a sample of 84 individuals exhibiting 72 different mtDNA types (Vigilant et al. 1989). The estimate of 2.00% was obtained by a different method and corresponds to a value of 2.14±0.19 obtained in our analysis. Until many more human sequences have been analyzed and are reported in more standardized formats, published values for within-human sequence divergence should be regarded as underestimates of unknown magnitude.

The amount of sequence diversity is high for the homologous segment of mtDNA in chimpanzees. We found within-chimpanzee diversity to be 8.63±0.94%, with a 95% confidence interval of 6.75% to 10.51%. These results agree with those of previous studies, which have shown that mtDNA D-loop sequence variation is three to four times greater in chimpanzees than in humans (Kocher, Wilson 1991).

Our estimate of the chimpanzee/human mtDNA sequence divergence is based on a neighbor-joining tree (not shown here) derived from data for the 14 human and 3 chimp sequences, edited to 692 bases. The observed sequence divergence estimate is 15.40±1.36%, and the corresponding 95% confidence interval is 12.68% to 18.12%. The previous estimate of 15.1%, which was reported without an associated error term (Vigilant et al. 1991), is within the 95% confidence interval in our estimate. In both instances, chimpanzee number 3 (C3) had been used to root the large mtDNA phylogenetic tree including all 135 known human types (Vigilant et al. 1991). Chimpanzee number 1 (C1) shows 10% fewer nucleotide changes than does C3 to the deepest node of the group of 14 humans used to construct our neighbor-joining tree. Therefore, merely changing the chimpanzee reference sequence from C3 to C1 would appreciably alter the chimpanzee-human mtDNA distance estimate and increase the estimated mtDNA coalescence time.

Transition-transversion ratio estimates

The multiple hit correction used to estimate the rate of control region sequence divergence (Vigilant et al. 1989) was based on previous work (Higuchi et al. 1989) that counted each transversion as equal to 10 transitions. More recently a transition-transversion ratio of 15:1 was used (Vigilant et al. 1991). Combined with a change in the observed measure of chimpanzee-human control region sequence divergencefrom 13.6% to 15.1%, this is a multiplier effect of shifting the estimated amount of control region sequence divergence from 42% (Vigilant et al. 1989) to 69.2% (Vigilant et al. 1991), an increase of 65%. The standard error of the estimate of the extent of human-chimpanzee sequence divergence (69.2%) was calculated (Nei 1992) to be 0.177, with a 95% confidence interval of 0.338 to 1.046.

Age estimates for the chimpanzee-human divergence

Chronologies based on molecular data commonly are calibrated by reference to one or more points in the fossil record. Recently, 4 to 6 million years was cited as the "best estimate" for the time of the chimpanzee divergence (Vigilant et al. 1991), but as earlier pointed out by Spuhler (1989), dates in this range

may be too shallow. The 4 to 6 million year range was based on calibration of a molecular clock by the branching of the orangutan from the African hominoids at 13 million years ago (Hasegawa and Kishino 1989; Hasegawa et al. 1990), but recent advances in zoogeography and geochronology (Bernor 1983; Steininger et al. 1985) support an earlier time of divergence.

Early Miocene dryopithecine apes are believed to be the common ancestors of the larger extant hominoids. They were initially restricted to Africa, and reached Eurasia as part of the mammalian faunal exchange that occurred 18.5–20 mya (Steininger et al. 1985). Large hominoid primates (*Sivapithecus*) ancestral to *Pongo* are known from Pakistan's Potwar Plateau by 12.5 to 13 mya (Barry 1986; Brown and Beecher 1989; Ward et al. 1991). Consequently, the ancestors of Asian lineages leading to *Pongo* and of African lineages leading to *Pan*, *Gorilla*, and *Homo* probably began phyletic differentiation 15 to 20 mya rather than 13 mya (Hasegawa and Kishino 1989; Hasegawa et al. 1990). These earlier dates accord with an estimate of 16.0 mya for the *Pongo-Homo* divergence and 9.2 mya for the *Pan-Homo* divergence times derived from a paleontologically-calibrated nonlinear molecular clock (Gingerich 1985). Although estimates for the time of the pongid-hominid divergence encompass extremes from 2.68 mya to 14 mya (Simons 1967), we have incorporated a moderate range estimated dates from 4 to 10 mya into our calculations of mtDNA coalescence times.

Variable age estimates for a common mtDNA ancestor

Table 1 presents estimates for within-human mtDNA variation, chimpanzee-human mtDNA divergence, and time for the phyletic separation of pongids and hominids, together with estimates of the error terms or ranges for these parameters. These values are combined here as in previous studies (Cann, Stoneking, Wilson

Table 2. Comparison of previously reported values and newly computed values contributing to calculation of a data of coalescence for human mtDNA types

Study	Year	Within-human variation, observed, %	Chimp-human sequence difference, observed, %	Transition-transversion ratio	Chimp-human sequence difference, adjusted, %	Chimp-human split, mya*	mtDNA divergence rate (%/my)	Human mtDNA coalescence date, years ago
(1)	1987a	0.57	NA	NA	NA	NA	2–4 (whole molecule)	140,000–280,000
(2)	1989	2.00	13.6	10:1	42	3–7	8.4	238,000
(3)	1991	2.87	15.1	15:1	69.2	4–6	11.5–17.3	166,000–249,000
(this paper)	1992+	1.97–3.85	12.69–18.13	9.6–20.4	33.8–104.6	4–10	3.4–25	79,000–1,139,000

* million years ago
Study 1 was based on restriction data. The others used sequence data (see text).
+ 95% confidence intervals are shown.

1987; Vigilant et al. 1989; Vigilant et al. 1991), to yield estimates of coalescence times for a common mtDNA ancestor by the formula (accumulated within-human mtDNA sequence difference in percent)/ adjusted chimpanzee-human sequence divergence in percent/estimated time for the chimpanzee-human divergence in millions of years).

When intrinsic sources of indeterminacy are incorporated into estimates of mtDNA coalescence time, there is inevitably a much greater range of dates compatible with the molecular data than has been reported (Cann, Stoneking, Wilson 1987; Vigilant et al. 1989; Vigilant et al. 1991). As noted above, the tree used to support an African origin for human mtDNA sequences (Vigilant et al. 1991) has been shown, in fact, not to give statistical resolution for the geographic origin of human mitochondrial DNA (Hedges et al. 1991; Maddison 1990; Templeton et al. 1992); our analysis demonstrates that, even accepting an African origin on independent grounds, the shallow coalescence times reported for a mtDNA ancestor still are not reliable. The outer ranges calculated here are from less than 80,000 to more than 1,100,000 years. Chimpanzee-human divergence dates in the range of 6 to 8 mya in combination with the calculated 95% confidence intervals for accumulated within-human diversity and the extent of chimp-human divergence yield hypothetical coalescence times ranging from less than 350,000 to more than 910,000 years ago.

An alternative approach is possible, not relying on the tree-based estimate of divergence rate, which has been questioned (Hedges et al. 1991; Maddison 1990; Templeton et al. 1992). This method uses an estimate of within-human sequence divergence, previously reported to be 2.00% (Vigilant et al. 1989). Based on analysis of a larger sample, our estimate for this variable is 2.14%±0.19%, with a corresponding 95% confidence interval of 1.76% to 2.52%. Even on this basis, human mtDNA coalescence times in excess of 745,000 years can be obtained.

Partial covariance in the error terms for within-human mtDNA variation and chimpanzee-human mtDNA divergence may exaggerate some of the deeper convergence time estimates. The magnitude of any covariance term is not calculated here, but the boundary conditions for its effects are estimable empirically by considering the coalescence time predicted, for example, with the upper limit of the 95% confidence interval for within-human mtDNA variation (3.85%) and without it (2.91%). Even in the latter case many of the values that can be estimated for mtDNA coalescence times still extend back beyond 687,000 years ago, substantially in excess of the previously stated outer limits of 50,000 to 500,000 years ago (Stoneking and Cann 1987).

The many alternative dates determinable from the data in Table 1 underestimate the actual age of a common mtDNA ancestor for several reasons: the full extent of within-human mtDNA control region diversity is yet to be determined, very few chimpanzee mtDNA control region sequences are presently available (and sequence variation among chmpanzees is substantial); the accumulation of sequence differences in the control region has been non-linear over the several million years separating humans from African apes, so that this region may not provide a reliable basis for estimating the time of a common mtDNA ancestor (Kocher, Wilson 1991); and the timing

of the chimpanzee-human divergence remains unresolved and possibly subject to substantial revision as new fossil evidence is recovered.

Discussion

An African origin for hominids is indicated by the fossil evidence

The mtDNA data (Spuhler 1988; Spuhler 1989) are consistent with an African origin for humans, which has long been accepted by paleontologists on the basis of fossil evidence (Thorne and Wolpoff 1981; Wolpoff and Thorne 1991). However, the existing mtDNA data do not require an African origin. (Avise et al. 1984; Hedges et al. 1991; Krüger and Vogel 1989; Maddison 1990; Saitou and Omoto 1987; Spuhler 1988; Templeton et al. 1992) and could be used to argue for an origin elsewhere, such as in New Guinea (Templeton et al. 1992). Although the fossil evidence has been largely overlooked or discounted in some recent treatments of this subject, it is pertinent (Thorne and Wolpoff 1992). Nearly a century ago, Darwin hypothesized an African origin for the earliest humans (Darwin 1896). Since then, fossil remains (Dart 1925; Johanson and White 1979; Wood 1992) have documented the existence of basal hominids in Africa at a time depth approximately three times greater than anywhere else in the world: from 2.6 to 3.6 million years ago compared with a million years or less in Asia or Europe.

Fossil evidence documents the spread of archaic hominids beyond Africa

A strong case can also be made from the fossil evidence for one early hominid expansion out of Africa. Members of *H. erectus* populations that were anatomically and culturally more advanced than their australopithecine predecessors appear in the African fossil record from 1.8 (MacDougall 1981) to 2.4 million years ago (Hill et al. 1992), in the Asian fossil record more than 800,000 years ago (Pope 1991), and in the European fossil record at about the same time as in Asia or slightly later (Thorne and Wolpoff 1992). One common source (Klein 1989) gives dates for Asian hominid fossils from Zhoukoudian ($\geq$0.50 mya), Chenjiawo (0.50 to 0.59 mya), Yuanamou ($\leq$0.73 mya), and Gongwangling (0.75 to 0.80 mya) in China and from Djetis and Trinil deposits ($\leq$0.80 mya) in Java; also, for less certainly dated European hominid fossils from Mauer and Petralona (*circa* 0.50 mya). To these might be added the recently-discovered hominid mandible from the Georgian Republic, provisionally dated at 0.90 mya or more (Gibbons 1992). In conventional terms all or most of the populations from which these specimens are sampled commonly are categorized as *H. erectus*, although the *erectus-sapiens* boundary is arbitrarily drawn. Formal taxonomic considerations aside, these specimens document the existence of ancient Eurasian populations coeval with the deeper coalescence times estimated from the mtDNA data. In formal taxonomic terms, they would be designated *H. erectus* rather than *H. sapiens*.

Multiregional continuity among hominid populations is not refuted by the mtDNA evidence

The fossil evidence and associated cultural artifacts can be explained in terms of a multiregional model of evolution (Weidenreich 1936), which first was referred to as a "theory of polycentic evolution"

(Weidenreich 1939). This model, developed in detail by Weidenreich (1940; 1943), now traces the ancestry of all anatomically modern humans back through a network of interrelated lineages to African ancestors that lived as much as a million years ago. Following the initial hominid expansion out of Africa, descendants of the earlier African populations spread over broad geographic areas of the Old World, where they developed into morphologically distinctive regional populations. It is hypothesized that these populations maintained sufficient genetic interchange to allow species-wide evolution into *H. sapiens* but not to eliminate all regional genetic differences. As a result, certain morphological features that now characterize anatomically modern *H. sapiens* are believed to have evolved in common over broad geographic areas, against the background provided by more ancient regional genetic heritages. Polytypic anatomical characteristics included a high frequency of prominently shoveled maxillary incisor teeth in east Asian populations and more pronounced nasal region development in European populations. Regional features such as these persisted even as widespread human populations shared temporal clines in neurocranial expansion, supraorbital bone reduction, and elaboration of a chin. The archeological record supports this pattern of multiregional continuity. Stone artifacts recovered from the earliest Asian Paleolithic sites continue to be found in late Pleistocene assemblages, while in Europe the late Saint Césaire Neanderthal skeleton was found in association with stone tool types formerly thought to be diagnostic of anatomically modern populations that replaced their *H. erectus* antecedents (Thorne and Wolpoff 1992). Juxtaposed to the well-documented record of biological and cultural continuity is the mtDNA-based interpretive framework that is said to require acceptance of a model incorporating total replacement of earlier Eurasian populations without genetic interchange (Cann et al. 1987; Vigilant et al. 1989; Vigilant et al. 1991). This model is not new; rather, it resurrects the earlier paleontological concept that modern humans arose recently in a single region, whence they spread to replace the previous hominid populations of other regions (Howell 1976). But whatever its origin, a hypothesis of recent total replacement is not warranted by the mtDNA evidence any more than by the fossil evidence. Half a century ago the fossil evidence supported Weidenreich's rejection of a single center for the origin of modern humans (Weidenreich 1936; 1939; 1940; 1943). Now it can be shown that many of the deeper estimates of mtDNA coalescence time are coincident with ages estimated independently for fossil hominid finds that are generally accepted as antedating anatomically modern humans. Beyond the limitations of the data, there are theoretical considerations that confound attempts to set specific chronological limits for hypothetical events such as populations migrating from one geographic region and replacing those elsewhere. When a phylogenetic tree is constructed from one genetic element (such as the D-loop of mDNA), the inferred tree is a gene tree (Nei 1987; Takahata and Nei 1985), not a population tree. Gene trees (including those constructed from mtDNA data) in finite populations are stochastically self-pruning, with the net effect that the frequency spectrum of times to common mtDNA ancestry is continually truncated (Avise et al. 1987). The deepest convergence time calculated

here by incorporating error terms could underestimate the chronology of events at the population level. Finally, one's confidence in the stochastic regularity of mtDNA evolutionary change is not enhanced by the changing rate estimates published thus far (Vigilant et al. 1989; Vigilant et al. 1991).

Concluding comments

Our analysis does not establish a single, deeper date for the time at which human mtDNA variants converge to a common archaic hominid ancestor, nor does it exclude shallower dates within the range of anatomically modern humans alone. What we have shown here is that, in fact, a very wide range of mtDNA coalescence times fit the existing data, many of the earlier dates also are compatible with evidence from the fossil record of hominid evolution which has been interpreted in terms of lineage continuity for over half a million years in Eurasia as well as Africa (Spuhler 1988; Thorne and Wolpoff 1991; Thorne and Wolpoff 1992; Wolpoff and Thorne 1991). The mitochondrial evidence does not require an interpretation in which human populations emerging from Africa over the last 140,000 to 280,000 years replaced previous Eurasian hominid populations. Gene trees reconstructed from human mtDNA molecules converge over a time range so deep that their roots may extend into populations of *Homo erectus*.

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there is in this paper, but all responsibility for its content, as well as the decision to publish it at all, and at this time, must be mine alone.

As in many past times in my career since the 1980s (e.g., Eckhardt, et al., 1988), Dr. David Eckhardt, a Professor in the Carnegie Mellon School of Computer Sciences, has stepped in to provide invaluable technical support. Here he took i-phone scans made by my wife, Dr. Caroline Eckhardt, of the two tables, and rendered them back into electronic form for incorporation, saving me many hours of tedious, duplicative effort. As this paper is being completed, I realize the wisdom of the observation, alleged by David to be apocryphal in Computer Science, that the first 90% of the task takes the first 90% of the time, and the last 10% of the task takes the second 90% of the time.

Last, this paper should be seen as a demonstration that what seems evident to many scholars at any given time often is not inescapable, but merely consensual. Again: "The greatest obstacle to knowledge is not ignorance; it is the illusion of knowledge." Indeed.

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