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Tales of Human Migration, Admixture, and Selection in Africa

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Abstract

In the last three decades, genetic studies have played an increasingly important role in exploring human history. They have helped to conclusively establish that anatomically modern humans first appeared in Africa roughly 250,000–350,000 years before present and subsequently migrated to other parts of the world. The history of humans in Africa is complex and includes demographic events that influenced patterns of genetic variation across the continent. Through genetic studies, it has become evident that deep African population history is captured by relationships among African hunter–gatherers, as the world's deepest population divergences occur among these groups, and that the deepest population divergence dates to 300,000 years before present. However, the spread of pastoralism and agriculture in the last few thousand years has shaped the geographic distribution of present-day Africans and their genetic diversity. With today's sequencing technologies, we can obtain full genome sequences from diverse sets of extant and prehistoric Africans. The coming years will contribute exciting new insights toward deciphering human evolutionary history in Africa.

1. GENETICS AS A TOOL FOR STUDYING HUMAN HISTORY

Multiple studies have shown that the human population is genetically structured and that individuals within certain groups are genetically more similar to each other than to individuals in other groups (e.g., 19, 60, 125, 136). These patterns of population structure are the result of a complex human history, including numerous population divergence, migration, and admixture events, resulting in frequency differences of genetic variants among extant human populations. The field of human evolutionary genetics examines these differences in order to unravel our collective history. By generating and analyzing population-genetic data, we can investigate population structure, population-expansion dynamics, and patterns of migration and admixture. The use of molecular genetics to study human history is relatively recent (19). Various other disciplines have been, and are still, actively researching human history and evolution. Historical and evolutionary linguistics, archaeology, and paleontology continually contribute to uncovering the history of humankind, and in order to understand our species' past, we need to synthesize interpretations from these fields together with genetic findings. Although this review has a genetic focus, we incorporate archaeological and linguistic findings to shed light on our species' deep and more recent history in Africa.

Anatomically modern humans (AMHs): members of the species *Homo sapiens* with an appearance consistent with the range of phenotypes classified as modern human

BP: years before present (where "present" is defined as the year 1950)

Early Stone Age (ESA): a period in African prehistory with earliest finds dating back to 3.3 million BP and ending between 400,000 and 250,000 BP; it is associated with specific lithic technologies

Middle Stone Age (MSA): a period in African prehistory that is generally considered to have begun around 280,000 BP and ended around 50,000–25,000 BP; it is associated with specific macrolithic technologies

Later Stone Age (LSA): a period in African prehistory that follows the MSA and is associated with modern human behavior and microlithic technologies; it started and ended at different times in different parts of Africa

2. THE EMERGENCE OF ANATOMICALLY MODERN HUMANS IN AFRICA AND THE PREFARMING POPULATION STRUCTURE

Genetic, paleoanthropological, and archaeological studies provide substantial support for an African origin of anatomically modern humans (AMHs) (e.g., 17, 60, 79, 86, 107, 134, 144), but the process by which they emerged has been vigorously debated (6, 11, 51, 56, 66, 110, 123, 125, 129, 132, 134). African groups show the greatest genetic diversity; genetic variation in Eurasia, Oceania, and the Americas is largely a subset of the African diversity (60, 107, 125), with small contributions from archaic humans in non-Africans (38, 82, 103, 109). In contrast to the many genetic studies focusing on the out-of-Africa migration [~80,000 years before present (BP)] and the events thereafter (e.g., 76, 86, 90, 107), fewer genetic studies have addressed early human history in Africa from 100,000 to 400,000 BP (47, 51, 123, 125, 129). Most of our knowledge about the emergence of AMHs in Africa is based on fossils and archaeological findings (12, 56, 84, 110, 134).

The fully modern AMH fossils from Omo Kibish and Herto, found in East Africa and dating to 160,000–180,000 BP, are often used to support an East African cradle of humankind (79, 134, 144), but East Africa is also the most extensively excavated area. However, continuous archaeological records exist in several places in Africa (6, 12, 29, 73), and transitional fossils with both archaic and modern features have been found in northern, eastern, and southern Africa (6, 12, 29, 56, 79).

Recent syntheses of the southern African archaeological and paleoanthropological records point to the occupation of southern Africa by the *Homo* genus from about 2 million BP (29), with major transitional phases 600,000–200,000 BP, from the Early Stone Age (ESA) into the Middle Stone Age (MSA), and around 35,000 BP, from the MSA into the Later Stone Age (LSA) (73). In southern Africa, transitional forms with a mosaic of archaic and modern features are found 300,000–100,000 BP, and AMHs appear in the record some 120,000 BP (29).

Although the MSA fossil record in North Africa is limited, some of the most important and interesting early human fossils have been discovered in the region, including the fossils from Jebel Irhoud, recently dated to ~300,000 BP (56, 110). These fossils may be the earliest ascribed to *Homo sapiens*, fulfilling most criteria for AMHs, including an anatomically modern cranial vault and face, but with some archaic morphological traits, such as heavy brow ridges and distinctly large teeth (55, 56, 119). Younger MSA fossils in North Africa dated to 100,000–60,000 BP have been described as retaining some of these archaic morphological traits but largely presenting anatomical modernity. Their presence suggests some level of population continuity across the MSA in North

Africa, including the Late Pleistocene populations in the Levant (at Skhul and Qafzeh) and in East Africa (at Aduma) (56, 111).

Central and western Africa generally have poor conditions for bone preservation, and few ancient human remains have been found in these areas. Although these are vast geographic areas, and pockets of better preservation conditions exist, they have been less excavated for various reasons, including political and economic conditions. There is more evidence in the archaeological record and material culture about human occupation of western Africa than there is in fossil remains. Although few in number, dated ESA, MSA, and LSA sites attest to human occupation at various time periods (120). The LSA burial at the Iwo Eleru rock shelter (southwestern Nigeria) is one of the few human skeletal remains in western Africa associated with a Pleistocene date (~13,000 BP, calibrated based on associated charcoal) (14, 48). The cranium displayed certain archaic aspects, morphology outside the range of modern human variability, and affinities to early AMHs from Skhul and Qafzeh (Levant) (48). Interestingly, the MSA, with its macrolithic stone tools, persists into the terminal Pleistocene in western Africa (the youngest examples of MSA technologies anywhere in Africa) before being replaced in a mosaic-like fashion by LSA microlithic industries (~12,000–13,000 BP). This replacement of MSA by LSA technologies seemed to have moved in a general direction from central to central-western to western Africa. Although Iwo Eleru was in an LSA context (48), the fossils date to the same time frame as the final MSA in Senegal, lending support to the possibility of admixture between late-surviving archaic populations and modern humans (120). More recent western African LSA human remains from, e.g., Shum Laka in Cameroon (7,000–3,000 BP) do not display these archaic features (68).

Today, the majority of people living south of a line from southern Nigeria in the west to southern Somalia in the east and as far south as the Eastern Cape province of South Africa speak languages belonging to the close-knit Bantu family (31, 39) and are genetically highly homogeneous (136). It is commonly assumed that this distribution of people with strong genetic affinities was accomplished by the gradual dispersal of expanding populations of sedentary farmers from western Africa (**Figure 1*b***) starting around 4,000 BP and reaching southern Africa by around 1,800 BP (25, 71, 91, 136) (for further discussion, see Section 3.1). In the course of this expansion, indigenous communities must have been displaced or absorbed (25, 71, 91, 136), and our current knowledge of the genetic landscape of sub-Saharan Africa prior to this recent population expansion (the so-called Bantu Expansion) is limited. Only a few populations—the hunter–gatherers of the central African rain forests (previously known as Pygmies, a name that now has derogatory connotations), the San populations of southern Africa, and the Hadza hunter–gatherers from eastern Africa—have retained their way of subsistence and their culture, albeit with different degrees of intermarriage with neighboring farming and herding populations. Today, they still display substantial stratification that is correlated with geography (92, 96, 125, 136, 141) (**Figure 1*a***). Central African rain forest hunter–gatherers comprise two geographically and genetically isolated groups of populations in the western and eastern parts of the Congo Basin (141), while San groups and their descendants live in scattered, often marginalized groups throughout present-day Namibia, South Africa, Botswana, and southern Angola. The southern and central African hunter–gatherer groups encompass some of the earliest divergences among modern humans (65, 123, 125) (**Figure 2**), and some may harbor genetic material from archaic humans (47, 54, 65).

Genetic studies of mitochondrial DNA (mtDNA) and the autosomes consistently identify southern African Khoe-San populations as carrying more divergent lineages than any other living human populations (5, 8, 17, 40, 51, 60, 96, 116, 122, 123, 125, 127, 136, 140). The deepest population split among modern humans—between the Khoe-San and other groups—has been estimated at around 100,000–160,000 BP, based on short sequence fragments (40, 140) and genome-wide single-nucleotide polymorphism (SNP) data (125). After recent revisions of the human mutation

Pleistocene: the geological epoch that preceded the Holocene and lasted from around 2,588,000 to 11,700 BP; the end of the Pleistocene indicates the end of the last glacial period

Rain forest hunter–gatherers: hunter–gatherer groups who live in the central African rain forests, which span several countries around the equator

Mitochondrial DNA (mtDNA): a relatively small stretch of DNA (16,569 base pairs in humans) that is located in the mitochondria of cells and is maternally inherited

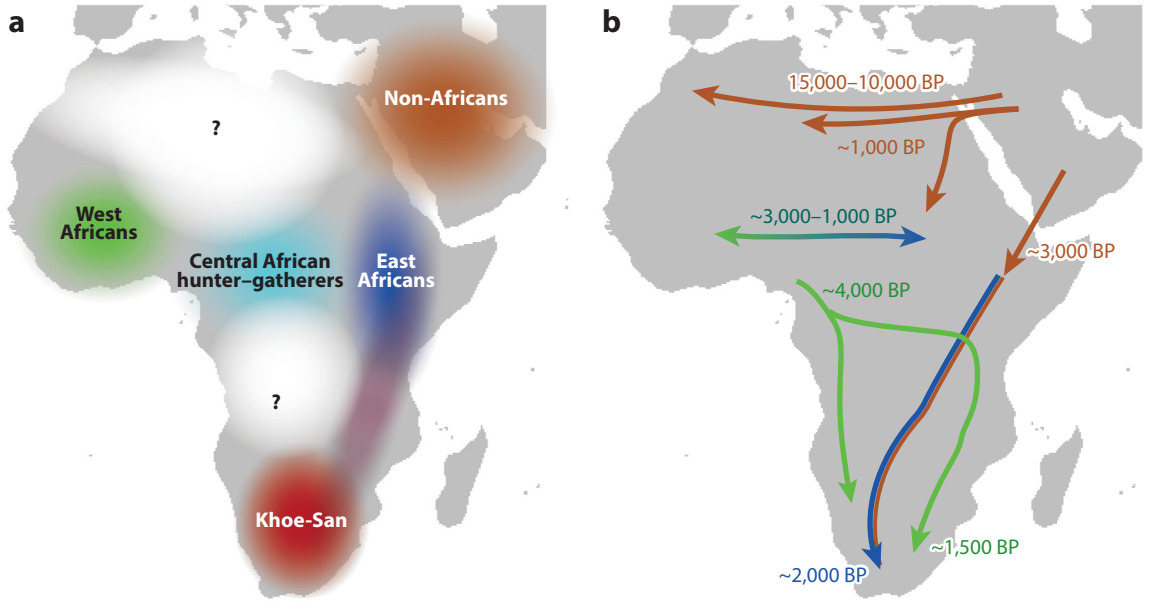

Figure 1

(*a*) Map of major prefarming population stratification across the African continent, showing non-Africans (*brown*), East Africans (*dark blue*), West Africans (*green*), central African hunter–gatherers (*light blue*), and Khoe-San (*red*). (*b*) Migration routes related to the expansion of herders and crop farmers during Holocene times. The green arrows represent the Bantu Expansion, the brown arrows represent the Eurasian back-migration, the brown/blue arrow represents the southward migration of mixed East African/Eurasian pastoralists, and the blue/green arrow represents bidirectional migration across the Sahel belt. Abbreviation: BP, years before present.

rate based on pedigree studies (117), rescaled estimates of the split ranged between 200,000 and 300,000 BP. This date has been pushed back even further by a recent study that sequenced the genomes of three 2,000-year-old southern African Stone Age hunter–gatherers (123) (**Figure 2**). The study found that all modern-day Khoe-San groups have between 9% and 30% genetic admixture from East Africans/Eurasians (for further discussion, see Section 3.2). Using genetic data from these Stone Age hunter–gatherers (who were not affected by recent gene flow from herders and farmers in the last two millennia), this study estimated the deepest human population divergence time at between 350,000 and 260,000 BP, separating the Khoe-San from all other extant humans (123) (**Figure 2**). This estimate is a lower bound for the emergence of modern humans, who must have emerged earlier than the estimated split time. Any (potential) additional gene flow between southern African hunter–gatherers and other groups before 2,000 BP would only lead to these dates underestimating the true population split time. Because the earliest diversification of modern humans involves the ancestors of the Khoe-San (123), the time prior to this event—a period exemplified by large morphological diversity in the fossil record (12, 41, 56, 79)—corresponds to a critical period for the origin of early modern humans.

Single-nucleotide polymorphism (SNP): a single-base-pair variable position at a defined genomic position or locus that segregates in a population (i.e., the locus is polymorphic in the population and has more than one variant, referred to as an allele)

The estimated divergence time of 260,000–350,000 BP for the ancestors of the southern African Khoe-San (123) coincides with the anatomical development of archaic humans into modern humans in the local southern African fossil record. Dated southern African MSA contexts of ~300,000–250,000 BP are few and include Florisbad (Free State Province, South Africa) (41) and Kathu Pan 1 (Northern Cape Province, South Africa) (99). At the Florisbad site, MSA artifacts were found together with human remains dating to 259,000 ± 35,000 BP (41), includ-

(Caption appears on following page)

Figure 2 (*Figure appears on preceding page*)

Demographic model of African history and estimated divergences. (*a*) Population split times, hierarchy, and population sizes (summarized from 123). Horizontal width represents population size; horizontal colored lines represent migrations, with down-pointing triangles indicating admixture into another group. (*b*) Population structure analysis at 5 assumed ancestries ($K = 5$) for 93 African and 6 non-African populations. Non-Africans (*brown*), East Africans (*blue*), West Africans (*green*), central African hunter–gatherers (*light blue*), and Khoe-San (*red*) populations are sorted according to their broad historical distributions. Data were obtained from several studies (4, 16, 44, 53, 70, 89, 125), and the details of the analysis are described in the **Supplemental Methods**. Abbreviation: BP, years before present.

Supplemental Material >

ing a partial cranium with a cranial volume similar to that of modern humans, interpreted as representing a combination of archaic and modern characteristics (28, 41). Human remains from Hoedjiespunt, South Africa, from ~300,000–200,000 BP were ascribed to *Homo heidelbergensis* because, although morphologically modern, they seemed larger than modern-day Africans (10). These records attest to the presence of humans on the southern African landscape at the time of the earliest modern human divergence, predating 260,000 BP, and the fossils deserve closer morphological scrutiny. Whether the Florisbad skull represents a modern human ancestor or an archaic form of human who contributed little or no genetic material to modern humans is an open question, as is modern humans' potential relationship with other southern African hominids, including the ~200,000–300,000-BP *Homo heidelbergensis* of Hoedjiespunt (10) and the archaic *Homo naledi* dated to ~236,000–335,000 BP (9). Although the ancestors of southern African Stone Age hunter–gatherers might have originated elsewhere in sub-Saharan Africa or might have mixed with other groups before 2,000 BP, archaeological, fossil, and genetic records increasingly point toward a modern human development that includes southern Africa. In this same period of earliest human population divergence, fossil evidence showing a morphological transition from archaic features to modern features has also been found in several other parts of Africa, including eastern and northern Africa (6, 12, 29, 56, 79). Therefore, both paleoanthropological and genetic evidence increasingly point to a multiregional origin of AMHs in Africa—i.e., *Homo sapiens* did not originate in one place in Africa but might have evolved from older forms in several places on the continent, with gene flow between groups from different regions.

High genetic diversity in the present-day Khoe-San was previously used to argue for a southern African origin of modern humans (51), although several different regions or groups within regions have also been suggested (as opposed to a single localized origin of modern humans) (123, 125, 134). From studies of southern African Stone Age human remains, we now know that it was likely the East African/Eurasian admixture into southern African Stone Age hunter–gatherers that resulted in the elevated diversity in present-day Khoe-San groups (123). The high levels of diversity of these groups likely arose because they represent the deepest split among humans and had recent admixture with a group in the other branch of the tree (i.e., the branch containing all other current-day human populations). This increased diversity resulting from admixture might also explain inflated past effective population sizes (78) in the Khoe-San and most likely implies that their (census) population size in prehistory was not much greater than those of other African groups (123).

Apart from rain forest hunter–gatherers and the Khoe-San, populations living in the area between southern and central Africa prior to the Bantu Expansion have not been investigated owing to the lack of knowledge of present-day groups extending back to before this expansion. A recent ancient DNA (aDNA) study (132) attested to this replacement of local hunter–gatherers in east-central African regions (today's Malawi and Tanzania). The study captured an array of SNPs (known to be variable in a human reference panel) in seven Stone Age Malawi hunter–gatherers (8,100–2,500 BP) and one prehistoric Tanzanian hunter–gatherer (~1,400 BP). Through comparisons with present-day Hadza hunter–gatherers from Tanzania, a 4,500-year-old ancient genome from Ethiopia (36), and the Dinka population from South Sudan, the study demonstrated a cline of geographically structured hunter–gatherer populations stretching from northeastern Africa

Ancient DNA (aDNA): DNA extracted from ancient remains

(present-day Ethiopia) to southern Africa (present-day South Africa), who were potentially connected to each other by gene flow between neighboring groups (132) or by shared ancestry—a link also previously seen from modern-day genetic variation (96, 125). This southern hunter–gatherer component, still present in the southern African San, contributed about two-thirds of the ancestry of Malawi hunter–gatherers (8,100–2,500 BP) and roughly one-third of the ancestry of Tanzanian hunter–gatherers (1,400 years BP) (132). Thus, before the great demographic changes that occurred in the last few thousand years owing to the introduction of farming and the migration of herding and farming groups, the genetic ancestry represented by present-day southern African San hunter–gatherers extended further, as a decreasing cline toward eastern Africa, with increasing genetic similarity to East African hunter–gatherers.

Although southern African Stone Age hunter–gatherers (who lived before the recent East African/Eurasian admixture) represent the most diverged human lineage, they still share significantly more alleles with eastern Africans (including the present-day Dinka and Hadza and the ancient Ethiopian Mota genome) than they do with present-day western Africans (as represented by the Yoruba and Mende) (123, 132) (**Figure 1**). There are two models that could explain this additional observation of deep structure. The first suggests that present-day western Africans have ancestry from two sources: a small fraction of their ancestry from a basal African lineage and the rest from a source related to eastern Africans (123, 132). In this model, the basal African lineage contributed more to the Mende than to the Yoruba. This model could support previous reports of evidence of archaic admixture in western and central Africans (47, 48, 54, 65, 98, 120) and is also consistent with larger estimates of effective population sizes among some western African groups (123). A low level of genetic drift between the basal African node and the rest of the tree (123) suggests a split time for the basal node not much earlier than the Khoe-San split and more recent than the Neanderthal split (132).

The second model suggests that continuous gene flow has connected southern and eastern African hunter–gatherer groups and that this cline of connected groups across the eastern part of the continent was also connected to western Africa (but with less gene flow toward the west). Furthermore, the eastern cline of groups was more connected to certain western African groups (e.g., Yoruba ancestors) than to other geographically more distant groups in western Africa (e.g., Mende ancestors). Generally, the second model equates to a model of isolation by distance, where groups are connected to surrounding groups but there are certain obstructions or barriers to gene flow in some directions (e.g., caused by terrain that is inaccessible, difficult to navigate, or uninhabitable). The rain forest is a known barrier to human movement in central Africa and could constitute such a barrier of gene flow to western Africa, while the easily navigable savanna grassland corridors in eastern Africa have reportedly led to clinal genetic relatedness in animals (74). These corridors of gene flow could have facilitated long-standing gene flow between hunter–gatherer populations in the eastern part of Africa, while the dense rain forests of central Africa could have hindered gene flow to the west (**Figure 1**). The inclusion of more representative (modern-day and ancient) central African groups could help with distinguishing between the different models of prefarming population structure within Africa. Until we have better genomic information from additional indigenous African groups and potentially from additional ancient human remains, our understanding of the deep human evolutionary history in Africa remains limited and is still based on interpretations of relatively limited data.

3. THE DEVELOPMENT OF FARMING IN AFRICA AND THE IMPACT ON POPULATION MIGRATION AND ADMIXTURE

The invention of farming not only caused dramatic transformations of the environment but also had a striking impact on the socioculture, health, and demography of human societies across the

globe. Population sizes increased drastically during the warmer Holocene epoch, and agriculture developed independently in several geographically dispersed regions (118). Farming societies outcompeted hunter–gatherer societies in temperate areas and rapidly expanded. Archaeological evidence indicates that farming practices spread rapidly over large distances, leading to continent-wide subsistence changes. It is, however, difficult to see in the archaeological record whether only the practices themselves spread to other places (cultural diffusion) or whether the people who practiced farming migrated (demic diffusion) (2). Genetic studies offer a unique opportunity to investigate the demographic effects of farming by comparing genetic variation within various farming populations and with remaining indigenous hunter–gatherer groups, allowing better inferences of human history with regard to population migration and cultural change.

Holocene: the geological epoch that began after the Pleistocene at approximately 11,700 years BP and continues to the present

Neolithic: the latest time period of the Stone Age, associated with new technology and the beginning of farming

Genetic studies have investigated the spread of farming (commonly called Neolithic expansions) on various continents. Arguably the most intensely investigated Neolithic event is the spread of farming into Europe from the Fertile Crescent and Anatolia (43, 86, 87, 130). Likewise, genetic studies contributed to the investigation of Neolithic expansions in East Asia (143), Oceania (145), the Americas (131), and Africa (15, 91, 136). However, the majority of research focusing on the spread of farming in Africa has been conducted using linguistic and archaeological approaches, with comparatively few investigations utilizing genetic information. Currently, it is believed that three regions in Africa developed agriculture independently: the Sahara/Sahel (around 7,000 BP), the Ethiopian highlands (~7,000–4,000 BP), and western Africa (~5,000–3,000 BP) (84). The Nile River Valley is thought to have adopted agriculture (~7,000–8,000 BP) from the Neolithic transition in the Middle East (~10,000–11,000 BP) (84). From these centers of origin, farmers or farming practices spread to the rest of Africa, with domesticated animals reaching the southern tip of Africa around 2,000 BP and crop farming around 1,800 BP (57, 83). Genomic investigations of both present-day and past humans hold great potential to generate, test, and contribute to hypotheses regarding the processes of neolithization in Africa.

3.1. The Expansion of the Bantu-Speaking Peoples

The Bantu Expansion is one of the largest expansion events of farmers globally and began around ~5,000–3,000 BP in western Africa (in the region of current eastern Nigeria and western Cameroon). It is visible in the archaeological record via increased sedentism, the spread of agricultural practices, and (later) the use of iron (39, 84, 85, 95, 139). Today, the majority of sub-Saharan Africans speak one of the ~500 closely related Bantu languages even though they are distributed over an area of ~500,000 km^2. Bantu languages form a subgroup of the Niger–Congo linguistic family, which, in turn, is one of the four independent major linguistic groups in Africa (the other three being Afro-Asiatic, Nilo-Saharan, and Khoisan). Earlier genetic studies have indicated that the current distribution of Bantu-speaking populations is largely a consequence of the movement of people (demic diffusion) rather than a diffusion of only language (71, 125, 136) (**Figure 3**). However, this huge migration event was likely complex and multifaceted, with initial and subsequent movements, replacements of different groups, and potentially admixture with local hunter–gatherer groups (57, 84). Most of the existing hypotheses about the migration routes of the Bantu Expansion are based on linguistics and archaeology.

Bantu languages are divided into three major groups: Northwestern Bantu, Eastern Bantu, and Western Bantu (45, 52, 139). Northwestern Bantu languages are spoken near the core region from where the expansion started, while the Eastern Bantu and Western Bantu language branches potentially spread out from their western African homeland in two separate migration routes (**Figure 1*b***; see also the **Supplemental Methods** and **Supplemental Figure 1**). Ancestors of Eastern Bantu–speaking groups are thought to have migrated eastward out of western Africa (either

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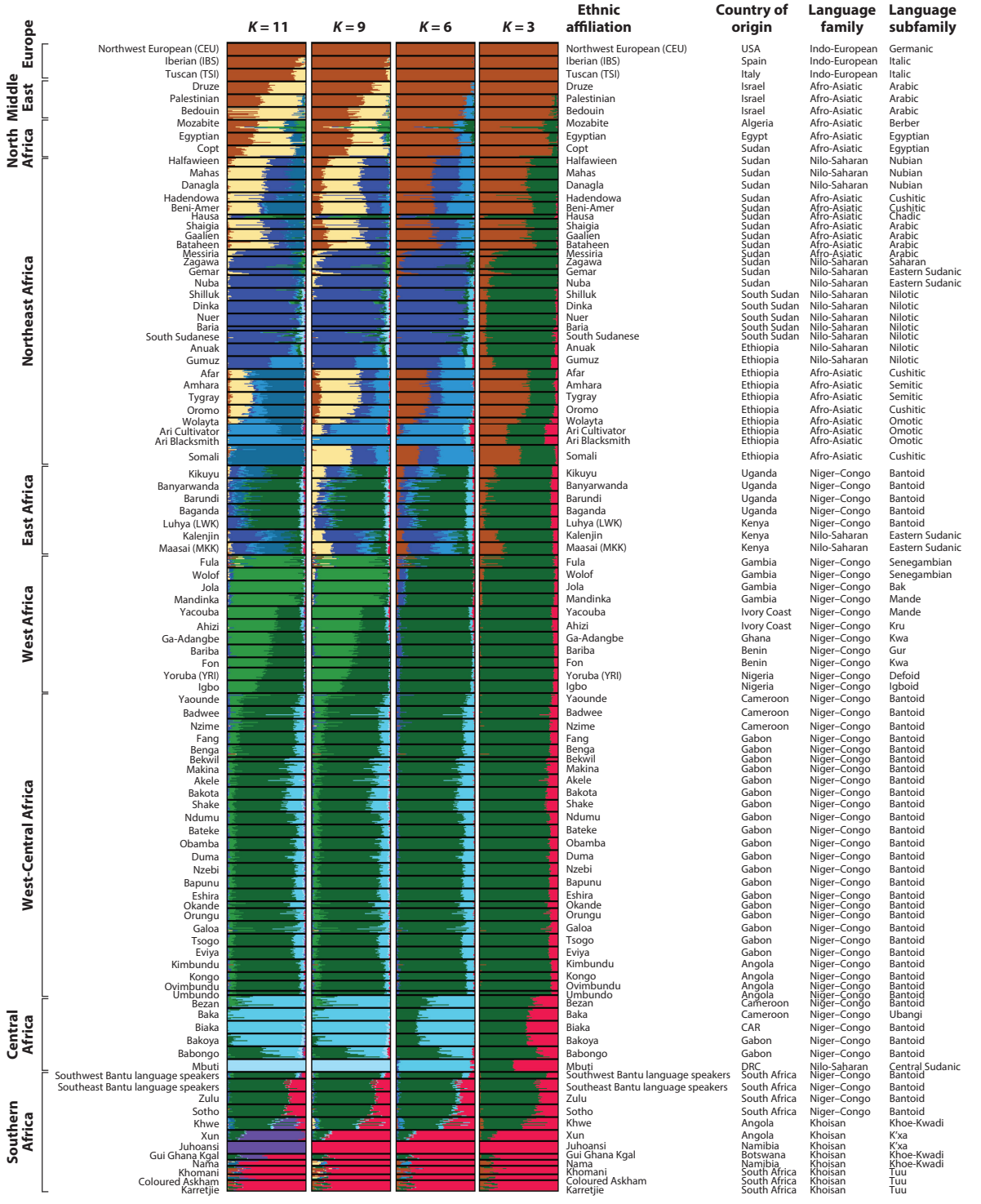

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Figure 3 (*Figure appears on preceding page*)

Population structure analysis and inferred ancestry components for selected choices of assumed number of ancestries ($K = 3$, 6, 9, and 11) for 93 African and 6 non-African populations. **Figure 2** displays the ancestry components for $K = 5$. The broad geographical distributions are indicated on the left. The columns on the right indicate ethnic affiliation, country of origin, language family, and language subfamily. Data were obtained from several studies (4, 16, 44, 53, 70, 89, 125), and the details of the analysis are described in the **Supplemental Methods**. Abbreviations: CAR, Central African Republic; DRC, Democratic Republic of the Congo.

Supplemental Material >

above or below the rain forests, forming the basis of the early-versus-late-split linguistic hypotheses), reaching the Great Lakes region in eastern Africa by ~3,000 BP (30). The linguistic theories suggest that they thereafter expanded further southward, reaching their current distribution across eastern and southern Africa around 1,300 BP. The ancestors of Western Bantu–speaking groups may have spread directly south through the rain forests from the Cameroon homeland, possibly following the Atlantic coast, forming the second major route of the Bantu Expansion (45, 52, 139). Therefore, in southern Africa, there are two main Bantu-speaking groups, southeastern and southwestern Bantu language speakers (**Figure 3**), who represent the edges of the two Bantu Expansion waves according to linguistic research.

Evidence from archaeology regarding migrations of Bantu language speakers does not necessarily support linguistic inferences (**Supplemental Figure 1**). According to archaeological theories, East African Bantu language speakers (possibly associated with traditions emerging from the Urewe ceramic tradition) spread south from the Great Lakes region in East Africa, through eastern and southern Africa, during the first millennium AD. The archeology of this group is distinct from that of the West African Bantu language speakers and is recognized by distinct pottery, use of iron, herding of domesticated livestock, and cultivation of cereal crops such as sorghum and millet (95). From the Great Lakes region, there seem to have been two main migration events southward, represented archaeologically by the split into two branches: the Nkope branch, which took an inland route, and the Kwale branch, which took a more coastal route (**Supplemental Figure 1*a***). Another ceramic tradition, Kalundu, is proposed to have come from the west, south of the equatorial forest, across central Africa (present-day Democratic Republic of the Congo and Zambia) into present-day Zimbabwe and South Africa. Southeastern Bantu language speakers who today live in South Africa, Mozambique, and Zimbabwe are therefore predicted to be a mix of these three different inferred dispersal routes from central Africa. Western Bantu languages (including southwestern varieties) could possibly be linked with a fourth ceramic tradition, Naviundu (**Supplemental Figure 1*a***).

Since the 1990s, genetic information has been utilized in deciphering the Bantu Expansion. These studies used a limited number of classical genetic markers and noted considerable genetic homogeneity among Bantu language speakers compared with the genetic differentiation between West African Niger–Congo language speakers and East African Nilo-Saharan language speakers (19). Studies using single-locus mtDNA (21, 116) and Y-chromosome markers (1, 3, 21, 24) have shown that specific haplogroups were associated with Bantu-speaking people. Recently, genome-wide typing and analyses of microsatellite markers (136) and SNPs (15, 91, 125) demonstrated the genetic similarity of geographically distant Bantu-speaking groups (**Figures 2** and **3**).

Genetic studies have also started to test specific hypotheses regarding the Bantu Expansion. De Filippo et al. (25) used autosomal genetic data to test a linguistic hypothesis regarding the early phases of the Bantu Expansion. Two hypotheses, based on linguistics, have been proposed for how the people speaking the eastern and western branches of Bantu languages spread from western Africa. In the first hypothesis (the early-split hypothesis), the people of the eastern and western branches split early into two separate migration routes. The alternative hypothesis (the late-split hypothesis) is that these two branches split later, after the people migrated through the central African rain forest (**Supplemental Figure 1*b***). The genetic data fit better with the

late-split linguistic hypothesis, suggesting a more recent development of Eastern Bantu languages out of Western Bantu languages (25). In accordance with this study, a recent extensive linguistic study found strong support for the late-split hypothesis (23), as did two genetic studies using dense genome-wide markers and additional populations (15, 91).

Another genetic study tested the larger-scale perspective of the linguistic hypothesis in connection with the eastern route of the Bantu Expansion by concentrating on the terminal southeastern Bantu-speaking groups (71). The study included selected Bantu-speaking populations from western, eastern, and southern Africa (136) and contrasted four different population histories with possible routes of dispersal of the eastern branch of Bantu language speakers on the African continent. In accordance with the linguistic hypothesis, the study found that the most likely model for the movement of the eastern branch of Bantu language speakers involved the migration of Bantu-speaking groups to the east followed by migration to the south (71). This model, however, was only marginally more likely than other models, which might indicate significant gene flow with the western branch of Bantu language speakers. Alternatively, it could also support the archaeological hypothesis and provide support for the existence of a migration route associated with the Kalundu ceramic tradition across central Africa.

Genetic studies of Bantu language speakers have thus far been limited owing to the amount of genetic data collected from each group (i.e., only mtDNA) and/or poor geographic coverage. The recent publication of full genome sequence data from Bantu language speakers is promising (4, 20, 44, 76), and the inclusion of more population groups across the continent in genome-wide studies should help to refine and extend hypotheses regarding large- and fine-scale movements of Bantu language speakers.

3.2. The Spread of Pastoralism from the East to the South

The Khoekhoe herders of southern Africa represent a lesser-known long-distance spread of pastoralist practices, originating from East Africa and spreading to the southern tip of the continent before, and independent of, the Bantu Expansion. During historical times in southern Africa (1600s and onward), the western parts of South Africa and the southern and central parts of Namibia were occupied by Khoekhoe herders and San hunter–gatherers. The eastern branch of Bantu language speakers (Xhosa speakers) reached as far south as the Fish River in the present Eastern Cape province of South Africa, whereas the western branch reached the north of Namibia, where they encountered the Khoekhoe herders (31, 57, 83).

Archaeological research suggests that a sheep-herding economy and ceramics were introduced to southern Africa from East Africa and arrived in Zambia and Zimbabwe around 2,100 BP (42, 115, 133). However, archaeological artifacts could not show whether the spread of pastoralism was associated with a demic diffusion of pastoralist populations or a diffusion of the practice on its own. Genetic studies of contemporary and ancient southern African Khoekhoe (herders) and San (hunter–gatherer) groups detected a mixed East African/Eurasian genetic component in all contemporary Khoe-San groups, but this component was present at higher frequencies in Khoekhoe groups (13, 75, 97, 123, 125, 132). The results suggested that herding practices were brought to southern Africa by the migration of a group of individuals with East African/Eurasian ancestry who were subsequently assimilated by one or more local southern African hunter–gatherer groups, which led to the ancestors of the Khoekhoe herders. The results showed that the post-2,000-BP admixture source in the modern-day Khoe-San was an already-admixed East African/Eurasian group (this group had 69% East African and 31% Eurasian ancestry), comparable to the present-day Amhara of East Africa (123) (see Section 3.3). The least admixed San group, the Ju|'hoansi (historical foragers), had 9–14% East African/Eurasian admixture; the Nama (Khoekhoe, historical

herders) had 23–30% admixture; and all modern-day Khoe-San groups had East African/Eurasian admixture levels ranging between 9% and 30%. The admixture events date to 1,500 and 1,300 BP (based on genetic data) for the Ju|'hoansi and Nama, respectively (123).

The Nama are only one of the many Khoekhoe pastoralist groups who occupied southern Africa during the 1600s, and it is not known whether the East African component occurred in all Khoekhoe groups. The Nama (most of whom are currently living in Namibia) were the northernmost group among the Khoekhoe herders (7). Following the European colonization, the South African Khoekhoe groups mostly lost their cultural identities and languages and became assimilated into a mixed-ancestry group, historically (and still used today by many individuals to self-identify) called the Coloured population (20, 125). Extending genetic studies to include more Khoekhoe and Khoekhoe-descendent populations as well as aDNA studies of ancient remains of herders (see Section 3.3) can help to clarify the extent and magnitude of East African admixture in different Khoekhoe groups. Such studies and data could lead to a better understanding of the population dynamics during the introduction of pastoralism to parts of southern Africa.

3.3. The Crop Farmers and Herders of Northeastern and Eastern Africa

It is currently believed that farming practices in northeastern and eastern Africa developed independently in the Sahara/Sahel (around 7,000 BP) and the Ethiopian highlands (7,000–4,000 BP), while farming in the Nile River Valley developed as a consequence of the Neolithic Revolution in the Middle East (84). Northeastern and eastern African farmers today speak languages from the Afro-Asiatic and Nilo-Saharan linguistic groups, which is also reflected in their genetic affinities (**Figure 3**, $K = 6$). In the northern parts of East Africa (South Sudan, Somalia, and Ethiopia), Nilo-Saharan and Afro-Asiatic speakers with farming lifeways have completely replaced hunter–gatherers. It is still largely unclear how farming and herding practices influenced the northeastern African prefarming population structure and whether the spread of farming is better explained by demic or cultural diffusion in this part of the world. Genetic studies of contemporary populations and aDNA have started to provide some insights into population continuity and incoming gene flow in this region of Africa.

For example, studies have shown that a back-migration from Eurasia into Africa affected most of northeastern and eastern Africa (36, 46, 53, 89, 132) (**Figure 1*b***). A genetic baseline of eastern African ancestral genetic variation unaffected by recent Eurasian admixture and farming migrations within the last 4,500 years has been suggested in the form of the genome sequence of a 4,500-year-old individual from Mota, Ethiopia (36). Based on comparisons with the ancient Mota genome, we know that certain populations from northeastern Africa show deep continuity in their local area with very limited gene flow resulting from recent population movements. For example, the Nilotic herder populations from South Sudan (e.g., Dinka, Nuer, and Shilluk) appear to have remained relatively isolated over time and received little to no gene flow from Eurasians, West African Bantu-speaking farmers, and other surrounding groups (53) (**Figures 2** and **3**). By contrast, the Nubian and Arab populations to their north show gene flow with Eurasians, which has been connected to the Arab expansion (53). The Nubian, Arab, and Beja populations of northeastern Africa roughly display equal admixture fractions from a local northeastern African gene pool (similar to the Nilotic component) and an incoming Eurasian migrant component (53) (**Figure 3**). The Eurasian component has been linked to the Middle East and the Arab migration, but only the Arab groups shifted to the Semitic languages; the Nubians and Beja groups kept their original languages. The Eurasian gene flow appears to have spread from north to south along the Nile and Blue Nile in a succession of admixture events (53).

Toward East Africa, the Ari (Blacksmiths) (36, 89) and Hadza (132, 136) seem to be remnant present-day populations of local hunter–gatherers who lived in these areas before the influence of Eurasian back-migrations and the migrations of farmers and herders. Genetic evidence suggests that prior to the introduction of farming, there existed a cline of relatedness between hunter–gatherers living in Ethiopia (represented by the Mota genome) and San hunter–gatherers from southern Africa (see Section 2). This cline stretched along East Africa in a north-to-south direction, and ancient Malawi and Tanzanian hunter–gatherers can be seen as intermediates in this cline, which reached from Ethiopia to southern Africa (132). The development and introduction of herding and farming in East Africa (around 3,000 years BP) and the ensuing southern migrations of mixed East African/Eurasian herders into southern Africa, followed by the Bantu Expansion, erased much of this preexisting cline of hunter–gatherer ancestry (132). In Malawi and Mozambique, the majority populations today are Bantu language speakers, and in East African countries farther north (e.g., Tanzania, Kenya, and Uganda), farmer populations are made up of a mix of these three ancestry components (East African, West African, and Eurasian) (36, 89, 132) (**Figure 3**, $K = 6$).

The timing of the Eurasian back-migration into East Africa has been estimated to (on average) 3,000 years BP based on genetic admixture signals in several Ethiopian populations (89, 97), and the source population had ancestry related to the ∼10,000-year-old prepottery farmers of the Levant (69, 132). There is significant archaeological evidence of intense contact and migration between Ethiopia and southern Arabia around 3,000 years BP (37, 61). During the first millennium BC, southern Arabians from the Saba territory established a polity in the Abyssinian highlands of Ethiopia, and a new conglomerate cultural landscape called the Ethio-Sabean society emerged (37, 61). This event overlaps with the timing of Eurasian genetic admixture signals in Ethiopian populations and is a good candidate for the source of the Eurasian admixture in East Africa. The southern spread of the mixed East African/Eurasian group into Tanzania was relatively rapid. A 3,100-BP individual from Luxmanda (Tanzania), associated with a Savanna Pastoral Neolithic archaeological tradition, had 38% ± 1% of her ancestry related to the prepottery farmers of the Levant and her remaining ancestry closely related to the Mota individual from Ethiopia. The southern movement of these East African/Eurasian pastoralists eventually reached southern Africa, where they admixed with local San hunter–gatherers. Today, all San hunter–gatherers show admixture from this East African/Eurasian group, and Khoekhoe herders, such as the Nama, have up to 30% admixture from this group (123) (also see Section 3.2). The admixture fractions in ancient southern African herders were higher than those in the Khoekhoe today, and a 1,200-BP pastoralist individual from the Western Cape had ∼40–50% ancestry related to the Tanzanian Luxmanda individual (Savanna Pastoral Neolithic individual) and the remaining ancestry component related to southern African San hunter–gatherers (132).

In addition to the Arabification of northeastern Africa, the recent north-to-south movements of mixed East African/Eurasian herders along the east coast of Africa, and the expansions of Bantu language speakers throughout sub-Saharan Africa, there were also east–west bidirectional migrations of nomadic herding groups throughout the Sahel Belt. In the Sahel Belt, which acts as a corridor of human migration and is fringed by the tropical rain forests to the south and the Saharan desert to the north, two lifeways of farming are practiced: nomadic pastoralism, where groups continually migrate to find pasture for their animals, and crop farming, where groups are sedentary and located in temperate areas. Triska et al. (138) found an increasing clinal differentiation between western and eastern Sahelian populations in genotype data from a large collection of populations from a region across the Sahel Belt into East Africa. Furthermore, there were strong signals of Eurasian admixture into central and eastern Sahelian populations but not into western Sahelian populations. Eurasian gene flow reaching into Chad has been reported (46).

The ~3,000-year-old Eurasian back-flow into Africa affected populations in northern Chad, such as the Toubou (who had 20–30% Eurasian admixture), but this event had no detectable genetic impact on other Chadian populations. Despite their Islamic faith, the Toubou do not harbor Middle Eastern admixture associated with the Arabification of northeastern Africa, suggesting cultural diffusion without genetic admixture (46).

3.4. Africa North of the Sahara: Migration Patterns and the Question of Population Continuity

Human demographic history in North Africa has a unique standing, with modern-day groups largely related to Eurasian populations in conjunction with modest gene flow from sub-Saharan Africa (50, 60, 76, 114), extreme climates and climate variability (26), important early human fossils, and a diverse record of archaeological artifacts (119). The North African climate oscillates between dry conditions during the interglacial periods and humid conditions, with savanna and river networks extending into the Sahara during glacial periods (18, 27). The coastal regions display less extreme variation, with forests and steppe plains existing even during the dry periods. The Saharan desert becomes hyperarid during the interglacial periods (covering a fourth of the African land mass), and during these times, the Nile River Valley forms the only major south-to-north fertile axis that transcends the Sahara (67).

The modern-day North African populations display clear genetic affinities to Middle Eastern and West Eurasian populations (50, 60, 76, 114) (**Figures 1*b***, **2**, and **3**), which is suggested to be the result of back-to-Africa migrations (50). A distinct genetic component, described as Maghrebi, is present in increasing frequency from the east to the west in North Africa (50), reaching as far as the Canary Islands (112). This Maghrebi component is dominant in early Neolithic individuals (~7,000 BP) from modern-day Morocco, who display strong genetic affinity with extant groups in the area (35). Among early Neolithic groups across western Eurasia, the Moroccan early Neolithic individuals are genetically most similar to prepottery Anatolian farmers and Natufians from the Middle East, suggesting a potential early migration of prepottery groups westward, potentially interwoven with some farming practices or, alternatively, predating farming practices (35). Local expressions of ceramics in North Africa have been used to argue for an indigenous development of farming, but the introduction of domesticated animals common for the early Neolithic Middle East complicates the interpretation. Whether earlier human groups in North Africa (potentially linking back to the groups found in the fossil record >40,000 BP or later epi-Paleolithic groups) contributed to the early Neolithic farmers of North Africa remains an open question. Later Neolithic groups in Morocco (~5,000 BP), however, display a distinct admixture component from Neolithic groups in Iberia, who were descendants of Anatolian early farmers (63), suggesting migration across the Mediterranean to North Africa, a process that does not appear to have happened in the earlier phase (35).

Genetic ancestry components related to populations on the Arabian Peninsula display an opposite pattern across North Africa to the Maghrebi genetic component, with greater fractions toward the east (50). A similar pattern is observed across northeastern Africa, with decreasing genetic affinities to groups on the Arabian Peninsula as distance increases toward the south, following the Nile River Valley, across Sudan and South Sudan (53). This genetic cline of admixture has been dated to coincide with the Arab expansion in both northern and northeastern Africa (53) (see Section 3.3). Gene flow across the Sahara has been rare and appears in relatively recent times, with limited gene flow from sub-Saharan groups in North Africa during the Neolithic (63), whereas earlier times appear to be represented by groups drawing ancestry from both sub-Saharan and Eurasian groups. The southwestern part of North Africa displays admixture with sub-Saharan

Africans, but the admixture proportions vary greatly across individuals, indicating recent and ongoing gene flow (50). People in classical Egypt also displayed less sub-Saharan admixture compared with present-day Egyptians, demonstrating that the gene flow is recent, at least in the easternmost part of North Africa (126).

It is possible that human occupation in North Africa has been interrupted at certain time points or is at least fragmented (119) owing to the specific climate conditions, with the Saharan desert extending over vast areas during periods spanning many millennia (27). For instance, archaeological investigations of stone-tool similarities (in Marine Isotope Stage 5) display correlations with geographic distance, in an isolation-by-distance pattern, with the exception of greater similarity along water sources (119, 121). Even if the early human populations of North Africa contributed little or no genetic material to the Neolithic groups, they may still have been related to and mixing with early East African groups who were related to the populations migrating out of Africa (90), first only to the Middle East (~120,000 BP) and then later (~80,000 BP) to eventually colonize every continent except Antarctica. They may also have contributed to the early human admixture into Neanderthals (81, 86, 100).

4. SELECTION AND ADAPTIVE INTROGRESSION IN AFRICAN POPULATIONS

Africa is a large continent with extreme environments. Habitats range from vast deserts (such as the Sahara, Namib, and Kalahari) to dense tropical rain forests in central Africa. These diverse environments offer unique challenges to human populations, yet humans have adapted to occupy all types of biomes in Africa. Signals of long-standing adaptation to the local environment and its challenges can be observed in the genomes of many African populations. The recent movement and migration of groups—for instance, because of the invention of pastoralism and farming in the Holocene—presented migrating groups with new environmental challenges. Even these recent events have left specific evidence of selection in the genomes of some groups. The cultural and dietary changes that accompanied the change from a hunter–gatherer lifeway to an agricultural and/or pastoralist lifeway also left signals of recent selection in the genomes. Here, we discuss several key examples of long-standing adaptation of African groups to their environments and evidence of recent selection in African groups caused by lifestyle changes, migration, and the challenges of new environments.

The African continent is centered on the equator with the Tropic of Cancer (23.5°N, going through, e.g., Algeria and Libya in North Africa) and the Tropic of Capricorn (23.5°S, going through South Africa). Human skin color varies with latitude, and close to the equator, dark skin color helps to protect against UV radiation from the sun. Farther away from the equator, lighter skin color is adaptive, allowing enhanced vitamin D_3 production (22, 33, 59). Skin color in Africa ranges from light in the San populations of southern Africa (comparable to skin color in Asian populations) to the darkest in the world in the Nilo-Saharan groups of eastern Africa (22). In an extensive study of the genetic basis of skin color variation in ethnically diverse African groups, Crawford et al. (22) found six genes to be strongly associated with skin color in Africa. Four of these genes contained alleles estimated to segregate for hundreds of thousands of years in the hominin lineages, suggesting long-standing local adaptation to UV radiation in African populations (22). The ancestral alleles at these loci are associated with light pigmentation, suggesting that dark pigmentation is a derived and adaptive trait in humans that arose from the need for UV light protection after human ancestors lost their body hair (59, 113). Aside from the six strongly associated loci, many additional loci were found to be weakly associated with pigmentation levels, and these loci are likely to contribute to skin color variation in Africans as well, with smaller effect sizes (22).

Selection on standing variation: selection that acts on a variant that is present in the population at the start time of selection; this variant was typically neutral before a change in, e.g., environment

Online Mendelian Inheritance in Man (OMIM): an online catalog that is continually updated with new studies concerning gene–phenotype associations

Major histocompatibility complex (MHC): a set of cell surface proteins that plays a crucial role in the immune system and is encoded by a set of genes on human chromosome 6

In addition to effects from the physical environment, such as solar radiation, humans are also exposed to challenges from the biological environment, such as various degrees of disease load. The distinctive climatic biomes of Africa present unique sets of pathogenic challenges to human population groups that inhabit these regions. In the tropical regions of Africa, diseases such as malaria, sleeping sickness, and leishmaniasis are widespread, while in the more temperate and dry regions of Africa, these pathogens are absent, and these regions generally have a lower disease load. Malaria is an infectious disease that has elicited one of the strongest selective pressures detected in humans (64, 80). Several studies have reported evidence of local adaptations that confer protection against malaria in various populations, with protective allelic variants in several genes, including *DARC*, *G6PD*, and *HBB* (the extensively studied sickle cell variant in the *HBB* gene has increased in frequency as a result of balancing selection among heterozygotes in the presence of malaria) (64). The *DARC* gene encodes a transmembrane receptor (Duffy antigen receptor) used by the malaria-causing protozoan *Plasmodium vivax* to infect red blood cells. Three alleles of this gene segregate in appreciable frequencies in human populations: FY*A, FY*B, and FY*O. The FY*B allele is ancestral and confers a susceptible phenotype in the presence of malaria (64). FY*O occurs on a FY*B background and protects against *Plasmodium vivax*, while the protective effect of FY*A is less clear. The FY*O allele is near fixation in western and central Africa, while FY*B and FY*A are common in Europe and Asia (64, 80). In southwestern parts of southern Africa, the environment is less suitable for the malaria parasite, and thus lower or no selection pressure is expected. The indigenous southern African ≠Khomani San display all three alleles (FY*A, FY*B, and, FY*O) at intermediate frequencies. The presence of two highly diverged (and malaria-protective) FY*O haplotypes in African populations suggests an ancient origin (>40,000 BP) of the protective variant(s) and selection on standing variation, rather than a recent hard selective sweep of a novel variant (80). Many other genes have been linked to protection against malaria. The Online Mendelian Inheritance in Man (OMIM) database reports 17 such genes, several of which have been linked to selection signals in African populations (15, 44, 91, 138). Studies have also linked numerous other infectious diseases to selection signals in several African populations; e.g., Gurdasani et al. (44) and Triska et al. (138) reported African-specific local adaptation to several endemic diseases, including malaria, Lassa fever, trypanosomes, and trachoma, and identified several allelic variants that might have been selected to protect against these diseases.

One of the largest migration processes in the Holocene involves Bantu-speaking groups from western Africa expanding to eastern and southern Africa, a process likely driven by farming subsistence strategies and, at least in the later phase, linked to iron working. These groups encountered new environments in which they had to survive. The strongest signal of selection in the genomes of Bantu language speakers that today live in or close to the central African rain forests is in the major histocompatibility complex (MHC) region of the genome, which mediates and controls immune responses (91). Among the Bantu-speaking groups, the MHC region is also the one that has the highest ancestry contribution from rain forest hunter–gatherers. Taken together, these two patterns suggest adaptive introgression. In other words, the genetic MHC variants in rain forest hunter–gatherers were likely better adapted to the specific disease conditions of the rain forests, and the expansion of Bantu language speakers into these areas was likely facilitated by gene flow from local populations (91).

Migrating farmer and pastoralist groups potentially also caused large increases in local disease burden, particularly zoonotic diseases. As a result, local hunter–gatherers may have been exposed to diseases associated with sedentary or herding lifestyles through interactions with immigrant groups and local groups that adopted those modes of subsistence. Owers et al. (88) found stronger and more abundant selection signals for immune genes in the southern African ≠Khomani San (who had abundant contact with other people migrating into the region, such as East African

pastoralist groups, Bantu language speakers, and European colonists) compared with the isolated Ju|'hoansi San group (88). The study provided evidence of how, through selection on multiple loci, the immune system can rapidly adapt in populations that come into contact with external groups and their unfamiliar diseases.

Lactase persistence (LP): the ability to digest lactose (milk sugar) into adulthood

Changing cultural practices, such as the adoption of a new subsistence strategy, directly cause changes in the human genome as a consequence of adaptation to the new lifeway (33, 86). Human groups in Africa are no exception, and one of the most striking examples is the adaptation of lactase persistence (LP)—the continued ability to digest lactose after weaning. The prevalence of LP varies among humans and is particularly common among populations that have traditionally practiced herding. LP is conferred to humans by a few mutations in a control element of the lactase gene (*LCT*) (135). Particular variants in the *LCT* control element situated in introns of an adjacent gene (*MCM6*) prevent the downregulation of the *LCT* gene in adults (32, 137). At least five variants are known that are responsible for the LP phenotype (128). These five variants occur on different haplotype backgrounds, which indicates that they evolved independently and in parallel (137). Three of these variants originated and underwent selection in African pastoralist groups: C–13907G (rs41525747) in Ethiopian groups, T–14009G (rs869051967) in African Arab groups, and G–14010C (rs145946881) in Kenyan and Tanzanian groups. The two remaining variants likely originated outside of Africa, in the Middle East (T–13915G, rs41380347) and Europe (C–13910T, rs4988235), but these variants are also present at appreciable frequencies in certain African groups owing to recent migration and admixture (62, 101, 108, 137).

The G–14010C variant is associated with LP in various East African groups from Tanzania and Kenya, and there is a strong signal for selection associated with this genomic region in some of these populations (124, 125, 137). The frequency of the C allele varies among different East African groups, occurring at frequencies of ~18–46% in Nilo-Saharan and Afro-Asiatic groups, while the variant is absent in the Hadza hunter–gatherers (137). This East African variant also occurs in southern African Khoe-speaking groups and has been connected with the introduction of herding practices to southern Africa (13, 75).

Both the –13907G- and –14009G-derived alleles occur in Sudan and East Africa (58, 62, 108, 137). The highest frequencies of these alleles are in the Beja populations (i.e., the Beni-Amer and Hadendowa) from Sudan. The –13915G LP-associated allele likely originated in the Middle East (32, 58, 102, 137) but occurs at appreciable frequencies in nomadic populations throughout northeastern Africa (102). The allele may have spread from the Middle East to Africa through nomadic Bedouin populations (58, 101). Frequencies in Sudan correlate with Middle Eastern admixture (N. Hollfelder, C.M. Schlebusch, H. Edlund, L. Granehäll, H. Babiker, et al., unpublished results) linked to the Arabification of northeastern Africa (53). The European LP allele (–13910T) has low frequencies in Africa but was introduced into certain African populations—i.e., the Fulani of Sudan, Mali, and Cameroon (49, 58, 72); the Shokrya of Sudan (49); and the Nama from southern Africa (13, 75)—as a result of European gene flow.

All five of these LP-associated SNPs are contained in the LP control region in intron 13 of the *MCM6* gene. However, potential additional LP variants have been identified farther away from this region—i.e., in intron 9 (137)—and it is possible that the upstream region of the *LCT* gene contains further LP variants (33). West African crop farmers (i.e., Yoruba from Nigeria) and central and southern African hunter–gatherers show no signature of selection at the *LCT* locus and do not carry any known LP variants at appreciable frequencies (60, 125, 142).

The LP region also has examples of adaptive introgression in various African population groups. Patin et al. (91) found an excess of East African ancestry in the *LCT* region of Bantu language speakers from East Africa. This region introgressed from local East African Afro-Asiatic or Nilo-Saharan groups into the genomes of Bantu language speakers, and the introgressed variants showed

evidence of strong positive selection. There is a correlation between the Middle Eastern variant and non-African ancestry in Sudanese populations, and the Middle Eastern variant has higher frequencies than genome-wide proportions, indicating adaptive introgression (N. Hollfelder, C.M. Schlebusch, H. Edlund, L. Granehäll, H. Babiker, et al., unpublished results). Similarly, the Nama herders from southern Africa showed higher East African ancestry in the LP region than genome-wide proportions (13). LP therefore has several independent strong signals of local adaptation in African pastoralist populations as well as several examples of adaptive introgression.

In addition to the LP control region, other genomic regions have been reported to be associated with selection pressures connected to lifestyle changes linked to farming. For example, copy numbers of the amylase gene (*AMY1*), associated with starch digestion, have been linked with selection in farmers (93, but also see 34). Other studies of farming groups identified selection signals in genes associated with celiac disease, fatty acid metabolism, vitamin absorption, and body mass (33, 77). More studies of African farmer and pastoralist groups could clarify the roles of these (and additional) genes in the adaptation of African farmers and pastoralists to new environments and lifeways.

5. CONCLUDING REMARKS

In the last few decades, genetic studies have increasingly contributed to hypotheses about the migration of farmers and herders across Africa during Holocene times. Studies have thus far been limited by the amount of genetic data collected from each group (i.e., many studies are based only on uniparental markers) and/or poor geographic coverage. Inclusion of more population groups in genome-wide autosomal studies will help to refine and extend hypotheses regarding large- and fine-scale movements of farmers and herders. However, since the true history is most likely a complex mix of events that has resulted in conflicting archaeological and linguistic interpretations, extensive coverage of sub-Saharan African groups in genetic studies (with regard to sample size and populations) is needed. Furthermore, genome sequencing studies of ancient human remains from across the African continent, especially of samples with good stratigraphic context and association with material culture, will further improve inferences by providing time-serial information on demographic changes. This will enable robust testing of the different hypotheses and possibly lead to the generation of new ideas of how farmers and herders moved across the continent, interacted with local hunter–gatherer groups, and possibly admixed with other branches of the same or other expansions.

For our species' deep history in Africa, both paleoanthropological and genetic evidence increasingly point to a multiregional origin of AMHs in Africa. However, many questions remain to be resolved, and several different (and possibly overlapping) scenarios could have resulted in the current-day patterns of genetic variation in humans. It is unclear whether modern humans originated from a single randomly mating population, originated from a geographically structured population (11), or exchanged genetic material with African archaic humans (47, 65, 86, 123, 132). It is also unclear which genetic changes were important for the transformation of archaic humans to AMHs (76, 94, 104–106, 125). African genomes will bring us closer to answering the main questions of human origins, and future aDNA studies and full genome sequences from hunter–gatherer groups will continue to clarify the picture of our deep genetic history in Africa.

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LITERATURE CITED

1. Alves I, Coelho M, Gignoux C, Damasceno A, Prista A, Rocha J. 2011. Genetic homogeneity across Bantu-speaking groups from Mozambique and Angola challenges early split scenarios between East and West Bantu populations. *Hum. Biol.* 83:13–38
2. Ammerman AJ, Cavalli-Sforza LL. 1984. *The Neolithic Transition and the Genetics of Populations in Europe*. Princeton, NJ: Princeton Univ. Press
3. Ansari Pour N, Plaster CA, Bradman N. 2012. Evidence from Y-chromosome analysis for a late exclusively eastern expansion of the Bantu-speaking people. *Eur. J. Hum. Genet.* 21:423–29
4. Auton A, Brooks LD, Durbin RM, Garrison EP, Kang HM, et al. 2015. A global reference for human genetic variation. *Nature* 526:68–74
5. Barbieri C, Vicente M, Rocha J, Mpoloka SW, Stoneking M, Pakendorf B. 2013. Ancient substructure in early mtDNA lineages of southern Africa. *Am. J. Hum. Genet.* 92:285–92
6. Barham L, Mitchell P. 2008. *The First Africans: African Archaeology from the Earliest Toolmakers to Most Recent Foragers*. Cambridge, UK: Cambridge Univ. Press
7. Barnard A. 1992. *Hunters and Herders of Southern Africa: A Comparative Ethnography of the Khoisan Peoples*. Cambridge, UK: Cambridge Univ. Press
8. Behar DM, Villems R, Soodyall H, Blue-Smith J, Pereira L, et al. 2008. The dawn of human matrilineal diversity. *Am. J. Hum. Genet.* 82:1130–40
9. Berger LR, Hawks J, Dirks PH, Elliott M, Roberts EM. 2017. *Homo naledi* and Pleistocene hominin evolution in subequatorial Africa. *eLife* 6:e24234
10. Berger LR, Parkington JE. 1995. A new Pleistocene hominid-bearing locality at Hoedjiespunt, South Africa. *Am. J. Phys. Anthropol.* 98:601–9
11. Blum MG, Jakobsson M. 2011. Deep divergences of human gene trees and models of human origins. *Mol. Biol. Evol.* 28:889–98
12. Brauer G. 2008. The origin of modern anatomy: by speciation or intraspecific evolution. *Evol. Anthropol.* 17:22–37
13. Breton G, Schlebusch CM, Lombard M, Sjödin P, Soodyall H, Jakobsson M. 2014. Lactase persistence alleles reveal partial East African ancestry of southern African Khoe pastoralists. *Curr. Biol.* 24:852–58
14. Brothwell D, Shaw T. 1971. A Late Upper Pleistocene proto-West African Negro from Nigeria. *Man* 6:221–27
15. Busby GB, Band G, Si Le Q, Jallow M, Bougama E, et al. 2016. Admixture into and within sub-Saharan Africa. *eLife* 5:e15266
16. Cann HM, de Toma C, Cazes L, Legrand MF, Morel V, et al. 2002. A human genome diversity cell line panel. *Science* 296:261–62
17. Cann RL, Stoneking M, Wilson AC. 1987. Mitochondrial DNA and human evolution. *Nature* 325:31–36
18. Castaneda IS, Mulitza S, Schefuss E, Lopes dos Santos RA, Sinninghe Damste JS, Schouten S. 2009. Wet phases in the Sahara/Sahel region and human migration patterns in North Africa. *PNAS* 106:20159–63
19. Cavalli-Sforza LL, Menozzi P, Piazza A. 1994. *The History and Geography of Human Genes*. Princeton, NJ: Princeton Univ. Press
20. Choudhury A, Ramsay M, Hazelhurst S, Aron S, Bardien S, et al. 2017. Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. *Nat. Commun.* 8:2062
21. Coelho M, Sequeira F, Luiselli D, Beleza S, Rocha J. 2009. On the edge of Bantu expansions: mtDNA, Y chromosome and lactase persistence genetic variation in southwestern Angola. *BMC Evol. Biol.* 9:80

22. Crawford NG, Kelly DE, Hansen MEB, Beltrame MH, Fan S, et al. 2017. Loci associated with skin pigmentation identified in African populations. *Science* 358:eaan8433
23. Currie TE, Meade A, Guillon M, Mace R. 2013. Cultural phylogeography of the Bantu Languages of sub-Saharan Africa. *Proc. Biol. Sci.* 280:20130695
24. de Filippo C Barbieri C, Whitten M, Mpoloka SW, Gunnarsdottir ED, et al. 2011. Y-chromosomal variation in sub-Saharan Africa: insights into the history of Niger-Congo groups. *Mol. Biol. Evol.* 28:1255–69
25. de Filippo C, Bostoen K, Stoneking M, Pakendorf B. 2012. Bringing together linguistic and genetic evidence to test the Bantu expansion. *Proc. Biol. Sci.* 279:3256–63
26. Drake NA, Breeze P. 2016. Climate change and modern human occupation of the Sahara from MIS 6-2. In *Africa from MIS 6-2*, ed. S Jones, B Stewart, pp. 103–22. Dordrecht, Neth.: Springer
27. Drake NA, Breeze P, Parker A. 2013. Palaeoclimate in the Saharan and Arabian Deserts during the Middle Palaeolithic and the potential for hominin dispersals. *Quat. Int.* 300:48–61
28. Dreyer TF. 1935. A human skull from Florisbad, Orange Free State, with a note on the endocranial cast, by CU Ariens Kappers. *Proc. K. Akad. Wet. Amst.* 38:3–12
29. Dusseldorp G, Lombard M, Wurz S. 2013. Pleistocene *Homo* and the updated Stone Age sequence of South Africa. *S. Afr. J. Sci.* 109:46–52
30. Ehret C. 1982. The first spread of food production in southern Africa. See Ref. 31, pp. 158–81
31. Ehret C, Posnansky M, eds. 1982. *The Archaeological and Linguistic Reconstruction of African History*. Berkeley: Univ. Calif. Press
32. Enattah NS, Jensen TG, Nielsen M, Lewinski R, Kuokkanen M, et al. 2008. Independent introduction of two lactase-persistence alleles into human populations reflects different history of adaptation to milk culture. *Am. J. Hum. Genet.* 82:57–72
33. Fan S, Hansen MEB, Lo Y, Tishkoff SA. 2016. Going global by adapting local: a review of recent human adaptation. *Science* 354:54–59
34. Fernandez CI, Wiley AS. 2017. Rethinking the starch digestion hypothesis for *AMY1* copy number variation in humans. *Am. J. Phys. Anthropol.* 163:645–57
35. Fregel R, Mendez FL, Bokbot Y, Martin-Socas D, Camalich-Massieu MD, et al. 2018. Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe. bioRxiv 191569. **https://doi.org/10.1101/191569**
36. Gallego Llorente M, Jones ER, Eriksson A, Siska V, Arthur KW, et al. 2015. Ancient Ethiopian genome reveals extensive Eurasian admixture throughout the African continent. *Science* 350:820–22
37. Gerlach I. 2011. *Yeha: an Ethio-Sabean site in the highlands of Tigray (Ethiopia) – new research in archaeology and epigraphy of South Arabia and its neighbours*. Presented at Recontres Sabeennes 15, Moscow, May 25–27
38. Green RE, Krause J, Briggs AW, Maricic T, Stenzel U, et al. 2010. A draft sequence of the Neandertal genome. *Science* 328:710–22
39. Greenberg JH. 1972. Linguistic evidence concerning Bantu origins. *J. Afr. Hist.* 13:189–216
40. Gronau I, Hubisz MJ, Gulko B, Danko CG, Siepel A. 2011. Bayesian inference of ancient human demography from individual genome sequences. *Nat. Genet.* 43:1031–34
41. Grün R, Brink JS, Spooner NA, Taylor L, Stringer CB, et al. 1996. Direct dating of Florisbad hominid. *Nature* 382:500–1
42. Güldemann T. 2008. A linguist's view: Khoe-Kwadi speakers as the earliest food-producers of southern Africa. In *Khoekhoe and the Origins of Herding in Southern Africa*, ed. K Sadr, F-X Fauvelle-Aymar, pp. 93–132. Pietermaritzburg, S. Afr.: South. Afr. Humanit.
43. Gunther T, Jakobsson M. 2016. Genes mirror migrations and cultures in prehistoric Europe-a population genomic perspective. *Curr. Opin. Genet. Dev.* 41:115–23
44. Gurdasani D, Carstensen T, Tekola-Ayele F, Pagani L, Tachmazidou I, et al. 2015. The African Genome Variation Project shapes medical genetics in Africa. *Nature* 517:327–32
45. Guthrie M. 1948. *The Classification of the Bantu Languages*. London: Oxford Univ. Press for Int. Afr. Inst.
46. Haber M, Mezzavilla M, Bergstrom A, Prado-Martinez J, Hallast P, et al. 2016. Chad genetic diversity reveals an African history marked by multiple Holocene Eurasian migrations. *Am. J. Hum. Genet.* 99:1316–24

47. Hammer MF, Woerner AE, Mendez FL, Watkins JC, Wall JD. 2011. Genetic evidence for archaic admixture in Africa. *PNAS* 108:15123–28
48. Harvati K, Stringer C, Grun R, Aubert M, Allsworth-Jones P, Folorunso CA. 2011. The Later Stone Age calvaria from Iwo Eleru, Nigeria: morphology and chronology. *PLOS ONE* 6:e24024
49. Hassan HY, van Erp A, Jaeger M, Tahir H, Oosting M, et al. 2016. Genetic diversity of lactase persistence in East African populations. *BMC Res. Notes* 9:8
50. Henn BM, Botigue LR, Gravel S, Wang W, Brisbin A, et al. 2012. Genomic ancestry of North Africans supports back-to-Africa migrations. *PLOS Genet*. 8:e1002397
51. Henn BM, Gignoux CR, Jobin M, Granka JM, Macpherson JM, et al. 2011. Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. *PNAS* 108:5154–62
52. Holden CJ. 2002. Bantu language trees reflect the spread of farming across sub-Saharan Africa: a maximum-parsimony analysis. *Proc. Biol. Sci.* 269:793–99
53. Hollfelder N, Schlebusch CM, Gunther T, Babiker H, Hassan HY, Jakobsson M. 2017. Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. *PLOS Genet*. 13:e1006976
54. Hsieh P, Woerner AE, Wall JD, Lachance J, Tishkoff SA, et al. 2016. Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. *Genome Res.* 26:291–300
55. Hublin JJ. 2000. Modern-nonmodern hominid interactions: a Mediterranean perspective. In *The Geography of Neandertals and Modern Humans in Europe and the Greater Mediterranean*, ed. O Bar-Yosef, DR Pilbeam, pp. 157–82. Cambridge, MA: Harvard Univ. Press
56. Hublin JJ, Ben-Ncer A, Bailey SE, Freidline SE, Neubauer S, et al. 2017. New fossils from Jebel Irhoud, Morocco and the pan-African origin of *Homo sapiens*. *Nature* 546:289–92
57. Huffman TN. 2007. *Handbook to the Iron Age: The Archaeology of Pre-Colonial Farming Societies in Southern Africa*. Scottsville, S. Afr.: Univ. Kwa-Zulu-Natal Press
58. Ingram CJ, Elamin MF, Mulcare CA, Weale ME, Tarekegn A, et al. 2007. A novel polymorphism associated with lactose tolerance in Africa: multiple causes for lactase persistence? *Hum. Genet.* 120:779–88
59. Jablonski NG, Chaplin G. 2017. The colours of humanity: the evolution of pigmentation in the human lineage. *Philos. Trans. R. Soc. Lond. B* 372:20160349
60. Jakobsson M, Scholz SW, Scheet P, Gibbs JR, VanLiere JM, et al. 2008. Genotype, haplotype and copy-number variation in worldwide human populations. *Nature* 451:998–1003
61. Japp S, Gerlach I, Hitgen H, Schnelle M. 2011. Yeha and Hawelti: cultural contacts between Saba' and D'MT—new research by the German Archaeological Institute in Ethiopia. *Proc. Semin. Arab. Stud.* 41:145–60
62. Jones BL, Raga TO, Liebert A, Zmarz P, Bekele E, et al. 2013. Diversity of lactase persistence alleles in Ethiopia: signature of a soft selective sweep. *Am. J. Hum. Genet.* 93:538–44
63. Kilinc GM, Omrak A, Ozer F, Gunther T, Buyukkarakaya AM, et al. 2016. The demographic development of the first farmers in Anatolia. *Curr. Biol.* 26:2659–66
64. Kwiatkowski DP. 2005. How malaria has affected the human genome and what human genetics can teach us about malaria. *Am. J. Hum. Genet.* 77:171–92
65. Lachance J, Vernot B, Elbers CC, Ferwerda B, Froment A, et al. 2012. Evolutionary history and adaptation from high-coverage whole-genome sequences of diverse African hunter-gatherers. *Cell* 150:457–69
66. Lahr MM, Foley RA. 1998. Towards a theory of modern human origins: geography, demography, and diversity in recent human evolution. *Am. J. Phys. Anthropol.* 107(27):137–76
67. Lamb HF, Bates CR, Coombes PV, Marshall MH, Umer M, et al. 2007. Late Pleistocene desiccation of Lake Tana, source of the Blue Nile. *Quat. Sci. Rev.* 26:287–99
68. Lavachery P. 2001. The Holocene archaeological sequence of Shum Laka Rock Shelter. *Afr. Archaeol. Rev.* 18:213–47
69. Lazaridis I, Nadel D, Rollefson G, Merrett DC, Rohland N, et al. 2016. Genomic insights into the origin of farming in the ancient Near East. *Nature* 536:419–24
70. Li JZ, Absher DM, Tang H, Southwick AM, Casto AM, et al. 2008. Worldwide human relationships inferred from genome-wide patterns of variation. *Science* 319:1100–4

71. Li S, Schlebusch CM, Jakobsson M. 2014. Genetic variation reveals large-scale population expansion and migration during the expansion of Bantu-speaking peoples. *Proc. Biol. Sci.* 281:20141448
72. Lokki AI, Jarvela I, Israelsson E, Maiga B, Troye-Blomberg M, et al. 2011. Lactase persistence genotypes and malaria susceptibility in Fulani of Mali. *Malar. J.* 10:9
73. Lombard M, Schlebusch CM, Soodyall H. 2013. Bridging disciplines to better elucidate the evolution of early *Homo sapiens* in southern Africa. *S. Afr. J. Sci.* 109:1–8
74. Lorenzen ED, Heller R, Siegismund HR. 2012. Comparative phylogeography of African savannah ungulates. *Mol. Ecol.* 21:3656–70
75. Macholdt E, Lede V, Barbieri C, Mpoloka SW, Chen H, et al. 2014. Tracing pastoralist migrations to southern Africa with lactase persistence alleles. *Curr. Biol.* 24:875–79
76. Mallick S, Li H, Lipson M, Mathieson I, Gymrek M, et al. 2016. The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. *Nature* 538:201–6
77. Mathieson I, Lazaridis I, Rohland N, Mallick S, Patterson N, et al. 2015. Genome-wide patterns of selection in 230 ancient Eurasians. *Nature* 528:499–503
78. Mazet O, Rodriguez W, Grusea S, Boitard S, Chikhi L. 2016. On the importance of being structured: instantaneous coalescence rates and human evolution—lessons for ancestral population size inference? *Heredity* 116:362–71
79. McDougall I, Brown FH, Fleagle JG. 2005. Stratigraphic placement and age of modern humans from Kibish, Ethiopia. *Nature* 433:733–36
80. McManus KF, Taravella AM, Henn BM, Bustamante CD, Sikora M, Cornejo OE. 2017. Population genetic analysis of the DARC locus (Duffy) reveals adaptation from standing variation associated with malaria resistance in humans. *PLOS Genet.* 13:e1006560
81. Meyer M, Arsuaga JL, de Filippo C, Nagel S, Aximu-Petri A, et al. 2016. Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins. *Nature* 531:504–7
82. Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, et al. 2012. A high-coverage genome sequence from an archaic Denisovan individual. *Science* 338:222–26
83. Mitchell P. 2002. *The Archaeology of Southern Africa*. Cambridge, UK: Cambridge Univ. Press
84. Mitchell P, Lane P, eds. 2013. *The Oxford Handbook of African Archaeology*. Oxford, UK: Oxford Univ. Press
85. Newman JL. 1995. *The Peopling of Africa*. New Haven, CT: Yale Univ. Press
86. Nielsen R, Akey JM, Jakobsson M, Pritchard JK, Tishkoff S, Willerslev E. 2017. Tracing the peopling of the world through genomics. *Nature* 541:302–10
87. Novembre J, Johnson T, Bryc K, Kutalik Z, Boyko AR, et al. 2008. Genes mirror geography within Europe. *Nature* 456:98–101
88. Owers KA, Sjödin P, Schlebusch CM, Skoglund P, Soodyall H, Jakobsson M. 2017. Adaptation to infectious disease exposure in indigenous Southern African populations. *Proc. Biol. Sci.* 284:20170226
89. Pagani L, Kivisild T, Tarekegn A, Ekong R, Plaster C, et al. 2012. Ethiopian genetic diversity reveals linguistic stratification and complex influences on the Ethiopian gene pool. *Am. J. Hum. Genet.* 91:83–96
90. Pagani L, Schiffels S, Gurdasani D, Danecek P, Scally A, et al. 2015. Tracing the route of modern humans out of Africa by using 225 human genome sequences from Ethiopians and Egyptians. *Am. J. Hum. Genet.* 96:986–91
91. Patin E, Lopez M, Grollemund R, Verdu P, Harmant C, et al. 2017. Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. *Science* 356:543–46
92. Patin E, Siddle KJ, Laval G, Quach H, Harmant C, et al. 2014. The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. *Nat. Commun.* 5:3163
93. Perry GH, Dominy NJ, Claw KG, Lee AS, Fiegler H, et al. 2007. Diet and the evolution of human amylase gene copy number variation. *Nat. Genet.* 39:1256–60
94. Peyregne S, Boyle MJ, Dannemann M, Prufer K. 2017. Detecting ancient positive selection in humans using extended lineage sorting. *Genome Res.* 27:1563–72
95. Phillipson D. 2005. *African Archaeology*. Cambridge, UK: Cambridge Univ. Press
96. Pickrell JK, Patterson N, Barbieri C, Berthold F, Gerlach L, et al. 2012. The genetic prehistory of southern Africa. *Nat. Commun.* 3:1143

97. Pickrell JK, Patterson N, Loh PR, Lipson M, Berger B, et al. 2014. Ancient west Eurasian ancestry in southern and eastern Africa. *PNAS* 111:2632–37
98. Plagnol V, Wall JD. 2006. Possible ancestral structure in human populations. *PLOS Genet.* 2:e105
99. Porat N, Chazan M, Grün R, Aubert M, Eisenmann V, Horwitz LK. 2010. New radiometric ages for the Fauresmith industry from Kathu Pan, southern Africa: implications for the Earlier to Middle Stone Age transition. *J. Archaeol. Sci.* 37:269–83
100. Posth C, Wissing C, Kitagawa K, Pagani L, van Holstein L, et al. 2017. Deeply divergent archaic mitochondrial genome provides lower time boundary for African gene flow into Neanderthals. *Nat. Commun.* 8:16046
101. Priehodova E, Abdelsawy A, Heyer E, Cerny V. 2014. Lactase persistence variants in Arabia and in the African Arabs. *Hum. Biol.* 86:7–18
102. Priehodova E, Austerlitz F, Cizkova M, Mokhtar MG, Poloni ES, Cerny V. 2017. The historical spread of Arabian Pastoralists to the eastern African Sahel evidenced by the lactase persistence −13,915*G allele and mitochondrial DNA. *Am. J. Hum. Biol.* 29:e22950
103. Prüfer K, Racimo F, Patterson N, Jay F, Sankararaman S, et al. 2014. The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature* 505:43–49
104. Racimo F. 2016. Testing for ancient selection using cross-population allele frequency differentiation. *Genetics* 202:733–50
105. Racimo F, Kuhlwilm M, Slatkin M. 2014. A test for ancient selective sweeps and an application to candidate sites in modern humans. *Mol. Biol. Evol.* 31:3344–58
106. Racimo F, Sankararaman S, Nielsen R, Huerta-Sanchez E. 2015. Evidence for archaic adaptive introgression in humans. *Nat. Rev. Genet.* 16:359–71
107. Ramachandran S, Deshpande O, Roseman CC, Rosenberg NA, Feldman MW, Cavalli-Sforza LL. 2005. Support from the relationship of genetic and geographic distance in human populations for a serial founder effect originating in Africa. *PNAS* 102:15942–47
108. Ranciaro A, Campbell MC, Hirbo JB, Ko WY, Froment A, et al. 2014. Genetic origins of lactase persistence and the spread of pastoralism in Africa. *Am. J. Hum. Genet.* 94:496–510
109. Reich D, Green RE, Kircher M, Krause J, Patterson N, et al. 2010. Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature* 468:1053–60
110. Richter D, Grun R, Joannes-Boyau R, Steele TE, Amani F, et al. 2017. The age of the hominin fossils from Jebel Irhoud, Morocco, and the origins of the Middle Stone Age. *Nature* 546:293–96
111. Rightmire GP. 2009. Out of Africa: modern human origins special feature: middle and later Pleistocene hominins in Africa and Southwest Asia. *PNAS* 106:16046–50
112. Rodriguez-Varela R, Gunther T, Krzewinska M, Stora J, Gillingwater TH, et al. 2017. Genomic analyses of pre-European conquest human remains from the Canary Islands reveal close affinity to modern North Africans. *Curr. Biol.* 27:3396–402
113. Rogers RA, Iltis DA, Wooding SA. 2004. Genetic variation at the MC1R locus and the time since loss of human body hair. *Curr. Anthropol.* 45:105–8
114. Rosenberg NA, Pritchard JK, Weber JL, Cann HM, Kidd KK, et al. 2002. Genetic structure of human populations. *Science* 298:2381–85
115. Sadr K. 1998. The first herders at the Cape of Good Hope. *Afr. Archaeol Rev.* 15:101–32
116. Salas A, Richards M, De la Fe T, Lareu MV, Sobrino B, et al. 2002. The making of the African mtDNA landscape. *Am. J. Hum. Genet.* 71:1082–111
117. Scally A, Durbin R. 2012. Revising the human mutation rate: implications for understanding human evolution. *Nat. Rev. Genet.* 13:745–53
118. Scarre C, ed. 2009. *The Human Past: World Prehistory and the Development of Human Societies*. London: Thames & Hudson
119. Scerri EML. 2017. The North African Middle Stone Age and its place in recent human evolution. *Evol. Anthropol.* 26:119–35
120. Scerri EML. 2017. The Stone Age archaeology of West Africa. In *Oxford Research Encyclopedia of African History*. Oxford, UK: Oxford Univ. Press. **https://doi.org/10.1093/acrefore/9780190277734.013.137**
121. Scerri EML, Drake N, Jennings R, Groucutt HS. 2014. Earliest evidence for the structure of *Homo sapiens* populations in Africa. *Quat. Sci. Rev.* 101:207–16

122. Schlebusch CM, Lombard M, Soodyall H. 2013. MtDNA control region variation affirms diversity and deep sub-structure in populations from southern Africa. *BMC Evol. Biol.* 13:56
123. Schlebusch CM, Malmstrom H, Gunther T, Sjödin P, Coutinho A, et al. 2017. Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. *Science* 358:652–55
124. Schlebusch CM, Sjödin P, Skoglund P, Jakobsson M. 2012. Stronger signal of recent selection for lactase persistence in Maasai than in Europeans. *Eur. J. Hum. Genet.* 21:550–53
125. Schlebusch CM, Skoglund P, Sjödin P, Gattepaille LM, Hernandez D, et al. 2012. Genomic variation in seven Khoe-San groups reveals adaptation and complex African history. *Science* 338:374–79
126. Schuenemann VJ, Peltzer A, Welte B, van Pelt WP, Molak M, et al. 2017. Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods. *Nat. Commun.* 8:15694
127. Schuster SC, Miller W, Ratan A, Tomsho LP, Giardine B, et al. 2010. Complete Khoisan and Bantu genomes from southern Africa. *Nature* 463:943–47
128. Segurel L, Bon C. 2017. On the evolution of lactase persistence in humans. *Annu. Rev. Genom. Hum. Genet.* 18:297–319
129. Sjödin P, Sjöstrand A, Jakobsson M, Blum MGB. 2012. No evidence for a human bottleneck during the penultimate glacial period. *Mol. Biol. Evol.* 29:1850–61
130. Skoglund P, Malmstrom H, Raghavan M, Stora J, Hall P, et al. 2012. Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. *Science* 336:466–69
131. Skoglund P, Reich D. 2016. A genomic view of the peopling of the Americas. *Curr. Opin. Genet. Dev.* 41:27–35
132. Skoglund P, Thompson JC, Prendergast ME, Mittnik A, Sirak K, et al. 2017. Reconstructing prehistoric African population structure. *Cell* 171:59–71
133. Smith AB. 1992. Origins and spread of pastoralism in Africa. *Annu. Rev. Anthropol.* 21:125–41
134. Stringer C. 2002. Modern human origins: progress and prospects. *Philos. Trans. R. Soc. Lond. B* 357:563–79
135. Swallow DM. 2003. Genetics of lactase persistence and lactose intolerance. *Annu. Rev. Genet.* 37:197–219
136. Tishkoff SA, Reed FA, Friedlaender FR, Ehret C, Ranciaro A, et al. 2009. The genetic structure and history of Africans and African Americans. *Science* 324:1035–44
137. Tishkoff SA, Reed FA, Ranciaro A, Voight BF, Babbitt CC, et al. 2007. Convergent adaptation of human lactase persistence in Africa and Europe. *Nat. Genet.* 39:31–40
138. Triska P, Soares P, Patin E, Fernandes V, Cerny V, Pereira L. 2015. Extensive admixture and selective pressure across the Sahel Belt. *Genome Biol. Evol.* 7:3484–95
139. Vansina J. 1995. New linguistic evidence and the Bantu expansion. *J. Afr. Hist.* 36:173–95
140. Veeramah KR, Wegmann D, Woerner A, Mendez FL, Watkins JC, et al. 2011. An early divergence of KhoeSan ancestors from those of other modern humans is supported by an ABC-based analysis of autosomal resequencing data. *Mol. Biol. Evol.* 29:617–30
141. Verdu P, Austerlitz F, Estoup A, Vitalis R, Georges M, et al. 2009. Origins and genetic diversity of pygmy hunter-gatherers from Western Central Africa. *Curr. Biol.* 19:312–18
142. Voight BF, Kudaravalli S, Wen X, Pritchard JK. 2006. A map of recent positive selection in the human genome. *PLOS Biol.* 4:e72
143. Wen B, Li H, Lu D, Song X, Zhang F, et al. 2004. Genetic evidence supports demic diffusion of Han culture. *Nature* 431:302–5
144. White TD, Asfaw B, DeGusta D, Gilbert H, Richards GD, et al. 2003. Pleistocene *Homo sapiens* from Middle Awash, Ethiopia. *Nature* 423:742–47
145. Xu S, Pugach I, Stoneking M, Kayser M, Jin L. 2012. Genetic dating indicates that the Asian-Papuan admixture through Eastern Indonesia corresponds to the Austronesian expansion. *PNAS* 109:4574–79

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Errata

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