

A weakly structured stem for human origins in Africa

Aaron P. Ragsdale¹, Timothy D. Weaver², Elizabeth G. Atkinson³, Eileen Hoal⁴, Marlo Möller⁴,
Brenna M. Henn^{2,5,†,*}, and Simon Gravel^{6,†,**}

¹Department of Integrative Biology, University of Wisconsin–Madison, WI, USA

²Department of Anthropology, University of California, Davis, Davis, CA, USA

³Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX, USA

⁴DSI-NRF Centre of Excellence for Biomedical Tuberculosis Research; South African Medical Research Council Centre for Tuberculosis Research; Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, Stellenbosch University, Cape Town, South Africa

⁵UC Davis Genome Center, University of California, Davis, Davis, CA, USA

⁶Department of Human Genetics, McGill University, Montreal, QC, Canada

[†]Co-Corresponding Authors

*bmhenn@ucdavis.edu

**simon.gravel@mcgill.ca

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Abstract

Despite broad agreement that *Homo sapiens* originated within Africa, considerable uncertainty surrounds specific models of divergence and migration across the continent¹. Progress is hampered by limited fossil and genomic data, as well as variability in prior divergence time estimates¹. To discriminate among such models, we consider linkage disequilibrium and diversity-based statistics, optimized for rapid, complex demographic inference². We infer detailed demographic models for populations across Africa, including representatives from eastern and western groups and newly sequenced whole genomes from 44 Nama (Kho-San) individuals. We infer a reticulated African population history in which contemporary population structure dates back to Marine Isotope Stage (MIS) 5. The earliest population divergence among contemporary populations occurs 120–135ka and was preceded by structure between two or more weakly differentiated ancestral *Homo* populations connected by gene flow over hundreds of thousands of years. Such *weakly structured stem* models better explain patterns of polymorphism that were previously attributed to contributions from archaic hominins in Africa^{3,4,5,2,6,7}. In contrast to models with archaic introgression, we predict fossil remains from coexisting ancestral populations should be genetically and morphologically similar, and that an inferred 1–4% of genetic differentiation among contemporary human populations can be attributed to genetic drift between stem populations. We show that model misspecification explains variation in previous divergence time estimates and argue that studying a suite of models is key to robust inferences about deep history.

Introduction

Decades of study of human genome variation have suggested a predominantly tree-like model of recent population divergence from a single ancestral population in Africa. It has been difficult to reconcile this finding with the fossil and archaeological records of human occupation across the vast African continent. For example, fossils such as those from the sites of Jebel Irhoud, Morocco⁸, Herto, Ethiopia⁹ and Klasies River, South Africa¹⁰ demonstrate that derived *Homo sapiens* anatomical features were found across the continent 300–100ka. Archaeological sites from the Middle Stone Age, of which some have been associated with *Homo sapiens*, are also widely distributed across Africa. It is unclear whether these fossils and archaeological sites represent populations which contributed to contemporary *Homo sapiens* as population precedents or were local “dead-ends”. Recently, attempts to reconcile genetic and paleoanthropological data include proposals

for a Pan-African origin of *Homo sapiens* by which populations in many regions of the continent contributed to the formation of *Homo sapiens* beginning at least 300ka^{11,12,13}.

Genetic models have been hampered in their contribution to this discussion because they primarily assume (or, at least, have been tested under) a tree-like model of isolation-with-migration. Alternative theoretical scenarios have been proposed, such as stepping stone models¹⁴ or population coalescence and fragmentation¹³, but these approaches are more challenging to interpret and fit to data. However, new population genetic tools now allow for inference involving tens to hundreds of genomes from multiple populations and greater complexity^{15,2,16}. Inspired by evidence for Neanderthal admixture with humans in Eurasia, several recent studies have shown that introducing an archaic hominin “ghost” population contributing to African populations in the period surrounding the Out-of-Africa migration event substantially improves the description of genetic data relative to single-origin models, mostly in western Africa^{3,4,5,2,6,7}, but also in southern^{4,6} and central African^{17,4,6,5} populations. This has driven speculation about the geographic range of this ghost population, possible links to specific fossils, and the possibility of finding ancient DNA evidence¹⁷. However, these prior studies share two weaknesses. First, they only contrast a single-origin model with an archaic hominin admixture model, leaving out other plausible models¹ (Figure 1). Second, they focus on a small subset of African diversity, either because of small sample sizes (2-5 genomes) or because they rely on 1000 Genomes data which only recruited populations of recent West African or Bantu-speaking ancestry (Figure 2C). While ancient DNA from Eurasia has helped to clarify early human history outside of Africa, there is no comparably ancient DNA to elucidate early history in Africa¹⁸.

We therefore aim to discriminate among a broader set of demographic models by studying the genomes of contemporary populations. We take as our starting point four classes of models (single population expansion, single population expansion with regional persistence, archaic hominin admixture, and multi-regional evolution, Figure 1), using 290 genomes of individuals from southern, eastern, and western Africa as well as Eurasia. By including geographically and genetically diverse populations across Africa, we infer demographic models that explain more features of genetic diversity in more populations than previously reported. These analyses confirm the inadequacy of tree-like models and provide an opportunity to directly evaluate a wide range of alternative models.

Results

We inferred detailed demographic histories using 4x-8x whole-genome sequencing data for four diverse African populations, comprising the Nama (Kho-San from South Africa, newly presented here, see Supplementary Information (SI) section 1.2 for ethical and practical aspects of participant recruitment), Mende (from Sierra Leone, MSL from the Phase 3 1000 Genomes Project¹⁹), Gumuz (recent descendants of a hunter-gatherer group from Ethiopia^{20,21}), and eastern African agriculturalists (Amhara and Oromo from Ethiopia²⁰). The Amhara and Oromo populations, despite speaking distinct Afro-Asiatic languages, are highly genetically similar^{22,21} and thus the two groups were combined for a larger sample size (Figure 2). We also included the British (GBR) from the 1000 Genomes Project in our demographic models as a representative source of back-to-Africa gene flow and recent colonial admixture in South Africa. Finally, we used a high-coverage ancient Neanderthal genome from Vindija Cave, Croatia²³ to account for gene flow from Neanderthals into non-Africans and gauge the relative time depth of divergence, assuming Neanderthals diverged 550ka from a common stem. We computed one- and two-locus statistics whose expectation within and across populations can be computed efficiently and that are well suited for both low- and high-coverage genomes^{2,24}. Using a maximum-likelihood inference framework, we then fit to these statistics a family of parameterized demographic models that involve population splits, size changes, continuous and variable migration rates, and punctuated admixture events, to learn about the nature of population structure over the past million years.

A Late Pleistocene common ancestry

We began with a model of geographic expansion from a single ancestral, unstructured source followed by migration between populations, without allowing for contribution from an African archaic hominin lineage or population structure prior to the expansion (Figure 1A or Figure 1D). As expected², this first model was a poor fit to the data qualitatively (Figure S10) and quantitatively (log-likelihood (LL) $\approx -189,300$, Table S3).

We next explored a suite of parameterized models in which population structure predates the differentiation of contemporary groups (SI Section 3). Depending on the parameters, these encompassed models allowing for ancestral reticulation, such as fragmentation-and-coalescence or meta-population models (Figure 1B), archaic hominin admixture (Figure 1C), and African multi-regionalism (Figure 1D). The recent expansion and the African multi-regional models (Figure 1A and D) have the same topology, so interpretation of the model depends on the specified or inferred divergence times.

Regardless of the model choice for early epochs, maximum-likelihood inference of human demographic history for the last 150ka was remarkably robust. In a reticulated model, we use “divergence” between populations to mean the time of their most recent shared ancestry. The earliest divergence among contemporary human populations differentiates the southern African Nama from other African groups between 110 – 135ka, with low to moderate levels of subsequent gene flow (Table 1). In none of the high-likelihood models which we explored did the divergence between Nama and other populations exceed ~ 140 ka. We conclude that geographic patterns of contemporary *Homo sapiens* population structure likely arise during MIS 5. Although we find evidence for earlier population structure in Africa (next section), contemporary populations cannot be easily mapped onto the more ancient ‘stem’ groups as only a small proportion of drift between contemporary populations can be attributed to drift between stems (SI Section 5.2, Figures 4 and S16–S19).

Given this consistency in inferred recent history and the numerical challenge of optimizing a large number of parameters, we fixed several parameters related to recent population history so as to focus on more ancient events (SI Section 3.1). These parameters were ones supported by multiple genetic and archaeological studies²⁵. Fixed parameters included the time of divergence between western and eastern African populations, set to 60ka, just prior to the split of Eurasians and East Africans set to 50ka. We also fixed the amount of admixture from Neanderthals to Europeans directly following the out-of-Africa migration to 1.5% at 45ka.

We quantify migration rates among populations after their divergence ~ 120 ka. Prior to agripastoralist expansion 5ka, migration between the ancestors of the Nama and other groups is an order of magnitude weaker than that observed between western and eastern Africans (Table 1). All models infer relatively high gene flow between eastern and western Africa ($m \approx 2 \times 10^{-4}$, the constant proportion of immigrant lineages per generation over 60ka). We further find that Back-to-Africa gene flow at the beginning of the Holocene primarily affected the ancestors of the Ethiopian agricultural populations²⁶, comprising over half of their genetic ancestry, estimated to be approximately 65%. We observe significant gene flow from the Amhara and Oromo into the Nama, a signal which is likely a proxy for the movement of eastern African caprid and cattle pastoralists^{27,28}, here estimated to constitute a 25% ancestry contribution 2,000 years ago. While this gene flow is not apparent from the ADMIXTURE plot (Figure 2), the ancestry is likely grouped into the Khoe-San component which has drifted appreciably from its ancestral eastern African source. Colonial period admixture from Europeans into the Nama was estimated at 15%, similar to proportions suggested by ADMIXTURE (Figure 2).

A weakly structured stem within Africa

To account for population structure prior to 135ka, three of our four models allowed for two or more “stem” populations which could diverge either before or after the Neanderthal split. We considered models both with and without migration between these stem populations, and in both cases we tested two different types of gene exchange during the expansion phase, as illustrated in Figure S6: 1) One of the stem population expands (splits into contemporary populations), followed by continuous symmetric migration with the other stem population(s); or 2) one or more of the stem populations expands, with instantaneous pulse (or “merger”) events from the other stem population, so that recent populations are formed by mergers of multiple ancestral populations. Depending on parameter values, this scenario encompasses archaic hominin introgression and fragmentation-and-coalescence models (such as Figure 1B and C). For many parameters, confidence intervals based on bootstrapping are relatively narrow (Tables S3–S7), reflecting an informative statistical approach. However, model assumptions have a larger impact on parameter estimates (and thus real uncertainty). To convey model uncertainty, we highlight features of the two inferred models with high likelihoods. These are referred to as the “multiple-merger” and the “continuous-migration” models. Both allow for migration between stem branches, but differ primarily in the timing of the early divergence of stem populations and their relative N_e (Figure 3). The two models also differ in the mode of divergence, with the multiple-merger

Likelihood	Label	Population Pair	Divergence Time (ka)	Migration rate per generation	Migration duration (kyr)
Continuous Model					
$LL = -115,300$ (Table S5)	a	Stem 1, Stem 2	1,223	6.26e-5	1,089
	b	Stem 2, Nama	NA	5.85e-5	129
	c, d	Stem 2, Other Africans*	NA	3.10e-5, 1.62e-4	129, 55
	e, f	Nama, Other Africans*	135	4.1e-5, 9.2e-6	134, 60
	g	Mende, East Africans	60	2.13e-4	60
	h	East Africans, British	50	4.16e-5	50
	i	Gumuz, Amhara/Oromo	12	3.37e-4	12
Merger Model					
$LL = -101,600$ (Table S7)	a	Stem 1, Stem 2	1,692	1.26e-4	1,213
	–	Stem 1S, Stem 1E	479	0 (fixed)	–
	b	Stem 2 to Nama	119	0.70	pulse
	c	Stem 2 to Stem 1E	98	0.52	pulse
	d	Stem 2 to Mende	25	0.19	pulse
	e, f	Nama, Other Africans*	119	4.5e-5, 9.8e-6	120, 60
	g	Mende, East Africans*	60	1.97e-4	60
	h	East Africans, British	50	3.82e-5	50
	i	Gumuz, Amhara/Oromo	12	3.59e-4	12

Table 1: **Migration and divergence parameters from best fit models.** Labeled migration rates correspond to symmetric continuous migration bands shown in Figure 3. Both the continuous migration and merger models inferred a relatively deep split of human stem branches, though they were connected by ongoing migration that maintained their genetic similarity. Bold text indicates migration rates above 10^{-4} . In both models, the branch ancestral to the Nama shares a common ancestral population with the other African groups $\sim 120 - 135$ ka. Following this divergence, the population ancestral to other African groups branches into West and East African groups 60ka. *Migration rates and durations are shown between branches ancestral to 1) Nama and East Africans and their ancestors, and 2) Nama and Mende, respectively. “Divergence times” correspond to the most recent common ancestral population and does not account for continuous migration or earlier reticulations.

featuring a population reticulation during the Middle Pleistocene.

Allowing for continuous migration between the stem populations substantially improved the fits relative to zero migration between stems ($LL \approx -101,600$ vs. $-107,700$ in the merger model, Tables S6 and S7, and $LL \approx -115,300$ vs. $-126,500$ in the continuous migration model, Tables S4 and S4). With continuous migration between stems, population structure extends back to up to 1.5Ma (Table 1). Migration between the stems in these models is moderate, with a fraction of migrant lineages each generation estimated as $m = 6.3 \times 10^{-5} - 1.3 \times 10^{-4}$. For comparison, this is similar to inferred migration rates between connected contemporary populations over the past 50ka (Table 1). This ongoing (or at least, periodic) gene flow qualitatively distinguishes these models from previously proposed archaic hominin admixture models (Figure 1C) as the early branches remain closely related, and each branch contributes large amounts to all contemporary populations (Figure 4). Because of this relatedness, only 1% to 4% of genetic differentiation among contemporary populations can be traced back to this early population structure (SI Section 5.2).

Under the continuous-migration model, one of the two stems diverges into lineages leading to contemporary populations in western, southern and eastern Africa, and the other (Stem 2) contributes variable ancestry to those populations. This migration from Stem 2 is highest with the Mende ($m = 1.6 \times 10^{-4}$) compared to the Nama and East African populations ($m = 5.9 \times 10^{-5}$ and 3.1×10^{-5} , respectively), with migration allowed to occur until 5ka. A sampled lineage from the Nama, Mende, and Gumuz have probabilities of being in Stem 2 at the time of Stem 1 expansion (135ka) of approximately 0.145, 0.2, and 0.13, respectively, though these probabilities change over time, precluding the notion of a fixed admixture proportion.

In contrast, under the multiple-merger model, stem populations merge with varying proportions to form the different contemporary groups. We observe a sharp bottleneck in Stem 1 down to $N_e = 100$ after the split of the Neanderthal branch. This represents the lower bound allowed in our optimization (i.e., an N_e of 100), although the size of this bottleneck is poorly constrained (95% confidence interval 100–851). After a long period of exchange with Stem 2, Stem 1 then fractures into “Stem 1E” and “Stem 1S” 478ka. The timing of this divergence was also poorly constrained (95% CI 276 – 478ka). These populations evolve independently until 119ka (101 – 125ka) when Stem 1S and Stem 2 combine to form the ancestors of the Nama, with proportions 30% and 70%, respectively. Similarly, Stem 1E and Stem 2 combine in equal proportions (50%

each) to form the ancestors of the western Africans and eastern Africans (and thus also all individuals who later disperse during the Out-of-Africa event). Finally, the Mende receive a large additional pulse of gene flow from Stem 2, replacing 19% (18–21%) of their population 25ka (22 – 26ka). The later Stem 2 contribution to the western African Mende resulted in better model fits ($\Delta LL \approx 60,000$). Speculatively, this may indicate that an ancestral Stem 2 population occupied western or central Africa, broadly speaking. The differing proportions in the Nama and eastern Africans may also indicate geographic separation of Stem 1S in southern Africa and Stem 1E in eastern Africa.

To assess robustness of the inferred models to analysis and reference population choices, SI Sections 6 and 7 present re-analyses changing the European and West African populations, as well as the recombination maps, filtering strategies and parameter optimization strategies. While we find some differences in the inferred parameters (see SI sections 7.1.1 and 7.2), the best fit models across all reanalyses are quantitatively consistent.

Reconciling lines of genetic evidence

Previous studies have found support for archaic hominin admixture in Africa using two-locus statistics^{17,2}, the conditional SFS (cSFS)⁷, and reconstruction of gene genealogies¹⁶. However, none of these studies considered a weakly structured stem. We validated our inferred models with additional independent approaches. We find that the observed cSFS (conditioned on the derived allele being carried in the Neanderthal sample) is very well-described by the merger model (Figures 5A-C and S20–S23), even though this statistic was not used in the fit. Our best-fit models outperform archaic hominin admixture models fit directly to the cSFS (for example, compare to Figure 1 in Durvasula and Sankararaman (2020)⁷). Specifically, it is the addition of migration between stems that results in a qualitative improvement of the agreement (compare Figures S22 and S23).

We used **Relate**¹⁶ to infer the distribution of coalescence rates over time in real data and data simulated from our inferred models. Many previous studies have found a reduction of coalescence rates between 1000ka and 100ka in humans, and thus inferred an increase in N_e during the same period²⁹. This increase in inferred N_e could be due to either an increase in population size or to ancestral population structure during the Middle Pleistocene³⁰. All models, including the single-origin model, recapitulate an inferred ancestral increase in N_e between 100ka–1Ma (Figure S26 and SI Section 7.3.2). Whereas the single-origin model achieves this by an increase in N_e during that period, the best-fit models recapitulate this pattern without corresponding population size changes.

Relative cross-coalescence rates (rCCR) have recently been used to estimate divergence between pairs of populations, as measured by the rate of coalescence between two groups divided by the mean within population coalescence. Simulations of rCCR accuracy, however, focus on a ‘clean split’ between populations whereby groups diverge without subsequent gene flow. Published estimates of the earliest human divergences with rCCR, which range from 150ka–100ka²⁵, may be significantly biased when compared to more complex models with gene flow as inferred here. We find that midpoint estimates of rCCR are poor estimates for population divergence, often underestimating divergence time by 50% or greater (e.g., Mende vs. Gumuz ~ 15 ka compared to a true divergence of 60ka), and recent migration can lead to the misordering of divergence events (Figure 5E). We suggest that rCCR analyses which do not fit multiple parameters including gene flow should be interpreted with caution.

Other studies have fit tree-like demographic models to African populations using distributions of allele frequencies or related statistics, finding inconsistent divergence times, some of which are older than those we find here^{1,25}. In the SI (Section 7.4), we show that this discrepancy can be explained by model misspecification: if divergence is estimated using an isolation with migration (IM) model with constant population sizes, but the correct model has ancient population growth or population structure, the divergence time in the inferred IM model is much deeper than in the correct model. Intuitively, growth or structure in the ancestral population will each increase coalescence times relative to a randomly mating population of constant size, so a model that assumes constant population sizes would require an older divergence time to fit the observed distribution of coalescence times and related statistics^{31,32}.

Discussion

Any attempt at building detailed models of human history is subject to model misspecification. This is true of earlier studies, which often assumed that data inconsistent with a single-origin model must be explained by archaic hominin admixture. This is also true of this study. While it remains prohibitive to fully explore the space of plausible models of early human population structure, we sought to capture model uncertainty by exploring multiple parameterizations of early history. The best fit models presented here include reticulation and migration between early human populations rather than archaic hominin admixture from long-isolated branches (Figure 1C). Elements of a recent single-origin or African multi-regionalism (Figure 1A,D) feature in our best fit models, as indicated in the recent time of contemporary population divergence or the gene flow between disparate stems, respectively.

We caution that we cannot rule out that more complex models involving additional stems, more complex population structure, or hybrid models including both weak structure and archaic hominin admixture may better explain the data. Because parameters related to the split time, migration rates, and relative sizes of the early stems were variable across models, reflecting a degree of confounding among these parameters, we refrained from introducing additional branches associated with more parameters during that period. Rather than interpreting the two stems as representing well-defined and stable populations over hundreds of thousands of years, we interpret the weakly structured stem as consistent with a population coalescence and fragmentation model¹³. Additional African populations such as those from Central Africa, other Khoe-San groups or pre-Holocene ancient DNA samples, could further test our proposed models.

Formation of population structure in Africa

Our inferred models paint a consistent picture of the Middle to Late Pleistocene as a critical period of change, assuming that estimates from the recombination clock accurately relate to geological chronologies (SI Section 8). During the late Middle Pleistocene, the multiple merger model indicates three major stem lineages in Africa, tentatively assigned to southern (Stem 1S), eastern (Stem 1E) and western/central Africa (Stem 2). Geographic association was informed by the present population location with the greatest ancestry contribution from each stem. For example, Stem 1S contributes 70% to the ancestral formation of the Khoe-San. The extent of the isolation 400ka between Stem 1S, Stem 1E and Stem 2 suggests that these stems were not proximate to each other. While the length of isolation among the stems is variable across fits, models with a period of divergence, isolation and then a merger event (i.e., a “reticulation”) out-performed models with bifurcating divergence and continuous gene flow.

A population reticulation involves multiple stems contributing genetically to the formation of a group. One way in which this can happen is through the geographic expansion of one or both stems. For example, if during MIS 5, either Stem 1S (Figure 3B) from southern Africa moved northward thereby encountering Stem 2, or Stem 2 moved from central/western Africa southward into Stem 1S, then we could observe disproportionate ancestry contributions from different stems in contemporary groups. We observed two merger events. The first, between Stem 1S and Stem 2, resulted in the formation of an ancestral Khoe-San population ~ 120 ka. The second event ~ 100 ka between Stem 1E and Stem 2, resulted in the formation of the ancestors of eastern/western Africans including the ancestors of “Out-of-Africans”. Reticulated models do not have a unique and well-defined “basal” human population divergence. We suggest conceptualizing the events 120ka as the time of most recent shared ancestry among sampled populations. However, interpreting population divergence times in population genetics is always challenging due to the co-estimation of divergence time and subsequent migration; methods assuming clean vs reticulated splits can infer different split dates (Figure S28 and Figure S36). Therefore, wide variation exists in estimates of divergence time in the literature^{25,1}.

Shifts in wet/dry conditions across the African continent 140ka to 100ka may have promoted these merger events between divergent stems. Precipitation does not neatly track interglacial cycles in Africa, and heterogeneity across regions may mean that the beginning of an arid period in eastern Africa is conversely the start of a wet period in southern Africa³³. The rapid rise in sea levels during the MIS 5e interglacial might have triggered migration inland away from the coasts, as has been suggested, e.g., for the Paleol-Agulhas plain³⁴. Following these merger events, the stems subsequently fractured into subpopulations which then persist over the past ~ 120 ka. These subpopulations can be linked to contemporary groups despite

subsequent gene flow across the continent; for example, a genetic lineage sampled in the Gumuz has a 0.70 probability of being inherited from the ancestral “eastern” subpopulation 55ka versus 0.06 probability of being inherited from the “southern” subpopulation (see Table S8 for additional comparisons).

We also find that Stem 2 continued to contribute to western Africans during the Last Glacial Period, indicative that this gene flow likely occurred in western/central Africa (Table 1). Such an interpretation is reinforced by the differential migration rates between regions, i.e., the gene flow from Stem 2 to western Africans is estimated to be five times that of the rate to eastern Africans during this period. We performed a variety of validation tests to explore sensitivity of our assumptions, including relaxing fixed parameters (SI Section 6). Most validation tests resulted in parameters similar to the models discussed above. However, one exception was the inferred Out-of-Africa and eastern/western African divergences which were 10–15ka younger than our fixed parameters. These younger dates are clearly at odds with the accepted timing of Out-of-Africa expansion at approximately 50ka, as based on archaeological, climatic and paleo-morphological information^{35,36,37,38}. We interpret the free estimate for eastern African vs. European divergence as reflecting our inclusion of only a single Out-of-Africa population in the model, the lack of a nearby source for back-to-Africa gene flow, and other regionally complex parameters. However, older pan-African features of our inferred models are weakly affected by this analysis choice (SI Section 3.1).

Contrasting ancestral structure models

Evidence for archaic hominin admixture in Eurasia has bolstered the plausibility of archaic hominin admixture having also occurred in Africa. Previous work that sought to explain patterns of polymorphism inconsistent with a single-origin model thus focused on archaic hominin admixture as an alternative model. The additional (or “ghost”) branches required to fit the data are systematically referred to as “archaic”^{3,4,5,2,6,7}, and assumed (or inferred) to be deeply diverged. We believe that this has strongly oriented the interpretation of these results (e.g., regarding selection³⁹ or the fossil record⁴⁰). Here, we have shown that a model of a weakly structured stem better captures the apparently inconsistent patterns of polymorphisms.

Preferring weakly-structured-stem models over archaic-admixture models potentially has a range of implications. First, with a weakly structured stem, there is no need to posit that an archaic hominin population in Africa stayed reproductively isolated from the ancestral human lineage for hundreds of thousands of years before the initiation of gene flow. Instead, there would simply have been continuous or recurrent contact between two or more groups present in Africa.

Second, there is evidence for both deleterious and adaptive archaic-hominin-derived alleles in contemporary genomes in the form of a depletion of Neanderthal ancestry in regulatory regions⁴¹ or an increased frequency of archaic-hominin-related haplotypes such as at *EPAS1* among Tibetans⁴². Under previous African-archaic-hominin admixture models, the estimated 8–10% introgression rate is much higher than Neanderthal gene flow, and would have plausibly been fertile ground for dramatic selection for or against archaic-hominin-derived haplotypes³⁹. By contrast, adaptation under a weakly structured stem would have occurred continuously over much longer periods. Patterns of polymorphism that are inconsistent with the single-stem model predictions have been used to infer putative archaic admixed segments^{3,17,39,7}, negative selection against such segments³⁹, and pervasive positive selection⁴³. However, such approaches are subject to high false positives in the presence of population structure with migration⁴¹, and their interpretation should be re-examined in light of a weakly-structured-stem model within Africa.

Third, multiple studies have shown a correspondence between phenotypic differentiation, usually assessed with measurements of the cranium, and genetic differentiation among human populations and between humans and Neanderthals^{44,45,46} (see also SI Section 5.4). This correspondence potentially allows predictions of our model to be related to the fossil record. The fossil record of Africa is sparse during the time period of the stems, but of the fossils that date to this time period, some are fairly similar overall in morphology to contemporary humans (e.g., Omo 1 from Omo Kibish, Ethiopia^{47,48}), others are similar in some morphological features to contemporary humans (e.g., Irhoud 1 from Jebel Irhoud, Morocco^{8,49}), and others are different enough in morphology to have been assigned to species other than *Homo sapiens* (e.g., DH1 from Dinaledi, South Africa^{50,51}). If, as our model predicts, the genetic differences between the stems were comparable to those among contemporary human populations, the most morphologically divergent fossils are unlikely to represent branches that contributed appreciably to contemporary human ancestries.

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Supplementary information

Available in the online version of the paper.

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Competing interests

The authors declare no competing financial interests.

Author contributions

APR, BMH, and SG designed the study. BMH, EH, and MM designed and conducted participant recruitment. BMH and EGA performed quality control of data. APR, BMH, and SG designed statistical analyses. APR conducted statistical analyses. APR, TDW, BMH, and SG interpreted the results and wrote the first draft of the article. All authors read and edited the article.

Methods

Data and sequencing

We generated a sequencing dataset by combining existing and newly recruited populations who are now part of the African Diversity Reference Panel (ADRP)^{20,22}, as well as Thousand Genomes Project populations (1KGP)¹⁹. These included the Amhara, Bakiga, Gumuz, Nama (newly generated), Oromo, Somali, and Zulu from ADRP, and ESN, GWD, LWK, MSL, YRI, CEU, GBR, CHB, and P JL from 1KGP. After filtering for relatedness and retaining Nama individuals with $> 70\%$ estimated Khoe-San ancestry, we focused on data from 289 individuals, including 44 Nama individuals. These were merged with the high-coverage Neanderthal genome from Vindija Cave²³. We kept variants from regions that fell within the 1KGP strict callability mask, overlapped with at least 100 continuously called base pairs in the Neanderthal genome, and were annotated as intergenic. ADMIXTURE and PCA analyses were conducted on a subset of variants filtered to remove variants in high LD (r^2 threshold of 0.1). See SI section 1 for additional details on data and sequencing.

LD and diversity statistics

We used multi-population LD and pairwise diversity statistics to fit parameterized demographic models to data². Unbiased LD statistics were computed from all variants in retained intergenic regions²⁴, for pairs of variants separated by recombination distances $r = 5 \times 10^{-6}$ to 5×10^{-3} . These were assigned to 16 recombination distance bins, and average statistics were computed within each bin (SI section 2.2). Expected statistics under each model were computed in **moments**, which also performed likelihood-based parameter optimization. Conditional site frequency spectra (cSFS) were computed conditioned on the Vindija Neanderthal carrying the derived allele relative to the ancestral allele determined by a six-primate alignment¹⁹.

Model specification and fitting

Model parameters include population sizes and size changes, split times, continuous migration rates, and admixture times and proportions. The simplest model we tested was a bifurcating tree-like structure, allowing for subsequent migrations and recent known admixture events. To include ancestral population structure, we tested models that included multiple stem groups, each of which were allowed their own population size and could be connected by continuous migration. We tested multiple scenarios of early population structure, including long-lasting continuous migration between stem populations and scenarios of periods of isolation with subsequent merger events (SI section 3). To avoid overfitting, we incrementally added complexity to our model optimization, and we fixed a number of parameters that are constrained by historical records or are consistently estimated across multiple models and previous studies (SI section 3.1). Likelihoods were computed using a composite multivariate Gaussian likelihood approach, and confidence intervals were

estimated by refitting each model to 200 block-bootstrap replicate datasets (SI section 3.2). We iteratively used gradient descent and L-BFGS-B optimization routines to fit each parameterized model (SI section 3.3).

Gene genealogy reconstruction

We used **Relate**¹⁶ to reconstruct genome-wide gene genealogies from the focal populations in the merged ADRP and 1KGP datasets (SI section 4). From reconstructed genealogies, we computed coalescence rates within and between populations, which provide an estimate for effective population sizes over time and the relative cross-coalescence rates between pairs of populations. To compare reconstructed genealogies from data to model predictions, we used **msprime**^{52,53} to simulate genomic data for equal numbers of samples for each population in our inferred models. We then applied **Relate** to these simulated datasets using the same mutation and recombination rates and generation time.

Data availability

Nama sequencing data are available from the European Genome-Phenome Archive (EGA), accession number: EGAD00001006198. The African Diversity Reference Panel can be found at accession: EGAS00001000960.

Code availability

Code for the software used in this paper is found at the following locations:

moments-LD (<https://bitbucket.org/simongravel/moments>),

Demes (<https://github.com/popsim-consortium/demes-python>),

Relate (<https://myersgroup.github.io/relate/>),

msprime (<https://github.com/tskit-dev/msprime>),

tskit (<https://github.com/tskit-dev/tskit>),

and scripts implementing analyses using each of these software are available at

<https://github.com/apragsdale/african-structure-paper>.

Figure captions

Figure 1: **Proposed conceptual models of early human history in Africa.** These models have been designed to translate models from the paleoanthropological literature into genetically testable demographic models¹. We used these conceptual models as starting points to build detailed parameterized demographic models (SI Section 3) that were then fit to genetic data.

Figure 2: **Genetic diversity across Africa.** (A) Select populations from the 1000 Genomes and African Diversity Reference Panels illustrate diversity from western, eastern and southern Africa. We chose representatives from each region (bold labels) to build parameterized models, including the newly-sequenced Nama from South Africa, Mende from Sierre Leone, Gumuz, Oromo and Amhara from Ethiopia, and the British and Vindija Neanderthal individual. (B, C) PCA highlights the range of genetic divergence anchored by western Africans, Nama, Gumuz and the British. Percentages show variance explained by each principal component. (D) **ADMIXTURE** with $K = 4$ illustrates signatures of recent gene flow in Africa which reflect colonial-period migration into the Nama, Back-to-Africa gene flow among some Ethiopians, and Khoe-San admixture in the Zulu.

Figure 3: **A weakly structured stem best describes two-locus statistics.** In the two best-fitting parameterizations of early population structure, continuous migration (A) and multiple mergers (B), models that include ongoing migration between stem populations outperform those in which stem populations are isolated. Most recent populations are connected by continuous, reciprocal migration that are indicated by double-headed arrows (labels matched to migration rates and divergence times in Table 1). These migrations last for the duration of co-existence of contemporaneous populations with constant migration rates over those intervals. The merger-with-stem-migration model (B, with $LL = -101,600$) outperformed the continuous-migration model (A, with $LL = -115,300$). Colors are used to distinguish overlapping branches and link to Figure 2.

Figure 4: **Structure among stems is weak and present-day structure is mostly recent.** From the best fit models of our two parameterizations (A and B: continuous migration, C and D: merger with stem migration), we predicted pairwise differences $H_{i,j}$ between individuals sampled from populations i and j existing at time t (A and C). (B and D) To understand how drift between stems explains contemporary structure, we also computed the proportion α^2 of drift between pairs of sampled contemporary populations that aligns with drift between past populations (here Nama and Mende, see SI Section S5.2 for details and additional comparisons in Figures S16–S19). Both models infer deep population structure with modest contributions to contemporary genetic differentiation. Most present differentiation dates back to the last 100ka.

Figure 5: **Model validation using independent statistics.** (A–C) Using our best fit models to linkage disequilibrium and pairwise diversity statistics, we simulated expected conditional site-frequency-spectra (cSFS) and compared to the observed cSFS from the data. Our inferred models provide a good fit to the data, even though these were not used in our inference. Across the three populations, ancestral state misidentification was consistently inferred to be 1.5 – 1.7% for intergenic loci (SI 6.2.2). (D, E) We used Relate¹⁶ to reconstruct genome-wide gene genealogies, which we used to estimate coalescence rate trajectories and cross-coalescence rates between pairs of populations. While coalescence rate distributions are informative statistics about past evolutionary processes, interpretation can be hindered by migration and population structure, and translating relative cross-coalescence rate curves (RCCR) into population divergence times is especially prone to misinterpretation. For example, the Mende-Gumuz comparison shows a more recent increased RCCR than either population with the British, a pattern that is recapitulated under our best-fit model, even though the Mende-Gumuz split occurs prior to the Gumuz-British split.