The mosaic genome of African cattle: a unique adaptive genetic resource

Olivier Hanotte & Sumaya Kambal

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Livestock Genetics – ILRI cattle, chicken, small ruminants

Understanding & meeting farmer needs

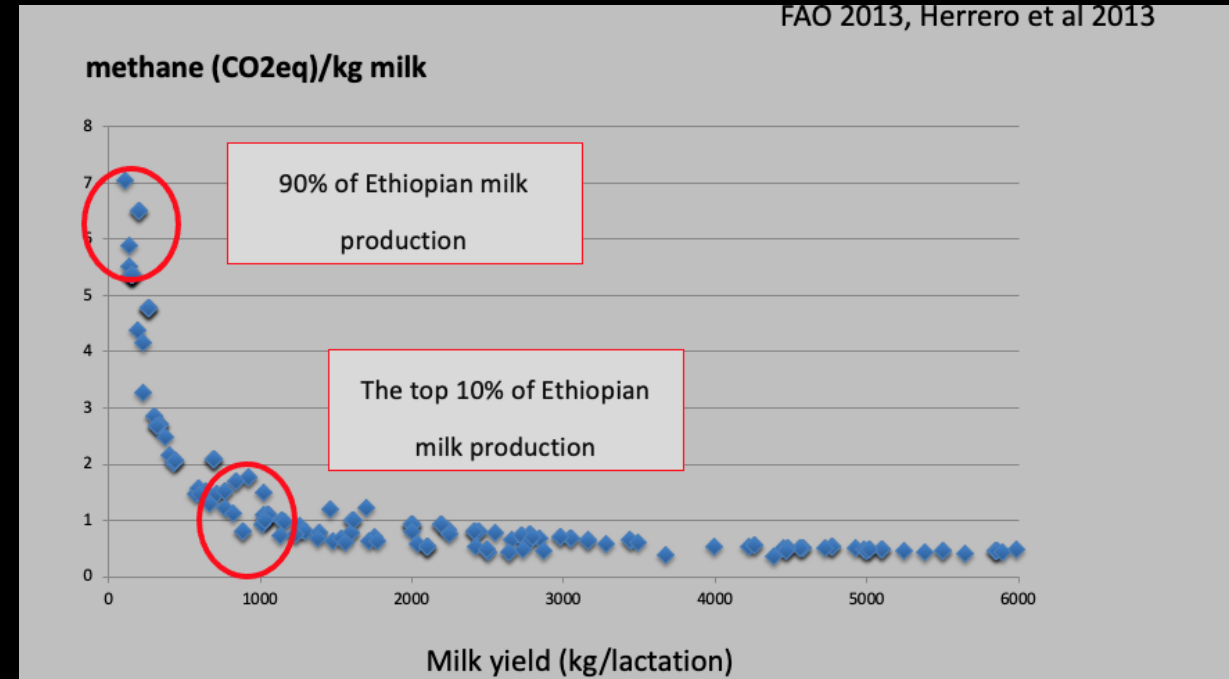The right genetics for the right environment

Adaptation

Climate is a key determinant of constraints – feed, disease, heat stress......

Performance

Improved resilience, productivity, profitability, human nutrition

Mitigation

Reduced environmental impact, including reduced GHG intensity

FAO 2013, Herrero et al 2013

methane (CO2eq)/kg milk

90% of Ethiopian milk production

The top 10% of Ethiopian milk production

Milk yield (kg/lactation)

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PLoS one

A Validated Genome Wide Association Study to Breed Cattle Adapted to an Environment Altered by Climate Change

Ben J. Hayes[1]*, Phil J. Bowman[1], Amanda J. Chamberlain[1], Keith Savin[1], Curt P. van Tassell[2], Tad S. Sonstegard[2], Mike E. Goddard[1,3]
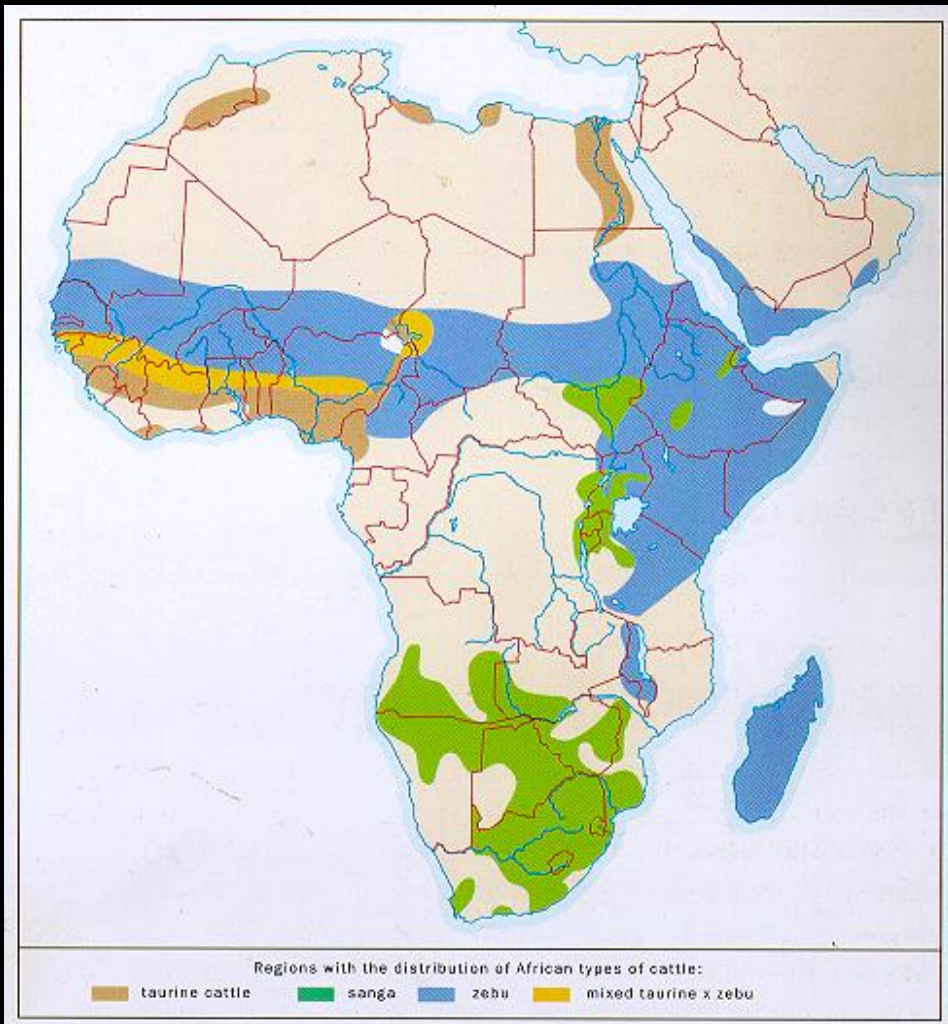
2009

Purpose: Within-breed selection of cattle adapted to predicted changes in the environment by studying the sensitivity of milk production to environmental conditions (feeding level and temperature humidity).

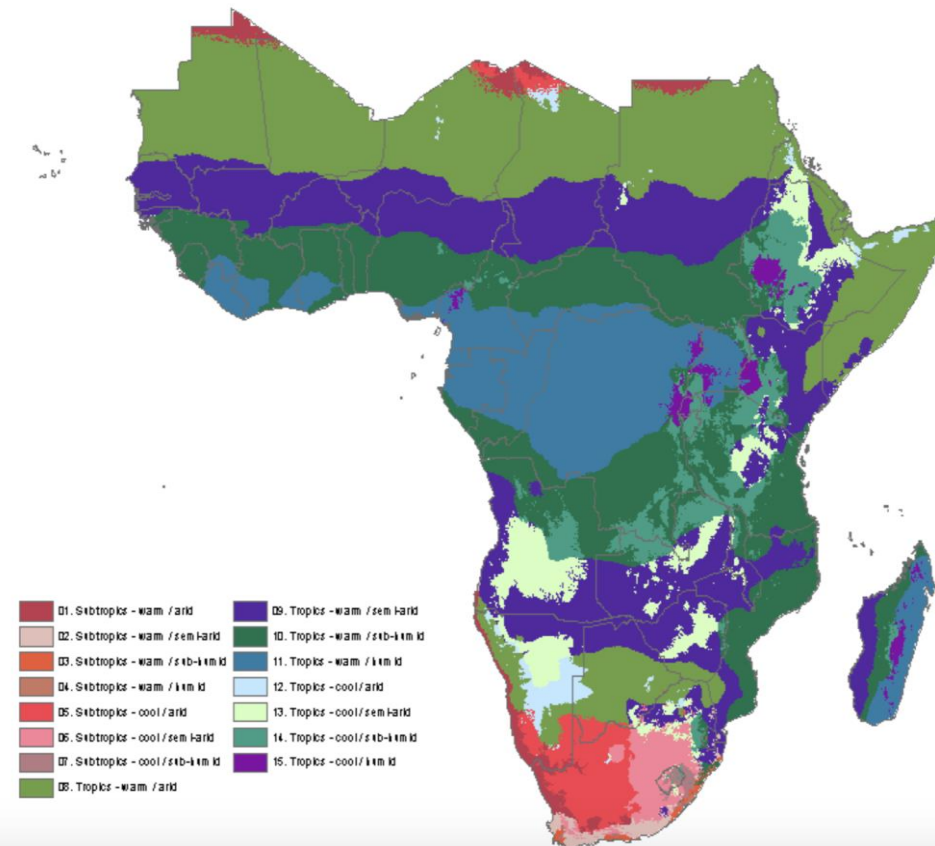But what about between breeds .....

Kuri cattle, Lake Chad

© Dan Bradley

Cattle distribution (Felius 1995)

African main agro-ecologies (HarvestChoice/IFPRI 2010)

- There are at least 150 recognized indigenous African cattle 'breeds', a fifth of world's cattle breeds; 300 million heads (Rege and Bester 1998; Dessie and Okeyo, 2019)

Nganda

Bos indicus

~4000 ya

~1500 ya

White Fulani

Ethiopian Boran

Red Fulani

Mursi

Fogera

Tuli

Kenya Boran

N'Dama

https://www.ilri.org/publications/story-cattle-africa-why-diversity-matters

Example of African cattle adaptation …….
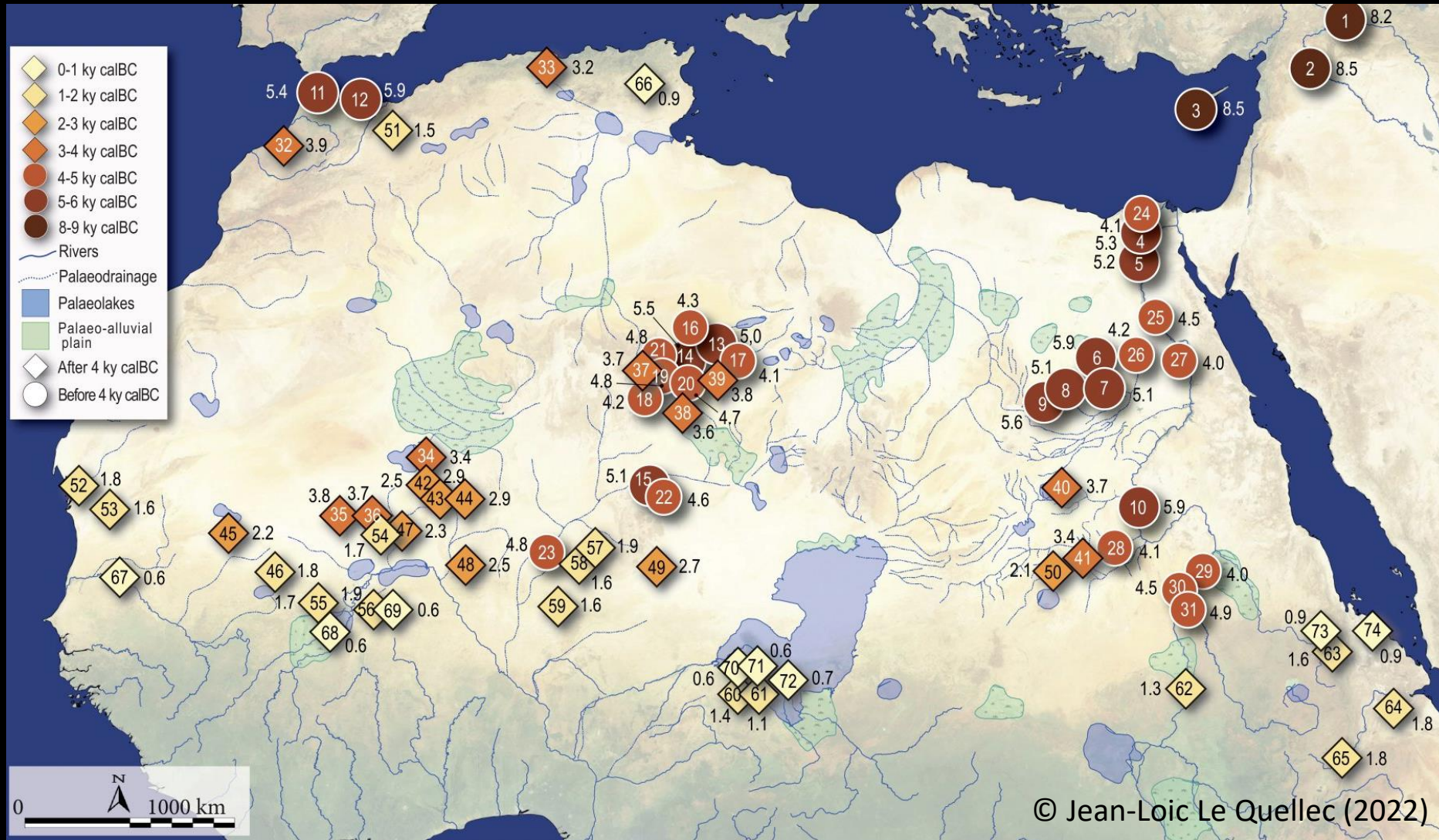
	N'Dama	Tolerance to trypanosomosis and cattle ticks
Humpless Shorthorns	Savanna Muturu	Sexual dimorphism on body size, well-fleshed body
	Sheko	Tolerance to trypanosomosis
Large East African Zebu	Barka	Active disposition
	Karamajong zebu	Adapted to a very dry climate
	Kenyan Boran	Walking ability, highly adapted to harsh conditions, herd instinct, mothering ability, longevity, large sex dimorphism
	Orma Boran	Tolerance to trypanosomosis
	Turkana	survive on very poor pasture and scarce water, walking ability
Small East African Zebu	Angoni	Adapted to browsing during dry season, variable coat color and size of horns
	Arsi	Poor milkers, extremely active and often very aggressive
	Jem-Jem	Well adapted to the wet and cold climate
	Mongolla	Expected tolerance to trypanosomosis, well fleshed
	Nuba Mountain Zebu	Dwarf, tolerance to trypanosomosis
	Ogaden	Good dairy and beef characteristics
	Ugogo Grey	Adapted to browsing during dry season
West African Zebu	Azaouak	Very well adapted to drought
	Red Fulani	Nervous and intractable temperament, poor milkers
	Sudanese Fulani	Good walking ability
	White Fulani	Good dairy and beef characteristics
	Yola	Expected tolerance to trypanosomosis, highly variable conformation
East African Sanga	Bahima*	Susceptible to rinderpest and trypanosomosis
	Raya-Azebo	Good draught power
South African Sanga	Afrikaner	Walking and grazing ability, good mothering ability, longevity
	Barotse	Docile temperament making it a good work animal
	Landim*	Well adapted to hot, humid weather as well as dry periods, very resistant to Foot and Mouth Disease
	Mashona	High fertility, strong maternal instinct, docile disposition
	Nguni	High fertility, early sexual maturity, good foraging and walking ability, good mothering ability
	Tswana	Tolerance to ticks, resistance to the endemic heartwater
	Tuli	High fertility, good mothering ability, low calf mortality
Zenga	Alur	Thought to have trypanotolerance

African Indigenous Cattle: Unique Genetic Resources in a Rapidly Changing World

O. Mwai , O. Hanotte, Y-J Kwon, S. Cho (2015) Asian Asian - Autralasian Journal of Animal Sciences

Etc……

North – African sites with early presence of African cattle

© Jean-Loic Le Quellec (2022)

https://twitter.com/Physiologos/status/1564712371884621824/photo/1

MOLECULAR ECOLOGY

2000

Geographic distribution and frequency of a taurine *Bos taurus* and an indicine *Bos indicus Y* specific allele amongst sub-Saharan African cattle breeds

O. Hanotte, C. L. Tawah, D. G. Bradley, M. Okomo, Y. Verjee, J. Ochieng, J. E. O. Rege

One *Y* micro

Bradley et al. PNAS 1996
Bofiglio et al. PloSOne 2012

D loop mtDNA

Science 2002

REPORTS

34. M. Ebihara, unpublished data.
35. We thank K. Shiraishi, H. Takeda, T. Hiroi, K. Keil, and T. Mikouchi for discussion, K. Hayano for technical assistance, and the Musée National D'Histoire Naturelle (Paris) for providing the sample of Juvinas. We acknowledge support by Grants-in-Aid for Scientific

Research from the Ministry of Education, Science, Culture, Sports, Science and Technology, Japan, Nos. 12740300 (A.Y.), 1144017 (M.E.), and 11640487 (K.N.), and NSF grant EAR9815338 (R.N.C.).

27 December 2001; accepted 6 March 2002

African Pastoralism: Genetic Imprints of Origins and Migrations

Olivier Hanotte,[1]* Daniel G. Bradley,[2] Joel W. Ochieng,[1]
Yasmin Verjee,[1] Emmeline W. Hill,[2] J. Edward O. Rege[3]

The genetic history of African cattle pastoralism is controversial and poorly understood. We reveal the genetic signatures of its origins, secondary movements, and differentiation through the study of 15 microsatellite loci in 50 indigenous cattle breeds spanning the present cattle distribution in Africa. The earliest cattle originated within the African continent, but Near East and European genetic influences are also identified. The initial expansion of African *Bos taurus* was likely from a single region of origin. It reached the southern part of the continent by following an eastern route rather than a western one. The *B. indicus* genetic influence shows a major entry point through the Horn and the East Coast of Africa and two modes of introgression into the continent.

Cattle pastoralism is widespread in Africa today and still forms the basis of life for millions across the continent. Two hypotheses for the origins of African domesticated cattle are currently debated. The North African subspecies of wild cattle or aurochs *Bos primigenius* (*1*) may have undergone an indigenous African domestication around 10,000 years ago, possibly in the northeast of

earliest evidence for humped cattle on the continent, provided by Egyptian tomb paintings of the XIIth Dynasty, do not appear until the second millennium BC (*11, 12*), which suggests that the Egyptian civilization may have played a role in the introduction of zebu into the continent. Today, most modern breeds have an appreciable zebu ancestry (*7, 8*), which attests to a major secondary intro-

15 microsatellite loci

Sumaya Kambal

OWSD – ILRI PhD fellow

Full genome high coverage sequencing of SNPs diversity

Breed	#Samples	Country
Abergelle	11	Ethiopia
Afar	9	Ethiopia
Arado	11	Ethiopia
Arsi	10	Ethiopia
Bagaria	10	Ethiopia
Bale	10	Ethiopia
Begait	20	Ethiopia
ET-Boran	40	Ethiopia
Choke	9	Ethiopia
Erob	8	Ethiopia
Fogera	9	Ethiopia
Goffa	9	Ethiopia
Horro	11	Ethiopia
Mursi	10	Ethiopia
Ogaden	9	Ethiopia
Raya	11	Ethiopia
Semien	10	Ethiopia
Sheko	9	Ethiopia
KE-Boran	16	Kenya
Aryashai	10	Sudan
Butana	36	Sudan
Gash	8	Sudan
Kenana	30	Sudan
Baggara	19	Sudan
Fulani	10	Sudan
Toupouri	15	Chad
Kuri	10	Chad
Gudali	1	Cameroon
Red Fulani	1	Cameroon
White Fulani	1	Cameroon
Kapsiki	1	Cameroon
Namchi	1	Cameroon
Zebu Gobra	12	Senegal
Zebu Maure	7	Senegal
Djakkore	11	Senegal
N'Dama	12	Senegal
Gourounsi	10	Burkina Faso
Baoule	16	Burkina Faso
Ankole	10	Uganda
Ghana Shorthorn	10	Ghana
F-Muturu	13	Nigeria
S-Muturu	10	Nigeria
N'Dama	17	Nigeria
N'Dama	13	Gambia
N'Dama	21	Guinea

537 Samples

45 Populations

Köppen-Geiger Climate Classification

BWh	Cwa
Bsk	Cwb
Bwk	Cwc
CSb	Dfa
AW	Cfa	Dfb
Af	Cfb	Dfc
Am	Cfc	Dfd
As	Csa	Dsa
BSh	Csc	Dsb

Centre for Tropical Livestock Genetics and Health

537 Samples   **45** Populations

Centre and West African zebu (CAZ)

Breed	Abbrev.	#IND	Country
Aryashai	ARY	10	Sudan
Butana	BUT	36	Sudan
Gash	GAS	8	Sudan
Kenana	KEN	30	Sudan
Baggara	BAG	19	Sudan
Fulani	FUL	10	Sudan
Toupouri	TOP	15	Chad
Gudali	GUD	1	Cameroon
Red Fulani	RFL	1	Cameroon
White Fulani	WFL	1	Cameroon
Zebu Gobra	ZGB	12	Senegal
Zebu Maure	ZMR	7	Senegal

African taurine (AFT)

Breed	Abbrev.	#IND	Country
Ghana Shorthorn	GSH	10	Ghana
Kapsiki	KAP	1	Cameroon
Namchi	NAM	1	Cameroon
Baoule	BAO	16	Burkina Faso
S-Muturu	SMT	10	Nigeria
F-Muturu	FMT	13	Nigeria
N'Dama	GND	13	Gambia
N'Dama	NND	17	Nigeria
N'Dama	SND	12	Senegal
N'Dama	UND	21	Guinea

East African zebu (EAZ)

Breed	Abbrev.	#IND	Country
Abergelle	ABR	11	Ethiopia
Afar	AFR	9	Ethiopia
Arado	ARD	11	Ethiopia
Arsi	ARS	10	Ethiopia
Bagaria	BAG	10	Ethiopia
Bale	BAL	10	Ethiopia
Begait	BEG	20	Ethiopia
ET-Boran	EBO	40	Ethiopia
Choke	CHK	9	Ethiopia
Erob	ERB	8	Ethiopia
Fogera	FOG	9	Ethiopia
Goffa	GOF	9	Ethiopia
Horro	HOR	11	Ethiopia
Mursi	MUR	10	Ethiopia
Ogaden	OGD	9	Ethiopia
Raya	RAY	11	Ethiopia
Semien	SEM	10	Ethiopia
KE-Boran	KBO	16	Kenya

African admixed (AAD)

Breed	Abbrev.	#IND	Country
Gourounsi	GOR	10	Burkina Faso
Kuri	KUR	10	Chad
Sheko	SHK	9	Ethiopia
Djakkore	DJK	11	Senegal
Ankole	ANK	10	Uganda

Köppen-Geiger Climate Classification

AW, Af, Am, As, BSh, BWh, Bsk, Bwk, CSb, Cfa, Cfb, Cfc, Csa, Csc, Cwa, Cwb, Cwc, Dfa, Dfb, Dfc, Dfd, Dsa, Dsb
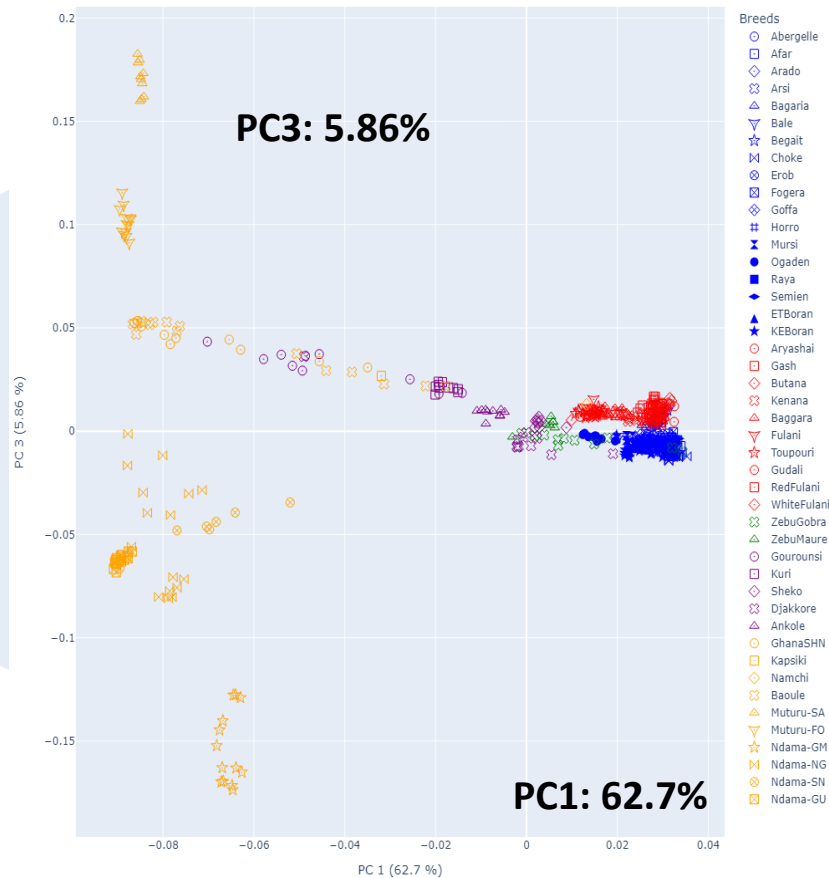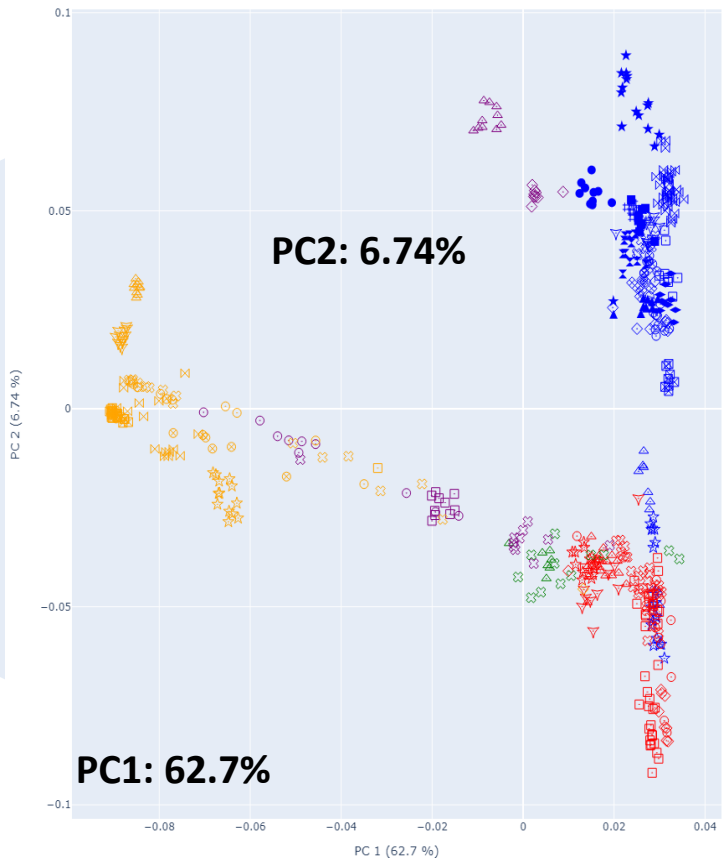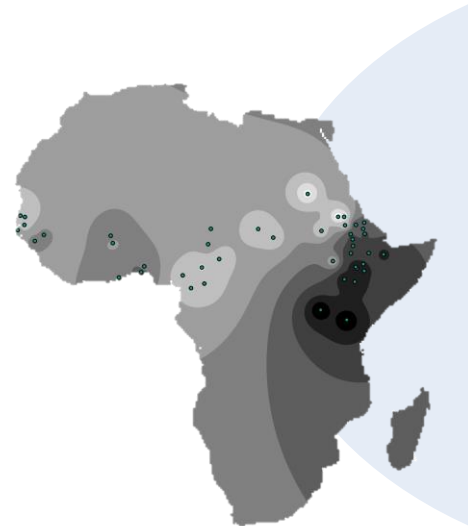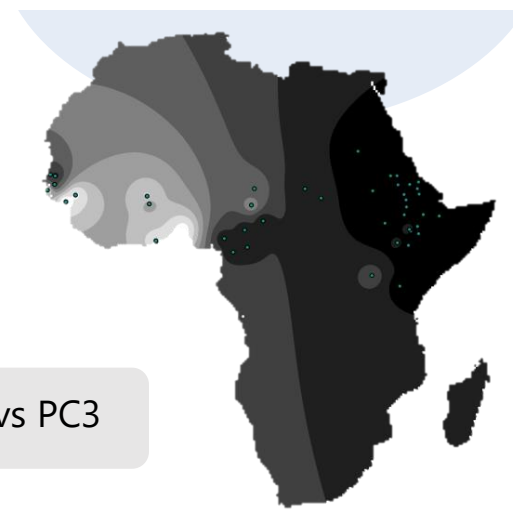
MAF and LD pruned data

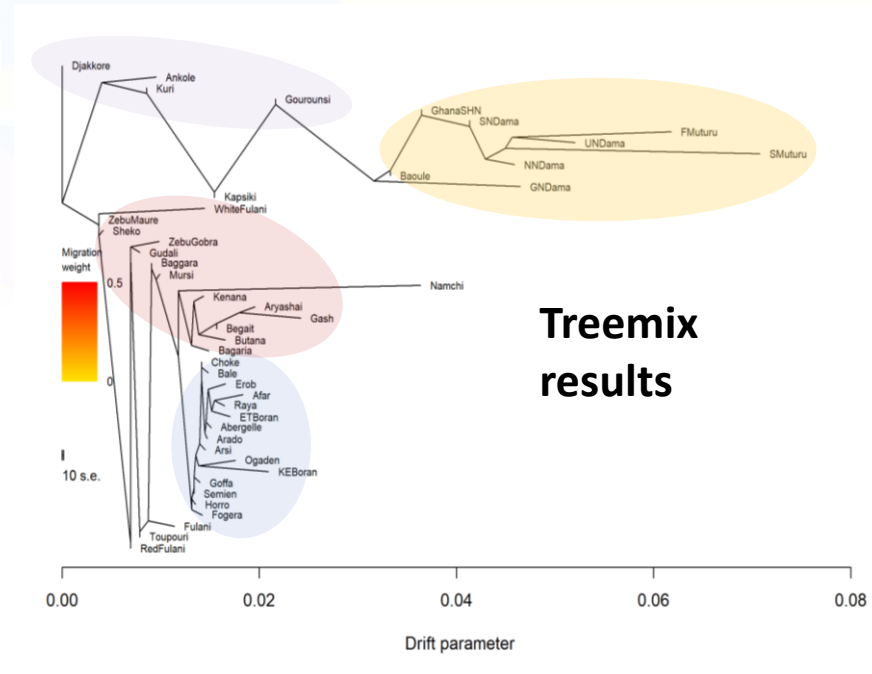2,994,996 SNPs

- MAF < 0.05
- r2 > 0.5

PC1 vs PC2

PC1 vs PC3
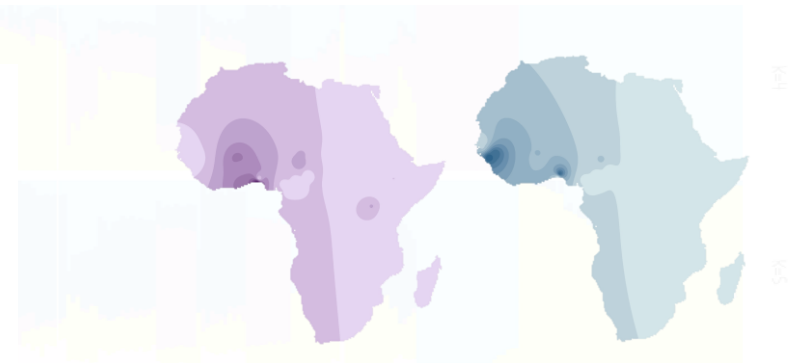
PC2: 6.74%

PC1: 62.7%

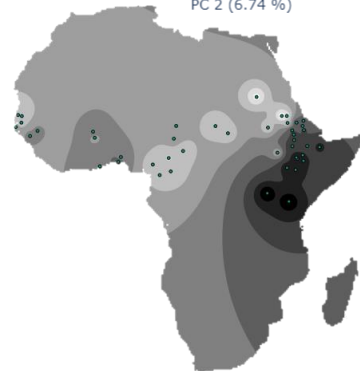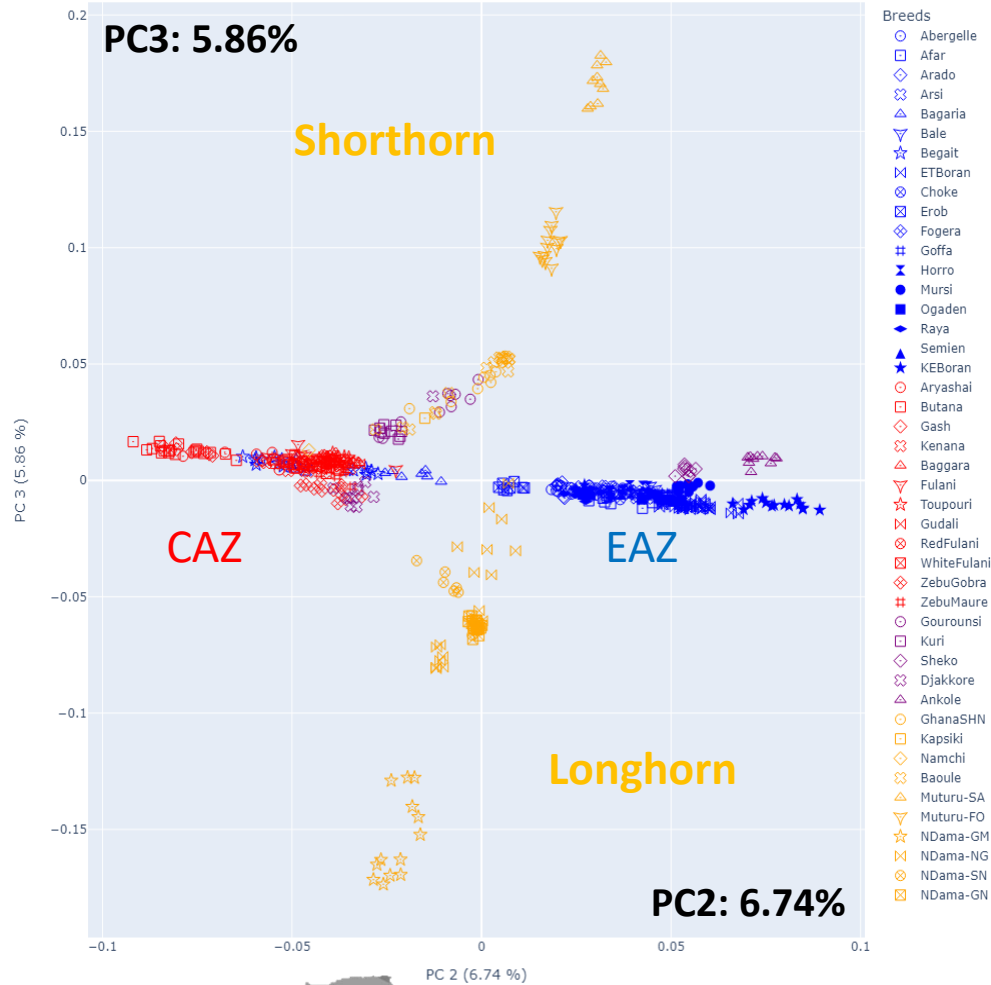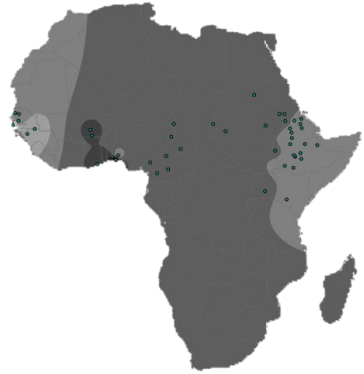PC3: 5.86%

PC1: 62.7%
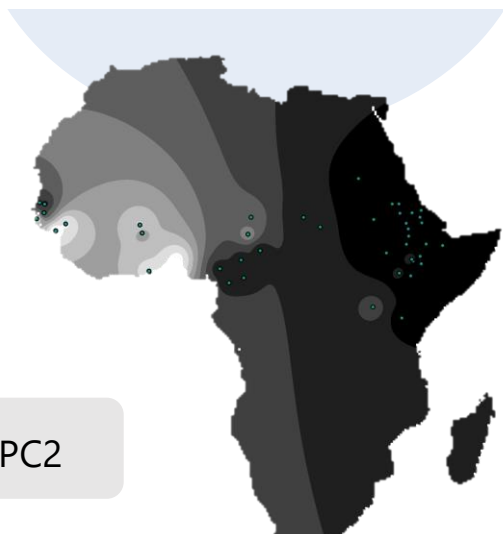
Population Admixture – K = 4
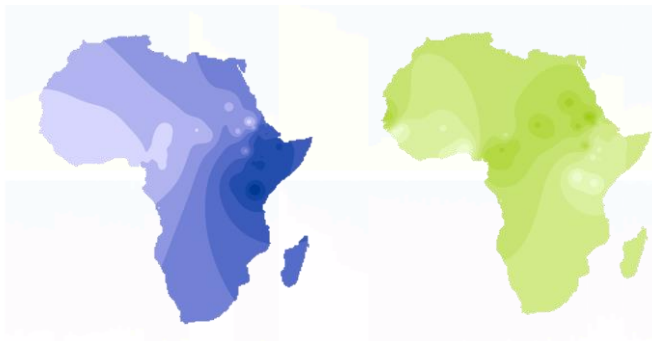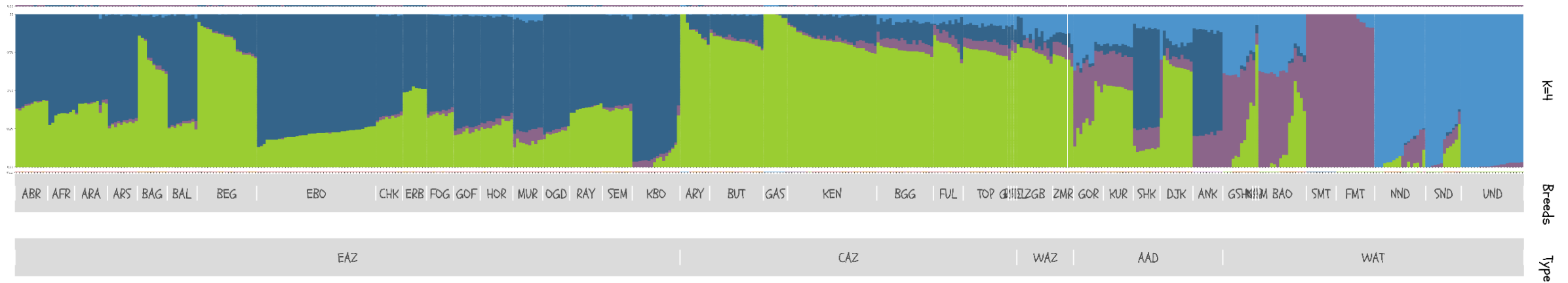
Zebu ancestries decreased as we move from **East** to the **West**

Treemix results

Small shared **Muturu** and **N'Dama** taurine ancestry background (**shorthorn/longhorn**) within zebu (**EAZ** and **CAZ**)

- Low genetic differentiation (*Fst* <= 0.01) within almost all EAZ and CAZ populations

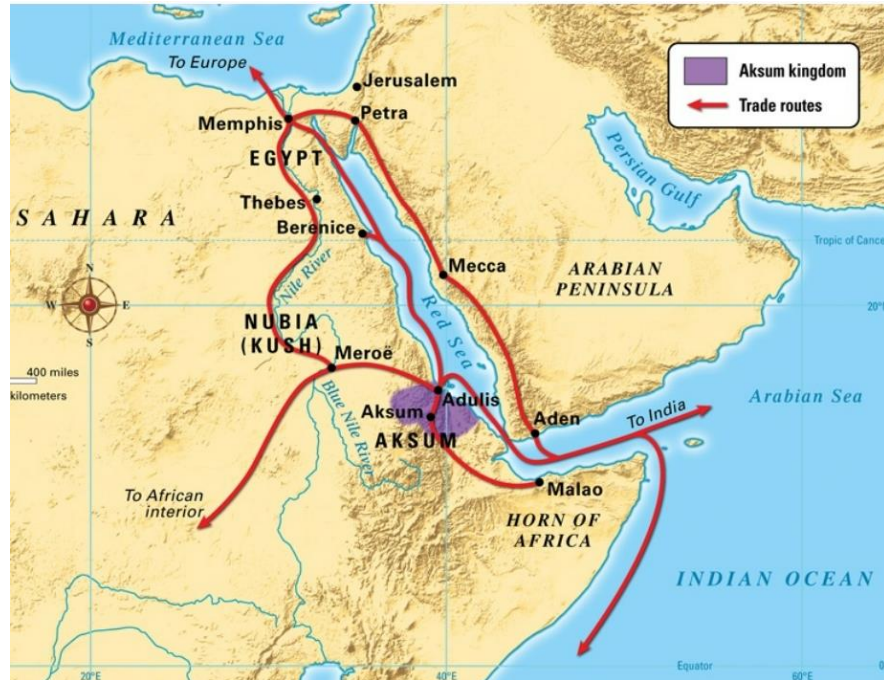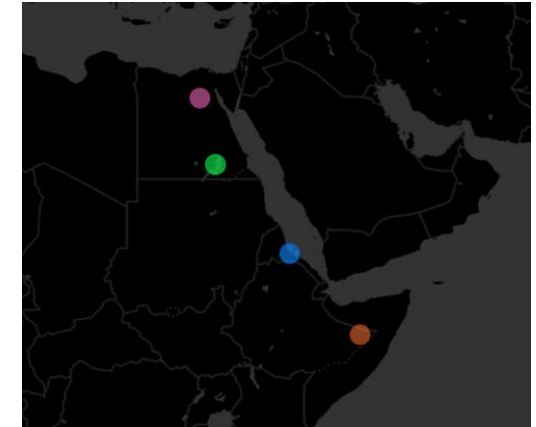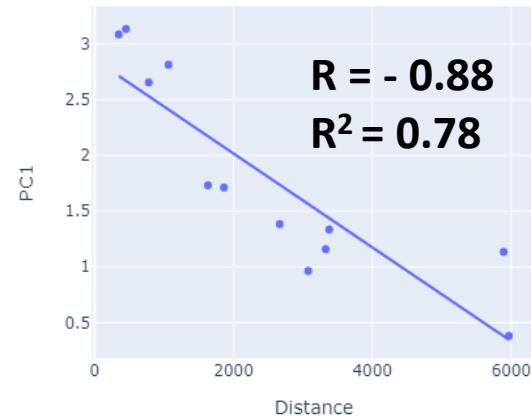- Moderate genetic differentiation (*Fst* = 0.02 to 0.04) between EAZ and CAZ populations
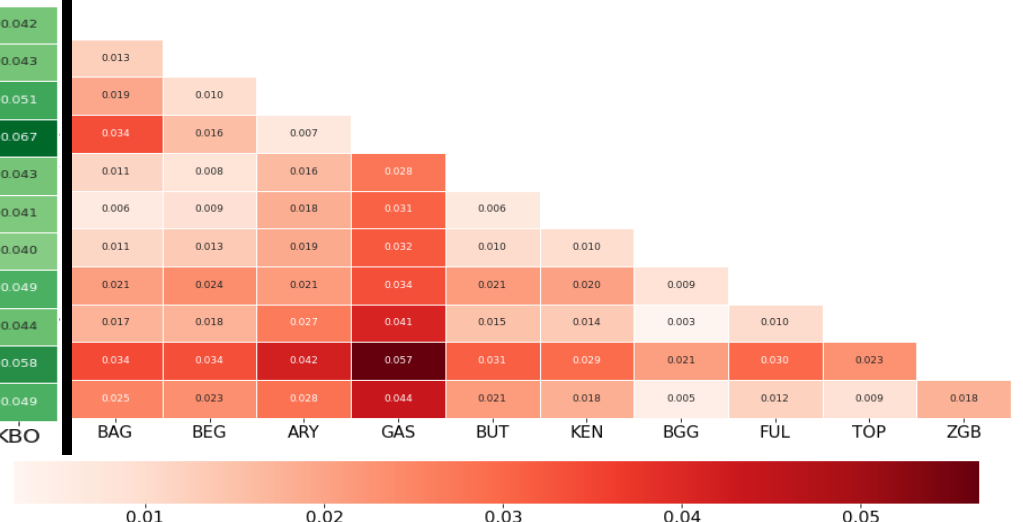
Entry points of the Zebu ancestral population on the African continent – Red Sea port Adulis (?)
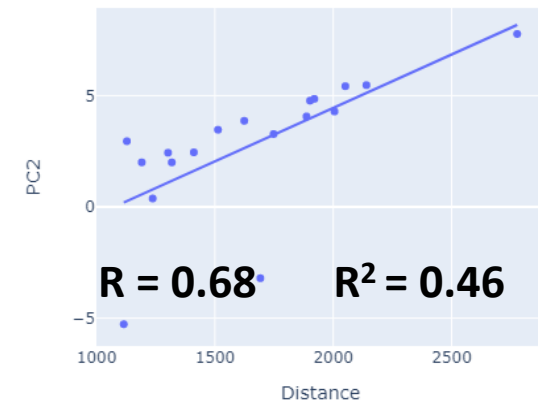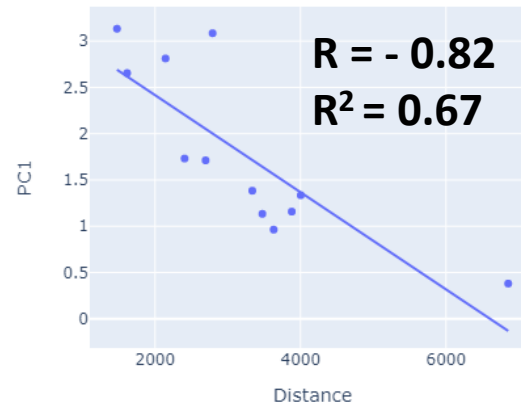

Adulis (Eritrea)

R = - 0.88
R² = 0.78

The Horn of Africa

R = - 0.82
R² = 0.67

Eastern Sahara (Nabta Playa)

R = 0.68   R² = 0.46

ECOLOGY

Time to Tap Africa's Livestock Genomes

> We need to better understand and exploit the genetic diversity of Africa's indigenous livestock breeds—before they fade away.

2010

Olivier Hanotte,[1] Tadelle Dessie,[2] Steve Kemp[3]

If you travel across rural Africa looking for livestock such as cows, pigs, and goats, rather than scenic or wildlife wonders, you will be struck by the extraordinary diversity of its indigenous breeds (*1*). But the visual wonders of coat color or horn shape are only the tip of the iceberg. Looking deeper, a world of Darwinian adaptations—from the ability to tolerate parasites to robust milk production—

Genetic studies are revealing the origins of today's African livestock. It is a complex history that includes human-driven migration, dispersion, crossbreeding, and trading (*2*). Africa's proximity to the major livestock domestication centers in the Near East, as well as oceanic currents and weather patterns linking the East African coast to South and Southeast Asia, have offered multiple opportunities for livestock introductions. Human migrations, such as the spread of Bantu-speaking people from their stronghold in western and Central Africa to the southern part of the continent, and the Islamization of eastern and northern Africa, further favored dispersion of livestock. Last but not least, European influences added a layer of livestock genetic diversity from the north.

Throughout its history, this diversity has been shaped by subtle combinations of

to pressure to increase short-term product ity, fueled by changing demography and ring demand for livestock products. The res is a livestock sector increasingly depend on external inputs such as veterinary interve tion and feed. This trend threatens to exclu a majority of rural farmers from livesto production and raises questions about lor term sustainability. Perhaps more seriously also drives an irreversible loss of the uniq adaptations of indigenous livestock, reduci options for future productivity improveme that could benefit local farmers.

Fortunately, the fields of genetics a genomics (*3–5*) offer a new start for the s tainable improvement of African livesto productivity. Landscape genomics lin genome-wide information to geo-enviro mental resource analysis to identify pote tially valuable genetic material. Typical researchers will perform a genome-wide sc on a number of animals from populations l ing in different habitats or across an ecolo cal cline (from dry to wet areas, for instanc Regions where livestock face selection pr sure from environmental conditions, such
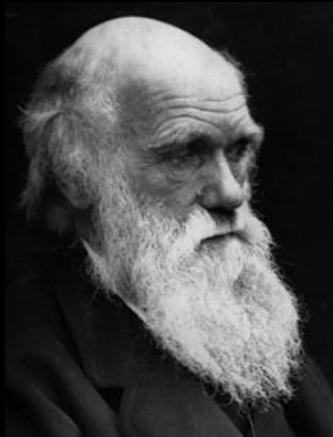
''I have often speculated on the probable cause through which each separate district in Great Britain came to possess in former times its own peculiar breed of cattle…..''
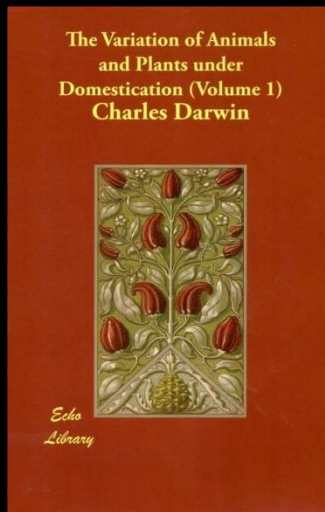
''… I conclude that, although slight differences in the nature of the climate, food, etc., as well as changed habits of life, aided by correlation of growth, and the occasional appearance from unknown causes of considerable deviations of structure, have all probably played their parts; yet the occasional preservation in each district of those individual animals which were more valued by each owner has perhaps been even more effective in the production of the several British breeds…''

1868

Genome Biology

CrossMark

The genome landscape of indigenous African cattle

2017

Jaemin Kim[1†], Olivier Hanotte[2,3†], Okeyo Ally Mwai[4], Tadelle Dessie[3], Salim Bashir[5], Boubacar Diallo[6], Morris Agaba[7], Kwondo Kim[1,8], Woori Kwak[1], Samsun Sung[1], Minseok Seo[1], Hyeonsoo Jeong[9], Taehyung Kwon[10], Mengistie Taye[10,11], Ki-Duk Song[12,18], Dajeong Lim[13], Seoae Cho[1], Hyun-Jeong Lee[8,14], Duhak Yoon[15], Sung Jong Oh[16], Stephen Kemp[4,17], Hak-Kyo Lee[12,18*†] and Heebal Kim[1,10,19*†]

Abstract

Background: The history of African indigenous cattle and their adaptation to environmental and human selection pressure is at the root of their remarkable diversity. Characterization of this diversity is an essential step towards understanding the genomic basis of productivity and adaptation to survival under African farming systems.

Results: We analyze patterns of African cattle genetic variation by sequencing 48 genomes from five indigenous populations and comparing them to the genomes of 53 commercial taurine breeds. We find the highest genetic diversity among African zebu and sanga cattle. Our search for genomic regions under selection reveals signatures of selection for environmental adaptive traits. In particular, we identify signatures of selection including genes and/or pathways controlling anemia and feeding behavior in the trypanotolerant N'Dama, coat color and horn development in Ankole, and heat tolerance and tick resistance across African cattle especially in zebu breeds.

Conclusions: Our findings unravel at the genome-wide level, the unique adaptive diversity of African cattle while emphasizing the opportunities for sustainable improvement of livestock productivity on the continent.
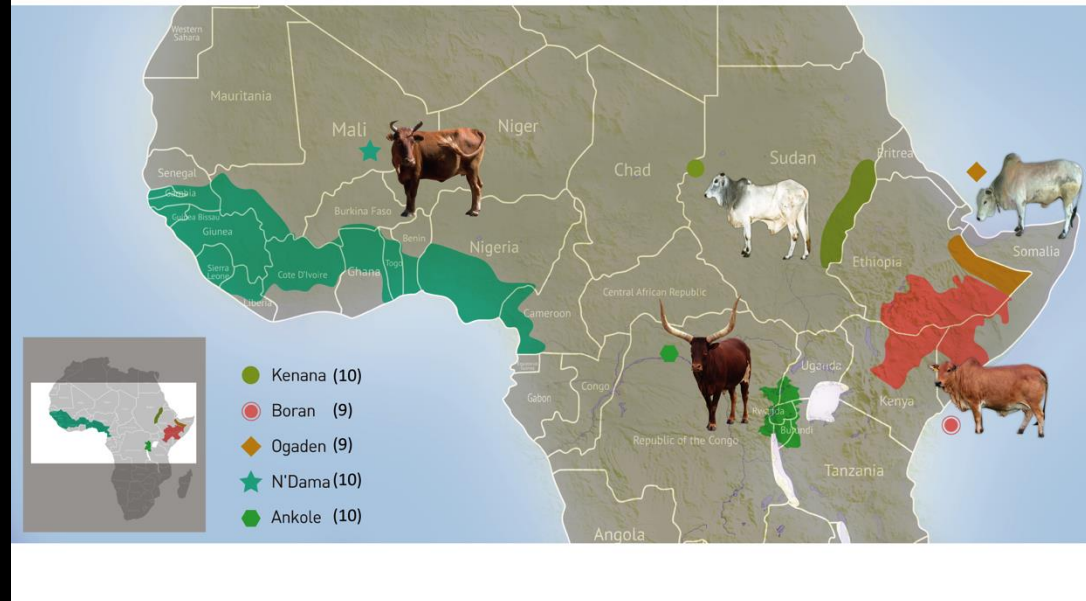
Keywords: African cattle, Genome, Adaptation, Diversity

The genome landscape of indigenous African cattle
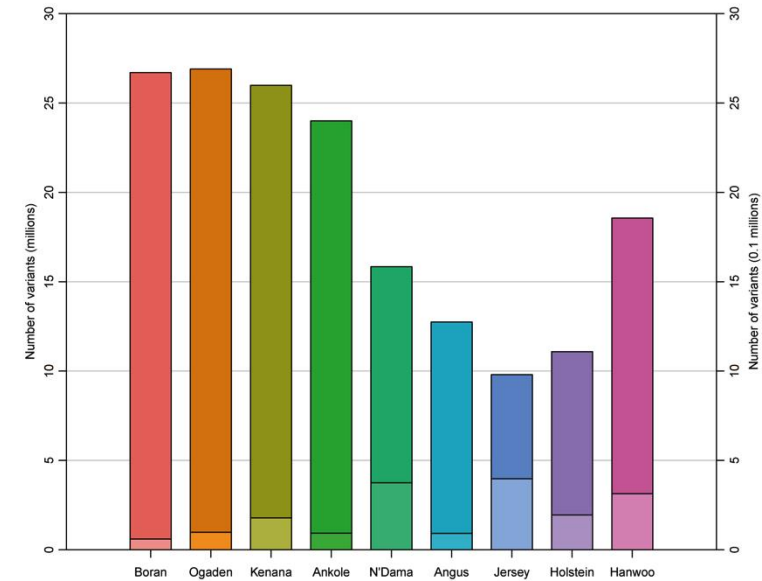## J. Kim, O. Hanotte *et al.* (2017) Genome Biology

Table 1 Summary of major candidate regions identified from XP-EHH and XP-CLR in each breed comparison (see Additional files 2 and 3 for summary values of all candidate genes)

Gene	CHR[a]	Max XP-EHH[b]	XP-EHH P value[c]	XP-CLR	Association	Candidate SNP position	Selected breed
HCRTR1	2	-	-	597.3	Circadian rhythm, feeding behavior		N'Dama
STOM	8	-	-	525.0	Anemia	112665146 (p.Met48Val)	N'Dama
SLC40A1	2	3.32	0.0002	831.1	Anemia	-	N'Dama
SBDS	25	2.91	0.0024	-	Anemia	-	N'Dama
EPB42	10	-	-	511.1	Anemia	38523031 (p.Arg503His)	N'Dama
RPS26	6	-	-	562.8	Anemia	-	N'Dama
KIT	6	1.80	0.0050	-	Coat color	-	Ankole
MITF	22	1.90	0.0032	-	Coat color	-	Ankole
PDGFRA	6	2.56	0.0001	319.3	Coat color	-	Ankole
FGF18	20	-	-	182.3	Horn development	-	Ankole
MC1R	18	-	-	295.0	Coat color	-	Ankole
SOD1	1	-	-	333.31	Thermoregulation	3116044 (p.Ile95Phe)	B. indicus
		-	-	186.33			African
PRLH	3	1.49	0.0014	-	Thermoregulation	117646610 (p.Arg76His)	B. indicus
		1.17	0.0039	-			African
BOLA	23	1.19	0.003	110.13	Tick resistance	-	African

Dash (−) indicates non-significant results
[a]Chromosome
[b]Maximum (positive) XP-EHH score of all SNPs within a window
[c]Rank-based empirical P value of genomic region

Kim, Hanotte et al. Genome Biology 2017

Functionally reciprocal mutations of the prolactin signalling pathway define hairy and slick cattle

Mathew D. Littlejohn[1,2,*], Kristen M. Henty[2,*], Kathryn Tiplady[1], Thomas Johnson[1], Chad Harland[1], Thomas Lopdell[1], Richard G. Sherlock[1], Wanbo Li[3], Steven D. Lukefahr[4], Bruce C. Shanks[5], Dorian J. Garrick[6], Russell G. Snell[2], Richard J. Spelman[1] & Stephen R. Davis[1]

Lactation, hair development and homeothermy are characteristic evolutionary features that define mammals from other vertebrate species. Here we describe the discovery of two autosomal dominant mutations with antagonistic, pleiotropic effects on all three of these biological processes, mediated through the prolactin signalling pathway. Most conspicuously, mutations in prolactin (*PRL*) and its receptor (*PRLR*) have an impact on thermoregulation and hair morphology phenotypes, giving prominence to this pathway outside of its classical roles in lactation.

PRL - Senepol
PRLR - Senepol
PRLH – African Zebu

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 animals showing an excess of taurine or indicine ancestry. These include immune-, heat-tolerance- and reproduction-related genes. Moreover, we identify one highly divergent locus in African taurine cattle, which is putatively linked to trypanotolerance and present in 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.

Admixture characterization → Signature of selection adaptation → Candidate ancestral selected gene identification

Admixture dating → Signature of selection ancestry

Identification of unique African ancestry candidates

a

~0.50 Ma

~4000 BC

~700 AD

Eurasian taurine
Reference population

African taurine
African population

African humped

Asian indicine
Reference population

● African indicine (AFI)

Arsi

Barka

Butana

Goffa

Ethiopian Boran

Kenya Boran

Kenana

Mursi

Ogaden

b

● African indicine
■ African taurine
◆ African sanga
▲ African zenga

◆ African sanga (AFS)

Afar

Ankole

■ Sheko

▲ African zenga (AFZ)

Fogera

Horro

■ African taurine (AFT)

Muturu

N'Dama

Whole-genome sequence analysis of 45 cattle breeds (16 indigenous African population, 172 animals), 35 billion reads or 3.5 terabytes of sequences

Population structure and admixture of indigenous African cattle
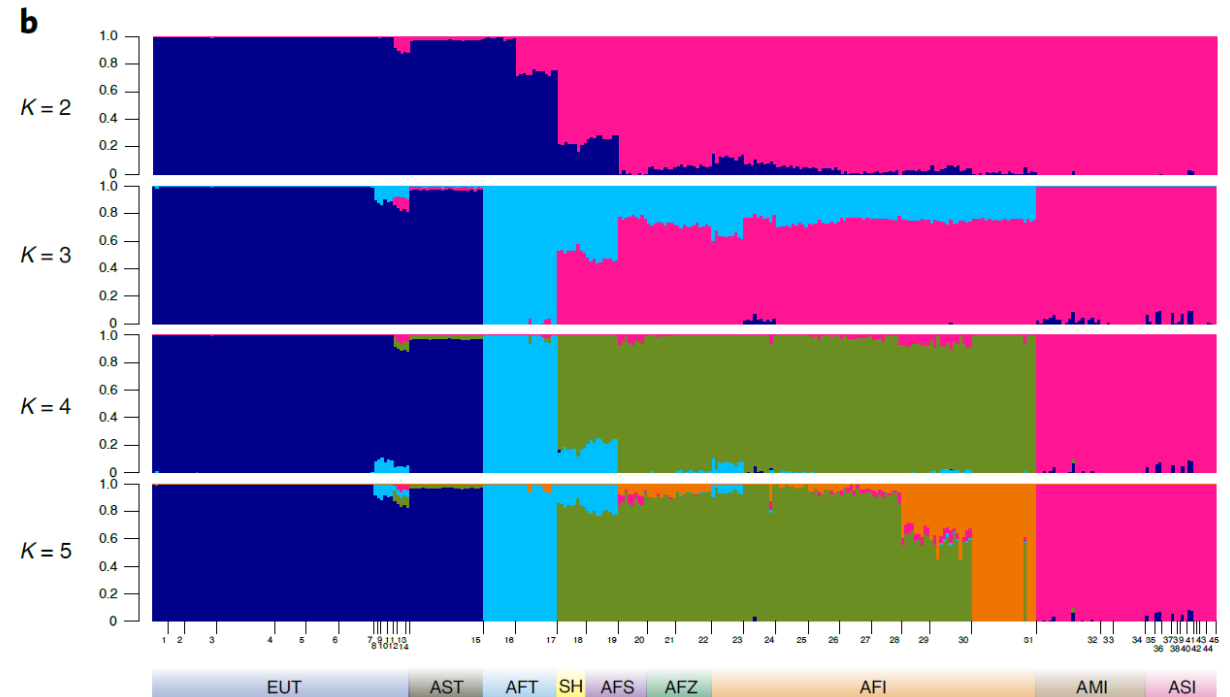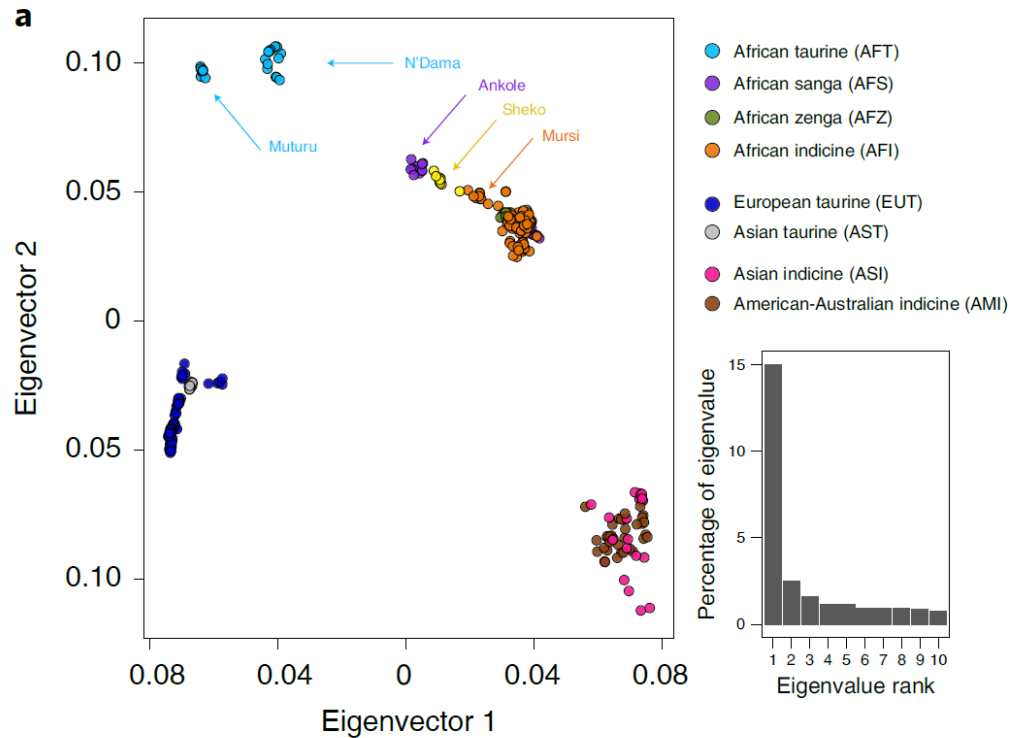
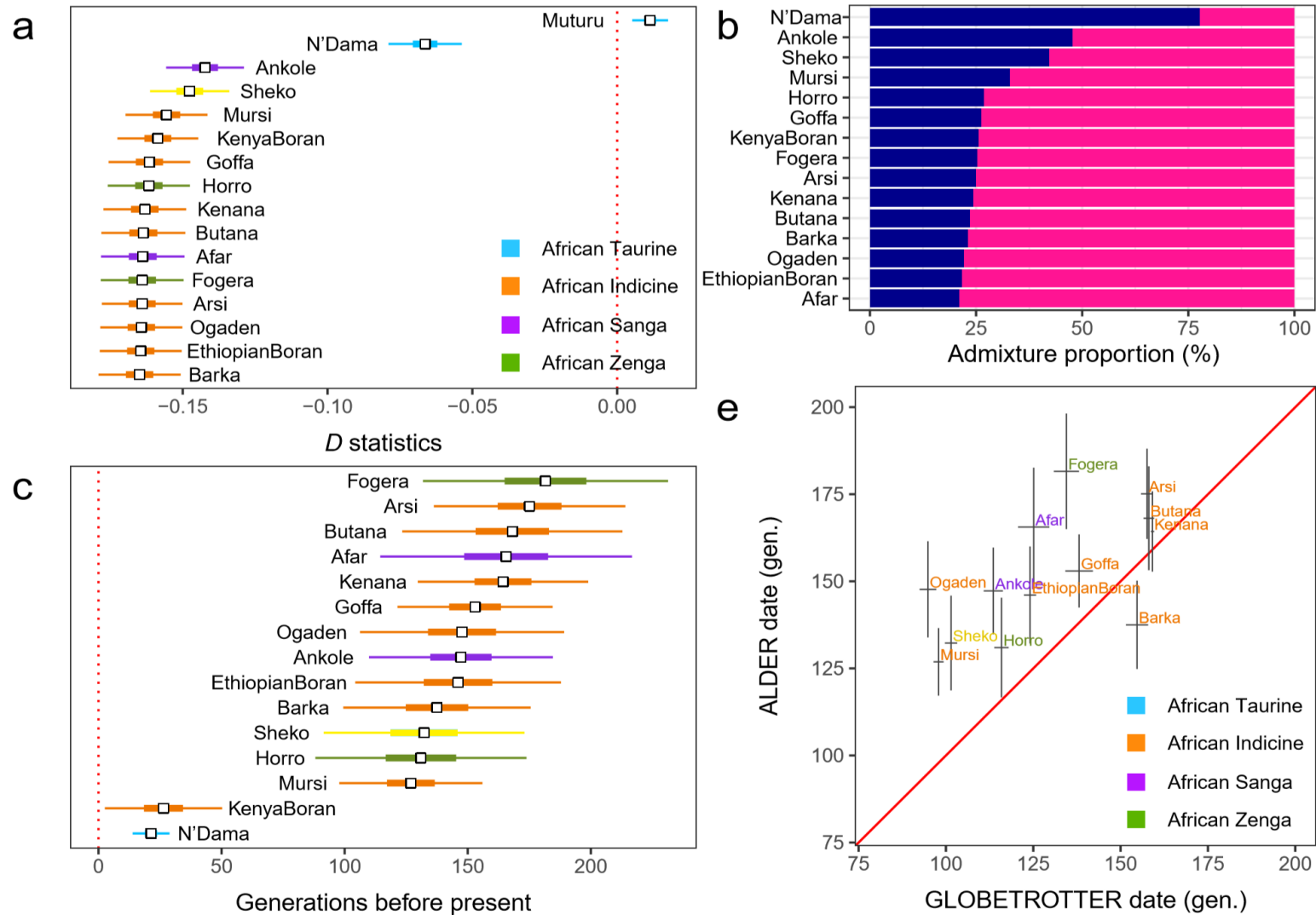**Whole-genome sequence analysis of 45 cattle breeds (16 indigenous African populations), 16 indigenous, 35 billion reads or 3.5 terabytes of sequences**

Admixture dating: Main taurine x indicine admixture events in East African cattle date back to around 150 generation ago (127 – 181), exception being Kenyan Boran and N'Dama, assuming a generation time of 5-7 years, it corresponds to 750 – 1050 years ago.
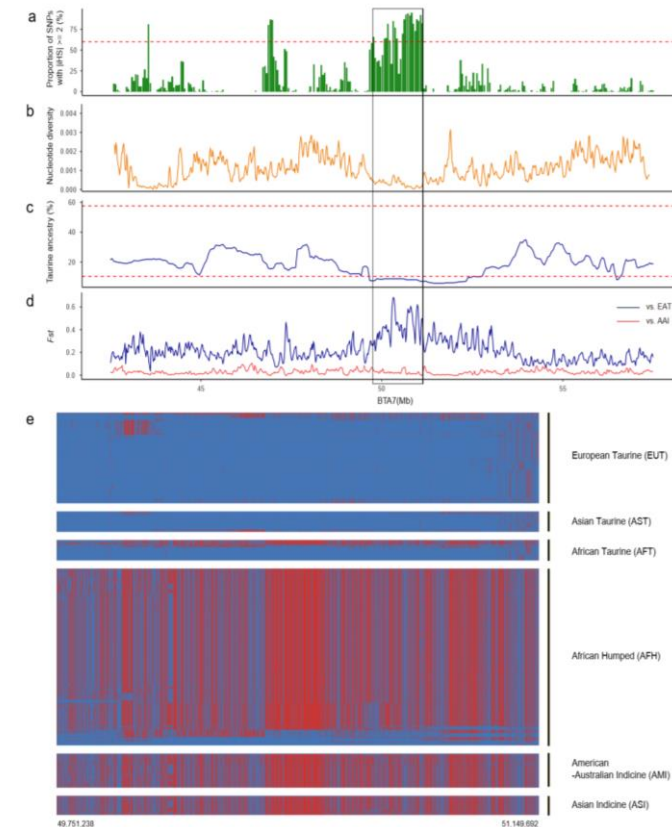
Signatures of selection analysis and signatures of selection ancestry

Table 1 | Common AFH candidate regions identified in the *iHS* and local ancestry (taurine or indicine) inference (LOTER, top 0.5% windows) analysis

BTA[a]	Region (Mb)	No. of windows	Proportion of SNPs with $|iHS| \geq 2$ (%)	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.[99]
3	120.60–120.65	1	79.35	92.62	0.2875	*FARP2, STK25, BOK*	Makina et al.[99]
3	120.70–120.80	2	83.36	92.62	0.2553	*ING5, D2HGDH, THAP4, ATG4B, DTYMK*	Kim et al.[31] Makina et al.[99]
3	120.85–120.90	1	79.25	92.62	0.3182	*RTP5*	Makina et al.[99]
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, LRRTM2, ENSBTAG00000004415*	Kim et al.[31] Gautier et al.[100]
7	50.30–50.45	3	75.17	91.28	0.6321	*SIL1*	Kim et al.[31] Gautier et al.[100]
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.[30] Kim et al.[31] Bahbahani et al.[76] Gautier et al.[100]
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	*PRELID3B, ATP5F1E, TUBB1, CTSZ, NELFCD, ZNF831, GNAS*	Kim et al.[31] Bahbahani et al.[76]
19	39.65–39.85	4	67.07	92.44	0.2982	*STAC2, FBXL20, MED1, PLXDC1, CACNB1, RPL19, ENSBTAG00000008368, ENSBTAG00000050597*	Bahbahani et al.[30] Gautier et al.[100]
Regions with an excess of taurine ancestry							
10	92.15–92.25	2	72.23	59.98	0.3211	*CEP128, ENSBTAG00000047322*	–
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, DPY30, SPAST, SLC30A6, NLRC4, ENSBTAG00000048521, ENSBTAG00000049576*	–

[a]*B. taurus* autosomes. The proportion (%) of SNPs ($|iHS| \geq 2$) 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.

Identification **of > 30 selective loci with an excess of taurine or indicine ancestry** underlying environmental adaptations, including heat tolerance and water reabsorption

An example of candidate selective loci on BTA7 with an excess of indicine (zebu) ancestry

MATR3, MZB1, STING1 (*TMEM173*): Immune related genes e.g. *STING1* essential for DNA-mediated type I IFN production and host defense against DNA viral pathogens

Unique selection signatures in African taurine
following their separation from the common ancestor with Eurasian taurine
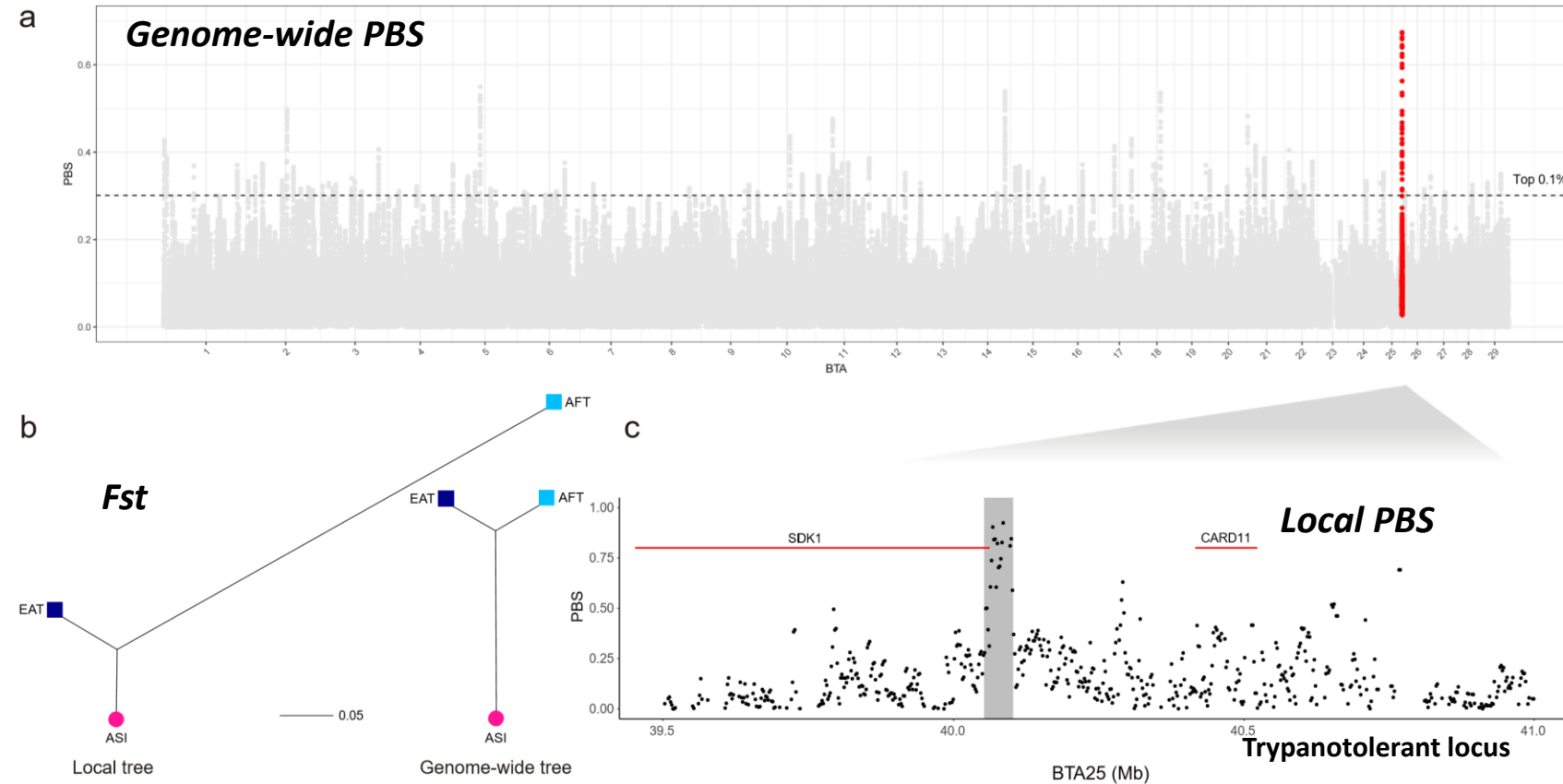
(a) Genome-wide distribution of PBS values with 50 kb window and 2 kb step. The dashed line indicates top 0.1% PBS value. (b) F_{st}-based phylogeny among AFT, EAT and AAI. The branch lengths are proportional to F_{st} values. (c) PBS values around the peak with the highest PBS value. The PBS values were calculated with 5 kb window and 2 kb step.

CARD11: protein essential for the signalling of T and B cells in innate and adaptive immunity, differentially expressed between trypanotolerant N'Dama and trypanosusceptible Kenya Boran (Noyes *et al*. 2011)

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GENOMICS

Original Article

Genomic signatures for drylands adaptation at gene-rich regions in African zebu cattle

Check for updates

Abdulfatai Tijjani [a,b,c,*], Bashir Salim [d], Marcos Vinicius Barbosa da Silva [e], Hamza A. Eltahir [f], Taha H. Musa [g], Karen Marshall [h,i], Olivier Hanotte [a,b,c,1,*], Hassan H. Musa [f,j,*,1]

A B S T R A C T

Background: Indigenous Sudanese cattle are mainly indicine/zebu (humped) type. They thrive in the harshest dryland environments characterised by high temperatures, long seasonal dry periods, nutritional shortages, and vector disease challenges. Here, we sequenced 60 indigenous Sudanese cattle from six indigenous breeds and analysed the data using three genomic scan approaches to unravel cattle adaptation to the African dryland region.
Results: We identified a set of gene-rich selective sweep regions, detected mostly on chromosomes 5, 7 and 19, shared across African and Gir zebu. These include genes involved in immune response, body size and conformation, and heat stress response. We also identified selective sweep regions unique to Sudanese zebu. Of these, a 250 kb selective sweep on chromosome 16 spans seven genes, including *PLCH2*, *PEX10*, *PRKCZ*, and *SKI*, which are involved in alternative adaptive metabolic strategies of insulin signalling, glucose homeostasis, and fat metabolism.
Conclusions: Our results suggest that environmental adaptation may involve recent and ancient selection at gene-rich regions, which might be under a common regulatory genetic control, in zebu cattle.

Zebu male-mediated introgression consequence …..

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BMC Biology

2022

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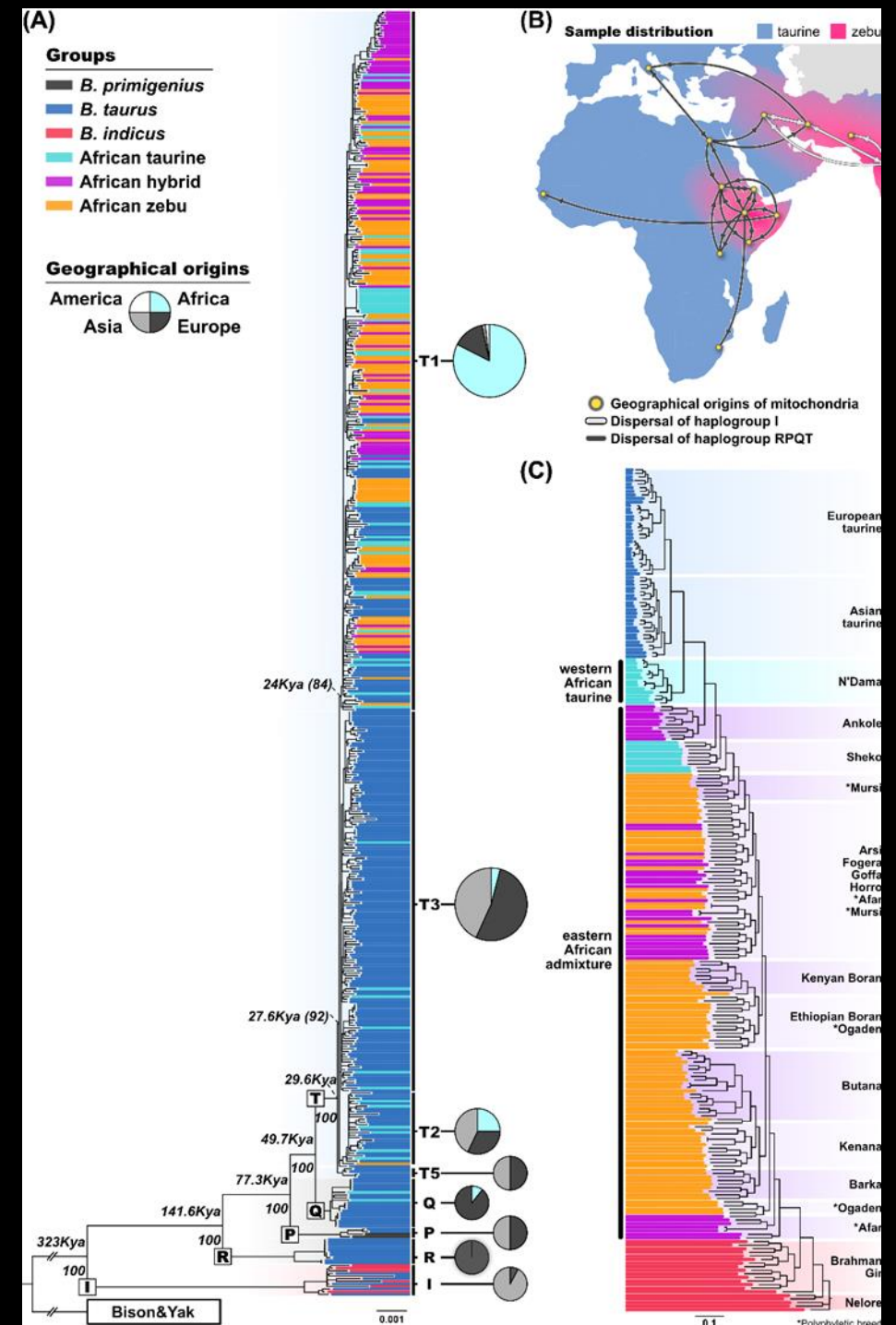
Mitonuclear incompatibility as a hidden driver behind the genome ancestry of African admixed cattle

Taehyung Kwon[1], Kwondo Kim[1,2], Kelsey Caetano-Anolles[3], Samsun Sung[2], Seoae Cho[2], Choongwon Jeong[4], Olivier Hanotte[5,6,7] and Heebal Kim[1,2,8*]

Results: By analyzing 494 mitochondrial and 235 nuclear genome sequences, we first confirmed the genotype discrepancy between mitochondrial and nuclear genome in African admixed cattle: the absence of *B. indicus* mitochondria and the predominant *B. indicus* autosomal ancestry. We applied approximate Bayesian computation (ABC) to assess the posterior probabilities of two selection hypotheses given this observation. The results of ABC indicated that the model assuming both male-biased *B. indicus* introgression and selection induced by mitonuclear incompatibility explains the current genomic discrepancy most accurately. Subsequently, we identified selection signatures at autosomal loci interacting with mitochondria that are responsible for integrity of the cellular respiration system. By contrast with *B. indicus*-enriched genome ancestry of African admixed cattle, local ancestries at these selection signatures were enriched with *B. taurus* alleles, concurring with the key expectation of selection induced by mitonuclear incompatibility.

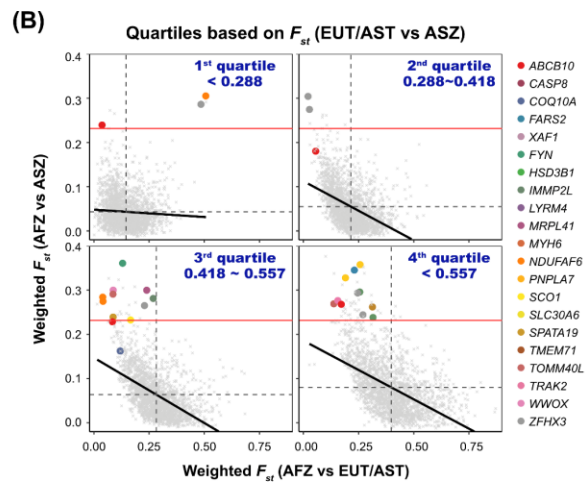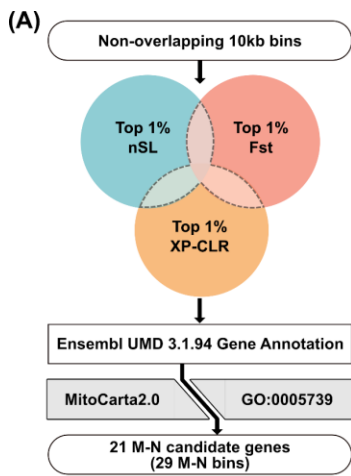**University of Seoul – ILRI - University of Nottingham**

(A) Non-overlapping 10kb bins → Top 1% nSL / Top 1% Fst / Top 1% XP-CLR → Ensembl UMD 3.1.94 Gene Annotation → MitoCarta2.0 / GO:0005739 → 21 M-N candidate genes (29 M-N bins)

(B) Quartiles based on F_{st} (EUT/AST vs ASZ)

Table 3 Selection scan results for 21 candidate genes

Gene symbol	Window (chr:start-end)	normalized XP-CLR	normalized nSL	weighted F_{st}	Functional description
LYRM4	23:49320001-49330000	9.29	0.64	0.18	To bind cysteine desulfarase and help free inorganic sulfur for Fe/S clusters
COQ10A	5:57390001-57400000	6.31	0	0.31	Required for the function of coenzyme Q in the respiratory chain
TOMM40L	3:8290001-8300000	8.26	0	0.29	To participate in the import of precursors into mitochondria as potential channel-forming protein
FARS2	23:49010001-49020000	5.54	0.65	0.16	To transfer phenylalanine to tRNA and to participate in mitochondria for mitochondrial protein translation
MRPL41	11:105590001-105600000	8.98	0	0.35	To participate in protein synthesis within the mitochondrion as ribosomal protein
SCO1	19:30290001-30300000	7.01	0	0.26	To incorporate two Cytochrome c oxidase subunits
ABCB10	28:490001-500000	7.00	0.73	0.23	To participate in transports of molecules across cellular membrane
NDUFAF6	14:71630001-71640000	5.95	0.55	0.27	To regulate of biogenesis of subunit ND1 that is crucial for assembly of the mitochondrial respiratory chain complex I
IMMP2L	4:57730001-57740000	5.18	0	0.28	To process signal peptide sequences used to direct mitochondrial proteins to the mitochondria
SPATA19	29:33750001-33760000	8.36	0.077	0.23	Possibly to participate in spermiogenesis
HSD3B1	3:23810001-23820000	6.16	0	0.27	To catalyze the oxidative conversion of steroid precursors for the production of steroid hormones
TRAK2	2:90350001-90360000	31.40	0.49	0.3	Possibly to regulate endosome-to-lysosome trafficking of membrane cargo
WWOX	18:5720001-5730000	4.96	0.10	0.27	To act as a tumor suppressor and to induce apoptosis
SLC30A6	11:14780001-14790000	0	0.69	0.27	To regulate cytoplasmic level of zinc
MYH6	10:21350001-21360000	4.58	0	0.24	To participate in muscle contraction
CASP8	2:90290001-90300000	5.52	0.036	0.24	To induce in apoptosis
FYN	9:39140001-39150000	4.02	0.27	0.36	To control cell growth and survival as tyrosine kinase
TMEM71	14:9630001-9640000	6.12	0	0.24	Putative transmembrane protein
PNPLA7	11:105600001-105610000	15.13	0	0.36	To regulate adipocyte differentiation
XAF1	19:25750001-25760000	9.76	0.24	0.29	To regulate apoptosis by binds to the inhibitor of apoptosis protein family
ZFHX3	18:38410001-38420000	5.58	0	0.29	To regulate myogenic and neuronal differentiation.
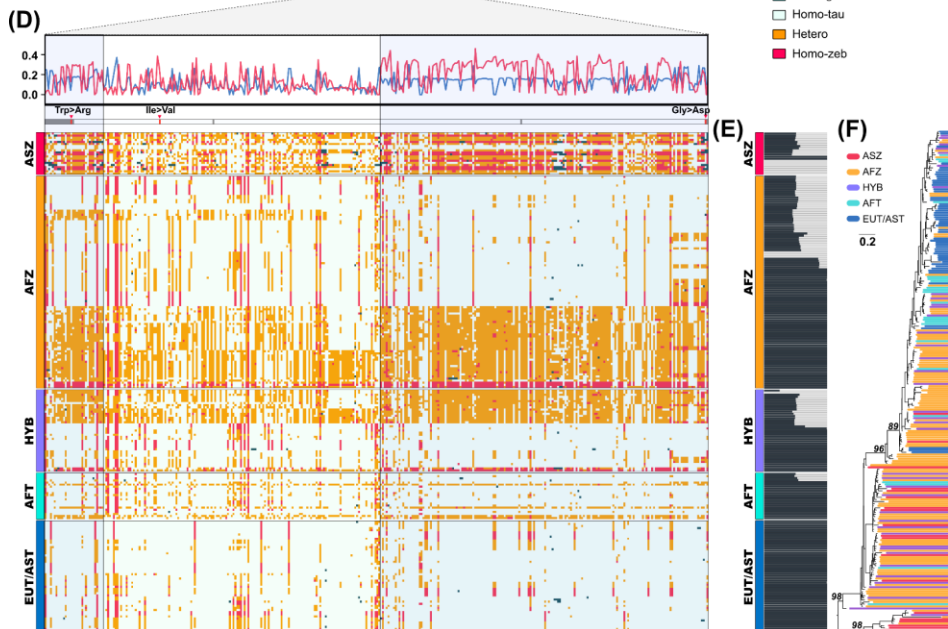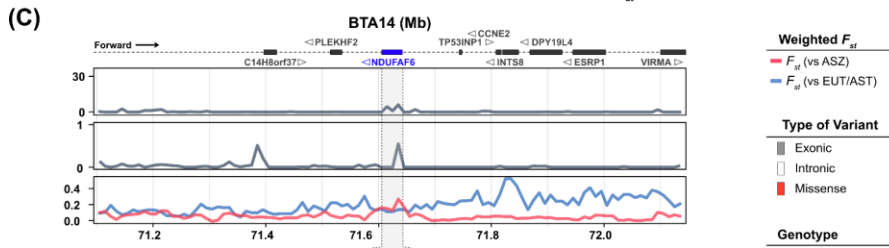
ABC simulation of admixture, indicates that mito-nuclear selection needed along with male-biased *Bos indicus* introgression.

- Mito-nuclear selection signatures enriched with *Bos taurus* ancestry in African *Bos indicus* cattle genome, the key expectation of the mito-nuclear incompatibility hypothesis.

Taehyung Kwon et al. (2022)

See also Ward et al. 2022 iScience. https://doi.org/10.1016/j.isci.2022.104672

2017

Kim *et al. Genome Biology* (2017) 18:34
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Genome Biology

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The genome landscape of indigenous African cattle

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Mitonuclear incompatibility as a hidden driver behind the genome ancestry of African admixed cattle

Taehyung Kwon[1], Kwondo Kim[1,2], Kelsey Caetano-Anolles[3], Samsun Sung[2], Seoae Cho[2], Choongwon Jeong[4], Olivier Hanotte[5,6,7*] and Heebal Kim[1,2,8*]

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 taurine × indicine admixture events followed by taurine 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.

**The future of African cattle production
is in ancient indigenous hybrids (composite)**

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The findings and conclusions contained within this presentation are those of the authors and do not necessarily reflect the positions or policies of any of these institutions.

We are recruiting two Post-doctoral positions: Statistical Geneticist (poultry) and Bioinformatician (livestock) o.hanotte@cgiar.org; t.dessie@cgiar.org