

Better lives through livestock

## Genetics and genomic approaches for sustainable dairy cattle improvement in smallholder dairy systems

Raphael Mrode, Chinyere Ekine-Dzivenu, Julie Ojango and Mwai Okeyo

Livestock Genetics Program International Livestock Research Institute, Nairobi Kenya

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Sustainable Dairy Cattle Improvement Program

Characteristics of a sustainable food system (FAO)

- Environmentally non-degrading
- Economically viable
- Conserves genetic resources
- Technically appropriate
- Socially acceptable







Sustainable Dairy Genetic Improvement Program

Components of a sustainable dairy genetic improvement program should include:

- Improvement in productivity with no adverse effect fitness
- Improve fitness reproductivity ability, disease resistance, robustness
- Improving welfare traits (body condition, sound feet etc.)
- Little or no negative impact on the environment







Some of the genetic approaches to achieve sustained dairy genetic improvement

Would include ...

- International efforts broadening breeding goals
- Harmonizing trait definitions
- Establishing data collection protocols for difficult to measure traits
- International dairy genetic evaluations leading to having a broader set of top bulls available to maintain genetic diversity
- Introgression of desirable alleles



Worldwide summary of the relative weights on various major traits in national economic indexes for dairy cows from 1917 to 2017 (Miglior et al., 2017).





Proportionate estimates of response world-wide for major traits in the national economic indexes for dairy cow from 1917 to 2017 (Miglior et al., 2017).



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Approaches for breeding dairy cattle sustainably in small holder systems need to address

Some of the following issues in dairy cattle breeding in the face of climate change

- Heat tolerance
- Feed resources and methane emission
- Conserving and utilization adaptive traits in indigenous breeds

Breeding for adaptation to heat stress Breeding for heat tolerance Breeding for reduction in methane emission Breeding for Feed efficiency Incorporating the genetic basis of adaptation





#### Breeding for adaptation to heat stress

• Dairy sires being selected in Australia based on resilience to heat stress measured on the basis of productivity using THI

Nguyen et al 2016 J.Dairy science: 99:2849– 2862



- Trait = rate of decline in milk yield with increasing THI;  $h^2 \approx 0.20$
- "how well does an animal cope?" ~ resilience



# Evaluating the impact of heat stress on milk yield using THI for small holder dairy system

(Ekine-Dzivenu et al. 2020, 2022)



The objectives of this study were to evaluate the effect of heat stress on milk production and describe the pattern of response of milk yield to increasing heat load as measured by temperature-humidity index (THI) on test day milk yield in small holder dairy cattle populations in the sub-Saharan African climate of Tanzania.

- Effect of heat stress on milk yield assessed using THI grouped 5 classes (61-66, 67-71, 72-78, 79-81, 82-86)
- Heat stress reduced milk yield by 4.16% to 14.42% across THI groups
- THI was non-linearly related with milk yield with significant negative and positive coefficients (-0.61, 0.004) for THI and THI<sup>2</sup>. No unique slope. Change in MY continuously changing through out the gradient



# Evaluating the impact of heat stress on milk yield using THI for small holder dairy system

Estimated breeding value (EBV) for a random sample of sires



The goal of this study, was to evaluate changes in genetic parameters for milk yield and heat tolerance in small holder dairy cattle population of Tanzania under different heat stress (THI) thresholds as a first step toward including this trait in selection indices for dairy cattle in the region.

THI thresholds				
Variance	69	71	78	
Components				
$\sigma_{a}^{2}$	9.83	9.16	7.52	
$\sigma^{2}_{aht}$	0.10	1.96	2.15	
$\sigma_{a (a. aht)}$	-1.00	-2.10	-0.24	
r <sub>g(a. aht)</sub>	-0.99	-0.50	-0.06	



# Breeding for heat tolerance through introgression of the slick gene

- The slick hair gene located on chromosome BTA20 in Senepol cattle is responsible for
  - a smooth and short hair coat
  - confers thermotolerance
  - associated with an improved capacity for heat dissipation.
- Introgression of the gene into some Holstein cattle has been shown
  - to produce animals with lower body temperatures
  - smaller declines in production under hot conditions (Dikmen et al., 2014; Ortiz-Colón et al., 2018)
- Some breeding companies are currently marketing bulls with the slick genes to farmers







#### Breeding for reduction in methane emission

Important as livestock is deemed a major contributor

- Heritability estimates vary from 0.12 to 0.45
- Difficult to measure routinely in large number of animals & lots of interest on indirect predictors
- A 20% reduction in methane emissions over 10 years feasible in Spanish Holstein with a weight of about 33% on methane in the total merit index and a reduction in gain for production traits by 6% 18% (González-Recio, et al, 2020)
- In Danish Holstein accuracy of genomic selection for methane was about 0.42 but including ECM and BW in both reference and validation populations increased accuracy by 92% (Manzanilla-Pech et al 2020)
- Selection for feed efficiency is good proxy for reduction in methane emission 26% reduction in methane over a 10-year period (de Haas et al. ,2011)





## Breeding for feed efficiency

- Feeds account for about 70% of production cost
  - Difficult and expensive to measure
- Genomics has allowed/enabled international evaluation of dry matter intake (DMI) using feed intake data pooled from 9 countries (Berry et al, 2014)



### Breeding for Feed efficiency

- Saved Feed =  $v_1 \times \text{GEBV}_{\text{Maintenance}} + v_2 \times \text{GEBV}_{\text{Metabolic efficiency}}$
- About one third of feed consumed is used for body maintenance and this is directly related to the body size.
- A number of countries have implemented the saved feed cost index for maintenance using genomic models
  - Nordic countries : EBVs based on indirect predictors- body weight and type traits
  - Netherlands : DMI or Indirect predictors :milk, fat and protein and body weight.
  - SFC accounts for 5% of the Dutch Total Merit index called NVI





# Improving efficiency in Tanzania Cows using milk yield and body weight Genetic parameters , forward validation and index

Trait	Method	Correlation	Regression
Milk yield	FRM-GBLUP	0.57	1.1
	FRM-ssGBLUP	0.59	1.0
	RRM-GBLUP	0.55	1.0
	RRM-ssGBLUP	0.53	0.92
Body weight	FRM-GBLUP	0.83	1.0
	FRM-ssGBLUP	0.77	1.1

Milk yield, h2=0.12, body weight, h2=0.22 and rg=0.34

This study examines the use of genomic best linear unbiased prediction (GBLUP) and single-step (ss)GBLUP for the estimation of genetic parameters and accuracy of genomic prediction for daily milk yield and body weight in Tanzania.

- Restricted index: improves the rate of milk production but with restrictions on body weight
- More efficient cows produce milk without increasing the amount of feed consumed.
- The moderate to high accuracy (0.53–0.83) indicates that selection on the basis of genomic prediction is feasible in smallholder dairy systems and is the most realistic pathway to realizing sustained genetic gains.



Incorporating the genetic basis of adaptation

- Indigenous breeds represent a unique set of genotypes adapted to surviving under harsh conditions and are disease/parasite resistance.
- Genomics provide the means for understanding the genetic basis of this adaptation
- Kwondo et al 2020 identified several loci in African cattle related to immunity, heat-tolerance trypanotolerance and reproduction-related genes.







Sustainable cattle breeding in developing countries: Incorporating the genetic basis of adaptation

- Small ruminants -- adaptation to arid environments and resistance to endoparasites in sheep from Tunisia (Ahbara et al, 2021)
- Paths for utilization
  - Incorporation of functional regions/genes in genomic prediction --- BayesR or BayesRC
  - Approach increased accuracy of prediction for heat tolerance for production traits by up 10% (Cheruiyot et al, 2022)
  - Gene editing & surrogate sires







Challenge of adequacy commercial SNP array: Examined in three African cattle

• Uniqueness of genotypes in indigenous breeds leads to another challenge; adequacy of commercial SNPs panels







#### Assessment of the 23 commercial Bovine SNP arrays in 3 cattle breeds



Genomics as a platform for collecting difficult to measure or expensive traits

- Genomics gives us the ability to undertake
  - Detailed phenotyping of difficult to measure traits in small cohort of animals
  - Enables prediction of gEBVs for a wider population connected to cohort with records
- Successfully used in Genomic Information Nucleus (Ginfo) project in Australia to capture fitness traits in few herds but connected to the national population. (Pryce et al, 2017)
  - Increased accuracy of prediction 5 to 7 % for fertility traits in the Holstein
- In developing countries, where data capture is a challenge, genomics may provide an opportunity to capture difficult or expensive traits







#### Conclusions

- For sustainable dairy cattle improvement in smallholder dairy systems genomics offers us a pathway especially if it is coupled with other technologies e.g. ICT for data capture, sensor-based technologies
- With genomics indexes for selection of genetically superior animals with incorporation of difficult to measure traits within the context of small holder systems is possible and starting to emerge and will ensure sustainability.
- Genomics provide the basis for understanding and utilizing adaptive traits in indigenous breeds to ensure sustainability



Genomics coupled with ICT offers a pathway...ADGG

• Ethiopia First dairy animal parade held on Tuesday March 30, 2020, Fikiru Regessa, State Minister of Agriculture (extreme left), Selam Meseret ADGG Ethiopia National Coordinator (middle), and Asrat Tera, Director General of National Animal Genetics Institute (NAGII) Ethiopia.





 ILRI director general, Jimmy Smith (left) and Minister for Livestock and Fisheries Luhaga Mpina (2nd to left) present the award for best bull at a special bull and cow show at the Nane Nane exhibition center in Dodoma, Tanzania, June 2019. Photo ILR









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