# Some Opportunities for informed & better utilization of AnGRs: Some Examples

#### Okeyo A. Mwai

AU-IBAR's Training Workshop on Empowering Livestock Breeders Associations for Competitive & Sustainable Use of AnGRs,

Harare, Zimbabwe, May-23-2017







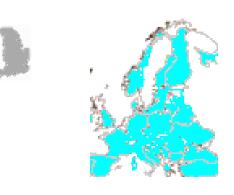


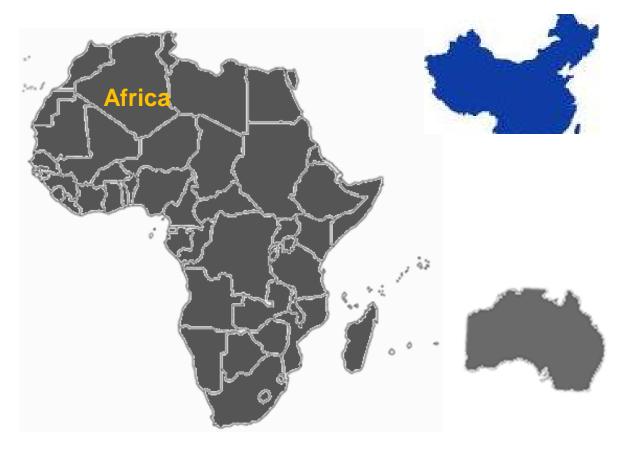


### Africa is not small?

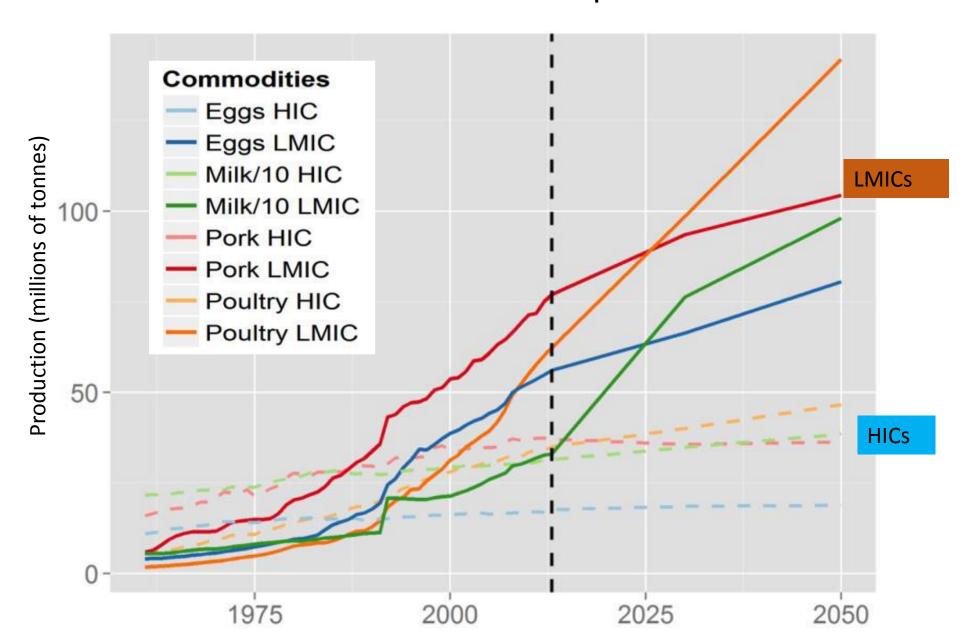




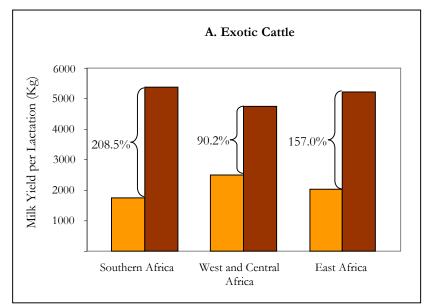


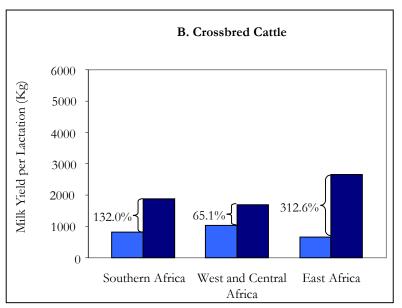


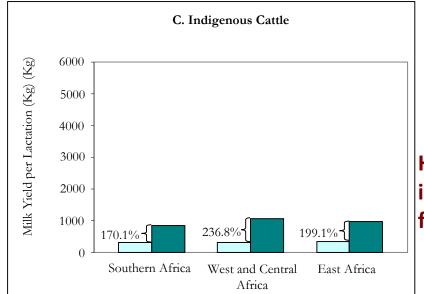
## Production of animal products



Huge Yield Gaps: Maximum (dark *coloured*) and minimum (*light coloured*) levels of milk production for different genotypes of cattle in Sub-Saharan Africa



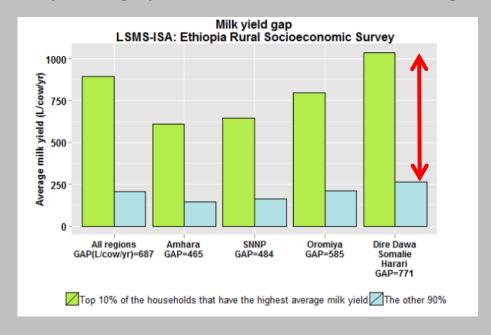


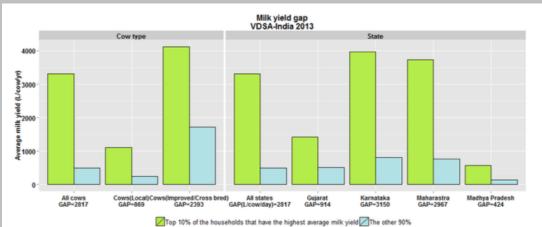


Better strategies are required & biotechnology is key

Huge opportunities for increased wealth creation, food & nutrition security

#### • The yield gap is self evident and huge cont..

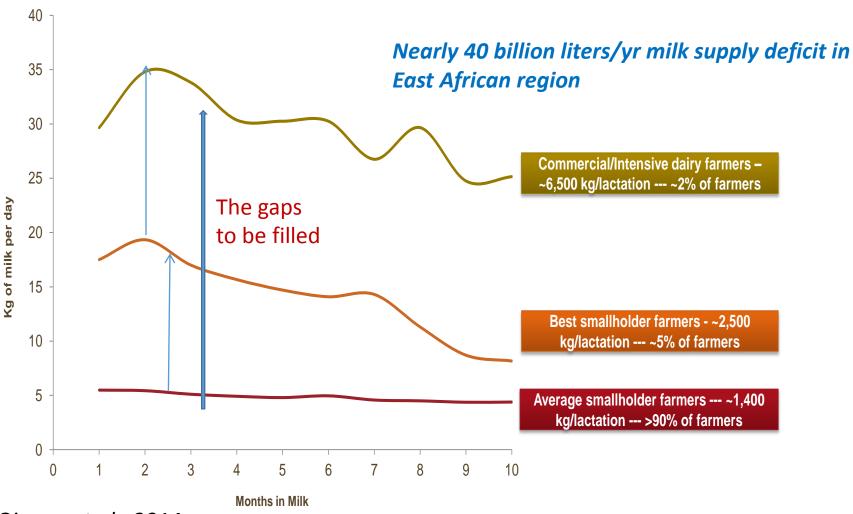






### Huge yield gaps-case of Kenya dairy cattle

Figure 1: Realized lactation curves of improved (crossbred or higher) dairy cows achieved by different farmer types in Kenya

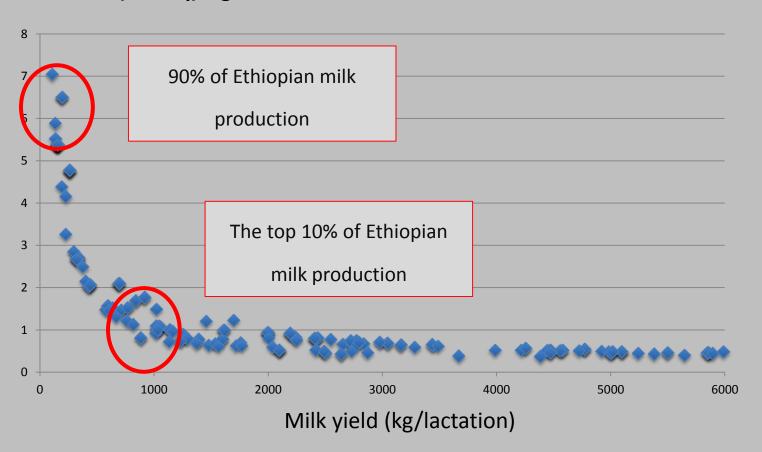


Source: Ojango et al., 2014

# But large and less productive herds have far reaching environmental implications

FAO 2013, Herrero et al 2013

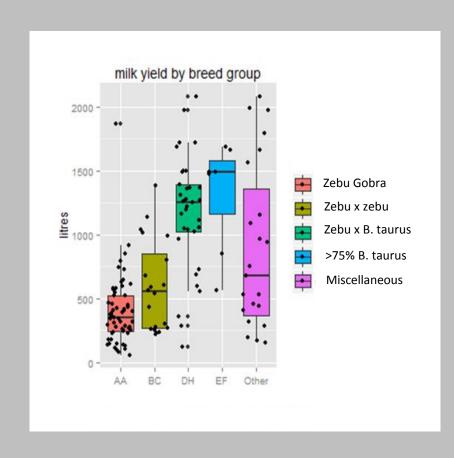
#### methane (CO2eq)/kg milk

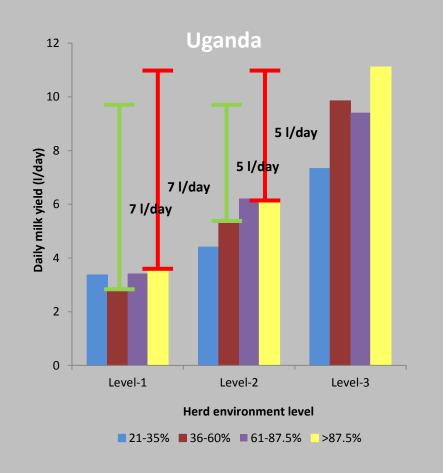




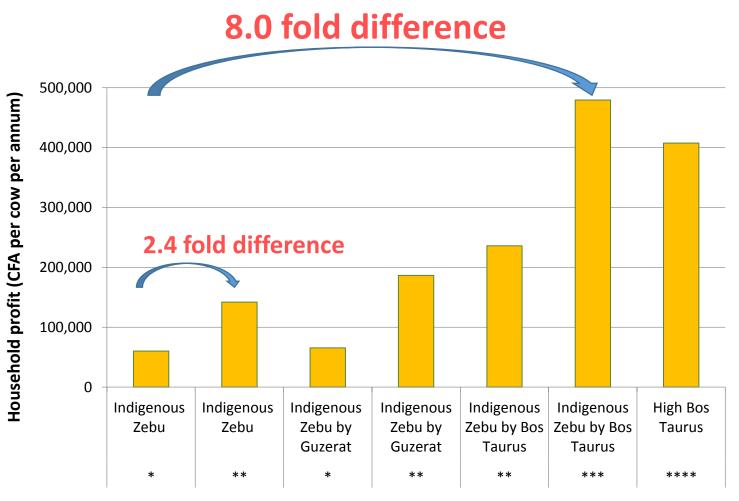


#### • Genetics is important



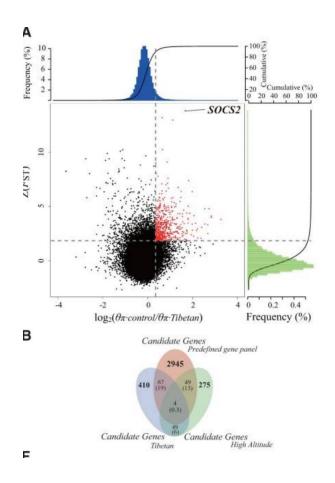


# Improved management matters & more comprehensive analyses needed!



**Breed type and management level** 

### The power of new genomic tools



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-





### A chance to skip a generation of technology

#### NextGen Phenotyping capacity:

- Remote sensing as proxy for phenotyping
- Use of Mid-Infra-red Spectroscopy as proxy for performance traits
- Ultra low cost sensors
- Farmer feedback systems
- GHG emission traits









# Evidence for innate resistance to ECF



#### T. parva Tolerance

				%	Fisher's
		Survived	Died	% Survived	Exact p
	- ·	Juiviveu	Dieu	Julviveu	LXact p
	Progeny of				
Trial 1	ZI3167	3	0	100	
IIIai I					
	Control	0	9	0	0.0045
	Progeny of				
Trial 2	ZI3167	4	6	40	
	Control	1	11	9	0.14
	Progeny of				
Trial 3	ZI3167	12	3	80	
	Control	0	8	0	3.4x10 <sup>-4</sup>
Combined	Progeny of 3167	19	9	68	Combined p (Stouffer's method)
	Control	1	28	4	2.11x10 <sup>-5</sup>

# Small is not always less efficient or less profitable

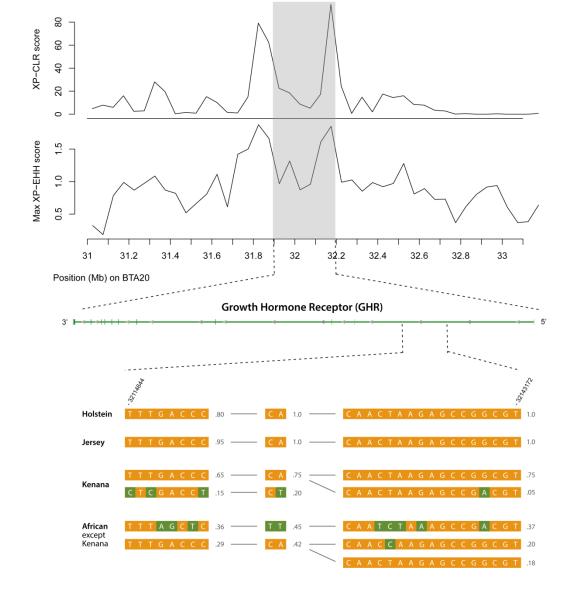
Α	Type of Kidding						
Location	Single	Twin	Triplet	Quadruplet	Sextuplet	Total	
Western Highland	23	74	58	4	1	160	
Forest	5	94	23	2	0	124	
otal (%)	28 (9.9)	168 (59.1)	81 (28.5)	6 (2.1)	1 (0.4)	284	

High Prolificacy can be profitable and **Green** (can reduce environmental impacts of goat production)

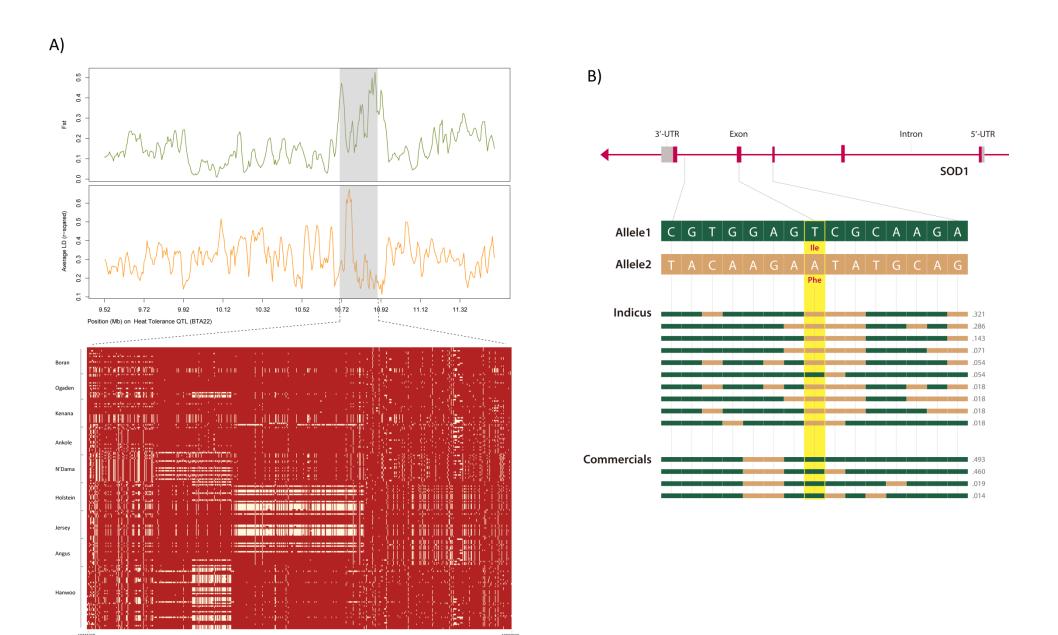
Prolificacy is expressed only in **does**, but efficient breeding requires use **bucks** with high potential.

The genomic region responsible has been identified

Total kg marketed (US\$)/female/year!!



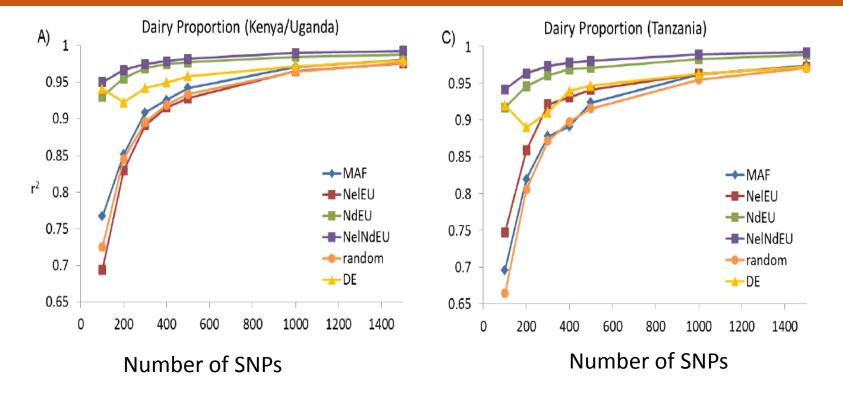
Selective sweep for milk production in Kenana cattle



Selective sweep for heat tolerance in African cattle

## Smatter tools are now becoming available: A low density SNP array gives same level of usefulness as a

780,000 array for estimates of dairy breed proportion and parentage testing



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





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## 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\*, †, 🏝 👱

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

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#### 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 this.











#### Community-based breeding programs-select under prevailing environments



Pool flocks & record performance



Use the records, indigenous knowledge & genomics to select young rams for breeding

Ruthlessly get rid of unwanted males



Bonga sheep in Bonga, Ethiopia







Thank you







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