Role of Biotechnology in Africa

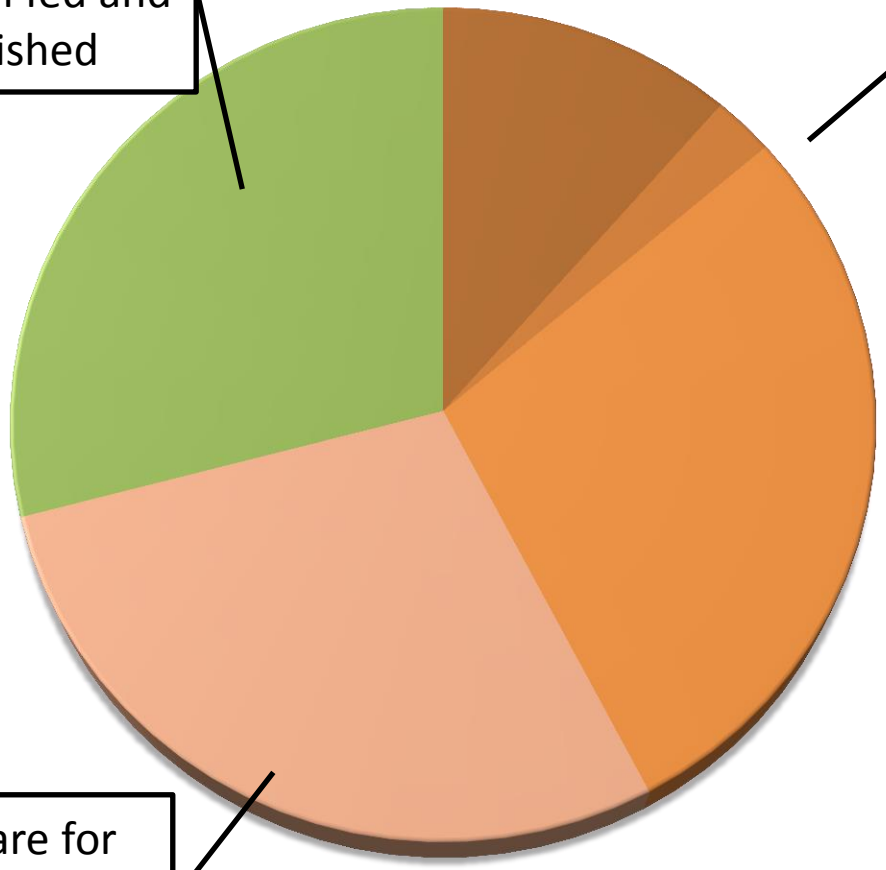
Steve Kemp

International Livestock Research Institute

Livestock is key to a balanced diet for 9 billion

- Much of the World's meat, milk and cereals comes from developing country livestock based systems
- Small amounts of livestock products – huge impact on cognitive development, immunity and well being
- **80%** of the poor in Africa keep livestock which contribute at least **one third** of the annual income and contribute a variety of other benefits. The role of women in raising animals, processing and selling their products is essential.

Nutritional divides among 7 billion people today



Less than one third well fed and nourished

11% of GNP lost annually in Africa and Asia from poor nutrition

- **Hungry people**
- **stunted children**
- **insufficient nutrients**
- **overweight/obese**
- **balanced diets**

Healthcare for obesity economic cost: $2 trillion

Opportunities and challenges in the livestock sector

Provides food and nutritional security

BUT overconsumption can cause obesity

Powers economic development

BUT equitable development can be a challenge

Improves human health

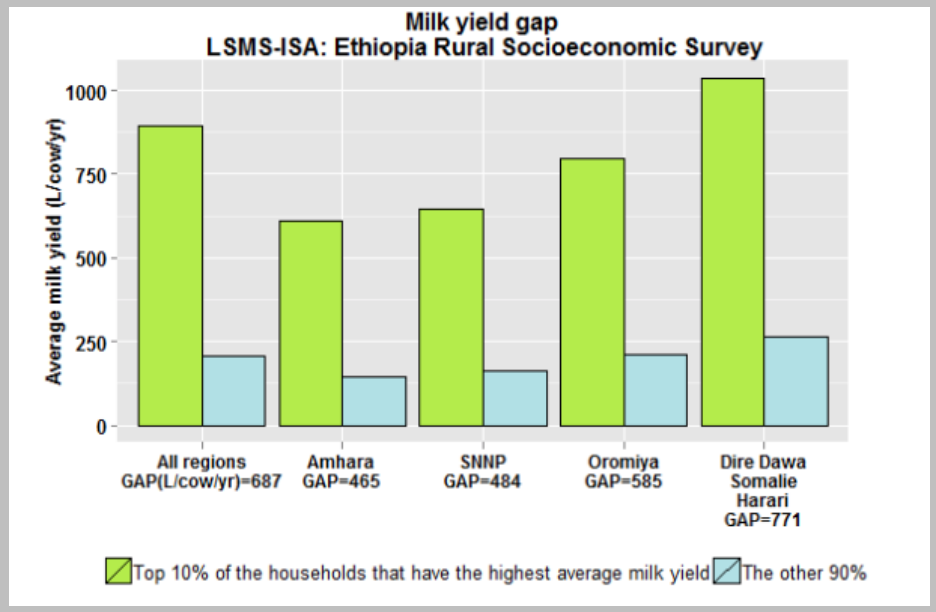
BUT animal-human/emerging diseases and unsafe foods need to be addressed

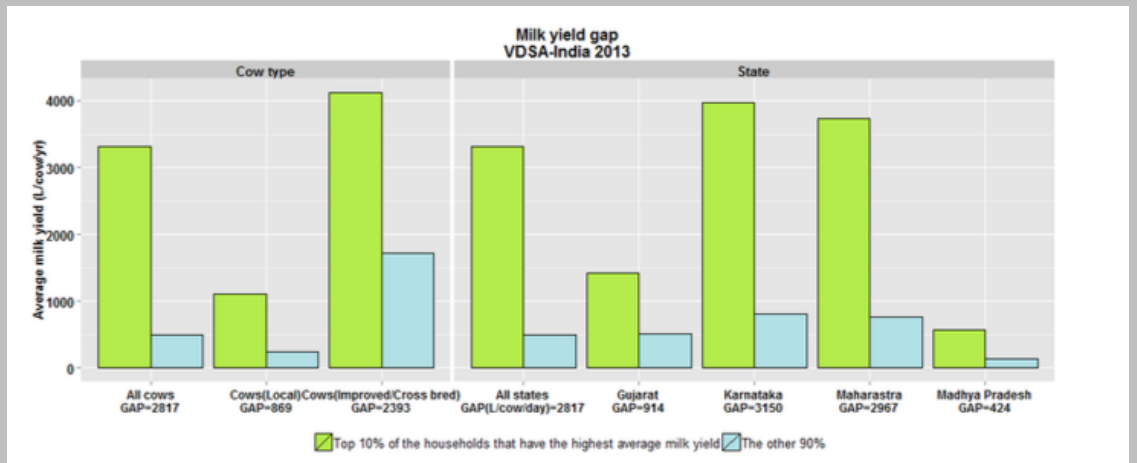
Enhances the environment

BUT pollution, land/water degradation, GHG emissions and biodiversity losses must be greatly reduced

Genetics Matters !

- The yield gap is self evident and huge





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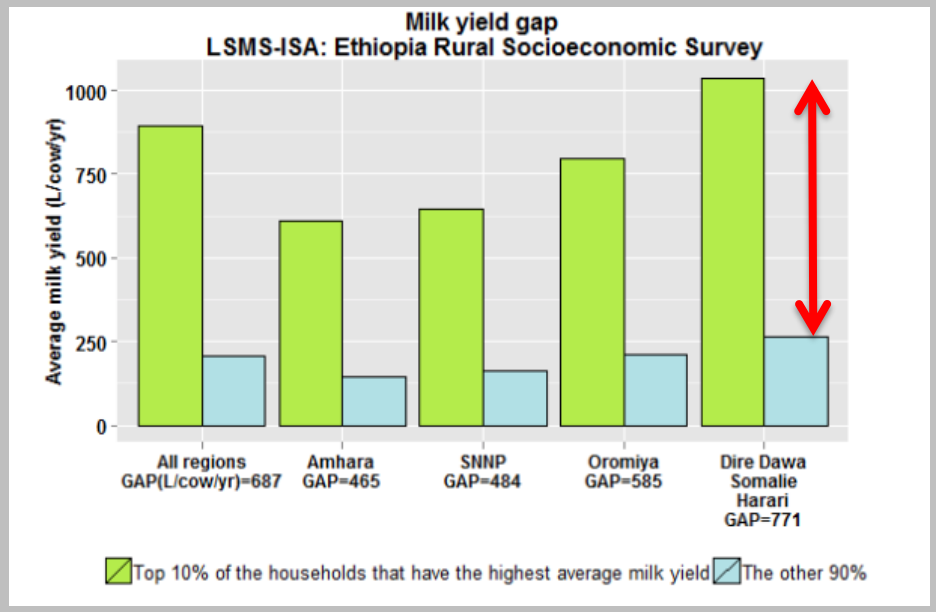
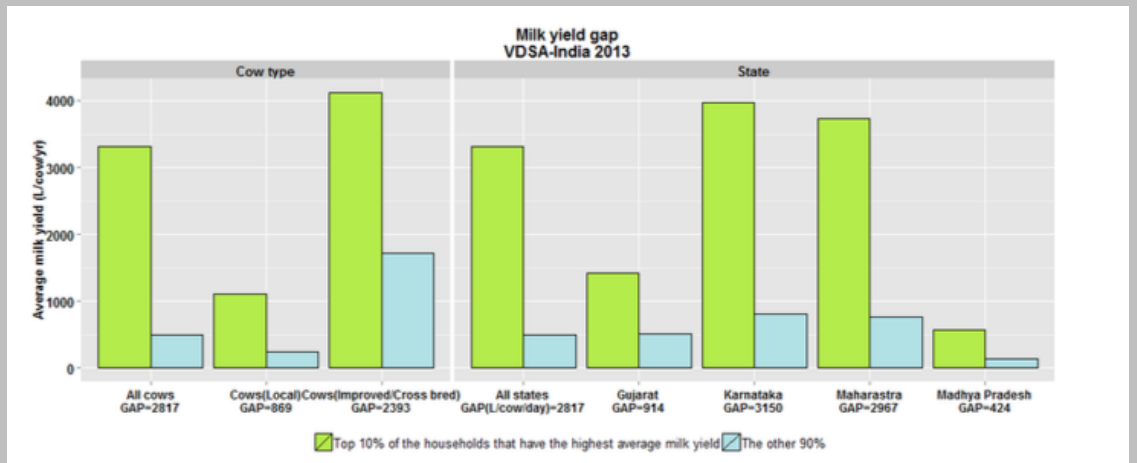
Genetics Matters !

- The yield gap is self evident and huge





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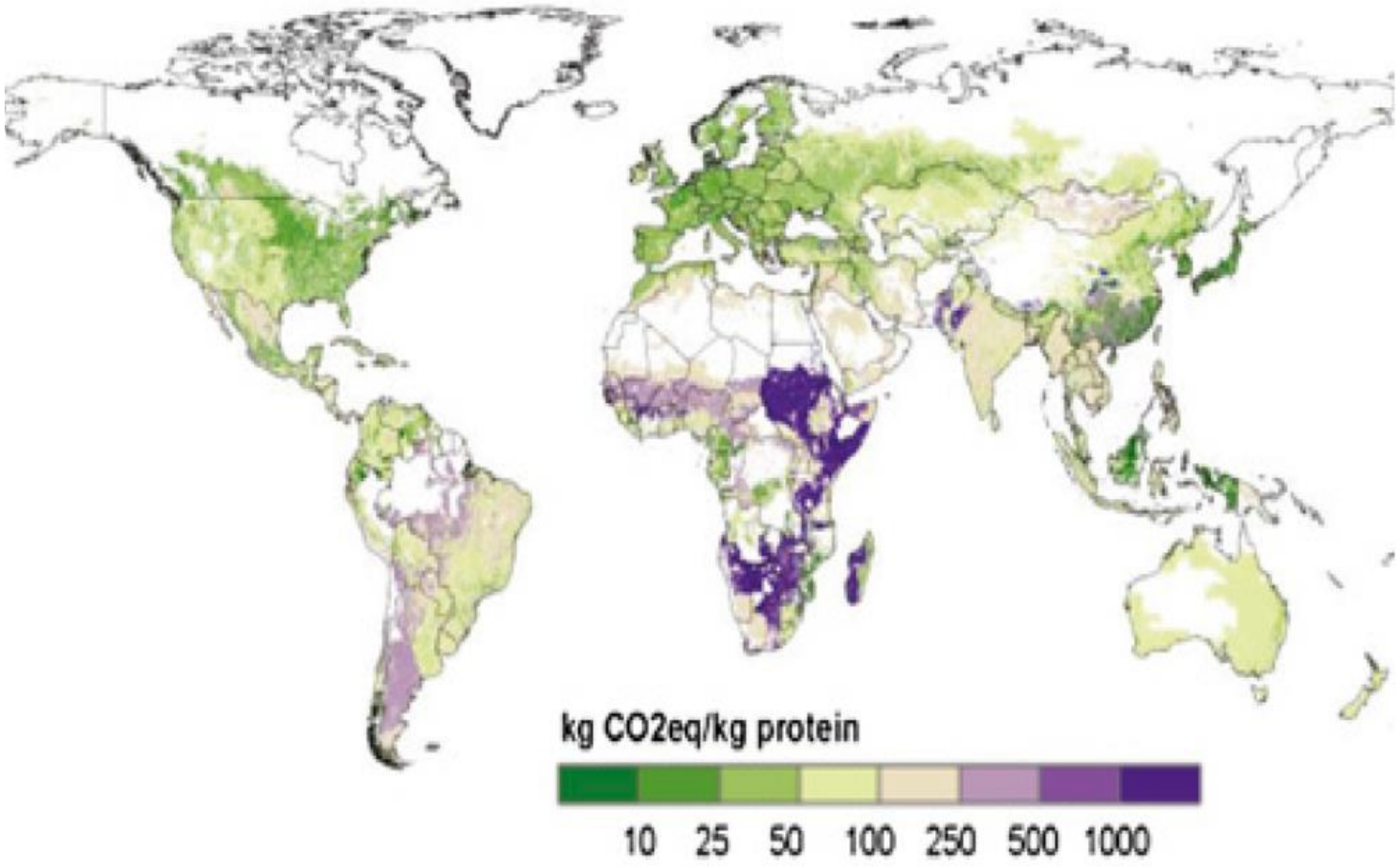
Livestock and Environment



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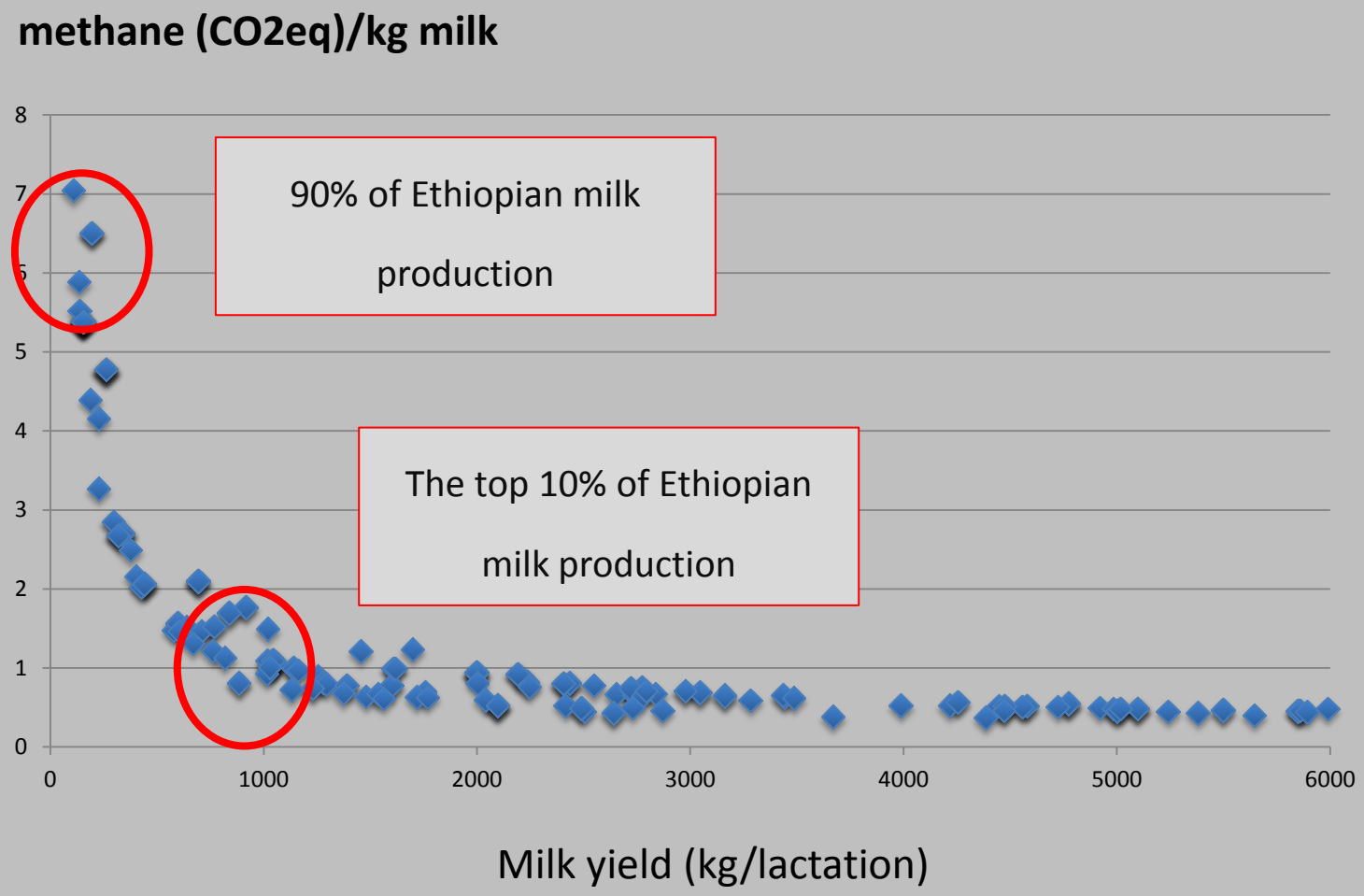
Genetics Matters !

- With far reaching implications

FAO 2013, Herrero et al 2013



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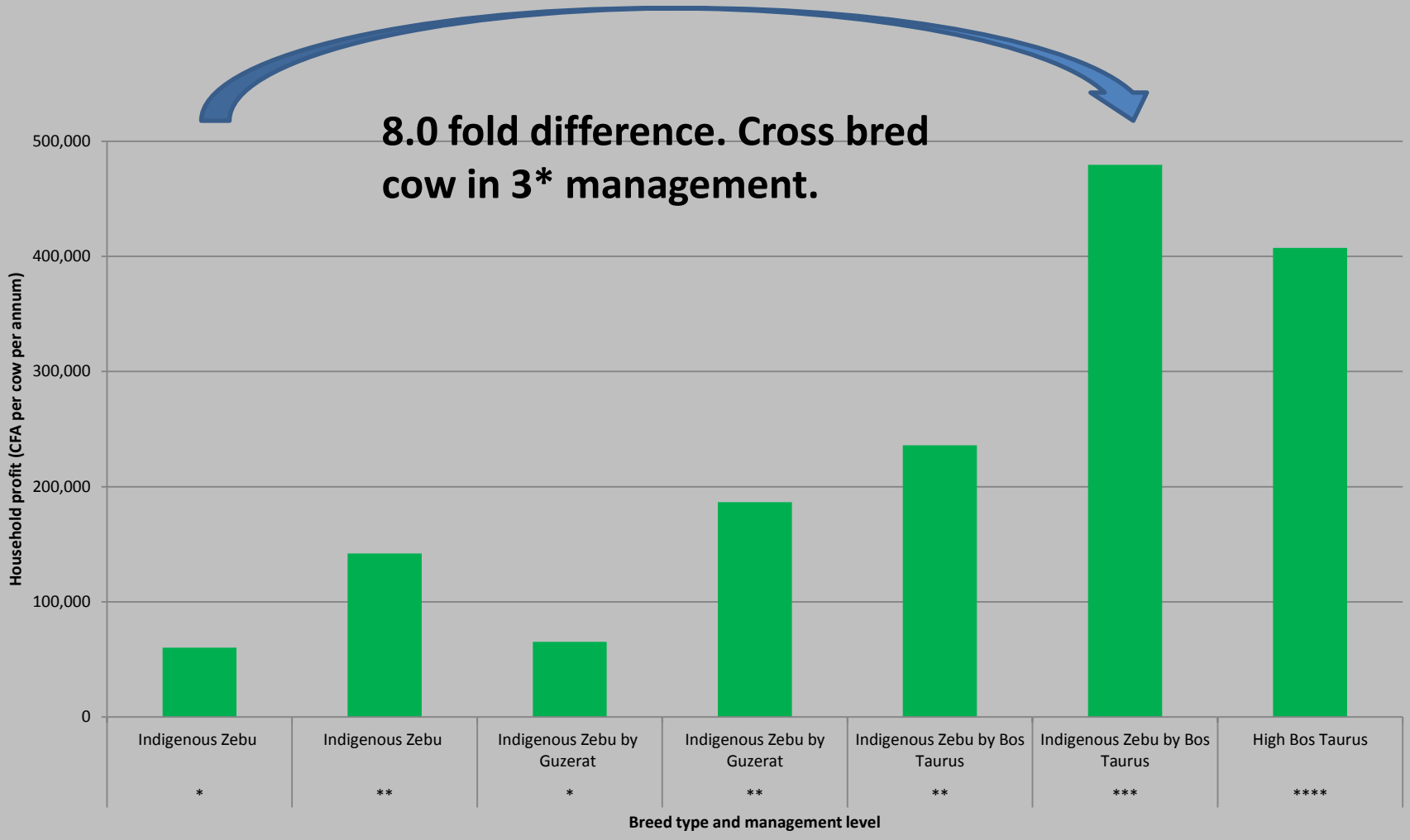
Why Genetics Matters

- But not everything. Genetics interacts with other aspects.



Constraints on Genetic Gains

- Extreme “environmental” heterogeneity with absence of infrastructure for the classic breeding pyramid.
- Limited ability to predict performance of different genetics in different systems
- Limited knowledge of mechanisms of adaptation and performance which limits the rate at which we can close productivity gap, especially in highly heterogeneous systems
- That adds-up to a limited capacity to define improved genetics
- Further constrained by a limited capacity to deliver improved genetics

Genetics Matters !

- So we need to match genetics to production system
- And *vice versa*

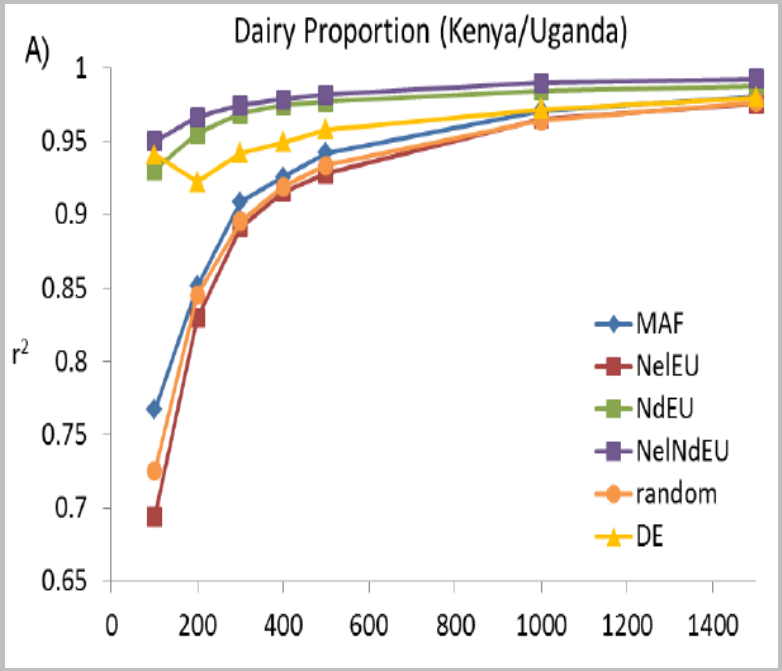
- A simple, but powerful measure of *genetics* is to determine breed mix

Why Genetics Matters

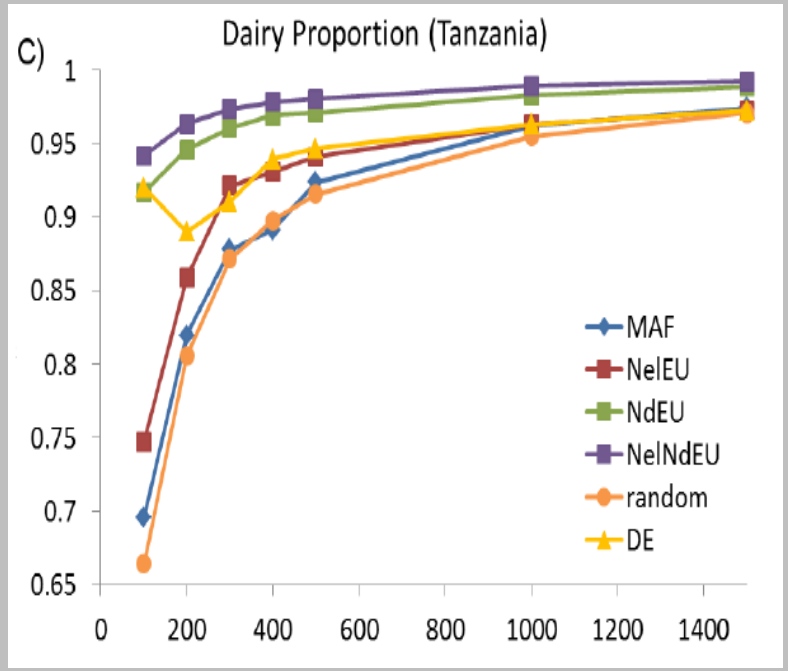
- Cross breeding is powerful but hard to sustain
  - We are working to develop tools to make crossbreeding more powerful and more sustainable

Genetics Matters !

- A simple, but powerful measure of *genetics* is to determine breed mix



Number of SNPs



Number of SNPs

A combined chip comprising 400 SNPs for both parentage and breed composition testing ready for field testing in from July, 2017.

ADGG
African Dairy Genetic Gains
More productive and profitable dairy cows

Why Genetics Matters

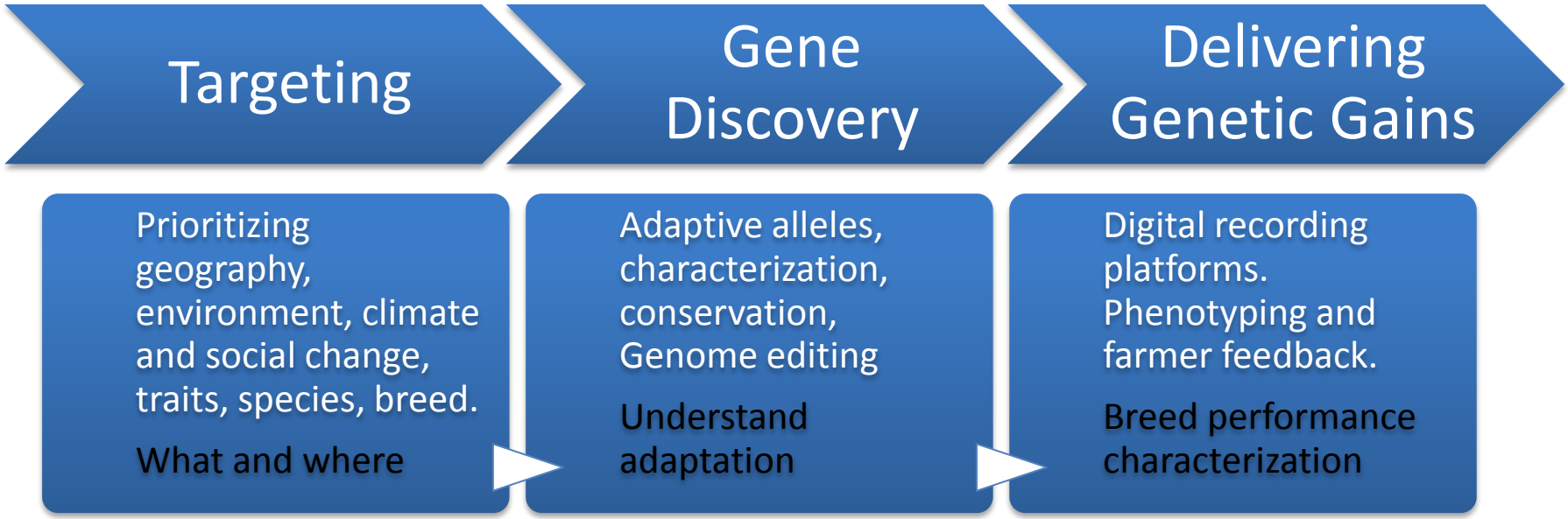
HOWEVER.

Cross breeding will never be the sustainable *game changer*

- What traits really matter?
  - Disease resistance/tolerance
  - Resistance to abiotic stress
  - Feed conversion (GHG production)
  - Growth rate
  - Milk production

- How do we identify, understand and exploit these in extremely heterogeneous environments ?

Using ‘Biotech’ to close the yield gap



Define and deliver

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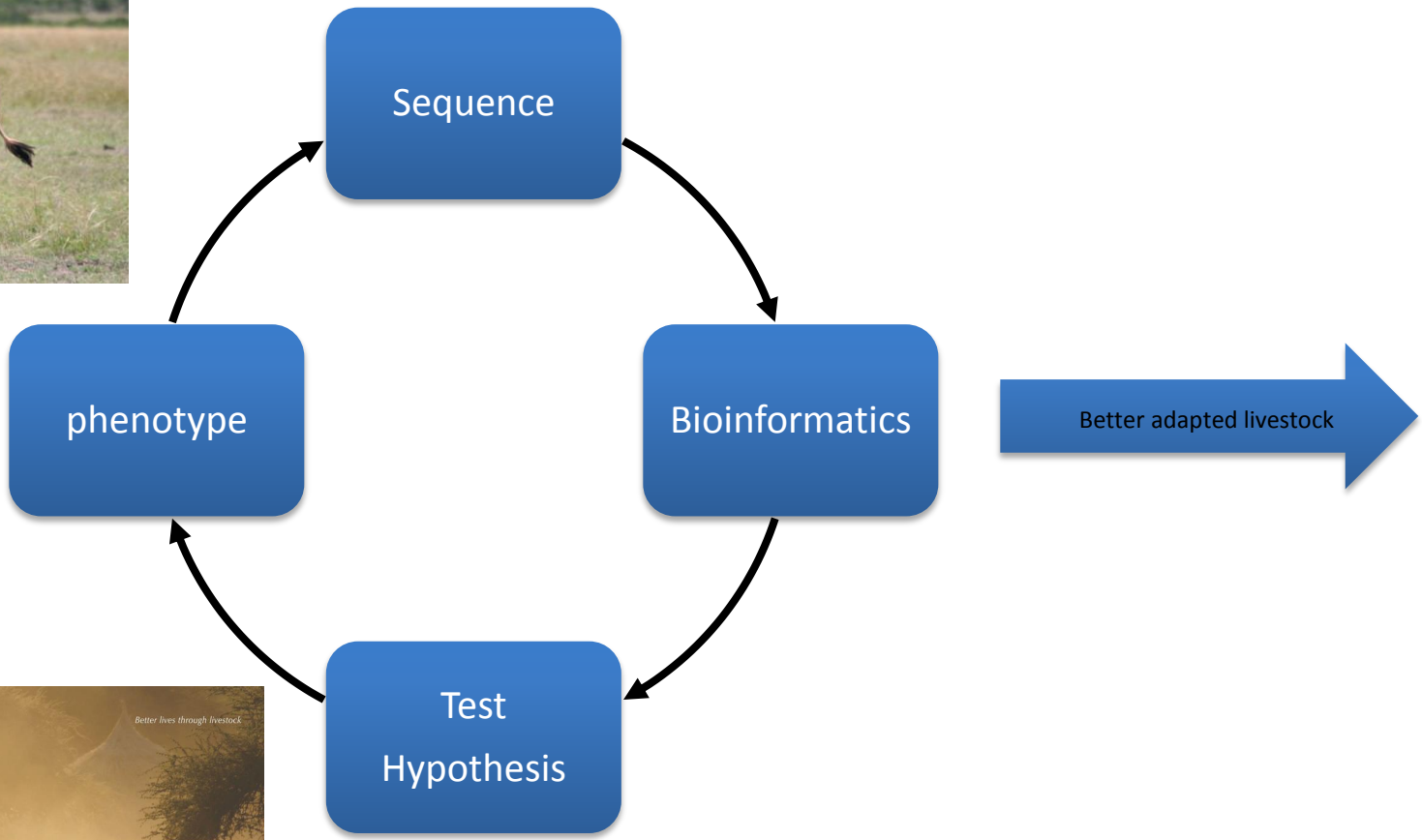
We need to understand livestock functional genomics



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

Genome Biology

RESEARCH Open Access

The genome landscape of indigenous African cattle

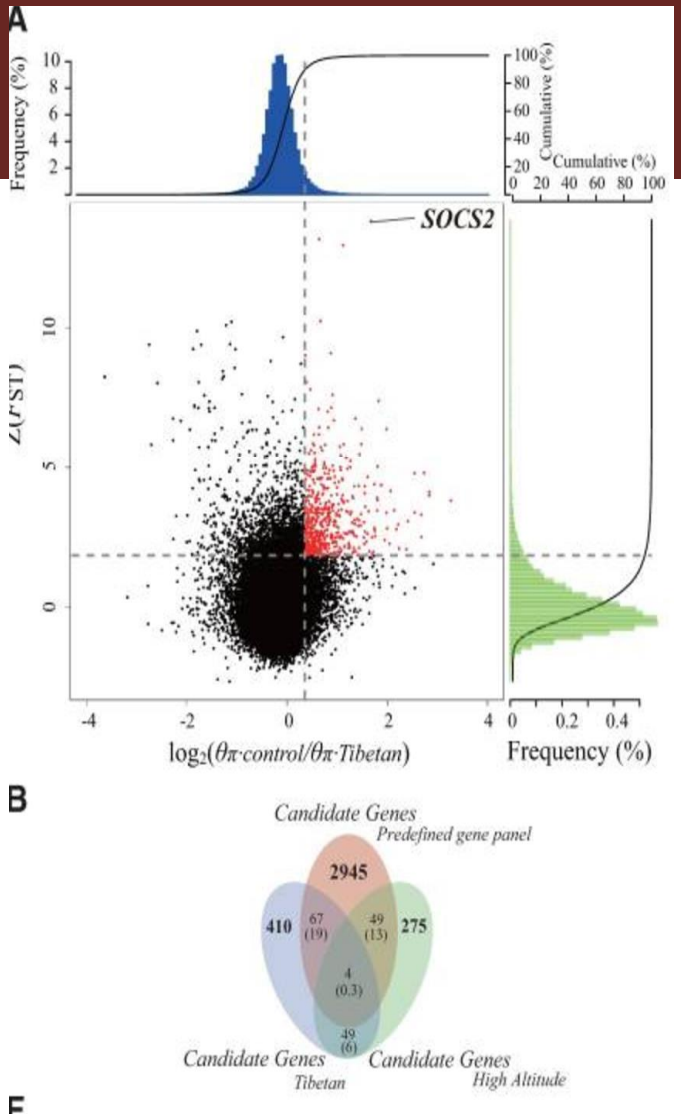
Jaemin Kim[1†], Olivier Hanotte[2,3†], Okeyo Ally Mwai[4], Tadelle Dessie[3], Salim Bashir[5], Boubacar Diallo[6], Morris Agaba[7], Kwondo Kim[1,8], Woori Kwak[1], Samsun Sung[1], Minseok Seo[1], Hyeonsoo Jeong[9], Taehyung Kwon[10], Mengistie Taye[10,11], Ki-Duk Song[12,18], Dajeong Lim[13], Seoae Cho[1], 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.



Yang J, Li WR, Lv FH, He SG, Tian SL, Peng WF, Sun YW, Zhao YX, Tu XL, Zhang M, Xie XL, Wang YT, Li JQ, Liu YG, Shen ZQ, Wang F, Liu GJ, Lu HF, Kantanen J, **Han JL**, Li MH, Liu MJ. (2016). Whole-genome sequencing of native sheep provides insights into rapid adaptations to extreme environments. Molecular Biology and Evolution, 33(10): 2576-

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Journal of Dairy Science

Volume 99, Issue 9, September 2016, Pages 7308–7312

Short communication: Genomic selection in a crossbred cattle population using data from the Dairy Genetics East Africa Project

A. Brown[*], J. Ojango[†], J. Gibson[‡], M. Coffey[*], M. Okeyo[†], R. Mrode[*,†]

Show more

http://doi.org/10.3168/jds.2016-11083

Abstract

Due to the absence of accurate pedigree information, it has not been possible to implement genetic evaluations for crossbred cattle in African small-holder systems. Genomic selection techniques that do not rely on pedigree information could, therefore, be a useful alternative. The objective of this study was to examine the feasibility of using genomic selection techniques in a crossbred cattle population using data from Kenya provided by the Dairy Genetics East Africa Project. Genomic estimated breeding values for milk yield were estimated using 2 prediction methods, GBLUP and BayesC, and accuracies were calculated as the correlation between yield deviations and genomic breeding values included in the estimation process, mimicking the situation for young bulls. The accuracy of evaluation ranged from 0.28 to 0.41, depending on the validation population and prediction method used. No significant differences were found in accuracy between the 2 prediction methods. The results suggest that there is potential for implementing genomic selection for young bulls in crossbred small-holder cattle populations, and targeted genotyping and phenotyping should be pursued to facilitate

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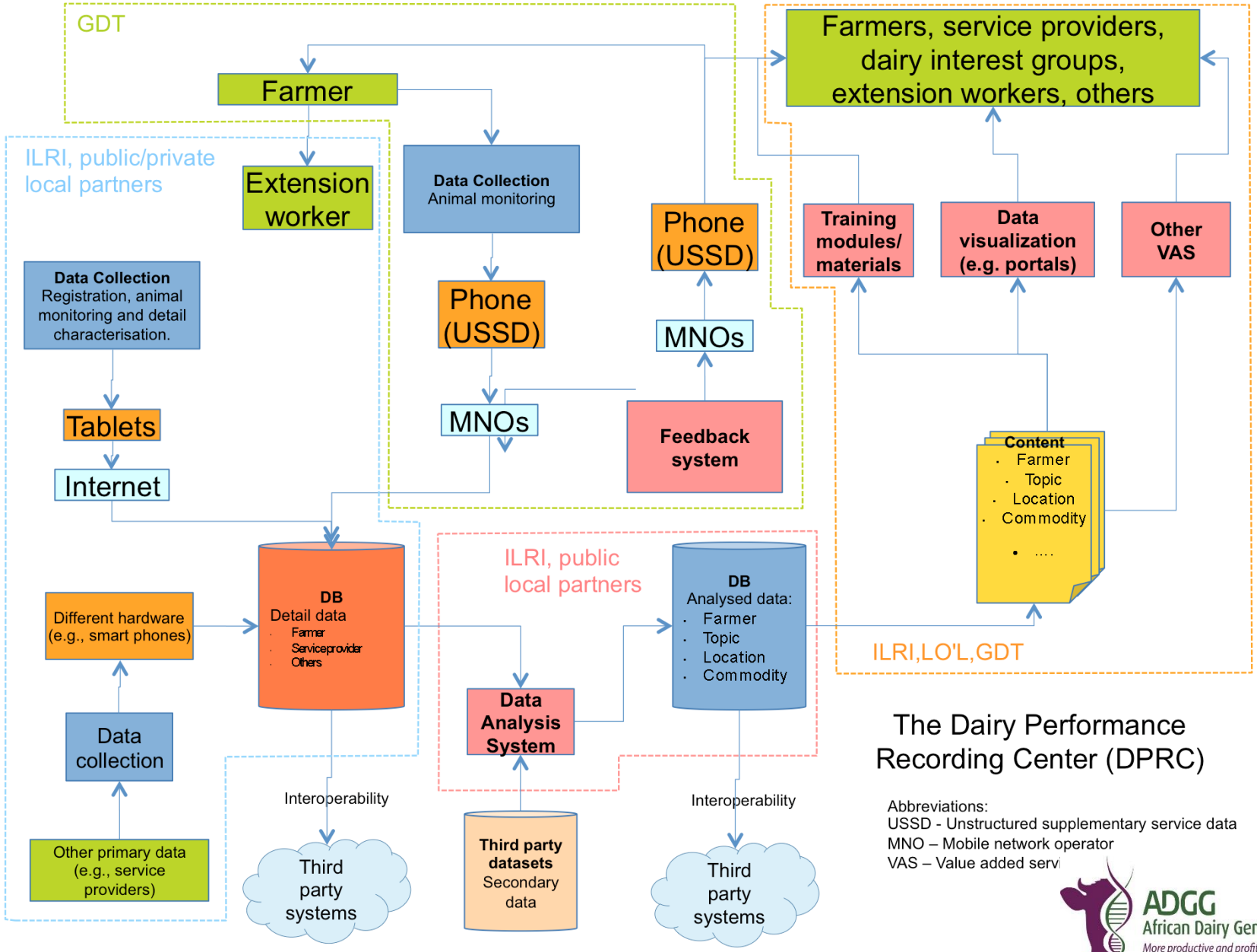
Phenotyping is harder – but essential

Identify, measure, understand and use diversity

Phenotyping is difficult and expensive !



The Dairy Performance Recording Center (DPRC)

Abbreviations:
USSD - Unstructured supplementary service data
MNO – Mobile network operator
VAS – Value added serv

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ADGG
African Dairy Genetic Gains
More productive and profitable dairy cows

Phenotyping Chickens! (ACGG partnerships)

African Chicken Genetic Gains

Kind Palms Ventures

Olorun Osun Farms

Possible targets

Evidence for innate resistance to ECF

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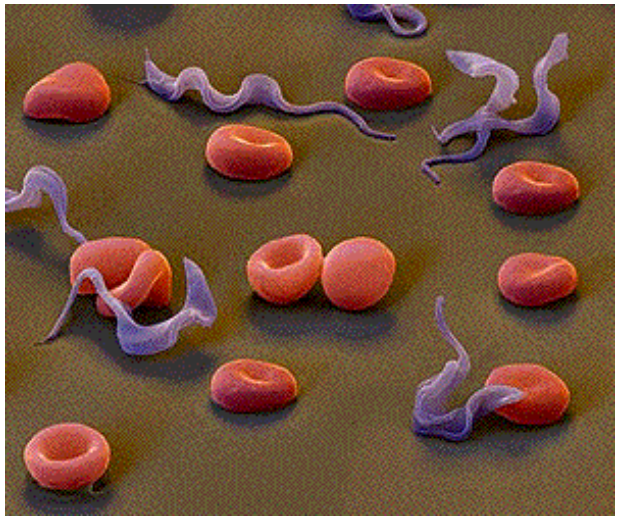
Centre for Tropical Livestock Genetics and Health

Possible targets

African Trypanosomiasis

- Caused by extracellular protozoan parasites – *Trypanosoma*
- Transmitted between mammals by Tsetse flies (*Glossina* sp.)
- Prevalent in 36 countries of sub-Sahara Africa.



In cattle

- A chronic debilitating and fatal disease.
- A major constraint on livestock and agricultural production in Africa.
- Costs US$ 1 billion annually.

In human (Human Sleeping Sickness)

- Fatal
- 60,000 people die every year
- Both wild and domestic animals are the major reservoir of the parasites for human infection.

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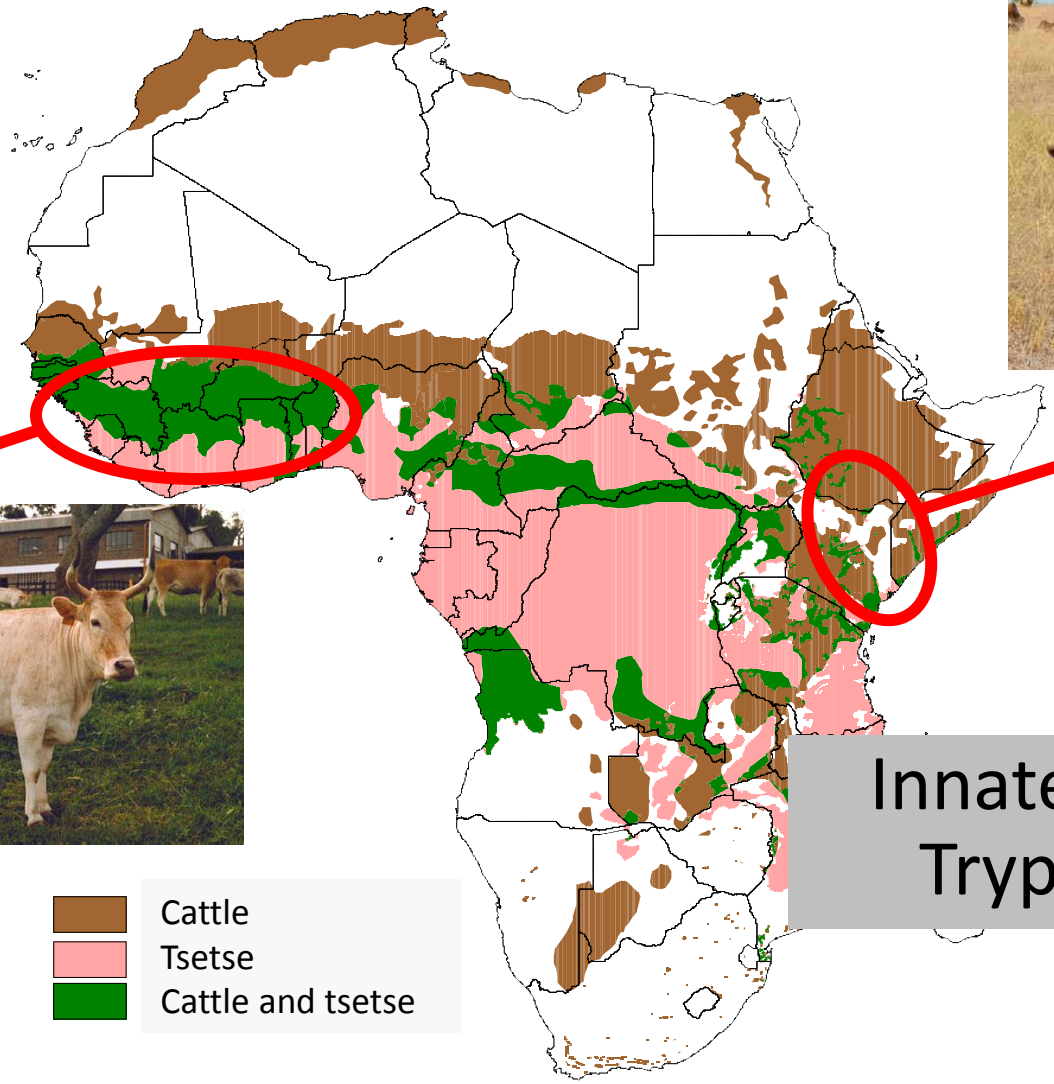
Possible targets

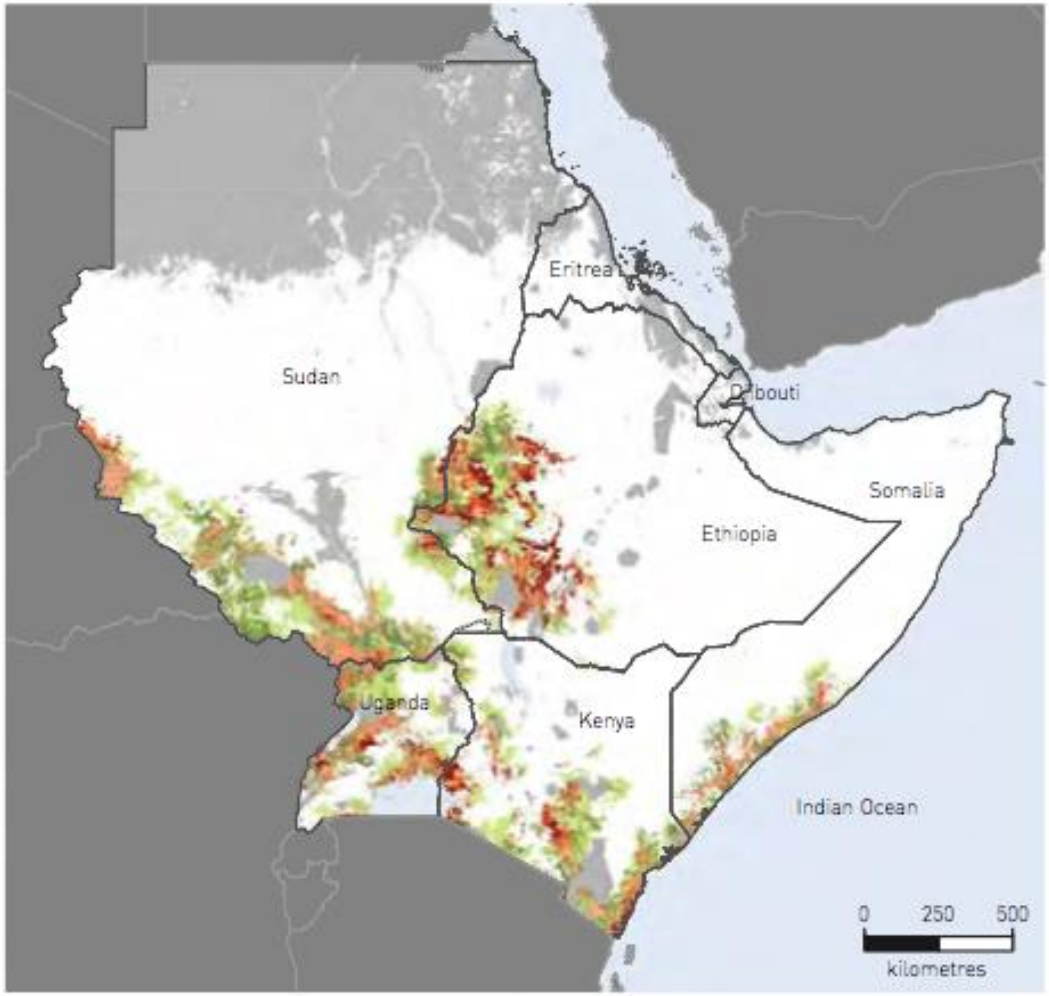
Boran

N'Dama



Innate resistance to Trypanosomiasis

7.4 THE MAPPED BENEFITS FROM THE REMOVAL OF AFRICAN ANIMAL TRYPANOSOMOSIS (AAT) IN THE HORN OF AFRICA

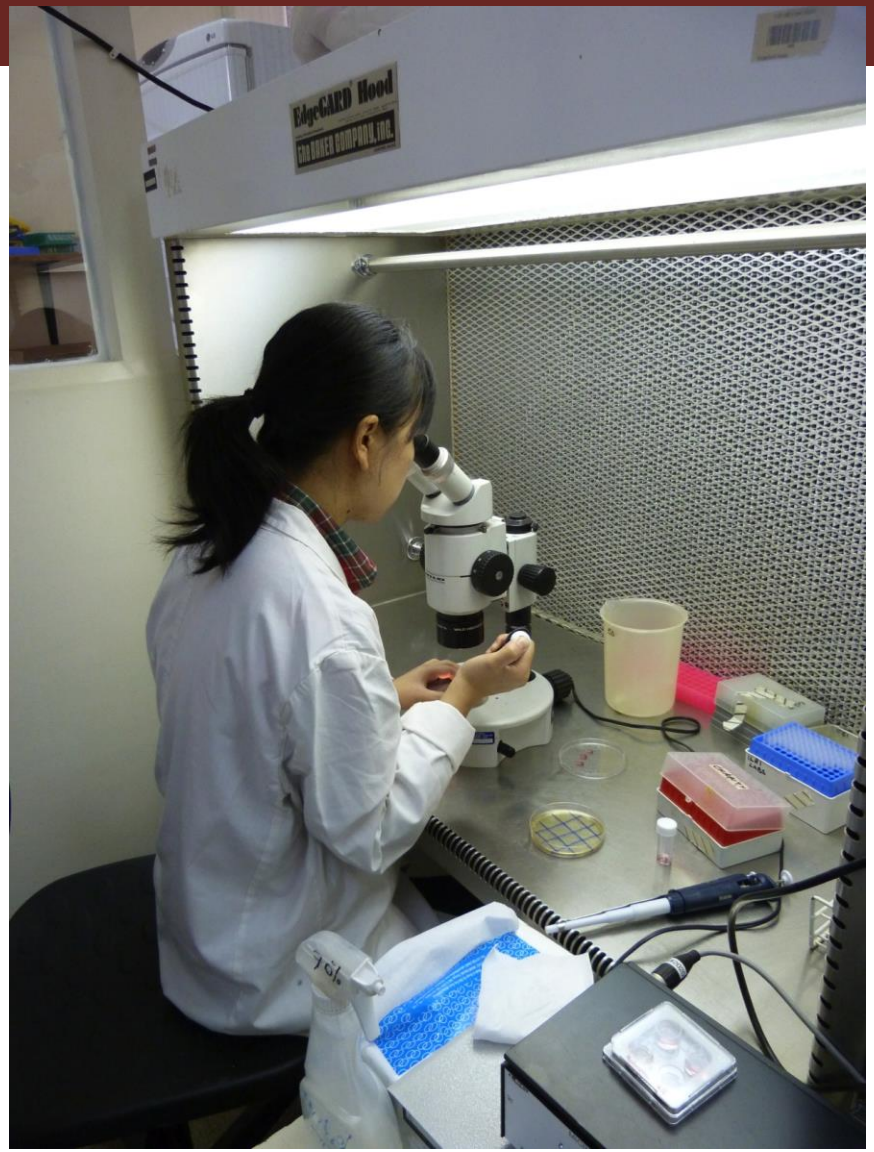


US$ per km² over a 20 year period

- > 12 500
- 10 000–12 500
- 7 500–10 000
- 5 000–7 500
- 2 500–5 000
- 1 000–2 500
- 500–1 000
- 10–500
- <10
- Unsuitable for ruminants

Source: adapted from Shaw *et al.* (in press).

Possible targets



Transgenic approaches to Trypanosomiasis resistance

Genetics for Africa – Strategies & Opportunities

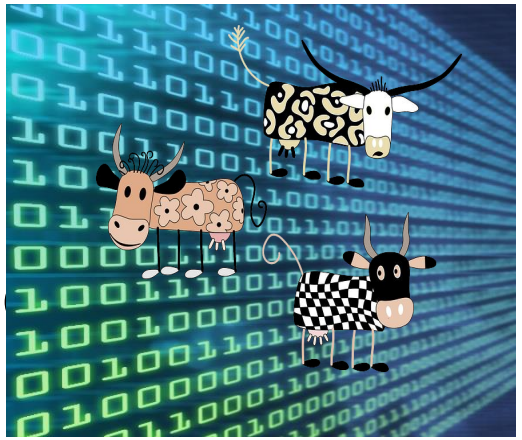
Mzima Cow Strategy & Theory of Change – Translating from Genetic Research in Africa to Adoption and Social Value: Workshop Report

January 18th – 19th 2017
International Livestock Research Institute
Nairobi, Kenya

Future approaches

Next Generation Phenotyping approaches:

- Remote sensing as proxy for phenotyping
- Ultra low cost sensors
- Farmer feedback systems
- 10K livestock genomes project – catal
  functional diversity
- Host - pathogen – nutrition
  interaction



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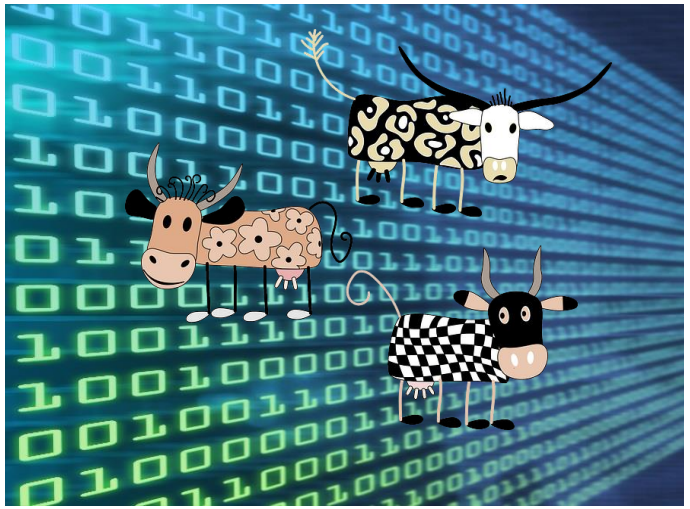
Future approaches

Big Data!

- Data exchange, integration, analysis, visualization
- Effective exchange and use of diverse data types is difficult and limiting
- Link real world livestock data into the models



- Evidence base
- Modeling
- foresight

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Asante

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Patron: Professor Peter C Doherty AC, FAA, FRS
Animal scientist, Nobel Prize Laureate for Physiology or Medicine–1996

Box 30709, Nairobi 00100 Kenya
Phone +254 20 422 3000
Fax +254 20 422 3001
Email ilri-kenya@cgiar.org

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Box 5689, Addis Ababa, Ethiopia
Phone +251 11 617 2000
Fax +251 11 667 6923
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