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Modern human origins: multiregional evolution of autosomes and East Asia origin of Y and mtDNA

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Abstract

Recent studies have established that genetic diversities are mostly maintained by selection, therefore rendering the present molecular model of human origins untenable. Using improved methods and public data, we have revisited human evolution and derived an age of 1.91-1.96 million years for the first split in modern human autosomes. We found evidence of modern Y and mtDNA originating in East Asia and dispersing via hybridization with archaic humans. Neanderthals and Denisovans were archaic Africans with Eurasian admixtures and ancestors of South Asia Negritos and Aboriginal Australians. Verifying our model, we found more ancestry of Southern Chinese from Hunan in Africans relative to other East Asian groups examined. These results suggest multiregional evolution of autosomes and East Asia origin of Y and mtDNA, thereby leading to a coherent account of modern human origins.

Key words: Multiregional, Out-of-Africa, Neutral theory, maximum genetic diversity (MGD) hypothesis, Neanderthals, Denisovans, Aboriginal Australians, Negritos

Running title: Origin of anatomically modern humans

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Background

There are two competing models of modern human origins termed "Multiregional" and the recent "Out-of-Africa" hypothesis (Stringer and Andrews, 1988). In the Multiregional model (Thorne and Wolpoff, 1981; Wolpoff et al., 1984; Wu, 2004), recent human evolution is seen as the product of the early and middle Pleistocene radiation of *Homo erectus* from Africa. Thereafter, local differentiation led to the establishment of regional populations which evolved to produce anatomically modern humans (AMH) in different regions of the world, made of four major differentiated groups (Africans, Europeans, East Asians, and Aboriginal Australians). *Homo* has been a single species since the genus first appeared in the fossil record ~2.3-2.8 million years (myr) ago. Support for this model is based on fossils and Paleolithic cultural remains but consistent molecular evidence has been lacking. While autosomal data have put a common ancestor of humans at ~1.5 myr ago, it is still far short of 2 myr (Blum and Jakobsson, 2011). In addition to regional continuity, the model further suggests hybridization among different groups (Wu, 2004). Major difficulties here however are the largely region-specific distribution of Y and mtDNA haplotypes, the clear separation between modern and archaic mtDNAs, the absence of archaic mtDNAs in modern humans, and the young age for the modern Y (~100,000 years) and mtDNA (~200,000 years) (Cann et al., 1987; Thomson et al., 2000; Wilder et al., 2004).

The single origin Out of Africa model assumes that there was a relatively recent common ancestral population for *Homo sapiens* which already showed most of the anatomical features shared by present day people. This population originated in Africa ~200,000 years ago, followed by an initiation of African regional differentiation, subsequent radiation from Africa, and final establishment of modern regional characteristics outside Africa (Cann et al., 1987; Stringer and Andrews, 1988). These modern Africans replaced the archaic *Homo* in Eurasia with limited genetic mixing (Fu et al., 2015; Fu et al., 2014; Green et al., 2010; Meyer et al., 2012; Vernot and Akey, 2014). Support for this model comes from the African location of the earliest fossils of modern humans (White et al., 2003) and the Neutral theory interpretation of the greater genetic diversity in Africans (Cann et al., 1987). The difficulties with this model include the discrepancy between autosomal and Y/mtDNA age, the Y haplotype A00 with age >300,000 years (Mendez et al., 2013), AMH fossils of ~100,000 years old in Hunan of China (Liu et al., 2015), and the generally weaker support from fossils and stone tools relative to the multiregional model. Most fatal to the Out of Africa model, however, is that the theoretical foundation for it, the Neutral theory, is widely known to be incomplete or has yet to solve the century old riddle of what determines genetic diversity (Leffler et al., 2012). Obviously, inferring human origins by using genetic diversity data must wait until one has a complete understanding of what genetic diversity means. The standard for such an understanding should of course be a complete and coherent account of all known puzzles related to genetic diversity.

The unusual admixed features of the Aboriginal Australians have yet to be explained by any model (Stringer and Andrews, 1988). A list of morphological features aimed at defining modern humans would exclude both modern Aboriginal Australians and Neanderthals, indicating some shared traits between the two (Wolpoff and Caspari, 2007). Also unexplained is the origin of Negritos in South Asia. Despite the obvious phenotypic similarities and close Y and mtDNA relationships, no special autosomal relationship has yet been found between Negritos and African pygmies or even among different Negrito groups in South Asia (Mondal et al., 2016).

In recent years, a more complete molecular evolutionary theory, the maximum genetic distance or diversity (MGD) hypothesis, has been making steady progress in solving both evolutionary and contemporary biomedical problems (Biswas et al., 2016; Huang, 2010, 2012, 2016; Zhu et al., 2015a; Zhu et al., 2015b; Zhu et al., 2015c; Zhu et al., 2015d). The core concept of the MGD theory, maximum genetic diversity, is a priori expected and supported by numerous facts (Huang, 2008b, 2009, 2016). In contrast, the Neutral theory and its infinite site

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model fail to take MGD into account and tacitly assumes that nearly all observed genetic distances/diversities could still increase with time with no limit defined (Kimura, 1968; King and Jukes, 1969). The MGD theory has solved the two major puzzles of genetic diversity, the genetic equidistance phenomenon and the much narrower range of genetic diversity relative to the large variation in population size (Huang, 2016; Leffler et al., 2012). The primary determinant of genetic diversity (or more precisely MGD) is in fact species physiology (Huang, 2016; Romiguier et al., 2014). The genetic equidistance result of Margoliash in 1963 is in fact the first and best evidence for MGD rather than linear distance as mis-interpreted by the molecular clock and in turn the Neutral theory (Hu et al., 2013; Huang, 2008a, 2010, 2012, 2016; Luo and Huang, 2016; Margoliash, 1963). Two contrasting patterns of the equidistance result have now been recognized, the maximum and the linear (Hu et al., 2013; Huang, 2012). The Neutral theory explains only the linear pattern, which however represents only a minority of any genome today. The link between traits/diseases and the amount of SNPs shows an optimum genetic diversity level maintained by selection, thereby providing direct experimental disproof for the neutral assumption for common SNPs (Yuan et al., 2012; Yuan et al., 2014; Zhu et al., 2015a; Zhu et al., 2015d). Others have also found experimental evidence invalidating the neutral assumption (Dunham et al., 2012).

One simple method to determine whether any sequence has reached MGD is to count the number of overlap sites (coincident substitutions) in a sequence alignment of three different species (Huang, 2010). Such sites represent positions where mutations leading to different residues had occurred independently at the same position in at least two species, which would be a low probability event under the Neutral theory or its infinite site assumption but common under the MGD theory (Huang, 2010). The Neutral theory is only valid for slow evolving genes yet to reach MGD, where its infinite sites assumption holds and the number of overlap sites follows calculation from probability theory (Huang, 2010). Unfortunately, however, nearly all existing phylogenetic results are from fast evolving sequences that were *assumed* to follow the infinite site model when they in fact do not as they have now been shown to be enriched with overlap sites (Huang, 2010).

Coincident substitutions at overlap sites do not contribute to genetic distance and make the relationship between distance and time hard if not impossible to model accurately. To overcome this, we developed the “slow clock” method that only uses slow evolving DNAs with zero or few overlap sites. The method has produced a separation time for the pongids and humans that is remarkably consistent with common sense and the original interpretation of fossil records and drastically different from the result of fast evolving DNAs (Huang, 2012). Here we used the MGD theory and its related methods to revisit the evolution of modern humans.

Results

Contrast between fast and slow evolving DNAs in genetic diversity patterns

Different human groups are well known to share ~85% of common SNPs (Lewontin, 1972). However, sharing may not necessarily mean genetic exchanges as saturation could also explain it. These two explanations could be distinguished by asking whether the fraction of shared SNPs is similarly distributed in the fast versus the slow evolving sequences. Since the majority of human genomes are made of non-coding sequences and hence faster evolving relatively to coding sequences, we randomly selected from the 1000 genomes project phase 3 (1kGP) data a set of 255K SNPs to represent the fast evolving SNPs or the average genome wide variation (Supplementary Table S1) (Auton et al., 2015). To find the slow evolving SNPs, we first identified the slow evolving proteins by aligning human and Macaca proteomes and then selected only the non-synonymous (nonsyn) SNPs located in these proteins as previously described (Yuan et al., 2012). Proteins that show the highest identity between human and monkey were considered the slowest evolving, including 423 genes > 304 amino acid in length

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with 100% identity and 178 genes > 1102 amino acid in length with 99% identity between monkey and human. We downloaded 1kGP data and obtained a list of ~15K nonsyn SNPs located in these slow evolving proteins as our slow set of SNPs (Supplementary Table S2 and S3).

To test the amount of sharing, we examined the SNP frequency files from 1kGP. For the three human groups, African (AFR), East Asian (ASN), and European (EUR), we considered a SNP as shared if it has frequency > 0 in more than one group and unique if it is present in only one group. We examined 3 different sets of SNPs, the slow set as defined above, syn SNPs in the slow genes as defined above (Supplementary Table S3), and the random set as defined above. The results showed a clear pattern of more sharing in fast evolving SNPs (Table 1), indicating saturation level of genetic diversity, which further confirmed previous findings of slightly higher genetic diversity in patients of complex diseases relative to normal matched controls (Yuan et al., 2012; Yuan et al., 2014; Zhu et al., 2015d).

We next examined the genetic diversity levels within each of the 5 major human groups as sampled by 1kGP, AFR, AMR (American), ASN, EUR, and SAS (South Asians), by calculating the average pairwise genetic distance (PGD) per group in different types of SNPs, including the slow set as defined above, the random set as defined above, and the stop codon gain/loss set (Figure 1). In our analysis here, we have excluded 4 highly admixed groups ASW, ACB, CLM, and PUR. Since certain deleterious SNPs may exist only in heterozygous (het) state rather than homozygous (hom) state, we calculated, in addition to total PGD contributed by both het and hom differences, also the hom PGD resulting from hom mismatches that should better represent neutral diversity. As shown in Figure 1, hom PGD showed different pattern from total PGD only in the slow SNPs, with the hom PGD level of AFR below the average of five groups while that of AMR being the highest. Remarkably, the stop codon set showed similar pattern as the random set, with AFR having the largest PGD. This indicates functionality rather than neutrality for the average genome wide SNPs since stop codon SNPs are definitely functional given its dramatic effect on protein structure (Prieto-Godino et al., 2016). To verify the results of stop codon SNPs, we also found similar PGD pattern in the splicing SNPs that are also expected to be functional (Supplementary Information 1 and Figure S1A-B). Overall, these results showed Europeans with the lowest diversity in stop codon and splicing SNPs and East Asians with the lowest diversity in random set. Africans have the highest genetic diversity level in all types of non-neutral SNPs examined, thereby deeming the Out of Africa model untenable.

To confirm if we have made the appropriate cut-off in selecting the slow SNPs as our phylogeny-informative set of neutral SNPs, we verified that the next set of just slightly less conserved nonsyn SNPs (total number ~13.7K, Supplementary Table S4) within 361 autosomal proteins already behaved like the random set or the stop codon set (800-1102 aa in length with identity between human and monkey >99% but <100%) (Supplementary Information 1, Figure S1 C-D). Furthermore, syn SNPs within the slow set of proteins as defined above (Supplementary Table S3) gave PGD patterns similar to the stop codon SNPs but unlike the nonsyn SNPs within the same set of proteins (Supplementary Information 1, Figure S1 E-F). Finally, we confirmed that these slow evolving proteins still have neutral nonsyn variations that are not under natural selection by showing that these proteins have fewer overlap or recurrent mutation sites than relatively faster evolving proteins (Supplementary Information 2 and Table S5), and that known positively selected genes are faster evolving (Supplementary Information 3). Together, these results suggest that only hom distance calculated from the slow nonsyn SNPs, hereafter referred as the slow SNPs, can be informative to phylogenetic inferences.

Divergence time between major human groups

Using hom distance measured by slow SNPs, we found, as expected, Africans as the outgroup to the other 4 groups as sampled in 1kGP because the non-African groups are closer to each other than to Africans (Supplementary Figure S2A). Also as expected from common

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sense but not from the existing model, Africans are closer to each other than to non-Africans. However, for the random set of SNPs, total distance within Africans was similar to that between Africans and non-Africans, which is well known from previous studies and reflects saturation as we now realize from the MGD theory (Supplementary Figure S2B). This result also established the maximum genetic equidistance phenomenon, previously known only at the inter-species level, at the intra-species level where groups with lower MGD are equidistant to the group with the highest MGD with the distance being equal to the MGD of the highest MGD group. The result independently confirms the difference between slow and fast SNPs and the fact that fast SNPs are at saturation level of genetic diversity.

To estimate the time of separation between major human groups, we determined the mutation rate of the slow evolving genes. We found 34 informative genes in the 178 slow evolving genes as defined above that showed gap-less alignment in any pair of comparisons among humans, chimpanzees, orangutans, and monkeys (Supplementary Table S6). Assuming gorilla and orangutan contributed similarly to their genetic distance since their split 12 myr as inferred from the fossil records (Suwa et al., 2007), we obtained a gorilla or orangutan mutation rate of 0.000173 aa per myr per aa for the 34 genes (47628 aa). Given a distance of 0.00385 aa per aa between human and orangutan and their separation time of 17.6 myr (Huang, 2012), we used the formula $0.00385 = R_{human} \times 17.6 + 0.000173 \times 17.6$ to obtain the human mutation rate as 4.46E-5 aa per myr per aa, which is 3.88 times slower than orangutan's. Given this mutation rate and the distance matrix (total distance including both het and hom distances) as shown in Table 2 (only the largest distance among groups are shown), we estimated the split time between ESN (Esen in Nigeria) and GBR (British in England and Scotland) as 1.96 myr, consistent with the known first migration out of Africa for the Homo species as shown by the fossil records. The split between ESN and CHS (Southern Han Chinese) was similar or slightly shorter at 1.91 myr and not significantly different from that between ESN and GBR. In fact, using hom distance as measured by the slow SNPs which represent neutral distance better, ESN is slightly closer to CHS (14.87) than to GBR (14.93).

Y chromosome phylogeny

The existing Y phylogenetic tree depends on inferring derived alleles and in turn requires the validity of the infinite site assumption, which means no maximum genetic distance and no recurrent mutations. However, this assumption can be proven invalid even just by the existing Y tree itself, since the tree shows numerous recurrent mutations that were simply ignored without valid reasons (Supplementary Table S7), especially for the early branches with some such as KxLT and HIJK contradicted by as much as 50% of all relevant SNPs (Poznik et al., 2013). That the existing tree may be unrealistic is also shown by the fact that while haplotypes with few sequence variations from the ancestor of F, C, D, E, NO, KxLT, or K are routinely found in present day people, none could be found for the putative ancestors of likely African origins, including BT, CT, or CF. Also, the branching pattern in Africans often involves one branch, such as A00, with few or no sub-branches while the other branch A0-T accounting for all of the remaining haplotypes on Earth, which is odd and against branching patterns known in experimental biology such as embryonic differentiation into three layers with each layer giving rise to multiple cell types.

Given functionality for genome wide autosomal SNPs as discussed above, it is easily inferred that most SNPs in Y chr are also non-neutral. We therefore redrew the Y tree based on shared alleles, which may mean common physiology more than common adaptations if physiology is the chief determinant of MGD. Using 58251 cleanly called SNPs (no individual with uncalled SNPs, Supplementary Table S9) and previously defined haplotypes for 1kGP samples (Poznik et al., 2016), we found a major megahaplogroup ABCDE (Figure 2). Megahaplotype F, defined as lacking any mutations that define other haplotypes, is the ancestor. All F-like or F* haplotypes sequenced so far are partial ABCDE carrying 4 (Lahu_HGDP01320),

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13 (Malay_SSM072) or 14 (KHV_HG02040) of the 151 mutations that group ABCDE (Figure 2) (Karmin et al., 2015; Mallick et al., 2016; Poznik et al., 2016). The F* haplotype is most common in East Asia, present in 5 of 7 (71.4%) Lahu males in Yunnan of South West China (Black et al., 2006), 10-15% of Han and other minority Chinese, and low percentages (<10%) in South Asians and French. Furthermore, the top 4 individuals among 1kGP closest to the ~45,000 year old Western Siberian Ust'-Ishim who carried NO haplotype and was expected to be most like the AMH ancestor were all East Asians with Asian haplotypes F and O (F2 in KHV_HG02040, O2 in CHB_NA18534, O3 in CHS_HG00559, O3 in KHV_HG02088), indicating least deviation from the ancestor for Asian haplotypes (Fu et al., 2014). These three O type East Asian individuals also were the closest to the three F* carrying individuals above. These results suggest the origin of F in East Asia with subsequent migration to other regions of the world (Supplementary Figure S3).

mtDNA phylogeny

The existing mtDNA phylogenetic tree has exactly the same problems as the existing Y tree as discussed above. Based on previously defined mtDNA haplotypes for 1kGP (Supplementary Table S8)(Poznik et al., 2016), we redrew the mtDNA tree using slow evolving SNPs, which alter amino acids or RNA sequences (Figure 3A, Supplementary Table S10). Fast SNPs are more involved in adaptation to fast changing environments and should not be used whenever possible. Two lines of evidence suggest haplogroup R as the ancestor of all modern haplogroups. First, ancient humans are expected to be closer to the ancestor and the oldest AMH, Ust'-Ishim, carried the R* haplotype (Fu et al., 2014). Second, R0 is the least differentiated haplotype and closest to the ancient haplotype in Ust'-Ishim (Figure 3B). That R0 is most common in Chinese among 1kGP indicates origin of R in East Asia (Figure 3B) and subsequent diversification in other regions of the world (Supplementary Figure S4). To confirm M giving rise to L, we examined mtDNA distance between African (YRI) L and South Asian (BEB) M and found L3e to be the closest to M (Figure 3C). Also, M of BEB or GIH is closer to L3e than M of CHS, indicating a more direct role for BEB or GIH in dispersing AMH mtDNA into Africa and a Southern route into Africa. Consistently, in autosome distance, BEB or GIH with M haplotype were closer to Africans than those with N (including R) haplotype (Figure 3D), despite the fact that people with M had larger autosomal nucleotide diversity than those with N (PGD: M_BEB = 8.59, N_BEB = 7.9, M_GIH = 8.42, N_GIH = 8.36).

Neanderthals and Denisovans

If major human groups have separated ~2 myr ago, Neanderthals and Denisovans with features more modern than *H. erectus* should be expected to belong to one of the modern groups today. However, previous studies have found Neanderthals to be outgroup to AMH and used D-statistics to show Neanderthal gene flow into non-Africans but oddly not Africans (Green et al., 2010; Meyer et al., 2012). The assumption of D-statistics is that all modern groups are equidistant to chimpanzees so that presence of derived alleles (different from chimpanzees) was due to gene flow from Neanderthal. If in fact Africans are closer to chimpanzees or carrying more ancestral alleles in general, the conclusion of gene flow into non-Africans would become invalid. We examined this by measuring genetic distance between 1000 genomes and 10 previously sequenced chimpanzee genomes (de Manuel et al., 2016). Using the random 255K SNPs set, we found closer hom distance between Africans and chimpanzees than between non-Africans and chimpanzees (Supplementary Figure S5). As presence of Neanderthal derived alleles in a non-African are mostly in het state (Fu et al., 2014), which could be observed to be biased toward non-Africans only if Africans are in hom ancestral state, the fact of more hom ancestral alleles in Africans (or closer hom distance between Africans and chimpanzees) therefore deems invalid the previous finding of Neanderthal gene flow into non-Africans. Furthermore, as already noted above for Y and mtDNA trees, the finding of saturated level of

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genetic diversity makes the infinite site assumption invalid, which in turn makes the assignment of ancestral and derived alleles unrealistic. Thus, the relationship between Neanderthals/Denisovans and present day populations remains to be determined.

Making use of the published Neanderthal genomes (Green et al., 2010; Meyer et al., 2012; Prufer et al., 2014), we calculated the genetic distance in slow SNPs between 1000 genomes and Neanderthals (Altai, Vindija 33.16, 33.25, 33.26, and Mezmaiskaya) or Denisovan (Figure 4A). These ancient genomes showed closer distance to Africans except Vi33.25 to ASN and Vi33.26 to AMR. Denisovan was closer to Africans than Neanderthals were (Figure 4A). The high coverage genomes of Altai and Denisovan allowed their African affinity, especially Denisovan, apparent on a principle component analysis (PCA) plot (Figure 4B-C). In contrast to the 5 Neanderthals studied here who were mostly found in Europe and yet who were no closer to Europeans or the related Indians than other groups, their contemporary AMH Ust'-Ishim from Western Siberia was closest to SAS followed by EUR (Figure 4). These results suggest that Neanderthals and Denisovans were Africans who migrated into Eurasia and admixed with local non-Africans. The observations of an East Asian like Neanderthal (Vi33.25) in Europe at >45,000 years ago and of a South Asian like Western Siberian (Ust'-Ishim) from ~45,000 years ago indicates migration of Asians into Europe around the time of AMH origin in South East Asia.

Origins of Negritos and Aboriginal Australians

The Andamanese and the African pygmies seem obviously related in multiple aspects, including traits, Y relationship with the African megahaplogroup ABDE, and mtDNA haplotype M being closely related to African L. However, previous studies have found Andamanese to be even more genetically distant to Africans than other Eurasians (Mondal et al., 2016). Using the published genomes of 10 individuals from the Jarawa (JAR) and Onge (ONG) populations in the Andaman Islands (Mondal et al., 2016), we found that Andamanese are relatively closer to Africans or have lower AFR/SAS(-BEB) distance ratio than other nearby populations such as BEB, with ONG more so than JAR, consistent with the known less admixture in ONG relative to JAR (Figure 5A). PC analysis also showed Andamanese closer to Africans than all five populations of SAS (Figure 5B). Relative to the distance to SAS, ONG showed smaller distance to Mbuti than to San or other Africans examined except LWK (Figure 5C). The Mbuti group here consists of 4 published genomes from the Simons project (Mallick et al., 2016) and the San group consists of 2 published genomes (Schuster et al., 2010). Given that Andamanese were closer to Africans than other Indians were (Figure 5A) but Mbuti pygmies were not closer to Andamanese than some other Africans were, it can be inferred that Andamanese came from Mbuti rather than the opposite.

The African affinity of Neanderthals prompted us to examine the distance between Neanderthals (with relatively higher coverage genomes, Vi33.16 and Altai) and several different Indian populations (ONG, JAR, BEB, and GIH) to see if ONG might have come from Neanderthals or related humans. Relative to the distance to the ~4500 year old African Mota (Gallego Llorente et al., 2015), ONG was closer to Neanderthals Vi33.16 and Altai, as well as to Ust'-Ishim who was known to have large amount of Neanderthal admixture, than other Indians were (Figure 5D). Also, if Andamanese came from Neanderthals, Neanderthals should be closer to Mbuti than to San and other Africans, since Andamanese are closer to Mbuti than to San (Figure 5C). This was indeed the case for the Altai individual who is the only Neanderthal with high coverage genome for this analysis to be informative (Figure 5E).

Since different Negrito groups in South Asia share similar traits, one expects them to be genetically related. The new Y tree grouping C with ABDE further suggests a common ancestry for different Negrito groups since the C haplotype is common in certain Negrito groups in Philippines while D is common in some others such as Onge. We therefore made use of a previously published SNPs genotyping data for a number of Oceanian groups including the Negrito group Mamanwa and its neighboring group Manobo in Philippines (Pugach et al., 2013).

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We measured the ONG/JAR distance ratio to look for the group that is closest to ONG relative to its neighbor JAR and the Mamanwa/Manobo distance ratio to look for the group closest to Mamanwa relative to its neighbor Manobo. Of the 13 groups examined, Mamanwa showed the smallest ONG/JAR distance ratio besides ONG; conversely, ONG showed the smallest Mamanwa/Manobo distance ratio besides Mamanwa (Supplementary Figure S6). These results suggest that the two Negrito groups are more closely related to each other than either is to other groups as examined here.

We also examined the Aboriginal Australian (AUA) samples in the Pugach et al (2013) dataset and a previously published ~100 year old AUA (AUA_100yr) who was unlikely to have admixed with European colonizers (Rasmussen et al., 2011). These AUA samples showed lower Mamanwa/Manobo ratio than other Oceanians (Supplementary Figure S7). The AUA samples from Pugach et al (2013) also showed lower AFR/ASN ratio than other Oceanians, representing 68% of the average ratio for the Oceanians (excluding AUA and NGH or New Guinea Highlanders). To examine if the African component of AUA had come from Neanderthals, we calculated the Altai/ASN distance ratio of AUA and found it to be 64% of the average ratio for the Oceanians in Pugach et al (2013) dataset, which was significantly lower than the 68% found for AFR/ASN ratio, indicating closer relationship of AUA to Altai than to AFR. These results showed similarity between AUA and Negritos, indicating similar ancestry in Neanderthals and Denisovans.

Testing the out of East Asia model

We next tested certain obvious predictions of the out of East Asia model. First, the model predicts lower diversity in people directly associated with the original AMH and higher diversity in people resulting from admixture of AMH with archaic humans. We calculated the hom PGD in slow SNPs as well as het numbers for each of the 25 groups totaling 2534 individuals in 1kGP. The lowest hom PGD level was found in LWK followed by slightly higher level in CHS (Supplementary Figure S8A). However, LWK has significantly higher numbers of het than CHS (Supplementary Figure S8B). As high level heterozygosity indicates high genetic diversity and would reduce hom distance, it is likely that CHS has lower genetic diversity than LWK. We further found that within CHS (made of 72 individuals from Hunan and 36 from Fujian), Hunan samples have lower hom PGD and het numbers than Fujian samples (Supplementary Figure S8CD). These results indicate that CHS, in particular Hunan people, have lowest genetic diversity levels among the 25 groups in 1kGP. Given that known admixed groups such as MXL and PUR showed the highest genetic diversity or PGD (Supplementary Figure S8A), it may be inferred that CHS or Hunan people may have the least amount of admixture and hence represent the original AMH group, at least among the 25 groups sampled here. That Africans, as human ancestor from ~2 myr ago according to the multiregional model, did not show the highest genetic diversity level may seem unexpected but is in fact consistent with a key role for admixtures as claimed by the multiregional model as well as our out of East Asia model here.

Second, we would expect Southern East Asian groups to be closer to Africans. Although CHS represent samples collected from Southern China (Hunan and Fujian), while CHB samples were from Northern China (Beijing), both in fact contain Southern and Northern Chinese. We therefore made use of the Hunan versus Fujian samples in CHS, where Fujian people are known to be mostly migrants from Central North China during the West Jin, Tang, and Song dynasties. We calculated the distance of each group to Hunan or Fujian and obtained the Hunan/Fujian distance ratio of each group. Consistently, groups known to have more Northern Chinese admixtures, such as CHB, MXL, PEL, JPT, had higher Hunan/Fujian distance ratio than Southern groups such as CDX, and KHV (Figure 6A). Of note, FIN is closest to Hunan people among EUR groups, suggesting that North Western migrations of Southern Chinese during the first wave of AMH dispersal from Hunan area may have contributed to the ancestry of

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FIN. Consistently, Western hunter-gatherers from the Paleolithic age also showed closer distance to Hunan (manuscript in preparation). All AFR groups showed lower Hunan/Fujian distance ratio than non-Africans with LWK in East Africa the lowest, consistent with migration of Southern Chinese into Africa and into the Horn of Africa first. That non-Africans had more Fujian admixtures is consistent with known migrations of Northern East Asians into both the West and the America in more recent times during the Neolithic and Bronze ages. We further found Hunan people to be relatively closer to Africans than other South East Asians such as Chinese Dai in Xishuangbanna (CDX) and Kinh in Ho Chi Minh City of Vietnam (KHV) (Figure 6B), indicating origin of AMH more likely in Hunan relative to other nearby regions.

Third, as migration of AMH from Hunan via the Southern route to East Africa must cross the Indian subcontinent, one would expect closer relationship with Africans for groups within South Asia that are more related to Chinese relative to those more related to Europeans or more Southern relative to more Northern. Indeed, relative to Fujian people, the distance of different Indian groups to Africans follows exactly their direct distance to Hunan people, as well as their direct distance to LWK, in the order of increasing distance, BEB, GIH, ITU, STU, and PJL (Figure 6BC). Also, Gujarati Indians (GIH) in Western India is closer to Africans than Punjabi people from Northern Pakistan (PJL) (Figure 6B). Consistently, relative to PJL, both BEB and GIH are closer to Africans with BEB closer than GIH (Figure 6B). The observation of lower BEB/Fujian distance ratio than Hunan/Fujian is consistent with Indians being in general closer to Africans than East Asians (Figure 6D) and being more recent ancestors to Africans than East Asians based on the migration route of the out of East Asia model.

Fourth, we hypothesized that the branching process of Y may involve AMH hybridization with archaic humans and subsequent adaptive co-evolution of Y and admixed autosomes. As the first major split resulted in ABCDE, G, and HIJK haplogroups, we tested whether the ABCDE megahaplogroup, whose sub-branches are mostly found in Africans and South Asians or Oceanians with African like features, may have resulted from admixture of F AMH with admixed archaic Africans such as Neanderthals who may have migrated to South East Asia. Using the Y chr sequence of a ~49,000-year-old Neanderthal from El Sidron Spain (Mendez et al., 2016), we found indeed closer genetic distance to this Neanderthal for haplotype A0, A1a, B, E, D and C, in the order of low to high distance which happens to correlate with degree of African ancestry, relative to G and HIJK (Supplementary Figure S9). These results indicate that admixture of F AMH with Neanderthals may have resulted in African-like descendants with ABCDE megahaplotype who largely preferred to live in the Southern hemisphere. Consistently, East Asians (JPT) with D or C haplotype showed closer autosomal distance to Andamanese (also with D haplotype) or African MSL (with E haplotype) than those with O haplotype did (Supplementary Figure S10).

Fifth, to similarly test whether mtDNA diversification from the original ancestor type to more African type may involve AMH hybridization with archaic humans, we examined the distance between archaic and modern mtDNAs in slow SNPs (Supplementary Table S10). Although archaic mtDNAs were nearly equidistant to the modern group consisting of Europeans (CEU), East Asians (CHS), and Africans (LWK), they were closer to Africans in SNPs found in archaic humans (sites that differ between archaic mtDNA and the rCRS), indicating more sharing of archaic alleles in Africans (Supplementary Figure S11). This is likely due to independent adaptive mutations since archaic mtDNAs are outgroups to modern mtDNAs as previous studies have shown. We also confirmed it by showing that the average distance between archaic and modern mtDNAs were larger than that within modern mtDNAs (Supplementary Figure S12A). The archaic mtDNAs are at least of two types, with Neanderthal Vi33.16 and Altai belonging to one type or close to each other than to other archaic mtDNAs while Denisovan and Heidelbergensis belonging to another type (Supplementary Figure S12B). Such results support the notion of multiple turnover events in mtDNA types in the past ~2 myr of modern human evolution.

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Finally, we used the common software, ADMIXTURE, to study ancestry relationships. However, in tests to see how well the software may perform, we did not obtain consistent results on the affinity of Mbuti or Ust'-Ishim to specific groups in the 1kGP (Supplementary Information 5 and Supplementary Figure S13 and S14). Therefore, this software may need further work before it can be routinely used.

Discussion

We have arrived at a new model of modern human origins based on a more complete understanding of genetic diversity (Figure 7b). While the autosomes in our model are largely consistent with the multiregional hypothesis, the mtDNA and Y have a single origin in East Asia. We also identified Negritos and Aboriginal Australians as direct descendants of Neanderthals/Denisovans who were African migrants with Eurasian admixtures.

Molecular and other types of evidence for the new model

The nonsyn SNPs in slow genes as defined here are neutral. They are not deleterious and unlike the stop codon and splicing SNPs. They are also not under positive selection as positively selected genes tend to be fast evolving. To the dramatic difference between slow and fast evolving DNAs as shown here, we cannot come up with a meaningful explanation using any known schemes other than the MGD theory (Huang, 2016). In highly conserved proteins, most mutations may hit functional sites and be negatively selected, and it would take many mutations and hence a long time before a neutral site is hit, thus giving the appearance of a slow mutation rate.

We have shown that there are only three major human groups, Africans, East Asians, and Europeans/Indians. Indians appear to give rise to Europeans as the oldest AMH Ust'-Ishim was Indian. Also, the Y haplotype H of Indians diverged before diversification of European haplotypes, which is consistent with our model as well as the non-inhabitability of Europe during the Last Glacial Period. Aboriginal Australians and the related Negritos, traditionally viewed as the fourth major group, in fact consist largely European/Indian and African genomes and their unique traits might have come from admixture of incoming Neanderthals with local archaic humans. Our calculation showed that the first major split of humans occurred 1.91-1.96 myr ago, well consistent with fossil evidence for the presence of *Homo* in Eurasia and the multiregional model. The coexistence at ~1.76 myr ago in Africa of both Olduwan and Acheulean technologies suggests the coexistence of multiple groups of humans distinguished by separate stone-tool-making behaviors (Asfaw et al., 2002; Lepre et al., 2011). The sudden appearance of Acheulean technologies and pro-Neanderthals at ~0.5 myr ago in Europe (Sima de los Huesos site of Atapuerca) can now be explained by a more recent out of Africa migration by the ancestors of Mbuti people (Bischoff et al., 2007; Lycett, 2009).

Mitochondrial DNA (mtDNA) and the non-recombination region of Y chr (NRY) lack recombination and provide records of history that are independent of autosomes. Most SNPs in these DNAs can be proven to be under selection, e.g. certain SNPs or haplotypes of mtDNA or Y chr are known to be related to human diseases or compatibility with nuclear genomes (Charchar et al., 2012; Picard et al., 2016; Shoffner et al., 1993; Sloan et al., 2016; van der Walt et al., 2003; Zhu et al., 2015b). Sharing of alleles of mtDNA or Y chr should mean similar selection, reflecting both environments and physiology or primarily physiology when saturation has been reached. Sharing of physiology should be informative for a phonetic approach of phylogeny. Coevolution of mtDNA, Y, and autosomes has been found by many previous studies (Gemmell and Sin, 2002; Osada and Akashi, 2012; Rand et al., 2004; Sloan et al., 2016; Zhu et al., 2015b), which may play a key role in the diversification into multiple haplotypes during AMH radiation from its place of origin to other regions by hybridization with archaic humans. People who have stayed relatively unchanged in physiology and living environments from the ancestor

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would be expected to have few deviations from the ancestor haplotype and their present day living place would indicate place of origin for the ancestor. It is through such reasoning that we have come to place the origin of modern Y and mtDNA in East Asia or South China. Our results showed that groups with the same Y or mtDNA haplotypes are also closer in autosomes and traits. Such a priori sensible results provide strong independent validation for our new phylogenetic method.

Given that most SNPs in Y and mtDNA are not neutral, one cannot use the molecular clock approach to determine the age of the haplotypes except for recent diversifications. We can only estimate the age of modern Y or mtDNA at ~50,000 years based on the first fossil appearance of AMH and the disappearance of Neanderthals. That the Y haplotype NO of the ~45,000 year old Ust'-Ishim differs from the putative ancestor F by only ~27 SNPs whereas a present day haplotype could differ from the F ancestor by as much as ~740 SNPs (Figure 2) indicates that the ancestor F should not be much older than ~45,000 years. This relatively young age is remarkably consistent with the time point for the replacement of Neanderthals by AMH but appears to contradict the oldest AMH fossils in Africa or in Hunan China (Liu et al., 2015). However, nearly all AMH fossils older than 40,000 years still have certain archaic features and independent evolution of modern features has been noted to occur periodically over the past 950,000 years since the time of *H. antecessor*(Bermudez de Castro et al., 1997; Wu, 2004).

The novel concept here of modern replacing archaic versions of Y and mtDNA but not autosomes is key to our model of out of East Asia. The lack of recombination in Y and mtDNA makes this idea biologically inevitable. The fact that Heidelbergensis, Denisovans, Neanderthals, and AMH all have distinct mtDNAs suggests that such replacements may have taken place multiple times in the past. Modern examples consistent with the replacement idea are the dominant presence of Asian Z mtDNA in the Saami people of Northern Europe and the wide presence of Asian Y haplotype N in Finnish, who are otherwise largely indistinguishable from Europeans in both autosomes and traits. Also consistent is the finding of three super-grandfather Y haplotypes in China that are relatively young in age (~5000-8000 years) but account for ~40% of Han Chinese males today (Yan et al., 2014). Admixture of incoming Asian AMH with archaic humans in Europe or Africa would lead to haplotype diversification in Y and mtDNA while still maintaining regional specificity in autosomes and hence traits as traits are mostly determined by autosomes.

The ~45,000-year-old AMH Ust'-Ishim from Siberia was previously found to have left no descendants among present populations and to be more related to East Asians than to Europeans/Indians (Fu et al., 2014). However, our results showed this individual as Indians. This discrepancy is to be expected. It has been routinely found as surprising in previous studies on ancient DNAs that there is no genetic continuity between ancient and present day people. Such unexpected anomalies can now be understood as artifacts of using non-informative SNPs.

Our finding of Neanderthals and Denisovans as primarily Africans with Eurasian admixture is well supported by fossil data indicating *H. heidelbergensis*, present in both Africa and Europe, as ancestors of Neanderthals. The taurodont teeth are common in Neanderthals, Heidelbergensis and certain South African fossils (Shaw, 1928). The occipital bunning of Neanderthals are also common in modern Africans (Liu et al., 2003).Neanderthals are known to share multiple traits with Europeans such as the prominent shape and size of the nose (Thorne and Wolpoff, 1992; Wolpoff and Caspari, 2007), which supports our finding that Europeans are often genetically the closest to Neanderthals (2/3 examined here) after Africans. Our result that Denisovan is nearly equally related to East Asians and Europeans (slightly more related to East Asians) is consistent with where Denisovan was found. Seemingly unexpectedly, certain Neanderthals found in Europe is most closely related to Asians (Vi33.25) or Americans (Vi33.26), and one of the three Neanderthals closest to Africans was closer to East Asians than

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to Europeans. However, this would be expected if Africans associated with the Neanderthal exit had also entered Asia via the Southern route. The general lack of Neanderthal fossils in this Southern route may reflect the relatively small effort so far invested in this region (with only few *Homo* fossil finds like Narmada from ~200,000 years ago). Indeed several fossils in China show Neanderthal features such as the teeth and an inner-ear formation in the 100,000 year old *Xujiayao* (Wu, 1988, 2004; Wu et al., 2014). Certain mysterious Southern China fossils such as the 11,500-15,500 year old 'Red Deer Cave' people with hybrid features of modern and archaic humans may also be candidates for Asian relatives of Neanderthals, especially considering their taurodont teeth (Curnoe et al., 2012). Early modern human fossils with typical Mongoloid features in South West China (Liujiang, Ziyang, Lijiang, and Chuandong) also have weak occipital buns commonly found in Neanderthals (Wu, 1988, 2004; Wu and Poirier, 1995). Mousterian stone tools commonly associated with Neanderthals also existed in Shuidonggou and Chenggong in South West China (Wu, 2004, 2006). Thus, although Neanderthals were mostly found in Europe and Middle East, they likely also made their way to North East Asia (Denisovan and Teshik-Tash) and South East Asia (Gunz and Bulygina, 2012).

Fossils or traits indicating AMH migration from East Asia into Africa or Europe have been noted before. First, native Africans such as Khoisans are well known to have certain East Asian features such as shoveling teeth, epicanthic fold, and lighter skins. Mbuti pygmies look very much like the Andamanese. The much lower frequency of shoveling teeth in African fossils and Khoisan relative to ancient and modern Chinese suggests that this type of teeth could only originate in China with its African presence due to migration. The type of shoveling teeth found in Neanderthals and Pleistocene *Homo* from Atapuerca-Sima de los Huesos may either be a different type from that of Asians and Africans or come from early disposal of *Homo* from Asia to Europe (Martinon-Torres et al., 2007; Wolpoff, 1996). Second, a combination of three features has been noted to be region-specific to China fossils with lower frequency also found in North Africa: a non-depressed nasal root, non-projecting perpendicularly oriented nasal bones and facial flatness (Brauer and Stringer, 1997). Third, Dali man of China (~250,000 years ago) had lower upper facial index and flat nasomolar angle, but these two modern features only first appeared in Europe in Cro Magnons (Xinzhi Wu, personal communication).

Insights on human traits

That humans have been a single species for more than ~2 myr is consistent with the unique feature of being human, i.e., creativity, which could be defined as constant creation of novelty. Intentionally made and constantly improved knife type stone tools, first appeared 2.3-2.8 myr ago, may be beyond the capabilities of non-humans and mark the first appearance of creativity in life on Earth.

The appearance of modern humans should be accompanied by new technologies just as the knife type stone tools were associated with the first appearance of the genus *Homo*. A technology just one step more advanced than stone tools is pottery making. Consistent with our model, the earliest pottery making intended for practical usage was found in Hunan and the neighboring Jiangxi in South China at 18,000-20,000 years ago (Boaretto et al., 2009; Wu et al., 2012). While future investigations could extend the time even earlier, one should not expect a new technology to appear simultaneously with the first appearance of AMH since it would take time for the first modern humans to grow into a large enough population to be able to invent new cultures. It is also remarkable to note that the next new invention after pottery, rice or agriculture, also likely came from Hunan (Zhang and Yuan, 1998). Hunan is also the site of earliest AMH fossils in Asia (Liu et al., 2015). Placing AMH origin in China is also in line with the observation that the best argument for regional continuity has been built using data from China (Wu, 2004). The observation here that different modern Chinese people could have independent genetic lineages separated by hundreds of thousands of years is consistent with the morphological observation that *H. erectus* and *H. sapiens* in Northern China are not identical to those in

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Southern China (Wu and Wu, 1999). Among all East Asians examined here, the genomes of Hunan people were found most enriched in Africans. Therefore, our model of modern human origins in East Asia, in particular Hunan Province in China, provides a satisfying account of all relevant data including the human specific trait of creativity and the related inventions.

The study here shows different genetic diversity levels in different human groups depending on different types of SNPs. Europeans show the lowest genetic diversity level in stop codon and splicing SNPs while Africans the highest, which has also been found in a recent study (Lek et al., 2016). However, East Asians show the lowest genetic diversity in genome average and hence in non-coding sequences. Thus, different populations encounter different selective pressures, the precise nature of which would require future research. Already, however, some tentative hints emerge on the genetic basis of certain complex traits that are commonly thought to be culturally shaped. The difference in selective pressure on non-coding or regulatory regions versus proteins or parts is reminiscent of the thinking style difference between the East and West in philosophy and medicine, i.e., the holistic versus the analytical (Nisbett et al., 2001).

Summary

The MGD theory provides a more complete understanding of the long standing puzzle of what determines genetic diversity, which makes inferring human origins from genetic diversity patterns realistically possible. By better identification of phylogenetically informative genes and constraining Neutral theory application to these genes, we provide strong molecular evidence for multiregional evolution of autosomes and for East Asia origin of modern Y and mtDNA. Further work utilizing the MGD theory is ongoing and may yield more surprising and yet satisfying results in human evolution.

Acknowledgements

We thank Shuhua Xu, Xitong Lu, Denghui Luo, Jie Liang and Xiaohua Tan for technical assistance. We thank Xinzhi Wu for sharing unpublished work. We are grateful to Mark Stoneking, Irina Pugach, David Reich, Joseph Pickrell, Arti Tandon, Sarah Tishkoff, Joseph Lachance, Philip Johnson, and Brenna Henn for sharing DNA datasets. Although not all analyses of these datasets were presented here, they have been helpful to make this work possible. We thank Xinzhi Wu and Joseph Daniels for critical reading of the manuscript. We thank Feng Gao, Xing Gao, Yamei Hou, Wu Liu, Erik Trinkaus, Lingxia Zhao, and Changqing Zeng for valuable discussions. Supported by the National Natural Science Foundation of China grant 81171880, the National Basic Research Program of China grant 2011CB51001, and the Furong Scholars program (S. H.).

Materials and Methods

Sequence download

We downloaded ancient and modern human genome sequences using publically available accession numbers. South Asian and Oceanian SNPs data from Pugach et al (2013) were obtained from the authors (Pugach et al., 2013). The Hunan and Fujian identity information of CHS sample of 1kGP were obtained from the Coriell Institute website.

Selection of SNPs

Random selection of 255K SNPs as fast evolving SNPs. We selected 255K SNPs from 1kGP data to represent the average variation of the genome (Supplementary Table S1). We first generated a random number for each SNP on a given chromosome followed by sorting the SNPs based on the random numbers, and then selected the top ranked set of SNPs with the

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number of SNPs in the set proportional to the size of the chromosome. SNPs from the slow set were removed. No consideration for SNP frequency was applied.

Slow evolving SNPs. The identification of slow evolving proteins and their associated SNPs were as previously described (Yuan et al., 2012). Briefly, to obtain non-synonymous SNPs located in the slowest evolving genes, we collected the whole genome protein data of Homo sapiens (version 36.3) and Macaca mulatta (version 1) from the NCBI ftp site and then compared the human protein to the monkey protein using local BLASTP program at a cut-off of 1E-10. We only retained one human protein with multiple isoforms and chose the monkey protein with the most significant E-value as the orthologous counterpart of each human protein. The aligned proteins were ranked by percentage identities. Proteins that show the highest identity between human and monkey were considered the slowest evolving (including 423 genes > 304 amino acid in length with 100% identity and 178 genes > 1102 amino acid in length with 99% identity between monkey and human). We downloaded the 1000 genomes phase 3 data and assigned SNP categories using ANNOVAR. We then picked out the nonsyn SNPs located in the slow evolving set of genes (Supplementary Table S2).

Calling SNPs from genome sequences

We used publically available software SAMTOOLS, GATK, and VCFTOOLS to call SNPs from either downloaded BAM files or BAM files we generated based on downloaded fastq data (Danecek et al., 2011; Li et al., 2009; McKenna et al., 2010).

Analysis of shared and unique SNPs

Shared and unique SNPs were identified by using downloaded allele frequency information from 1kGP.

Imputation

Because commonly used SNPs chips for genome wide genotyping have only a fraction of the slow SNPs defined here, we performed imputation to obtain more coverage of the slow SNPs on the South Asian and Oceanian datasets of Pugach et al (2013). We used the SHAPEIT2 software to do phasing for the SNP chip data (Delaneau et al., 2013) and the IMPUTE2 software to impute based on 1kGP data (Howie et al., 2009).

Genetic distance calculation

We used the custom software, dist**,** to calculate pairwise genetic distance (PGD) or number of SNP mismatches from SNP data (Yuan et al., 2012). This software is freely available at https://github.com/health1987/dist and has been described in detail in previous publications (Zhu et al., 2016; Zhu et al., 2015c). We obtained PGD for each of the 25 human groups in the 1kGP data and obtained average PGD per group for groups within each of the 5 major continents as represented by the 1kGP. We excluded highly admixed groups ASW, ACB, CLM, and PUR in calculating the continental average.

PC analysis

We utilized GCTA to analyze data in the PLINK binary PED format to generate two files (*.eigenvec and *.eigenva). We drew PCA plot using *.eigenvec file (Purcell et al., 2007; Yang et al., 2011). One sample BEB_HG04131 was found on PC2-PC3 plot to be an outlier and was hence excluded from the PC analysis and most distance calculations presented here.

Other methods

Other common statistical methods used were Student's t test, chi square test, and Fisher's exact test, 2 tailed.

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Tables:

Table 1. Sharing of different types of SNPs among three different groups in 1kGP, AFR, ASN, and EUR. Shared SNPs are present in more than one group and unique SNPs are present in only one group. Shown are fractions of each type of SNPs. SNPs that are not found in any of the three groups are grouped as no variations (No var.).

	Shared	**Unique**	**No var.**	**#SNPs**
Nonsyn slow	0.05	0.66	0.29	15422
Syn slow	0.11	0.64	0.24	16591
Random set	0.24	0.52	0.24	254489

Table 2. Time of divergence between human populations. The separation time and average pairwise genetic distance (total distance including both het and hom distances) between human populations (ESN, GBR, CHS) in 9578 slow evolving autosome SNPs located in the 178 genes (>99% and <100% identity between human and Macca) with total length 291083 aa. The human mutation rate was estimated as 4.46E-5 aa/myr/aa x 291083 aa = 13.0 aa/myr.

	Myr (total distance, #aa mismatches)		
Groups	ESN	GBR	CHS
ESN	1.82 (47.21)	1.96 (51.03)	1.91 (49.62)
GBR		1.56 (40.65)	1.65 (42.8)
CHS			1.43 (37.19)

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Figure legends:

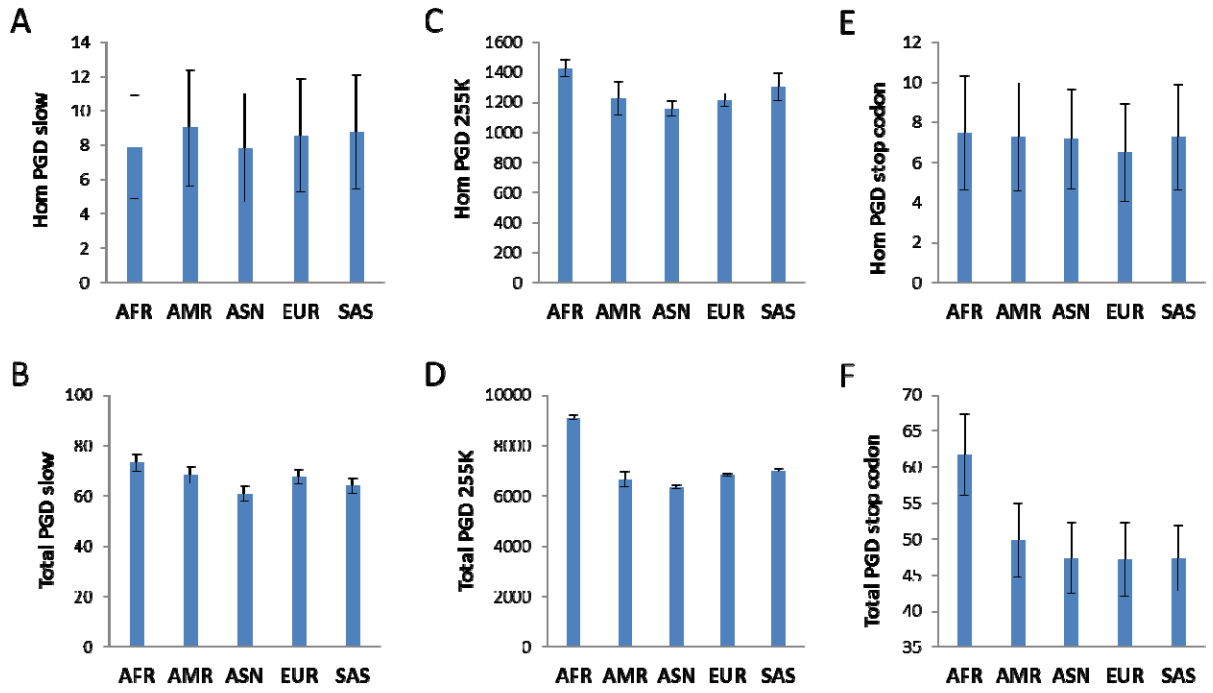

Figure 1. Pairwise genetic distance as measured by different types of SNPs. Pairwise genetic distance (PGD), either by homozygous mismatches (Hom) or by both homozygous and heterozygous mismatches (Total), as measured by three different types of SNPs is shown for each of the 5 major human groups in the 1000 genomes project. Known heavily admixed groups such as ASW and ACB in the African group or CLM and PUR in the American group were excluded in the analysis. Data are means with standard deviation.

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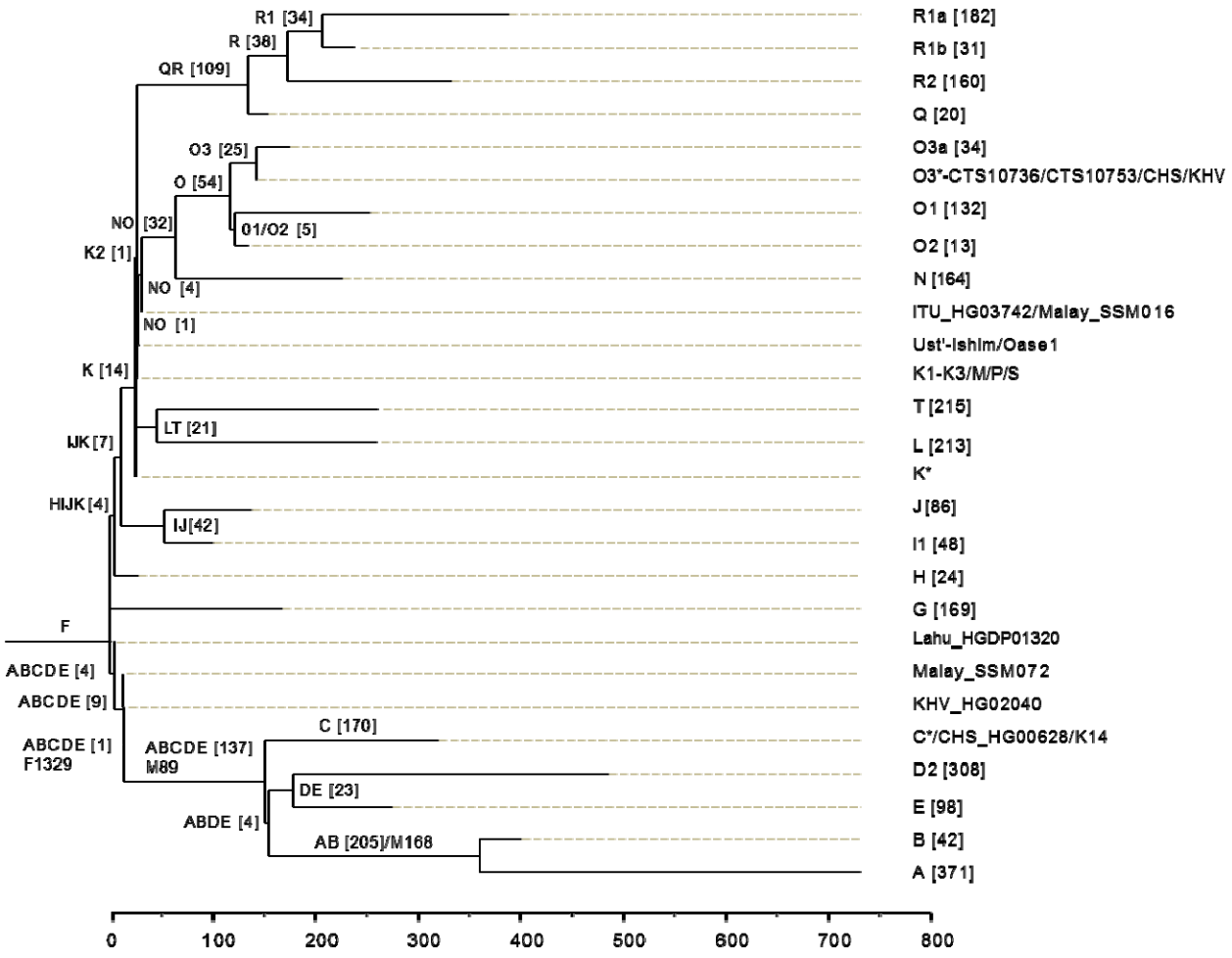

Figure 2. New Y chromosome phylogeny. Branch lengths are drawn proportional to the number of SNPs. Only major haplogroups are shown with defining SNPs indicated for some. Numbers in parenthesis indicate the number of SNPs defining a haplogroup among the 58251 cleanly called SNPs (no individual with uncalled SNPs) in the 1000 genomes. Individuals with few changes from an ancestor haplotype are also listed as shown.

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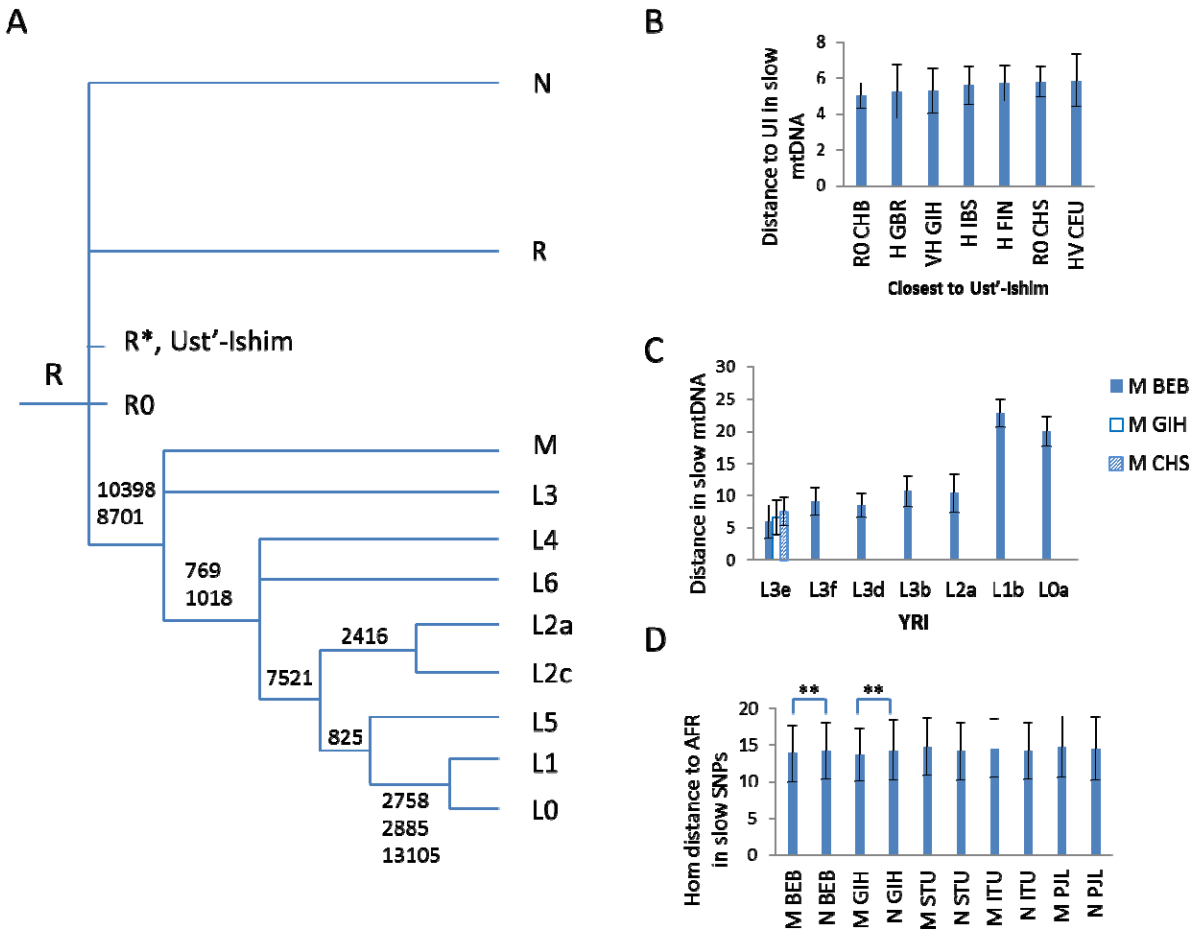

Figure 3. New mtDNA phylogeny and evidence for it. A. The mtDNA tree was drawn using slow evolving SNPs as indicated with the common ancestor haplotype defined as being closest to the ~45,000 year old Ust'-Ishim. Only major branches are shown and no slow SNPs could be found to separate N and R. **B.** Genetic distance in slow mtDNA SNPs to Ust'-Ishim mtDNA for haplotypes in the 1000 genomes. Only the closest few are shown. **C.** Genetic distance in slow mtDNA SNPs to the M haplotype in BEB, GIH, or CHS for different L haplotypes in the YRI group. **D.** Genetic distance in slow autosomal SNPs to individuals of South Asian BEB (or GIH, STU, ITU, PJL) carrying either the M or N haplotype. Data are means with standard deviation.

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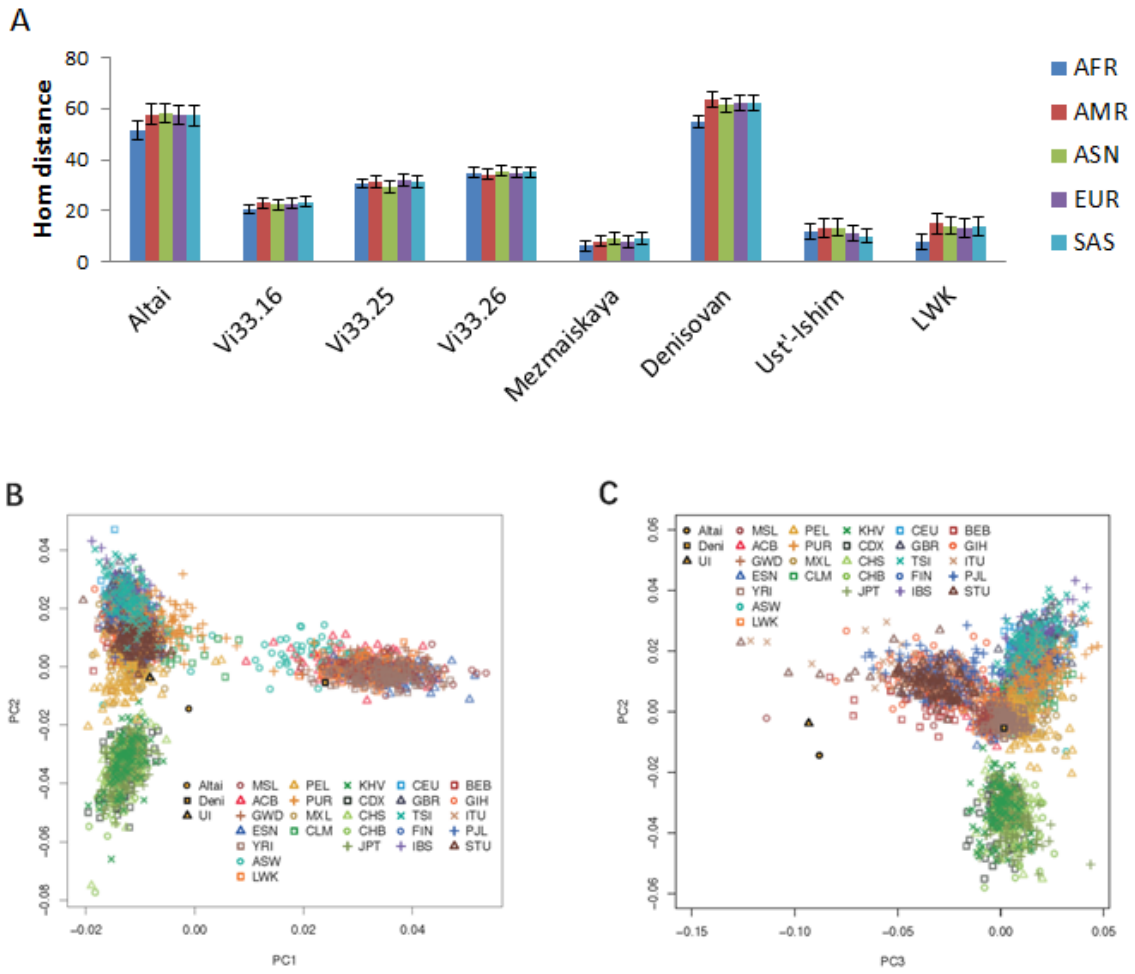

Figure 4. Autosomal relationship between archaic and modern humans. A. Shown are the genetic distances between the 5 groups of the 1000 genomes and Neanderthals, Denisovan, Ust'-Ishim, or the modern African group LWK. Data are means with standard deviation. **B and C.** Shown are PCA plot analyses for Denisovan, the Altai Neanderthal, Ust'-Ishim, and the 1000 genomes.

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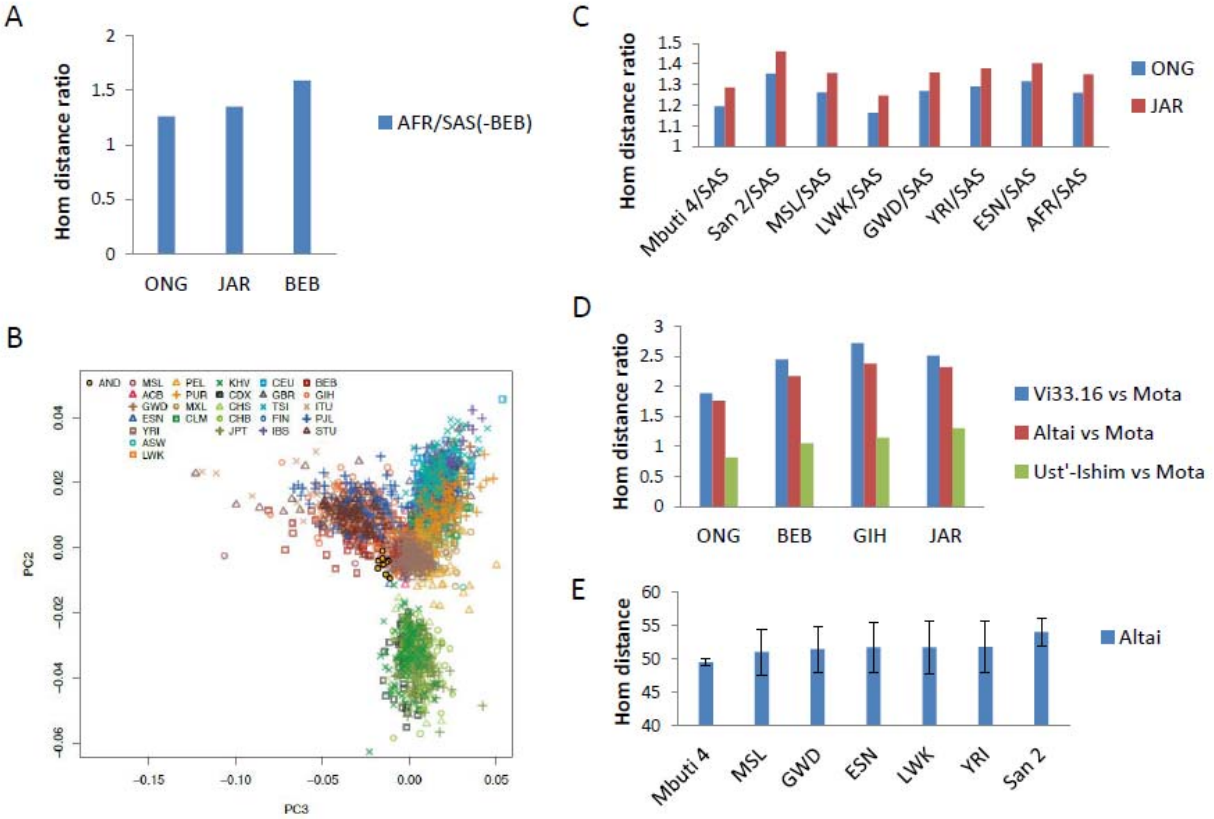

Figure 5. Origin of Negritos. A. Shown are the ratios of ONG, JAR, or BEB autosomal distance to AFR versus SAS(-BEB). SAS (-BEB) excluded the BEB group from SAS groups. **B.** PCA plot (PC3-PC2) analysis of 10 Andamanese and 1000 genomes using slow autosomal SNPs. **C.** Shown are the ratios of ONG or JAR autosomal distance to African groups versus SAS. **D.** Hom distance ratio of ancient humans versus the Mota African for four South Asian groups (ONG, BEB, GIH, JAR). **E.** Autosomal distance between Altai and various African groups. Data are means with standard deviation.

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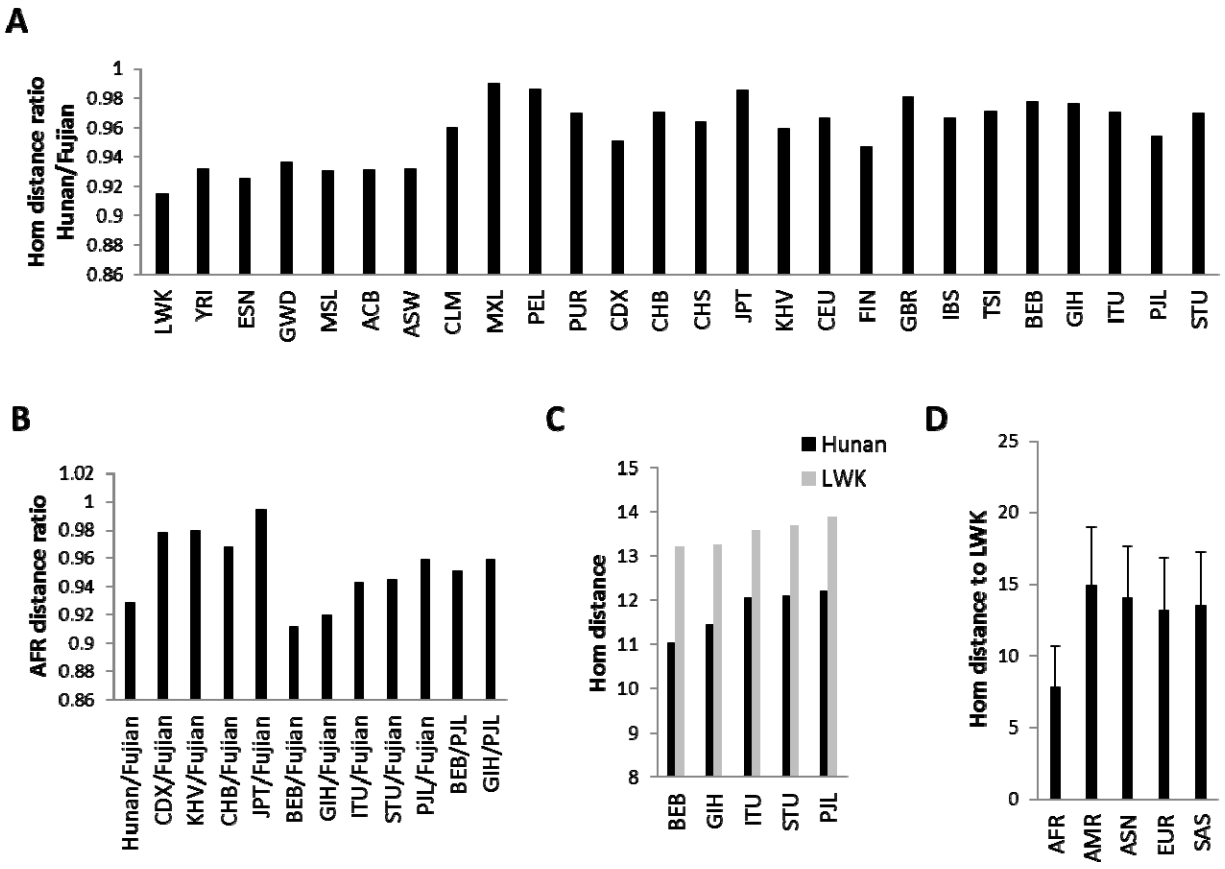

Figure 6. Hunan ancestry in Africans. A. Ratios of autosomal distance to Hunan versus Fujian for each of the 25 groups in the 1000 genomes project. **B.** Ratios of autosomal distance to Hunan (or other East Asian and South Asian groups in the 1000 genomes) versus Fujian. **C.** Autosomal distance to Hunan or LWK for various South Asian groups. **D.** Autosomal distance to LWK for the 5 groups in the 1000 genomes project.

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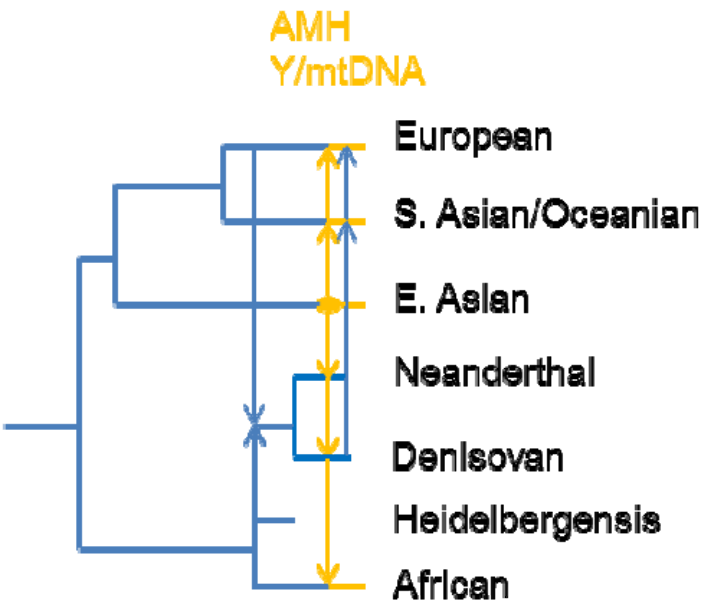

Figure 7. Model of human evolution. A schematic tree showing the phylogenetic relationship of major human groups, including Africans, East Asians, South Asians/Oceanians, Europeans, Heidelbergensis, Neanderthals, and Denisovans.