

Invest in livestock diversity

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Forever Initiative: Biodiversity for Resilient Food Systems
Abu Dhabi UAE, 9th -10th December 2019

ILRI
INTERNATIONAL
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TODAY

THE VIEW FROM MALAPA

Lee Berger's team suggests that the clearest line to *Homo* links *A. sediba* directly to *H. erectus*. If true, more primitive East African *Homo* fossils would represent a lineage that went extinct.



Homo sapiens
Worldwide

H. heidelbergensis
Old World

H. neanderthalensis
Europe and Middle East



H. erectus
Old World



H. habilis
East Africa

H. rudolfensis
East Africa

Hadar jaw
Ethiopia

A. garhi
Ethiopia



A. afarensis
East Africa

Kenyanthropus platyops
Kenya

A. anamensis
East Africa

Ardipithecus ramidus
Ethiopia

- *Homo*
- *Kenyanthropus*
- *Australopithecus*
- *Ardipithecus*

1 MILLION YEARS AGO (M.Y.A.)

Australopithecus boisei
East Africa

A. robustus
South Africa

PROPOSED VIEW OF HOMO ORIGINS

PREVAILING VIEW

A CROWDED FIELD

Two or possibly three species assigned to *Homo* coexisted in East Africa around 1.8 million years ago. (Some researchers view a few *H. habilis* fossils as a separate species, *H. rudolfensis*.) Larger brained *H. erectus* eventually gave rise to our own species.

2 M.Y.A.

A. sediba
South Africa

EARLIEST TRACES?

A few fragments older than the Malapa fossils, notably a jawbone from Hadar in Ethiopia, have been described as *Homo*—calling into question a link between *A. sediba* and our genus. But Berger's team has challenged both the age of these fossils and their assignment to *Homo*.

3 M.Y.A.

A. africanus
South Africa

A. aethiopicus
East Africa

4 M.Y.A.



Animals and Climate Change: Dazed and Confused?

Does livestock rival transportation as a greenhouse gas emitter?	Not in high income countries: California livestock contributes 5.4 % of GHG emissions & transport 36.9 %.
Not all meat is the same when it comes to GHG emissions	Compared to beef cattle, pig meat and poultry emit about 1/7th GHG per 100g
Food Waste is one of the biggest food related emissions of GHGs	>30% of the world's food is lost or wasted
Not all cows are created equal	US cows produce 1/20th of the GHG, per unit of cow output, compared to Indian cows
Does Livestock take up land that could be used to grow crops?	Livestock occupies 70% of agricultural land, but occupies only a very small % of land that could be used to grow crops

Based on Porter et. al. 2016, Poore et. al. 2018, and Mitloehner 2018

Let them eat meat? A solution or or a problem for a sustainable healthy future?

Lawrence Haddad
Global Alliance for Improved Nutrition
International Tropical Agriculture Conference
Brisbane, Australia
November 11-13, 2019

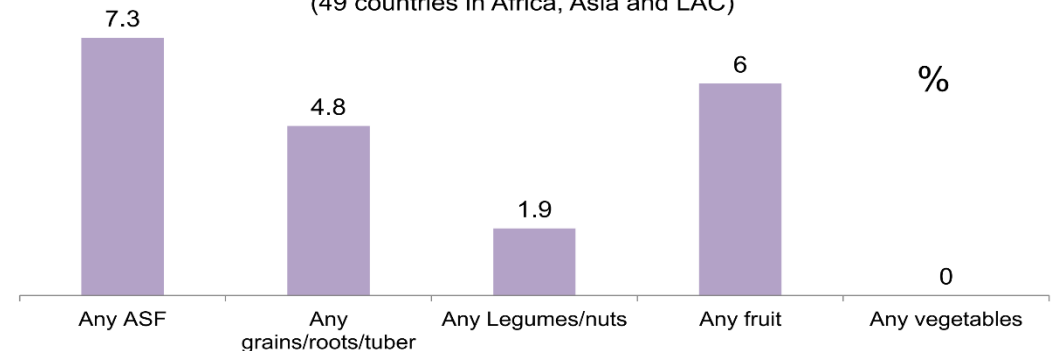


Simple message:
Animal source foods are essential for infant and young child growth

ASF: Animal Source Food

State of the World's Children 2019, UNICEF

Percentage reduction in stunting rates from consuming a food from the food groups below in the previous 24 hours
(49 countries in Africa, Asia and LAC)



Animal Sourced Foods and Child Stunting
D. Headey, K. Hirvonen, and J. Hoddinott (2018) Amer. J. Agr. Econ. 100(5): 1302-1319

Huge increases over the 2005/7 amounts of cereals, dairy and meat will be needed by 2050

From 2bn to 3bn tonnes cereals each year

From 664m to 1bn tonnes dairy each year

From 258m to 460m tonnes meat each year



Huge opportunity and impact for local livestock diversity

Africa's total food import bill in 2016 - USD 55 billion

Imports for milk, meat and eggs in 2016 were USD 8 billion (11% of all food imports), rising to USD 43 billion (21% of all food imports) in 2050

Africa's livestock sector will be worth USD 150 billion in 2050

Livestock contribute on average 40% of agricultural GDP

Over 70% livestock production from farms < 20 ha

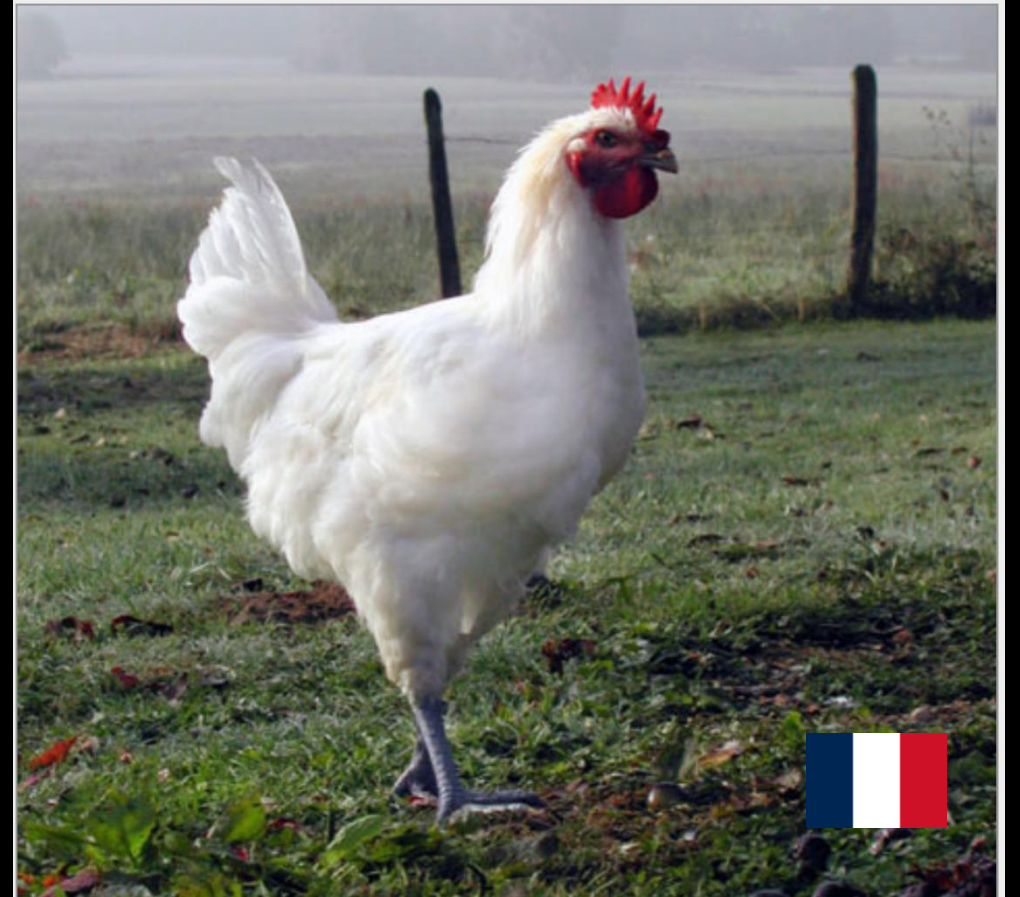
About 250 million people directly engaged in livestock production, 55% of sub-Saharan Africa's workforce is employed in agriculture



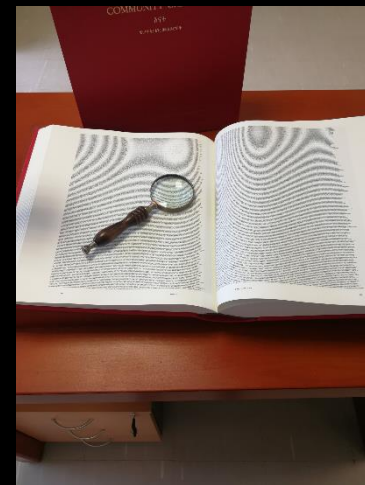
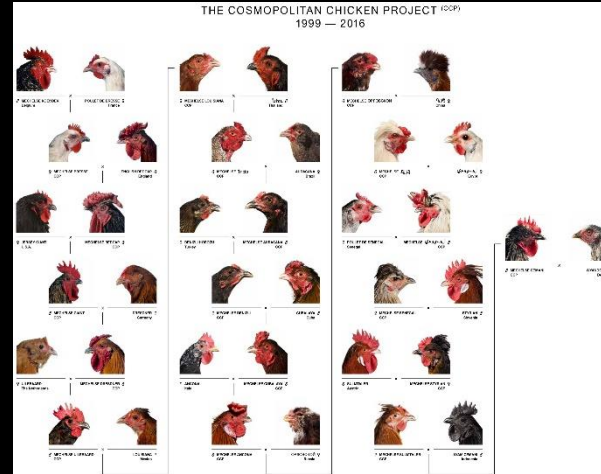
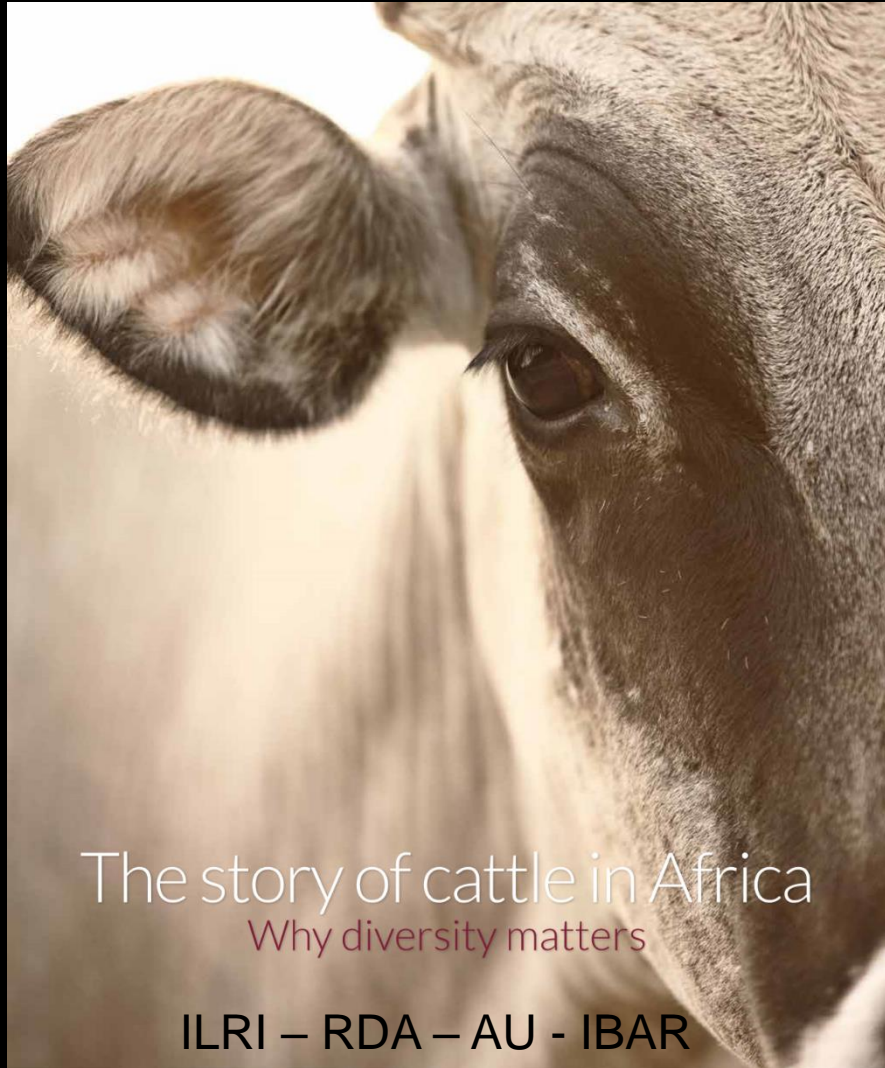
The culture values



POULET DE BRESSE CHICKEN: THE FOURTH
GASTRONOMIC WONDER OF THE WORLD



Invest in people awareness, connect to all actors



Koen Vanmechelen

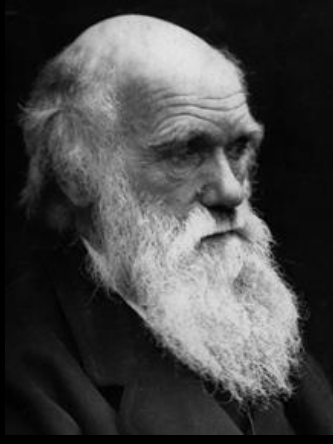
Labiomista
www.labiomista.be



Mouth Foundation

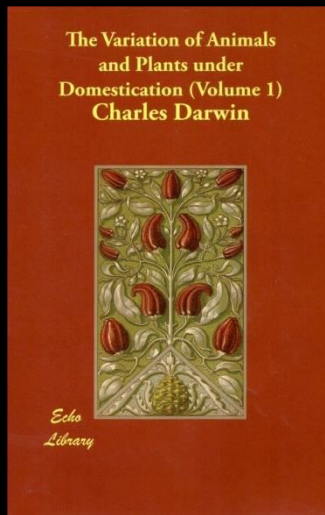
art – science –
diversity

Invest in diversity characterization for sustainable Improvement, climate mitigation



Charles Darwin

“ 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.....”

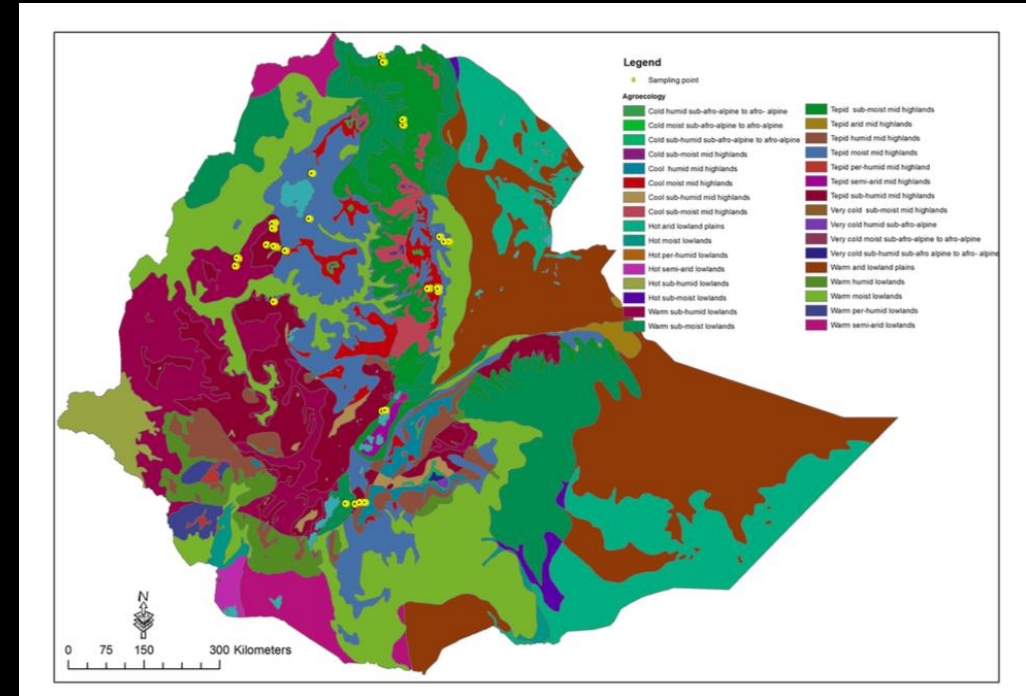
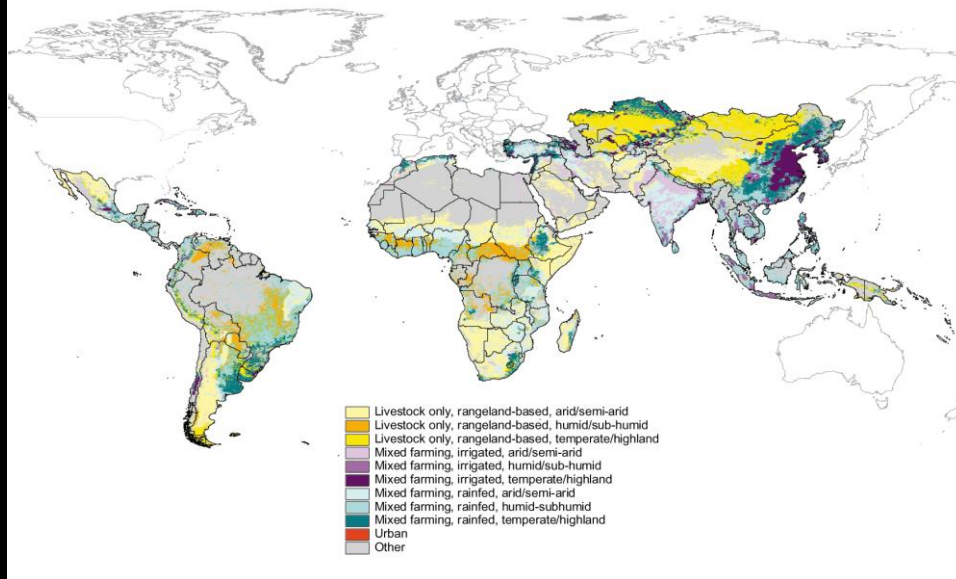


1868

“... 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...”

Invest in diversity *characterization* for sustainable Improvement, climate mitigation

Map 3. Global Livestock Production Systems



PERSPECTIVES

ECOLOGY

Time to Tap Africa's Livestock Genomes

Olivier Hanotte,¹ Tadelle Dessie,² Steve Kemp³

Science 2010

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



The 10,000 livestock genome project

LiveGene



80 - 90 millions US\$

Exploring genome diversity to enhance agricultural productivity

Rationale

With nearly 9,000 recognized breeds, indigenous livestock populations are a treasure trove of unique adaptation shaped by the environment and human selection. For centuries, livestock have met our demands for food, traction, transport, clothing etc. Today, a handful of commercial breeds provide most animal commodities in the developed world, with for example, most indigenous breeds now extinct or only surviving thanks to the enthusiasm of a few breeders in Europe.

The situation is different in the developing world. Here, a large proportion of livestock populations, though not catalogued as breeds, represent distinct ecotypes that display large phenotypic and genotypic diversity. Locally adapted, they represent major and unique repositories of livestock diversity and adaptation. Under pressure

from population growth, urbanization, changes and evolution of agro-systems leading to breed replacement and crossbreeding programs, this diversity is now in danger. It is estimated that 17% of breeds are at risk of extinction with 58% of unknown status. Diversity is being lost before the world has an opportunity to unravel, understand and use it. We are losing adaptive capacity of today livestock jeopardizing the sustainable livestock production of tomorrow.

Efforts to partially address these issues through *in-situ* and *ex-situ* conservation of animal genetic resources have largely failed, or at best only captured an arbitrary and tiny subset of this diversity. Indeed, they face several major hurdles, such as lack of a rational basis to prioritize breeds/populations for conservation, lack of infrastructure and technologies (e.g. for cryopreservation), relevant with in-country expertise, and weak supportive policies etc. Consistent methodologies to assign the phenotypes necessary to infer function are also lacking. We need to act now before this irreplaceable diversity fades away. The 10,000 livestock genome project proposes to do this.

Towards a complete genome characterization of all African indigenous cattle

*Abdulfatai Tijjani^{1,3}, Karen Marshal^{2,3}, Heebal Kim⁴, Han Jianlin^{2,5}, Olivier Hanotte^{1,3,6}

*Contact : A.Tijjani@cglar.org

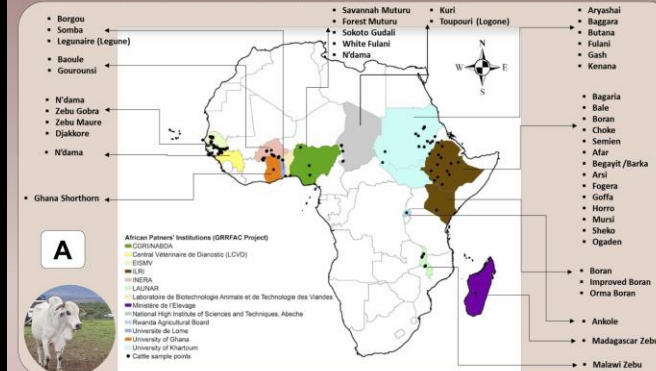
¹ILRI - Addis Ababa, Ethiopia, ²ILRI - Nairobi, Kenya, ³CTLGH, Roslin Institute, University of Edinburgh, Scotland, UK, ⁴Seoul National University, Seoul, Republic of Korea, ⁵ILRI - CAAS Joint Laboratory on Livestock and Forage Genetic Resources, Beijing, China, ⁶University of Nottingham, Nottingham, UK



Project Objectives

We aim to develop a genomic reference resource for African cattle through a consortium of African partners. Our current objectives include:

- Identification of most informative SNPs for designing African reference SNP genotyping arrays
- Identification of selection signatures underpinning adaptation and productivity traits
- Pan-genome analyses of African cattle including *de novo* sequencing and transcriptomic analyses
- Facilitate bioinformatics capacity building among African Scientists



Genomic Reference resource for African cattle (GRRFAC) project

- An initiative of the dairy genomics program of CTLGH
- A strategic alliance of ILRI, Roslin Institute, SRUC and African research partners
- Aims to facilitate the generation of a collated set of sequences and genotype information on African cattle
- For use by African and international research and breeding communities in cattle genomics for the ultimate benefit of African livestock keepers
- Facilitate the capacity building of African researchers in the field of genomics
- More partners especially from North and South of Africa are welcome
- Signed MTA and country ABS permit are required

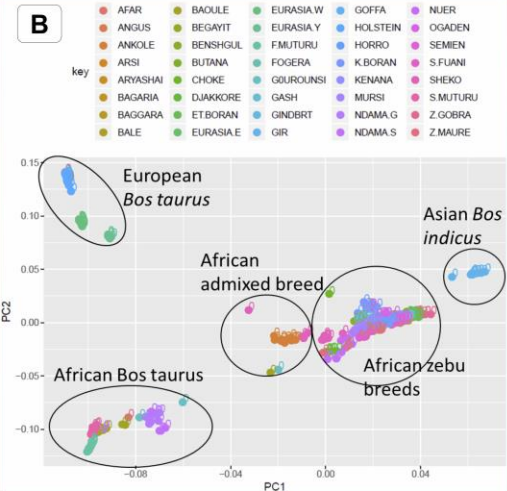
Project update

- 12 African partners, 45 African cattle breeds and about 1500 samples (Figure A)
- Whole genome sequences of up to 380 samples is already in our database and the generation of new sequences is on-going
- Sequences are being mapped to the latest reference genome assembly (ARS-UCD1.2) for variants discovery and further analyses

- About 38 million SNPs identified in 346 samples and PCA of these samples shown in Figure B

Expected outcome

- Design of tailored African SNP array(s)
- Define and characterize important cattle adaptability, resilient and productivity traits
- Project consortium, database and website
- Bioinformatics trainings targeted at African partners



Invest in utilization of diversity

Genomic selection of cross-bred bulls in East Africa

The Challenge

Farmers extracting low profits from their dairy animals

High and intermediate grade cows are reared in low and average production environments

No pedigree records are kept so most farmers do not know the genetic make up of their animals

Heifers and crossbred bulls with breed composition that is appropriate to farmers' circumstances are needed, but are not readily available

Genomic prediction

Accuracies of genomic prediction for young bulls with no records are reasonable (about 40% across a wide range of cross-bred bulls)

The SNP chip could be used initially to eliminate the worst bulls and select the best young bulls for AI

Genomic prediction can be achieved using a low density (3-4K) SNP chip combined with imputation exploiting the covariance between SNPs



A Optimizing productivity and adaptation

Identify genomic regions associated with productivity and resilience (i.e. number of times animals are treated, reproductive performance and longevity)

Incorporate GWAS results into GEBVs computation to optimize productivity and functionality

B Screening Exotic bulls for adaptability in Africa

Use the information from **A** to develop a genomic tool to screen exotic bulls for adaptability and performance in Africa

Design strategic mating plan for selected bulls and indigenous cows and select progeny with optimum combination of desired traits

Use AI to deliver **millions** of semen doses with the aim of establishing tropically adapted cattle

Invest in building the national capacity for ex - situ conservation



- Establishing Primordial Germ Cell Cell (PGC) culture protocols
- Cryopreservation of 400 chicken, 13 ecotypes, 3 countries (Ethiopia, Kenya, Tanzania)
- Training courses, workshop, support of the National Livestock GeneBank
- National Ownership of AnGR

Continuing investing in the best of science valuing diversity

African Pastoralism: Genetic Imprints of Origins and Migrations Science 2002

Olivier Hanotte,^{1*} Daniel G. Bradley,² Joel W. Ochieng,¹ Yasmin Verjee,¹ Emmeline W. Hill,² J. Edward O. Rege³

ARTICLES

<https://doi.org/10.1038/s41893-018-0150-9>

nature
sustainability

The role of local adaptation in sustainable production of village chickens 2018

Judy M. Bettridge^{1,2,3}, Androniki Psifidi^{4,5}, Zelalem G. Terfa^{1,2}, Takele T. Desta^{2,6}, Maria Lozano-Jaramillo⁷, Taddelle Dessie², Pete Kaiser^{4,8}, Paul Wigley¹, Olivier Hanotte^{2,6} and Robert M. Christley^{1*}

Kim et al. *Genome Biology* (2017) 18:34
DOI 10.1186/s13059-017-1153-y

Genome Biology

2017, IP: 13.21

RESEARCH

Open Access

The genome landscape of indigenous African cattle

Jaemin Kim^{1†}, Olivier Hanotte^{2,3†}, Okeyo Ally Mwai⁴, Taddelle Dessie³, Salim Bashir⁵, Boubacar Diallo⁶, Morris Agaba⁷, Kwondo Kim^{1,8}, Woori Kwak¹, Samsun Sung¹, Minseok Seo¹, Hyeonsoo Jeong⁹, Taehyung Kwon¹⁰, Mengstie Taye^{10,11}, Ki-Duk Song^{12,16}, Dajeong Lim¹³, Seoae Cho¹, Hyun-Jeong Lee^{8,14}, Duhak Yoon¹⁵, Sung Jong Oh¹⁶, Stephen Kemp^{4,17}, Hak-Kyo Lee^{12,18†} and Heebal Kim^{1,10,19†}



The mosaic genome of indigenous African cattle as a unique genetic resource for African pastoralism (Kwondo Kim et al. (Nature Genetics under review)



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ILRI thanks all donors and organizations who globally supported its work through their contributions to the [CGIAR system](#)

Patron: Professor Peter C Doherty AC, FAA, FRS

Animal scientist, Nobel Prize Laureate for Physiology or Medicine—1996

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SDG target 2.5

“by 2020 maintain genetic diversity of seeds, cultivated plants, farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks at national, regional and international levels, and ensure access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge as internationally agreed”