The mosaic genome of indigenous African cattle as a unique genetic resource for African pastoralism

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Cattle pastoralism plays a central role in human livelihood in Africa. However, the genetic history of its success remains unknown. Here, through whole-genome sequence analysis of 172 indigenous African cattle from 16 breeds representative of the main cattle groups, we identify a major taurine × indicine cattle admixture event dated to circa 750–1,050 yr ago, which has shaped the genome of today’s cattle in the Horn of Africa. We identify 16 loci linked to African environmental adaptations across crossbred cattle living in trypanosomosis-infested areas. Our findings indicate that a combination of past taurine and recent indicine admixture-derived genetic resources is at the root of the present success of African pastoralism.

Cattle play an important role across African economies and societies as a primary source of wealth1,2. They provide nutrition, manure and draught power, and are often used to pay as bride wealth3. Today, at least 150 indigenous cattle breeds have been recognized across the different agro-ecologies of the African continent4, each with unique phenotypic and adaptive characteristics5,6.

Previous studies5,6 have indicated that the dispersion and diversity of African cattle followed the history and development of African pastoralism. It is understood that the humpless Bos taurus and the humped Bos primigenius originated from domestications of distinct aurochs Bos primigenius subspecies with an ancestral divergence time of ~200,000 to less than 1 million yr ago7–10. The oldest uncontroversial evidence of domestic cattle in Africa dates back to circa 5750–4550 bc in Egypt's Western Desert at Naba—Keseiba and circa 7000 bc in Kerma, Sudan11. These B. taurus cattle were introduced through North Africa and reached the Western and Eastern continent. They remained largely confined to the Saharan–Sahelian belt12,13, until circa 4,000–3,000 yr ago, when they reached the Tlemssi Valley tributary of the Niger River in West Africa14, the Lake Turkana basin of East Africa15,16 and the Horn of Africa17. The main arrival of B. indicus started around 700 ad along the Red Sea and the Indian Ocean coastal areas, at the outset of the Swahili civilization18,19 (Fig. 1a), which subsequently led to crossbreeding between B. indicus and already established African taurine.

However, the timing of the taurine × indicine admixture event(s) and their impacts on the development of African pastoralism remain unknown. Archeological evidence indicates that the development of sub-Saharan cattle pastoralism was a complex process that may not have proceeded as smoothly as its modern prevalence suggests20,21. In particular, environmental climatic and infectious disease challenges (for example, bovine malignant catarrhal fever, East Coast fever, foot-and-mouth disease, Rift Valley fever and trypanosomosis) likely have led to patchy and delayed establishment of herding across East Africa22,23.

Today, the majority of African cattle are B. taurus × B. indicus humped populations of diverse phenotypes. They are classified as African Sanga (crossbred between Taurine and Zebu cattle), African Zenga (crossbred between Sanga and Zebu) and African Zebu23,24. The African Sanga, an Abyssinian word meaning bull, likely originated in North-East Africa with subsequent dispersion in the Central Lake Region and Southern Africa14. A few taurine populations found within the tsetse-belt in West Africa are the only pure African taurine cattle left on the continent14,25.

African humped cattle carry only taurine mitochondrial DNA haplotypes24,25. The Y-chromosome microsatellite indicates the presence of both indicine and taurine Y chromosomes on the continent26,27. Furthermore, autosomal genome-wide analyses show that African humped cattle contain taurine background with
different levels of genetic contributions across populations, but with little variation within a population\textsuperscript{28–31}. These analyses suggest that selection played a role in shaping the \textit{B. taurus} × \textit{B. indicus} admixture proportion in African cattle, with admixture increasing diversity and providing new genetic resources for human and natural selection\textsuperscript{32}. This may have facilitated dispersion and colonization of new habitats\textsuperscript{33}. Several recent studies have addressed the effects of admixture and introgression among the \textit{Bos} species. They have identified loci derived from donor species, which have contributed to the adaptation of recipient species\textsuperscript{34–36}. However, admixture and introgression also have a cost, as they may reduce the reproductive fitness due to genome incompatibility\textsuperscript{37}.

Here, we generated whole-genome sequences of 114 cattle that belong to 12 indigenous African cattle populations and two African buffalo. We combined these with the previously sequenced genomes of 58 cattle from four additional African populations\textsuperscript{31,38}. These populations represent the main African cattle groups (Supplementary Note). Using this unique set, we date a main taurine × indicine admixture event and assess the present genome ancestry of African cattle, supporting that a combination of these two ancestries is at the root of the success of African pastoralism.

**Results**

**Sequencing, mapping and identification of SNPs.** Individual genomes of 114 indigenous African cattle and two African buffalo, \textit{Syncerus caffer caffer} (AFB), were sequenced to an average of ~9.91× depth coverage and jointly genotyped with 217 publicly available genomes. A total of 45 cattle breeds or populations...
including 331 samples were classified according to their phenotypes as follows: African Taurine (AFT), African Humped cattle (AFH) (including African Indicine (AFI), African Sanga (AFS), African Zenga (AFZ)) and Sheko, Eurasian Taurine (EAT) (including European Taurine (EUT) and Asian Taurine (AST)) and American-Australian-Asian Indicine (AAI) (including American-Asian Indicine (AAI) and Asian Indicine (ASI)) (Fig. 1, Supplementary Note and Supplementary Table 1).

Population structure and relationships. To characterize the structure of the African populations, we performed principal component analysis (PCA) of the 331 animals (Fig. 2a). All AFH position between EAT and AAI, along eigenvector 1, which explains ~1% of the total variation. AFT Muturu and N’Dama are close to EAT along the eigenvector 1. Most of the AFH cattle cluster together regardless of their breed memberships, leaving only Ankole, Mursi and Sheko outside the main cluster toward the AFT Muturu and N’Dama. The PCA results also show that Muturu and N’Dama, our representative of the AFT population, are separated from the other cattle groups (eigenvector 2, ~2.5% of total variation). Sheko positions close to the AFH, as similarly reported in previous studies.

Genetic clustering analysis using ADMIXTURE corroborates the pattern found in PCA (Fig. 2b and Extended Data Fig. 2). Most of AFH show a similar proportion of taurine ancestry, around 25% on average. Only a few AFH breeds have elevated taurine ancestry: Ankole (53.37 ± 1.49%), Sheko (46.28 ± 2.03%) and Mursi (35.90 ± 2.16%) (Fig. 2b; K = 3, light blue).

Genetic distance and diversity. Pairwise fixation index ($F_{st}$) values were calculated to estimate the genetic distances between populations ($n = 38$) (Extended Data Fig. 3). Taurine populations (EUT, AST and AFT) show $F_{st}$ values of 0.1568 and 0.3287 on average against AFH and AAI, respectively. Across AFH, the pairwise $F_{st}$ between breeds is close to zero, regardless of their phenotypic classification as African Zebu, Sanga or Zenga. Muturu and N’Dama show an $F_{st}$ value of 0.1769, 0.1847 and 0.3734 against AFH, EAT and AAI, respectively.

The genome-wide autosomal SNPs show reduced levels of heterozygosity in the taurine (0.0021 ± 0.0005 per base pair (bp)) compared with all other populations (0.0048 ± 0.0008 per bp). Heterozygosity values of AFH are similarly higher across populations (0.0046 ± 0.0003 per bp). AAI shows a higher level of heterozygosity compared with AFH (0.0052 ± 0.0014 per bp) (Extended Data Fig. 4). The degree of inbreeding measured by runs of homozygosity (ROH) shows that taurine populations, including Muturu and N’Dama, have a higher level of inbreeding compared with the other populations. AAI shows a similar pattern of ROH distribution to AFH (Extended Data Fig. 5).

Genome-wide admixture signatures in African cattle. Evidence of intensive admixture across African cattle. To further analyze and quantify admixture levels in African cattle, we examined patterns of allele sharing using $f_1 D$ and $f_2$ ratio statistics. In the group-based analyses, we used EAT and AAI as a single group considering their genetic similarity compared with the African populations. Only Muturu and N’Dama show no evidence of admixture in $f_1$ analysis assuming EAT and AAI as proxies for unadmixed taurine and indicine cattle, respectively. For the $D$ statistics, which are more robust to the effect of population-specific drift, this is only the case for the Muturu (Fig. 3a and Supplementary Tables 4 and 5). The positive $f_1$ statistic in N’Dama is likely due to a recent population bottleneck and subsequent allele frequency changes by genetic drift, as suggested by its high ROH counts and lengths (Extended Data Fig. 5). As Muturu shows no evidence of admixture (Supplementary Tables 4 and 5), we recalculated $f_1$ and $D$ statistics using Muturu as a proxy for unadmixed taurine. These showed consistent results compared with those when EAT was the proxy (Supplementary Tables 4 and 5). The admixture proportions estimated by $f_1$ ratio statistics
Dating taurine×indicine admixture across African cattle. Having established the level of taurine×indicine admixture among African cattle, we then estimated the timing of its generation using admixture LD decay. We first employed a single-pulse admixture model using ALDER. Across all AFH populations, excluding the Kenya Boran, admixture times range from 126.88 (Mursi) to 181.58 (Fogera) generations ago (mean 153.67) (Fig. 3c and Supplementary Table 7). Additionally, we analyzed our data using MALDER to assess the possibility of multiple admixture events. After fitting a single-pulse model, MALDER analysis did not add a new admixture event with enough significance. Also, the lower significance (Z-score) and larger standard errors of the double-pulse model fitting compared with the single-pulse model fitting support the single-pulse admixture model for our data (Fig. 3d). When we combined AFH populations, excluding Ankole, Kenya Boran, Mursi and Sheko, we obtained a similar result (Supplementary Table 8).

Only the Kenya Boran has a different timing of admixture among the AFH populations, with a very recent admixture signal and similar significances for both the single- and double-pulse model fittings (Fig. 3d). These results support recent and admixture signals in Kenya Boran (Extended Data Fig. 6). The Kenya Boran originates from the Ethiopian Boran. After they migrated from Ethiopia to Kenya, they underwent selection and improvement with European taurine in the early twentieth century. These recent crossbreeding events most likely correspond to the admixture signal (12.77 ± 12.96 generations ago) of the Kenya Boran (Extended Data Fig. 6). We also detect an ancient admixture signal (132.28 ± 13.60 generations ago) in the Sheko.

In N’Dama, we detected only a recent admixture signal (21.36 ± 2.50 generations ago) (Supplementary Table 7). Previous studies have shown that the N’Dama is composed of several subpopulations with varying degrees of indicine ancestry. The N’Dama population here is from The Gambia, where an indicine ancestry has previously been documented by ADMIXTURE analyses. Our results now provide a timescale for this recent admixture event.

We also performed GLOBETROTTER analysis, based on haplotype sharing, as an alternative method to estimate admixture time. The 14 African cattle populations, excluding Muturu and N’Dama, show robust evidence of admixture (bootstrap P < 0.01) (Supplementary Table 9). In addition, admixture time estimates from the populations with best-guess model ‘one-date’ range from 94.85 to 158.08 generations ago, in agreement with the results from ALDER (Fig. 3c). The exceptions are the Kenya Boran and Kenana, with best-guess model ‘multiple-dates’ (Supplementary Table 9).

Selection signatures with an excess of taurine or indicine ancestry in African humped cattle. Our genome-wide analysis shows that all sampled African cattle breeds, except Muturu, have taurine and indicine ancestry, with little variation within a population. In such crossbreeds, a haplotype of either taurine or indicine ancestry may confer a relative adaptive advantage following selection pressures. Accordingly, such haplotypes will be selected in the admixed African cattle population over time.

We employed two approaches to identify such loci and haplotypes. We first explored ongoing selective sweep using the integrated haplotype score (iHS). Taking the top 1% windows in terms of the proportion of SNPs with |iHS| ≥ 2 (260.00%), we obtained a total of 496 windows of 50 kilobase (kb) length as candidates under selection (Extended Data Fig. 7a). The 494 protein-coding genes overlapped with these windows show significant enrichment in ‘defence response to bacterium’ (GO:0042742) and ‘keratinization’ (R-BTA-6805567) (false discovery rate–adjusted P < 0.05) (Supplementary Table 10). These 496 windows have a lower average taurine ancestry (26.14%) than other iHS percentiles as well as the whole genome (32.49%) (Extended Data Figs. 8 and 9). Also, the average taurine ancestry of the windows is outside the empirical distribution generated by resampling (Extended Data Fig. 10). This indicates that the overall ancestry of these selected loci is more skewed toward indicine than the whole genome.

We then inferred local ancestry across the genome using LOTER and selected the top 0.5% windows with the highest taurine or indicine ancestry (Extended Data Fig. 7b). Of these 496 windows, 63 windows identified in the previous iHS analysis were further considered. After filtering out windows with pairwise Fst value between the reference populations (EAT and AAI) less than the genome-wide level (<0.2296) and merging adjacent windows, 16 genomic regions were retained, of which three and 13 show an excess of taurine and indicine ancestry, respectively. Eleven of the regions with an excess of indicine ancestry have been identified as selection signal in previous African cattle studies (Table 1). To our knowledge, none of the regions with an excess of taurine ancestry was previously reported under selection in African cattle. The taurine and indicine excess regions overlap with nine and 51 protein-coding genes, respectively.

The longest region, 600 kb in length, is observed at BTA7 (Table 1). It includes 12 significant windows with 92.05% average indicine ancestry, which is much higher than the 67.51% genome-wide average. Downstream of this region, we found three smaller regions of 150-, 200- and 50-kb length with high average indicine ancestry of 91.28%, 91.28% and 92.62%, respectively (Table 1). This cluster of four candidate regions spans 1.40 megabases (Mb) of BTA7 (49.75–51.15 Mb). It shows a reduced level of diversity within AFH and an increased level of genetic differentiation between AFH and EAT.
Shared haplotypes are more commonly observed between AFH and AAI than AFH and EAT (Fig. 4). In this cluster, we identified 18 protein-coding genes, three related to the host immune (MATR3 (ref. 52), MZB1 (ref. 53) and STING1 (ref. 54)) and one to the environmental thermal stresses (heat shock protein gene DNAJC18 (ref. 55)) responses. We also found one more heat shock protein gene (HSPA9 (ref. 51)) with an excess of indicine ancestry (BTA7: 49.85–49.95 Mb; 91.30% average indicine ancestry), but here the iHS (36.98%) does not reach the significance threshold. Two protein-coding genes linked to reproduction (PAIP2 (ref. 56) and SPATA24 (ref. 57)) are also found in this region, together with SEPTIN2 (ref. 58) on BTA3 (Table 1).

The region with the highest taurine ancestry (61.34%) is of 200-kb length (BTA11: 14.65–14.85 Mb) (Table 1). As for the BTA7 region, it shows reduced genetic diversity (Fig. 5). However, we observe an increased level of genetic differentiation between AFH and AAI as well as extended haplotype sharing between EAT and AFH (Fig. 5). This region overlaps with seven protein-coding genes (Table 1), one of which linked to the inflammatory response59–61 and tick infestation62 (NLRC4).
**Table 1 | Common AFH candidate regions identified in the iHS and local ancestry (taurine or indicine) inference (LOTER, top 0.5% windows) analysis**

| BTA* | Region (Mb) | No. of windows | Proportion of SNPs with $|\text{iHS}| \geq 2\%$ (%) | Ancestry (%) | $F_{st}$ | Genes identified | Previous studies |
|------|-------------|----------------|-----------------------------------------------|---------------|------|-----------------|-----------------|
| **Regions with an excess of indicine ancestry** | | | | | | | |
| 3 | 120.30–120.40 | 2 | 67.74 | 93.02 | 0.3390 | PASK, PPP1R7, SNED1, MTERF4 | Kim et al.31 |
| 3 | 120.45–120.55 | 2 | 63.33 | 92.86 | 0.2913 | SEPTIN2, FARP2, HDLBP | Makina et al.29 |
| 3 | 120.60–120.65 | 1 | 79.35 | 92.62 | 0.2875 | FARP2, STK25, BOK | Makina et al.29 |
| 3 | 120.70–120.80 | 2 | 83.36 | 92.62 | 0.2553 | INGS, D2HGHDH, THAP4, ATG4B, DTYMK | Kim et al.31 |
| 3 | 120.85–120.90 | 1 | 79.25 | 92.62 | 0.3182 | RTPS | Makina et al.29 |
| 7 | 49.75–49.80 | 1 | 65.74 | 92.62 | 0.3817 | KDM3B | Gautier et al.100 |
| 7 | 50.05–50.25 | 4 | 67.90 | 91.28 | 0.4179 | CTNNA1, LRRM2, ENSBTAG00000004415 | Kim et al.31 |
| 7 | 50.30–50.45 | 3 | 75.17 | 91.28 | 0.6321 | SII | Kim et al.31 |
| 7 | 50.55–51.15 | 12 | 86.06 | 92.05 | 0.4861 | PSD2, NRG2, DNAJC18, ECSCR, SMIM33, STING1, CXXC5, UBE2D2, MATR3, PAIP2, SLC23A1, MZB1, PROB1, SPATA24 | Bahbahani et al.90 |
| 13 | 56.95–57.00 | 1 | 82.80 | 93.58 | 0.3090 | – | – |
| 13 | 57.05–57.10 | 1 | 73.94 | 93.76 | 0.2685 | EDN3 | – |
| 13 | 57.15–57.65 | 10 | 81.95 | 92.69 | 0.3114 | PRELD38, ATPSFLIE, TUBB1, CTSS, NELFCD, ZNF831, GNAS | Kim et al.31 |
| 19 | 39.65–39.85 | 4 | 67.07 | 92.44 | 0.2982 | STAC2, FBXL20, MED1, PLD1C1, CACNB1, RPL19, ENSBTAG00000008368, ENSBTAG00000010S597 | Bahbahani et al.90 |
| **Regions with an excess of taurine ancestry** | | | | | | | |
| 10 | 92.15–92.25 | 2 | 72.23 | 59.98 | 0.3211 | CEP128, ENSBTAG00000047232 | – |
| 11 | 14.40–14.45 | 1 | 67.08 | 61.19 | 0.4337 | – | – |
| 11 | 14.65–14.85 | 4 | 78.31 | 61.34 | 0.2870 | MEMO1, DPD30, SPAST, SLC30A6, NLRCC4, ENSBTAG00000048521, ENSBTAG000000009576 | – |

* BTA: bovine chromosome. Proportion (%) of SNPs with $|\text{iHS}| \geq 2\%$ and ancestries are averaged values over windows. The $F_{st}$ values are pairwise values between reference populations (EAT and AAI) averaged over windows. Dashes (–) indicate that no genes have been annotated within the region or have not overlapped with candidate selection signals in African cattle from previous studies.

African taurine-specific loci and their distribution in African humped cattle. Taurine cattle are the most ancient African cattle population. They have adapted to the local environmental challenges, as exemplified by the trypanotolerance traits of West African taurine cattle. Accordingly, their unique genetic components may confer a selective advantage in crossbreed animals facing similar environmental challenges to the West African taurine.

To identify such loci, we performed population branch statistics (PBS) analysis, comparing AFT and EAT using AAI as an outgroup. After filtering out windows with less than 10 SNPs, we remained with 1,239,021 autosomal windows (50-kb sliding windows with 2-kb overlapping step). PBS values ranged from $-0.1156$ to 0.8341, with a mean of 0.0314. After removing windows with $F_{st}$ value (AFT versus EAT) less than 0.1 (Supplementary Fig. 1) from the highest 0.1% PBS windows, we considered the remaining windows as candidate selection signal specific to AFT (Supplementary Table 11).

The strongest PBS signal (0.6740) overlaps with SDK1 on BTA25 (40,052,001–40,102,000), approximately 300 kb upstream of CARD11 (Fig. 6). At this region, $F_{st}$ values between AFT and EAT ($F_{st}=0.5173$) or AAI ($F_{st}=0.5308$) are much higher than the genome-wide level ($F_{st}=0.1106$ and $F_{st}=0.1825$, respectively) (Fig. 6b). We observe a unique AFT haplotype pattern compared with EAT and AAI, which is present in some AFH breeds (Supplementary Figs. 2 and 3).

**Discussion**

In this study, we first highlighted the taurine × indicine admixture characteristics of 16 indigenous African cattle populations, 14 of them living in the Horn of Africa, the main entry point of Asian zebu on the African continent. Then, we identified and dated the main taurine × indicine admixture event, which has shaped today’s genome of these crossbreeds, to around 150 generations ago. We also identified candidate selected regions in these admixed populations, including immune-response- and heat-tolerance-related genes in haplotypes of indicine origins and inflammatory-response-related genes in haplotypes of taurine origins. Last, we identified a locus of African taurine origin putatively linked to trypanotolerance. Together, these results support our hypothesis that the present success and dispersion of African pastoralism followed the arrival of indicine cattle and their crossbreeding with local taurine cattle.

Our estimation under a single-pulse admixture model dates back the admixture time of AFH to around 150 generations ago. Assuming a cattle generation time of 5–7 yr (refs. 63,64), it corresponds...
Fig. 4 | Example of candidate selective loci on BTA7 with an excess of indicine ancestry. a, Proportion of SNPs with $|iHS| \geq 2$ in each nonoverlapping 50-kb window around the candidate locus (BTA7: 49.75–51.15 Mb, the black square) including MATR3, MZB1, STING1 and DNAJC18. The red dashed line indicates the top 1% proportion of SNPs with $|iHS| \geq 2$ (60.00%). b, Nucleotide diversity calculated using VCFtools v.0.1.17 (ref. 102) for each 50-kb window with 20-kb step around the candidate locus. c, Average taurine ancestry (%) in each nonoverlapping 50-kb window around the candidate locus. The lower and upper dashed red lines indicate the lowest and highest 0.5% of average taurine ancestry, respectively (10.31% and 57.67%). d, Pairwise $F_{st}$ values calculated using VCFtools v.0.1.17 (ref. 102) for each 50-kb window with 20-kb step around the candidate locus. The blue line indicates the pairwise $F_{st}$ values between AFH and EAT. The red line indicates the pairwise $F_{st}$ values between AFH and AAI. e, Haplotype sharing at the candidate locus. The haplotypes were hierarchically clustered within each cattle group. The major allele in EAT (allele frequency $\geq 50\%$) is indicated in blue.
Fig. 5 | Example of candidate selective loci on BTA11 with an excess of taurine ancestry. 

a. The proportion of SNPs with |iHS| ≥ 2 in each nonoverlapping 50-kb window around the candidate locus (BTA11: 14.65–14.85 Mb, the black square) including NLRC4. The dashed red line indicates the top 1% proportion of SNPs with |iHS| ≥ 2 (60.00%).

b. Nucleotide diversity calculated using VCFTools v.0.1.17 (ref. 102) for each 50-kb window with 20-kb step around the candidate locus.

c. Average taurine ancestry (%) in each nonoverlapping 50-kb window around the candidate locus. The lower and upper dashed red lines indicate the lowest and highest 0.5% of average taurine ancestry, respectively (10.31% and 57.67%).

d. Pairwise $F_{ST}$ value calculated using VCFTools v.0.1.17 (ref. 102) for each 50-kb window with 20-kb step around the candidate locus. The blue line indicates the pairwise $F_{ST}$ values between AFH and EAT. The red line indicates the pairwise $F_{ST}$ values between AFH and AAI.

e. Haplotype sharing at the candidate locus. The haplotypes were hierarchically clustered within each cattle group. The major allele in EAT (allele frequency ≥ 50%) is indicated in blue.
to about 750–1050 yr ago at the beginning of the second millennium AD (950–1250 AD). According to historical records, Asian zebu arrival along the Horn of Africa started earlier, around 700 AD, following the Islamization of the East African coast and the onset of the Swahili civilization, in agreement with the earliest noncontroversional archeological evidence in the Horn of Africa for African humped cattle, dated around the mid-first millennium AD. Therefore, our results suggest that indicine cattle remained initially confined to the East African coastal areas for at least 2–3 centuries before crossing extensively with taurine cattle. Then, during the second millennium AD, the complex human history of the Horn of Africa, characterized by multiple human population movements and dispersion as well as climatic fluctuation, would have further contributed to the landscape of today’s genome admixture in East African cattle. Interestingly, a previous study indicates an admixture event in two West African zebu populations at around 500 yr ago. This timing is in agreement with our earlier East African dating of taurine×indicine crossbreeding, which would have been followed by the movement of East African humped cattle along the Sahelian belt and crossbreeding with local taurine cattle in West Africa. The same study identified a more recent admixture event in the West African Borgou around 20 generations ago. This is at approximately the same time as the one identified in our study in the N’Dama from The Gambia. These more recent admixture events may have been linked to the rinderpest epidemics of the end of the nineteenth century.

We cannot exclude the possibility that more ancient taurine×indicine admixture events have contributed to the genetic composition of the AFH population from the Horn of Africa. Indeed, the haplotype sharing-based and LD-based admixture dating have limited power to detect admixture signals older than about 200 generations ago. However, if this was the case, their admixture signals would have been likely erased by the more recent ones identified here.

The ancestry of the selection signatures in AFH was found to be more skewed toward indicine than the genome-wide average. Domestic cattle are not native to the African continent; African taurine cattle originate from the Near East, while indicine cattle were introduced into Africa after their domestication on the Indian subcontinent. On reaching the African tropical environments, the Near East taurine cattle must have faced major environmental challenges. However, indicine cattle found across the tropical Indian subcontinent may have been better preadapted to African environments and, in particular, to its climatic characteristics. These preadaptations would have facilitated indicine introgression into local indigenous cattle populations and the dispersion of crossbred animals. However, African livestock diseases (for example, trypanosomosis, bovine malignant catarrhal fever, East Coast fever and Rift Valley fever) would have represented major constraints to the dispersion of indicine×taurine crossbred cattle. Here, the tolerance of African taurine cattle to trypanosomosis as well as the resistance of indicine cattle to infestation with ticks and to heat stress have proven advantageous.

Heat tolerance, a characteristic of zebu cattle, is a candidate for indicine preadaptations to climatic challenges. We found two heat shock protein genes (HSPA9 and DNAJC18) at BTA7, which were previously reported as candidate selective loci in African and Asian indicine cattle. We also found a water-reabsorption-related gene, GNAS, at BTA13. The protein encoded by GNAS mediates antidiuretic hormone arginine vasopressin (AVP) to aquaporin-2 (AQP2) water channels, contributing to the water conservation pathway of the kidney. Considering the adaptation of Asian zebu cattle to the arid environments, we infer that the indicine haplotype of GNAS contributes to the local adaptation of AFH to the arid areas of the continent. Also, the immune-related genes at BTA7 (MATR3, MZB1 and STING1) and BTA3 (ATG4B) (ref. 49) (Table 1) might be related to the resistance of indicine cattle to...
ticks and tick-borne diseases, such as East Coast fever. STING is essential for DNA-mediated type I interferon production and host defense against DNA viral pathogens, and therefore might confer some tolerance to viral infections such as Rift Valley fever and foot-and-mouth disease.

The identification of an autosomal taursine background in all African cattle leads us to expect a contribution of local taursine ancestry to environmental adaptation and thus its contribution to the success of African cattle pastoralism. One example is the candidate region at BTA11, which overlaps with NLRCA4 (ref. 90) involved in the inflammatory response. It shows extensive haplotype sharing between AFT and taursine cattle (AFT and EAT). Considering the lack of EAT ancestry in AFH cattle, this haplotype likely originates from AFT. Its presence in AFH may have resulted from selection for a better control of the inflammatory response following infections with diseases such as East Coast Fever and Rift Valley Fever.

Similarly, across large areas of sub-Saharan Africa, cattle have been exposed to the challenge of trypanosomiasis, a severe obstacle to livestock productivity in Africa. African taursine cattle show tolerance to Trypanosoma sp infection, controlling both the effect of infection (for example, anemia and weight loss) and the level of blood parasites. Accordingly, we expect to detect selection signals in some of the humped cattle exposed to trypanosomiasis challenges.

In our PBS analysis, a selection signature in AFT was found upstream of CARD11, which encodes a protein essential for the signaling of T and B cells in the innate and adaptive immune systems. Importantly, it was reported as a differentially expressed gene between the trypanotolerant N'Dama and trypanosusceptible Kenya Boran. We suggest that this candidate region plays a role in regulating CARD11 expression and contributes to the adaptation of AFT and AFH populations to trypanosomiasis challenge. Accordingly, this taursine region is expected to be observed in cross-breeds (Sheko, Horro and Mursi), whose natural habitats are infested with tsetse flies. However, as a complex quantitative trait involved in trypanotolerance, the potential regulatory element upstream of CARD11 should be regarded as one of many genetic factors contributing to trypanotolerance. Accordingly, it is worth mentioning that the windows within the highest 0.1% PBS value include several genes (FAAP24 (ref. 91), WDR48 (ref. 92), LRRC8A (ref. 93) and JFNAR1 (ref. 94)) related to anemia and immune response (Supplementary Table 11).

In conclusion, despite the environmental complexity of the African continent, and cattle domestication outside its geographic area, we currently find domestic cattle across all African agro-ecologies. The results presented here support that taursine x indicine admixture events followed by taursine and indicine ancestry selection across the genome is at the root of the success of African cattle pastoralism. These findings are far-reaching in today’s context of improving livestock productivity to respond to the needs of the growing human populations, with further cross-breeding of indigenous African cattle with exotic cattle recommended as one of the pathways for the continent’s food security. A complete characterization at the genome level of African cattle unique adaptations will open the door to sustainable crossbreeding programs combining local environmental adaptation and increased exotic productivity.

Online content
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Methods

Ethics statement. Blood samples were collected during routine veterinary treatments with the logistical support and agreement of relevant agricultural institutions in each country: the International Trypanotolerance Center, The Gambia; the International Livestock Research Institute (ILRI), Kenya (NDama, Kenya Boran); the Ministry of Animal Resources, Sudan (Kenana and Butana); the OI Pejeta Conservancy, Kenya (Ankole, African Buffalo); and the Ethiopian Ministry of Agriculture, Ethiopia (Afar, Arsi, Barka, Ethiopian Boran, Fogera, Gofa, Horro, Mursti, Ogaden and Sheko). No further ethics permissions were required for this study. For European and Asian taurine, all animal work was approved by the Institutional Animal Care and Use Committee of the National Institute of Animal Science in Korea under approval numbers 2012-C-005 (Holstein and Hanwoo) and NIAS-2014-093 (Angus and Jersey). All animals were handled in strict accordance with good animal practice.

Sequencing and variant calling. All sequenced samples (n = 116) were prepared according to the Illumina protocols (TruSeq DNA Sample Prep Kit v.2 Support (FC121-2001)). Briefly, 1 μg of genomic DNA was fragmented using a Covaris Focused-Ultrasonicator, and repaired. An 'A' was ligated to the 3′ end of the fragments, followed by Illumina adapter ligation. The product was further size-selected for 400–500 bp, PCR amplified and validated using the Agilent Bioanalyzer. Finally, the DNA was sequenced using the HiSeq2000 platform (Illumina) by Macrogen.

Our previously published data of 53 commercial taurine105,106 and 48 African cattle, as well as publicly available data of 10 African taurine, 30 European taurine, 34 African and 22 Asian zebu, were used in this study in addition to the generated data. We generated genotype data following the 1000 Bull Genomes Project Run 8 guideline (17 October 2019) (http://www.1000bullgenomes.org/). We first examined a per-base sequence quality for the raw sequence reads using the fastQC software v.0.11.8 (ref. 107), and removed low-quality bases and array sequences using Trimmomatic v.0.39 (ref. 108). The high-quality sequence reads were mapped against the bovine reference genome (ARS-UCD1.2) using bwa mem v0.7.17 (ref. 109) with default parameters. We then used Samtools v1.1.9 (ref. 110) to sort bam files and create index files. For the mapped reads, potential PCR duplicates were identified using the 'MarkDuplicates' of Picard v2.20.2 (http://broadinstitute.github.io/picard). The 'BaseRecalibrator' and 'PrintReads' of the genome analysis toolkit (GATK) v.3.8 (GATK) were used to perform base quality score recalibration (BQSQR). The known variants file (ARS1.2PlsUSy_BQSR_v3.vcf.gz) provided by the 1000 Bull Genomes Project was used for masking known sites for all individuals except the two African buffalos (AFB). The before/after BQSQR reports were checked by running 'AnalyzeCovariates' to ensure that base quality scores were corrected as expected. For the two AFB samples, we performed an initial round of variant calling on unrecalibrated data. We then performed BQSQR by feeding the variants obtained from the initial variant calling as known sites to BaseRecalibrator and finally checked the improvement of base quality information.

For the calling of the candidate SNPs from the bam files, we created GVCF files using 'GenotypeCaller' in GATK with ‘ERC GVCF’ option. Individual GVCF files were merged by breeds using ‘CombineGVCFs’ in GATK. We called and selected candidate SNPs from these combined GVCF files using ‘GenotypeGVCFs’ and ‘SelectVariants’, respectively. To avoid possible false-positive calls, we used ‘VariantFilter’ of GATK as recommended by GATK best practice: (1) SNP clusters with ‘clusterWindow’ size > mean depth (for all individuals) <1× and >3× (x, overall mean sequencing depth across all SNP sites); (2) quality by depth, QD < 2; (4) phred-scaled variant quality score, QUAL < 30; (5) strand odds ratio, SOR > 3; (6) Fisher strand, FS > 60; and (7) mapping quality, MQ < 40; (8) mapping quality rank sum test, MQRankSum < -12× and (9) read position rank sum test, ReadPosRankSum< -8 were filtered. We then filtered out nonbiallelic SNPs or SNPs with missing genotype rates >0.01. For the remaining SNPs, genotype refinement, imputation and phasing were simultaneously performed using BEAGLE 4.0 (113990), while excluding AFB individuals. After filtering out SNPs with minor allele frequency <0.01, the remaining high-quality SNPs were annotated according to their positions using SnpEff v.4.3 (ref. 112) and were used in the downstream analysis (Supplementary Tables 12 and 13).

To check the confidence of variant calls from the resequencing analysis, we additionally genotyped 69 cattle samples using the BovineSNP50 Genotyping BeadChip (Illumina). After filtering out SNPs based on GeneCall score <0.7, common loci of SNP chip and DNA resequencing data were extracted and examined to assess concordance between genotypes from the two different platforms. We also incorporated the genotype data of 45 samples from our previously published study11 into this assessment to check the reliability of our current pipeline.

Population differentiation and structure. For PCA, we used the Genome-wide Complex Trait Analysis (GCTA)11 tool v.1.93.0 to estimate the eigenvalues and eigenvectors, incorporating genotype data from 331 individuals, excluding two African Buffalos. For admixture analysis, we performed LD-based pruning for the genotype data using PLINK v1.19 (ref. 114) with ‘—indep-pairwise 50 10 0.1’ option as recommended by the developer. Admixture v1.3.0 (ref. 115) was run, increasing K from 1 to 10, where K is the assumed number of ancestral populations. The delta K method was used to choose the optimal K. Genetic distances between cattle breeds were estimated with the Fst estimator as described by Weir and Cockerman116 using PLINK v1.19 (ref. 117).

Phylogenetic reconstruction and genetic diversity. For the most significant candidate region in PBS analysis (BTA25: 40,052,001 – 40,102,000), we split the phased variant call format and generated reference-based consensus sequences for the 50-kb window using becftools v.1.8 (http://samtools.github.io/bcftools/bcftools.html). A maximum-likelihood tree for the generated 666 haplotypes was reconstructed using IQ-TREE v.1.6.12 (ref. 118) with the following options: ModellierPlus + msf phylm, -cm 4, -cm 6 and -msf phylm. The best-fit model was determined to TVM + F + I + G4 (TVM, transversion model; F, empirical base frequencies; I + G4, invariant site plus discrete Gamma model with default four rate categories) under the Bayesian information criterion. The reconstructed trees were visualized using FigTree v.1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

Individual heterozygosity (theta) based on Felsenstein’s model of substitutions119 was estimated using the ATLAS v.0.9 (ref. 120) program, which takes into account the depth coverage and sequencing error of each locus. ROH were analyzed using VCFTools v.0.1.17 (ref. 121), filtering out ROH segments of <50 kb.

Test for admixture and estimation of admixture proportion. We used the f and D statistics in African cattle populations. We used our variant calls (~17.7 million SNPs) and the linearly interpolated recombination map derived from a large US Department of Agriculture dairy cattle pedigree122. All statistics were computed using ADMIXTOOLS v.5.1 (ref. 123) with standard errors obtained from a block jackknife with 5-cM block size. Z-score was calculated on the standard errors. Three types of statistics were used in these analyses with the following notations. Normal distribution was replaced with the approximate function when the test statistic, f, did not always mean there is no admixture, as a high degree of drift specific to the X population can mask the negative signal124.

The f statistic was used to test for evidence that African cattle populations are derived from the admixture of two populations (EAT and AAI). X is the target African population of interest and EAT and AAI are populations close to the source populations. A significant negative f statistic is considered evidence of historical admixture in the population. In contrast, a positive value does not always mean there is no admixture, as a high degree of drift specific to the X population can mask the negative signal124.

The D statistic was used to evaluate gene flow between different cattle populations. X is the target African population. If we ascertain AFB as an outgroup, a significant positive value indicates gene flow between EAT and AAI and a significant negative value indicates gene flow between X and AAI. 

\[ f(X; EAT, AAI) \]

The f statistic was used to test for evidence that African cattle populations are derived from the admixture of two populations (EAT and AAI). X is the target African population of interest and EAT and AAI are populations close to the source populations. A significant negative f statistic is considered evidence of historical admixture in the population. In contrast, a positive value does not always mean there is no admixture, as a high degree of drift specific to the X population can mask the negative signal124.

\[ D(EAT, X; AAI, AFB) \]

The D statistic was used to evaluate gene flow between different cattle populations. X is the target African population. If we ascertain AFB as an outgroup, a significant positive value indicates gene flow between EAT and AAI, and a significant negative value indicates gene flow between X and AAI.

\[ f = f(EATA, AFB, X; AAI) / f(EATA, AFB; EATB, AAIB) \]

The f statistic was used to test for evidence that African cattle populations are derived from the admixture of two populations (EAT and AAI). X is the target African population of interest and EAT and AAI are populations close to the source populations. A significant negative f statistic is considered evidence of historical admixture in the population. In contrast, a positive value does not always mean there is no admixture, as a high degree of drift specific to the X population can mask the negative signal124.

Estimation of admixture time. The time of admixture was first estimated with ALDER v1.03 (ref. 125), which provides an LD-based admixture time, using the default parameters with a minimum genetic distance (mindis) of 0.5 cM. For this, we used our variant calls (~17.7 million SNPs) and the linearly interpolated recombination map derived from a large US Department of Agriculture dairy cattle pedigree122. A population is derived from an admixture between two source populations close to the reference populations, the pairwise LD in this population, weighted by the allele frequencies in the reference populations, shows an exponential decay as a function of the genetic distance. ALDER fits this decay and then infers the admixture time from the decay rate of the fitted curve.

We additionally used the modified version of ALDER (MALDER v1.10 (ref. 126), which allows multiple admixture events, to compare the agreements of single- and double-pulse admixture models with our data. For estimating admixture time using ALDER and MALDER, we performed two analyses for each African cattle population using two sets of reference populations (EAT and AAI, Muturu and AAI). The fitted curve of both the single- and double-pulse admixture models for Kenya Boran was visually checked using the ‘nlq’ function implemented in R. For all of the admixture time estimations, standard errors were estimated from a leave-one-chromosome-out jackknifing.

In addition, we used GLOBETROTTER127 on 14 African cattle populations (APF) to estimate haplotype-sharing-based admixture time. The
GLOBETROTTER method uses a coancestry curve, in which a measure of how often pairs of haplotypes separated by a genetic distance X come from each respective source population is plotted as a function of the genetic distance X (ref. 13). Given a given event, haplotypes inherited from each source population theoretically have an exponential size distribution, which leads to an exponential decay of the coancestry curve13. GLOBETROTTER fits this curve, allowing us to estimate the rate of the exponential decay, which is an estimate of the admixture time14.

We specified the 14 African humped cattle populations and the other non-African cattle populations as target and donor populations, respectively. This specification indicates that target haplotypes are allowed to be copied from the donor haplotypes, not from the other target haplotypes. This is recommended when a similar admixture history is shared across the target populations15.

To reduce the computational load, we performed LD-based pruning for the phased data using PLINK v.1.9 (ref. 16) with ‘-indep-pairwise 50 10 0.1’ option. The known genetic map17 was interpolated against this reduced data, not allowing interpolation for gaps larger than 50 kb. Using the loci of the LD-pruned data, for which the recombination rates are available on the interpolated genetic map (≈0.72 million SNPs), we performed GLOBETROTTER analysis as the following: (1) first, we ran ten rounds of the expectation–maximization iterations for BT1A, 2, 7 and 12 using ChromoPainter v2 (ref. 18) with ‘-im’ and ‘—im’ switches, which result in estimates of the switch rate and global mutation rate parameters; (2) we then averaged the estimated parameters from (1) over all individuals and chromosomes, and used these as fixed estimated values (>514,030-M.005127882) for the second running of ChromoPainter v2 (ref. 18); (3) we summed the ‘chunk length’ output from (2) across chromosomes using ChromoCombine, and obtained a single ‘chunk length’ output; (4) we also obtained ten painting samples for each target individual by running ChromoPainter v2 (ref. 18) with the fixed parameters averaged over all target individuals (n 632,949-M.006601492); (5) using the summed chunk length from (3) and ten painting samples from (4), we ran GLOBETROTTER with the ‘prop.ind: 1’ and ‘null.ind: 1’ options; and (6) to check the significance of admixture evidence, bootstrapping was performed with 100 replicates using ‘prop.ind: 0’ and ‘bootstrap.date.ind: 1’ options. In the bootstrap replicates, the proportion of inferred generations(s) that were between 1 and 400 was considered as evidence of detectable admixture17.

Detection of selection signatures in African humped cattle. To detect ongoing selection signatures in AFH genomes (n = 149), we employed the iHS19 implemented in HAPBIN v1.3.0 (ref. 18) using the default settings except for the ‘-f 0.01’ option. For each SNP, the ancestral allele was defined as the allele fixed in the AFH outgroup. After computing iHS values for each SNP, they were grouped into 2% frequency bins and standardized. The proportion of SNPs with |iHS| > 2 was then calculated in each nonoverlapping window of 50 kb. In this step, windows with less than 10 SNPs were removed. We considered windows within the highest 1% of the empirical distribution for the proportion of SNPs with |iHS| > 2 as candidate regions with selection signal.

Local ancestry inference in African humped cattle. Using the genotypic data phased in the iHS analysis, we performed local ancestry inference implemented in the LOTER package20 to infer taure–indicine ancestry along the AFH genomes. We specified 103 individuals of EAT and 56 individuals of AAI as reference individuals; assuming that a haplotype of an admixed AFH consists of a mosaic of assigned taure or indicine ancestry within AFH. The resulting frequencies were then averaged over each nonoverlapping window of 50 kb. For the windows with the highest or lowest 0.5% of the empirical distribution for averaged taure ancestry, we additionally filtered out windows with pairwise FST values between reference populations less than genome-wide level (<0.2296) to reduce false positives from the admixture in each reference population. The remaining windows were considered as candidate regions with excess or deficiency of taure ancestry. In light of the history of indicine cattle on the Indian subcontinent and in the Americas, it is possible that they contain some taure background, although at low frequencies21–23. However, this will not result in false positives. Rather, it could lead to few false negatives since there are similar haplotypes to select in the LOTER algorithm, which may mask an excess of a particular ancestry.

Detection of selection signatures in African taure cattle. To detect selection signatures in AFT after divergence from EAT, we employed the PBS developed by Yit et al.24. For each window with 50-kb size and 2-kb step, we calculated the PBS as follows:

\[ T = \log(1 - F_A) \]

\[ PBS = \frac{P_{\text{AF}} + P_{\text{A}} - P_{\text{F}}}{2} \]

where \( P_{\text{AF}} \) represents estimated branch length between \( i \) and \( j \) populations based on pairwise Weir and Cockerham25, \( F_A \) estimated by VCFTools v0.1.17 (ref. 18). A represents the target population (AFT), while \( E \) and \( O \) represent the control population (EAT) and the outgroup (AAI), respectively. A population PBS value conceptually represents the amount of allele frequency change at a given locus since its divergence from the other two populations. From this statistic, we intended to discover selection signatures in AFT cattle following their ancestral migration into the African continent.

Annotation and functional enrichment analysis. The annotation of the candidate regions was based on the ARS-UCD1.2 Gene Transfer Format file (.gtf) from Ensembl release 99 (ref. 18). For functional enrichment analysis of a candidate gene set, a statistical overrepresentation test in PANTHER v.15.0 (ref. 19) was used based on the GO-Slim Biological Process terms and REACTOME pathway26 with default settings. A false discovery rate–adjusted P value of 0.05 was used as the threshold for statistical significance.

Reporting Summary. Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability. The newly generated sequences for 114 African cattle and two African buffalo samples are available from the Sequence Read Archive (SRA) with the BioProject accession number PRJNA574857. The publicly available sequences were downloaded from the SRA and the China National GeneBank (CNGB) with the following project accession numbers: CPN0000189 (Achai, Bhagnari, Cholistani, Dajal, Dhanni, Gabrali, Hariana, Lohani, Red Sindhi, Sahiwal and Tharparkar), PRJNA318087 (Angus, Anokole, Jersey, Kenya Boran, Kenana, N’Dama and Ongole), PRJNA514217 (Bos frontalis, Limia, Maremmana, Maronese, Pajuna, Podolica and Sayaguessa), PRJNA324822 (Brahman), PRJNA433626 (Brahman, Gir, Hereford, Nelore and Simmental), PRJNA432125 (Bosindicus), PRJEB28185 (Eastern Finn and Western Finn), PRJNA210523 (Hanwoo), PRJNA379859 (Hariana, Sahiwal and Tharparkar), PRJNA210521 (Holstein), PRJSTSN602 (Holstein), PRJNA3797239 (Nelore). The known variants file (.ARSLiptranslation_BSRQ_v3.vcf.gz) for base quality score recalibration was provided in the 1000 Bull Genomes Project (http://www.1000bullgenomes.com/). The annotation of the candidate regions was based on the ARS-UCD1.2 Gene Transfer Format file (.gtf) from Ensembl release 99 (http://www.ensembl.org/). The PANTHER database (http://pantherdb.org) was used for functional enrichment analysis of a candidate gene set.

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Author contributions

K.K. and O.H. devised the main conceptual ideas. O.H. and H.K. managed the project. D.L., S.C., S.J.O., H.-K.L., O.A.M., T.D., S.K., O.H. and H.K. conceived of and designed all of the described experiments. O.A.M., T.D., B.S., G.M.T. and A.T. contributed to sample collection and laboratory work. K.K., T.K., D.Y., J. Jang, S.S., S.L., J. Jung and H.J. analyzed the data. K.K., C.J., J.K. and O.H. drafted the manuscript. All authors read and approved the final manuscript.

Competing interests

The authors declare no competing interests.

Additional information

Extended data is available for this paper at https://doi.org/10.1038/s41588-020-0694-2. Supplementary information is available for this paper at https://doi.org/10.1038/s41588-020-0694-2. Correspondence and requests for materials should be addressed to O.H. or H.K. Reprints and permissions information is available at www.nature.com/reprints.
Extended Data Fig. 1 | Improvement in genotype concordance after genotype refinement using BEAGLE as a function of depth coverage. The y-axis shows the concordance between genotypes called from sequencing data compared to genotypes obtained using the BovineSNPSO Genotyping BeadChip.
Extended Data Fig. 2 | Delta K of cluster number K in genetic clustering analysis using ADMIXTURE. A subset of ~1.6 million SNPs (linkage disequilibrium (LD)-based pruning using PLINK v1.9 with '-indep-pairwise 50 10 0.1' option) was used for K from 1 to 10. The delta K analysis suggests K = 2 as the most likely number of distinct genetic ancestries among the 10 Ks (delta K = 31.02).
Extended Data Fig. 3 | Mean pairwise Fst values between cattle breeds represented by more than one animal. Sheko is indicated as yellow.
Extended Data Fig. 4 | Estimated heterozygosity of cattle breeds. The lower and upper bounds of box correspond to the first and third quartiles (the 25th and 75th percentiles), respectively. The horizontal line in the box represents the median value. The upper and lower whisker extend from the bounds to the largest and lowest value no further than 1.5 * interquartile range (IQR), respectively. The number of biologically independent animals used in this analysis for each breed is as follows: Achai (2), Afar (9), Angus (10), Ankole (10), Arsi (10), Barka (9), Bhagnari (3), Boskarin (1), Brahman (20), Butana (20), Cholistani (2), Dajal (1), Dhanni (2), Eastern Finn (5), Ethiopian Boran (10), Fogera (9), Gabrali (2), Gir (4), Goffa (10), Hanwoo (23), Hariana (3), Hereford (18), Holstein (10), Horro (11), Jersey (10), Kenya Boran (10), Kenana (13), Limia (1), Lohany (1), Maremmana (3), Maronesa (1), Mursi (10), Muturu (10), N'Dama (13), Nelore (10), Ogaden (9), Pajuna (2), Poldolica (1), Red Sindhi (1), Sahiwal (2), Sayaguesa (2), Sheko (9), Simmental (11), Tharparkar (3) and Western Finn (5). Sheko is indicated as yellow.
Extended Data Fig. 5 | Runs of homozygosity patterns of cattle breeds. Sheko is indicated as yellow.
Extended Data Fig. 6 | Weighted LD decay in the Kenya Boran breed before and after fitted with a double-pulse admixture model. The red curve shows the exponential fit to the data. a, Weighted LD fitted by a single-pulse admixture model, when using EAT and Muturu as a reference population separately. b, Weighted LD fitted by a double-pulse admixture model, when using EAT and Muturu as a reference population separately.
Extended Data Fig. 7 | Distribution of proportions of SNPs with $|\text{iHS}| \geq 2$ and taurine ancestry in each 50-kb window. **a**, Distribution of proportions of SNPs with $|\text{iHS}| \geq 2$. **b**, Distribution of taurine ancestry. The windows with SNPs less than 10 were removed. Dashed lines indicate the highest 1% for **a**, and highest or lowest 0.5% in **b**.
Extended Data Fig. 8 | Distribution of taurine ancestry in the candidate regions (the highest 1% for proportion of SNPs with $|iHS| \geq 2$), and whole genome windows. Dashed lines indicate mean (top 1% in iHS analysis: 26.14%, and whole genome: 32.49%).
Extended Data Fig. 9 | Distribution of taurine ancestry according to quantiles of proportions of SNPs with $|iHS| \geq 2$ in each 50-kb window. The lower and upper bounds of box correspond to the first and third quartiles (the 25th and 75th percentiles), respectively. The horizontal line in the box represents the median value. The upper and lower whisker extend from the bounds to the largest and lowest value no further than 1.5 * interquartile range (IQR), respectively. Asterisk indicates the highest 1% with proportions of SNPs with $|iHS| \geq 2$. $n = 149$ (African humped cattle) biologically independent animals were used in this analysis.
Extended Data Fig. 10 | Distribution of average taurine ancestry generated by resampling random windows (same number of windows as the candidate) for 0.1 million times. Asterisk indicates average taurine ancestry of the candidate windows from iHS analysis.
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Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection No software was used in data collection.

Data analysis
- Raw sequence quality check: FastQC v0.11.8
- Raw sequence trimming: Trimommatic v0.39
- Read mapping: bwa mem v0.7.17
- Mark duplicates: Picard v2.20.2
- Sort and indexing bam files: Samtools v1.9
- Base quality score recalibration, variant calling and filtering: Genome analysis toolkit (GATK) v3.8
- Haplotype phasing: BEAGLE v4.0 (r1396)
- SNP annotation: SnpEff v4.3
- Principal component analysis: Genome-wide complex trait analysis (GCTA) v1.93.0
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- Tree visualization: FigTree v1.4.4
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- Runs of homozygosity and Population Branch Statistics (PBS) analysis: VCFtools v0.1.17
- F3, D, F4 ratio statistics calculation: ADMIXTOOLS v5.1
- Chromosome painting: ChromoPainter v2
- Admixture time estimation: ALDER v1.03, MALDER v1.0, GLOBETROTTER v1.0
- Integrated haplotype score (iHS) analysis: HAPBIN v1.3.0
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The newly generated sequences for 114 African cattle and 2 African buffalo samples are available from Sequence read archive (SRA) with the Bioproject accession number PRJNAS74857. The publicly available sequences were downloaded from SRA and China National GeneBank (CNGB) with following project accession numbers;
CNP0000189 (Achai, Bhagnari, Cholistani, Dajal, Dhanni, Gabrali, Hariana, Lohani, Red Sindhi, Sahiwal, and Tharparkar), PRJNA318087 (Angus, Ankole, Jersey, Kenya Boran, Kenana, N’Dama, and Ogaden), PRJNAS14237 (Boskariin, Limia, Maremmana, Maronesa, Pajuna, Podolica, and Sayaguesa), PRJNA324822 (Brahman), PRJNA343262 (Brahman, Gir, Hereford, Nellore, and Simmental), PRJNA432125 (Brahman), PRJEB28185 (Eastern Finn, and Western Finn), PRJNA210523 (Hanwoo), PRJNA379859 (Hariana, Sahiwal, and Thaparkar), PRJNA210521 (Holstein), PRJNA386202 (Muturu), and PRJNAS07259 (Nelore)
The known variants file (ARS1.2PlusY_BQSR_v3.vcf.gz) for base quality score recalibration is provided by the 1000 bull genomes project (http://www.1000bullgenomes.com/). The annotation of the candidate regions was based on the ARS-UCD1.2 Gene Transfer Format file (.gtf) from Ensembl release 99 (http://www.ensembl.org/). PANTHER database (http://pantherdb.org/) was used for functional enrichment analysis of a candidate gene set.

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| Sample size | A minimum sample size of 9 animals per breed or 18 autosomal chromosomes was chosen under the expectation that for a biallelic locus of equal frequency for each allele (50%), random fixation of one allele in a breed will have a sufficiently low probability (0.5 to the power of 18) to indicate selection signal. There are no further consideration in determining sample size than the one described. Note that we collected samples, excluding 1st or 2nd degree of relatives based on the pedigree or farmer interview. |
| Data exclusions | We did not exclude any data. |
| Replication | To assess the confidence of SNPs identification, we performed SNP genotyping for a subset of whole samples (n = 114), all of which were successful. |
| Randomization | No randomization was required as no analyses involved in selection of subset of animals or informative SNPs. |
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| Laboratory animals | The study did not involve laboratory animals. |
|--------------------|---------------------------------------------|
| Wild animals       | This specific study did not involve the capture of any wild animals. |
| Field-collected samples | International Livestock Research Institute (ILRI) livestock biorepository provided the cattle samples. The samples of each breed were collected at a single time point within the geographic area of the breed or in the research station as follows; Breed (sample location, country, latitude, longitude, altitude (m))
Afar (Melka Werer, Ethiopia, 09.78217, 040.44031, 804), Arsi (Bekoji, Ethiopia, 07.58051, 039.27933, 3300), Barka (Humera, Ethiopia, 14.09885, 037.21861, 895), Butana (Tamboul, Atabara, Sudan, N/A, N/A, N/A), Ethiopian Boran (Dida Tuyura ranch, Ethiopia, 04.55188, 38.10037, 1569), Fogera (Andassa Livestock Research Centre, Ethiopia, 11.30020, 37.28463, 1735), Goffa (Gamo Goffa, Ethiopia, 06.21423, 37.07276, 1100), Horro (Bako, Ethiopia, 09.07076, 37.03412, 1405), and Sheko (Masha, Ethiopia, 07.64703, 35.50526, 2240). From N'Dama cows in The Gambia, embryos were collected in 1983, with the assistance of the International Trypanotolerance Center (Banjul, The Gambia). They were implanted into recipient cows, and five N'Dama males and five N'Dama females were born in 1984. The N'Dama animals in this study are the offsprings of them.
As these samples were collected for different purposes, they were collected across several years. Animals at the village level were under traditional management system of each community holding them. Animals at the research station were kept indoor at night or in grazing areas at daytime. |
| Ethics oversight | Blood samples were collected during routine veterinary treatments with the logistical support and agreement of relevant agricultural institutions in each country: International Trypanotolerance Center, The Gambia and International Livestock Research Institute (ILRI – Kenya) (N'Dama, Kenya Boran); Ministry of Animal Resources, Sudan (Kenana, and Butana); Ol Pejeta Conservancy, Kenya (Ankole, African Buffalo); Ethiopian Ministry of Agriculture, Ethiopia (Afar, Arsi, Barka, Ethiopian Boran, Fogera, Goffa, Horro, Mursi, Ogaden, and Sheko). No further ethics permissions were required for this study. For European and Asian taurine, all animal works were approved by the Institutional Animal Care and Use Committee of the National Institute of Animal Science in Korea under approval numbers 2012-C-005 (Holstein and Hanwoo) and NIAS-2014-093 (Angus and Jersey). All animals were handled in strict accordance with good animal practice. |

Note that full information on the approval of the study protocol must also be provided in the manuscript.