Better lives through livestock

# Application of nuclear and genomic technologies for improving livestock productivity in developing world: Challenges and opportunities

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# Outline of the talk

- Major drivers for the success of genomic technologies in developed countries
- Opportunities in developing countries
    - Limited data infrastructure, genomic tools
    - Understanding and utilization of genetic basis of adaptation in indigenous livestock
    - Indirect opportunities for improving animal feeds
- Challenges
    - Data capture, Cost efficiency
    - Adequacy of commercial genomic tools and delivery of superior genetics
- Conclusions

# Benefits of genomic technologies in developed countries

- Benefits of genomic selection have well been demonstrated in developed countries
- Higher rates of genetic gain
  - Reduced generation interval especially in dairy cattle
  - Accuracies of above 70% for production traits reported for young genomic proven bulls
  - High accuracies for cows for low heritability traits
- Enabled genetic improvement in difficult to measure traits/predictive traits which are of global importance

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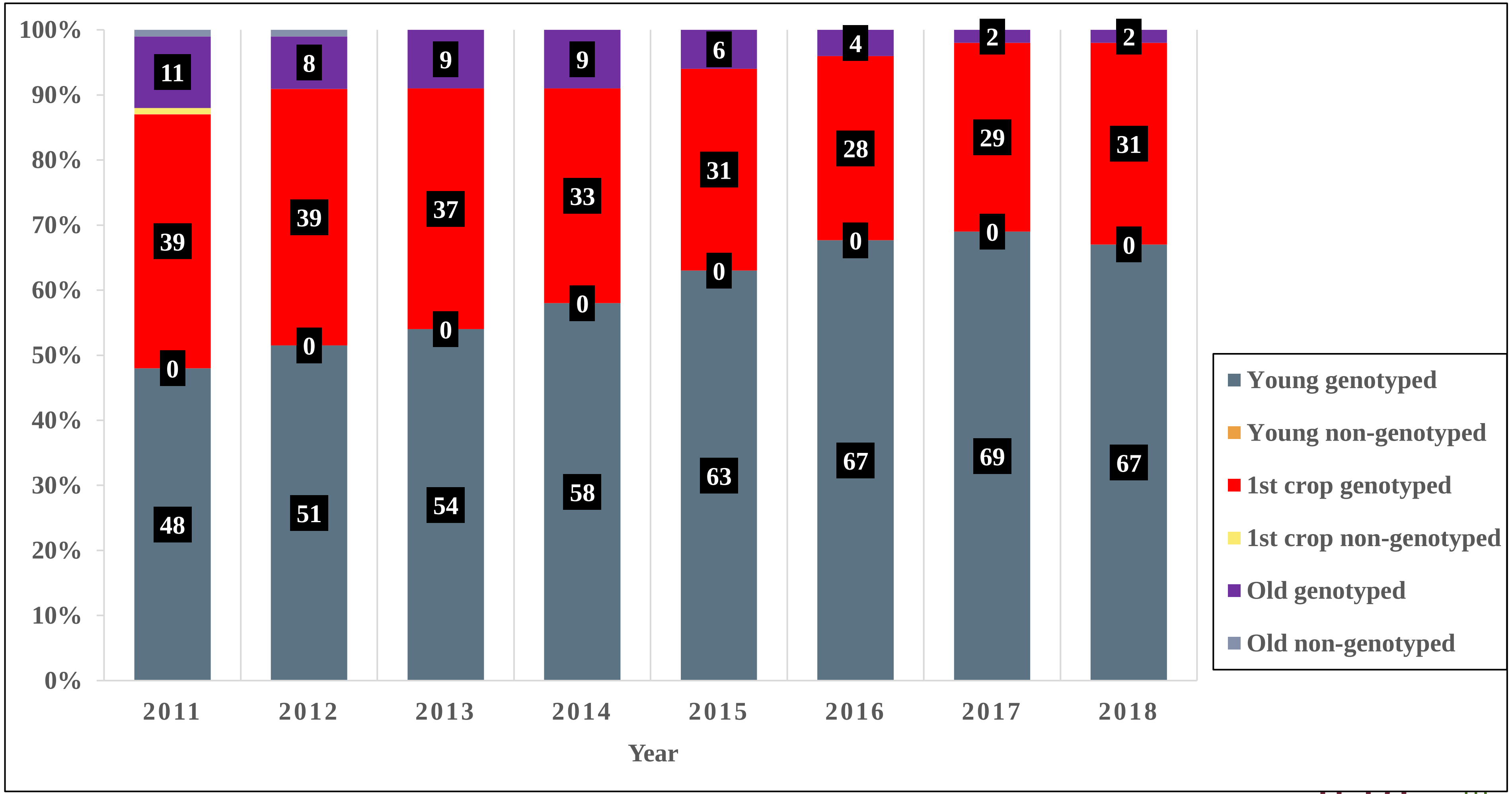
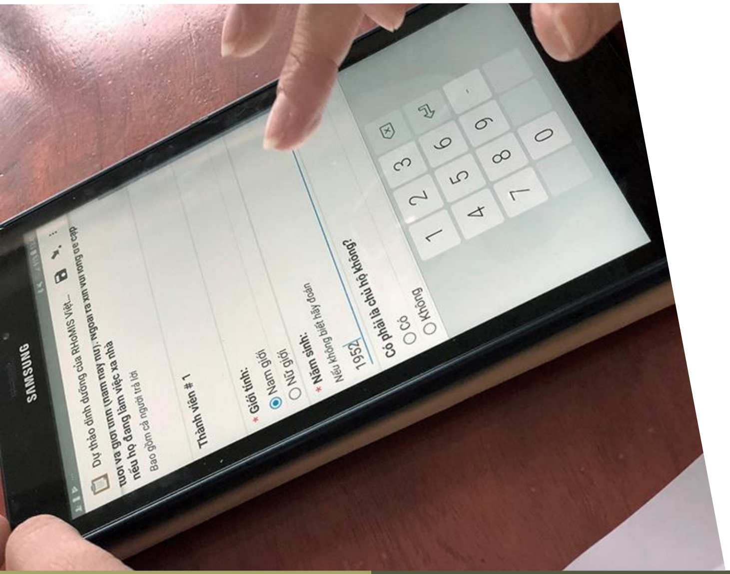
# Proportion of inseminations to various categories of bulls: 2011-2018 in USA (Wiggans, 2019)

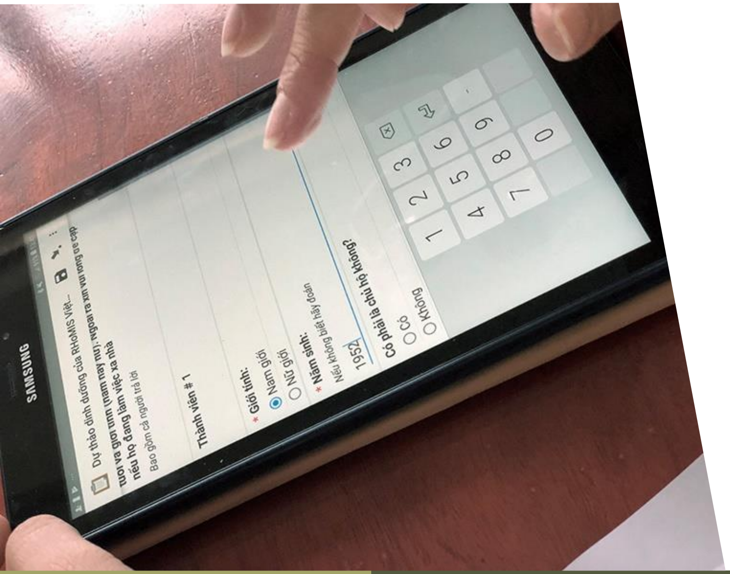




# Enabling factors for huge success in genomic selection in developed countries

- Existence of well-established infrastructure
  - Routine data capture systems ⟷ Genetic evaluation ⟷ Delivery system for superior genetics
  - Major drivers : Dairy Cattle - multi-national AI companies; Beef cattle &Sheep - driven by breed societies; Pigs and Poultry -- driven private breeding companies

# Enabling factors for huge success in genomic selection in developed countries



- Organization and design
    - Across country collaboration: Euro-Genetics , North America Consortium
    - Inter-genomics : Brown Swiss
    - Strategic genotyping of connected herds to handle difficult to measure traits – Australia AGIN
- Huge role of farmer: genomics designed to address farmer's needs
    - USA genotyped cows: 2015 =350K & 2020 = 900K
    - Selection - which calves to keep, cows to flush, breed with sexed semen ; Pedigree validation/determination; mating

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# Opportunities and challenges of genomic technologies in developing countries

- Should be examined:
- Not only in terms of the direct application of the principles of genomic technologies
- But also, the important associated factors: infrastructure, design, organization, and farmers' role

# Some limiting data infrastructure in developing countries & quick wins of genomics

- Lack of routine pedigree recording system
- Genomic prediction using the G matrix—less reliance on pedigree

- Limited herd sizes - animal effect confounded with herd effects
- Use of haploblocks from G matrix from common sires used across herds (Powell et al, 2018)

# Quick wins of genomics: Illustration with using Tanzania data

- The African Dairy Genetics Gain (ADGG) Project at ILRI funded by BMGF and working in several African countries
- Tanzania data to illustrate of quick wins of genomics
- Genomic prediction on about 2000 animals genotyped with HD SNP chip
- Limited pedigree: 88%, 11.4%and 0.6% with no, one and both parents identified
- More than 50% cows in one herd


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# Genetic parameters from a fixed (FRM)and random regression (RRM) model with **G** matrix for Tanzania data

| Trait | Model | | Heritability | Variance due to Pe | Variance due to herd | Phenotypic Variance |
|---|---|---|---|---|---|---|
| Milk Yield | FRM | GBLUP | 0.12±0.03 | 0.10±0.03 | 0.23±0.02 | 9.73±0.19 |
| | | ssGBLUP | 0.12±0.03 | 0.12±0.03 | 0.22±0.02 | 9.68±0.16 |
| | RRM | GBLUP | 0.22 | 0.14 | 0.21 | 9.76 |
| | | ssGBLUP | 0.24 | 0.15 | 0.21 | 9.72 |
| Body Weight | FRM | GBLUP | 0.24±04 | 0.20±0.04 | 0.22±0.03 | 1287.6±33.2 |
| | | ssGBLUP | 0.22±04 | 0.22±04 | 0.26±03 | 1338.4±29.9 |

# Forward validation results for daily milk yield(kg) and body weight(kg)

| 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 |

# Similar genomic predictions in Beef cattle

- Fernandes Júnior et al. (2016) examined genomic prediction for carcass traits (rib eye area (REA) ,back fat thickness (BF), and hot carcass weight (HCW) in Brazilian Nellore cattle
  - Total of 1756 steers genotyped with 777K HD Chip.
  - Accuracies estimates were of low-medium 0.21 (BT), 0.37 (HCW) and 0.46 (REA) when using YD

- Silva et al 2016--- GS in experimental farm with 788 Nellore animals genotyped with HD but with 9551 with pedigree
  - Accuracies for FCR and RFI : 0.30 to 0.45 from ssGBLUP compared to 0.29 to 0.23 from BLUP

# Some limiting data infrastructure in developing countries & quick wins of genomics

- Inadequate data structure ( small data sets and small sire progeny size)
- The application appropriate genomic methodologies
- Incorporation of external genomic information

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# Some limiting data infrastructure : The application appropriate genomic methodology

- Inadequate data structure
  - For example, the Simmental-Simbrah beef cattle population is one of the largest under genetic evaluation in Mexico
  - In the 2010 run, 5,159 bulls were evaluated but only 703 Simmental and 387 Simbrah with more than 10 daughters
- The application of Single step methodology implies bulls with reliable evaluations are not critical

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# Some limiting data infrastructure : The application appropriate genomic methodology

- Cows can now be genotyped to
    - Increase reference populations
    - Strategically handle difficult to measure traits
- Single Step genomic methods can be used to compute evaluations using both pedigree and genomic information.
- Bayesian methods could also be considered

# Some limiting data infrastructure :Incorporation external  information

- Across  country or regional opportunities :  Brown swiss model   or  SNP-BLUP model or consortium model

- Incorporating genotypes from foreign sires

# Across country or regional opportunities

- Pool genotypes to form a single reference population
  - InterGenomics : Brown Swiss populations from 7 main countries
  - InterGenomics-Holstein: Countries with small Holstein populations (Israel, Ireland, Slovenia, South Korea)
- Share genotypes: Eurogenetics & North America Consortium with UK & Italy
- Pooling genomic data across countries may be critical for GS in developing countries

# Incorporating genotypes from foreign sires

- Li et al 2016 examined the improvement in prediction reliabilities for 3 production traits in Brazilian Holsteins that had no genotypes
  - adding information from Nordic and French Holstein bulls that had genotypes.
  - Increases in reliabilities in some traits varied from 4 to 64%
- Similar studies in China Holstein with increase in reliabilities from 0.266 to 0.330 from incorporating Nordic bulls (Ma et al 2014)

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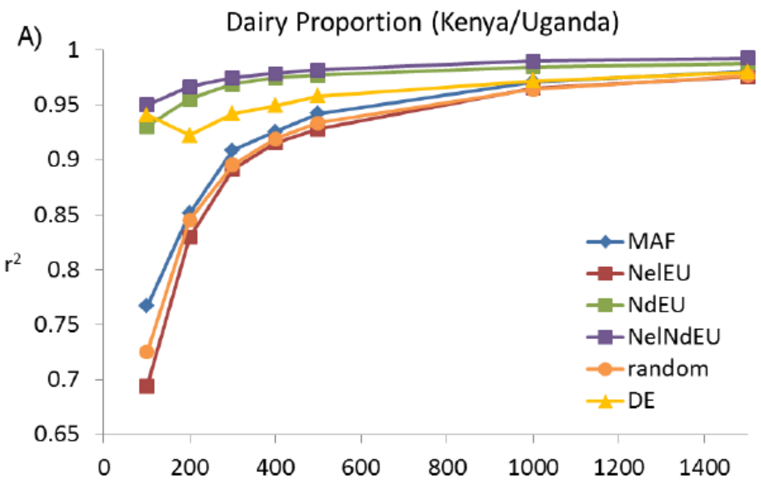
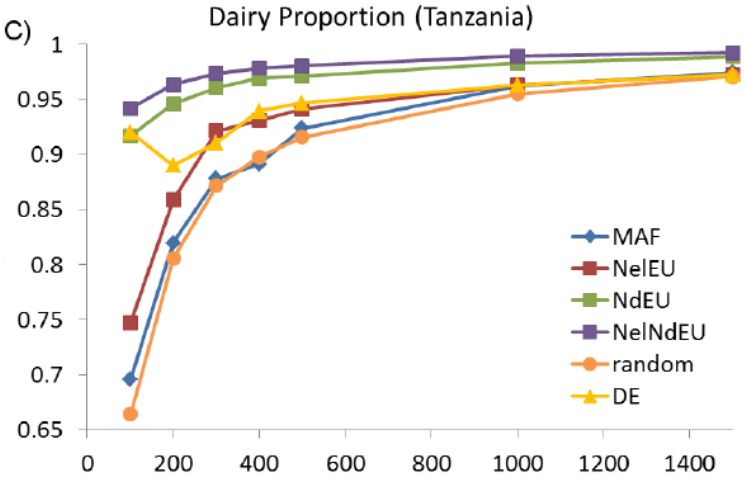
# Genomic tools: Breed composition and parentage verification

- Low density SNP assay (200) developed for breed composition determination (Strucken et al , 2017)
- If parentage verification is included, assay expands to 400 SNPs





# Understanding and utilization of genetic basis of adaptation in indigenous livestock

- Indigenous breeds represent a unique set 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 - Several loci in African cattle related immunity, heat-tolerance trypanotolerance and reproduction-related genes.

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# Understanding and utilization of genomic basis of adaptation in indigenous livestock

- 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
  - Gene editing & surrogate sires

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# Validated selection for stover quality without cost to grain yield

- Using genomic prediction as a tool to improve stover traits- (in-vitro organic matter digestibility (IVOMD) and metabolizable energy (ME))
- Supports the development of new dual-purpose maize varieties.

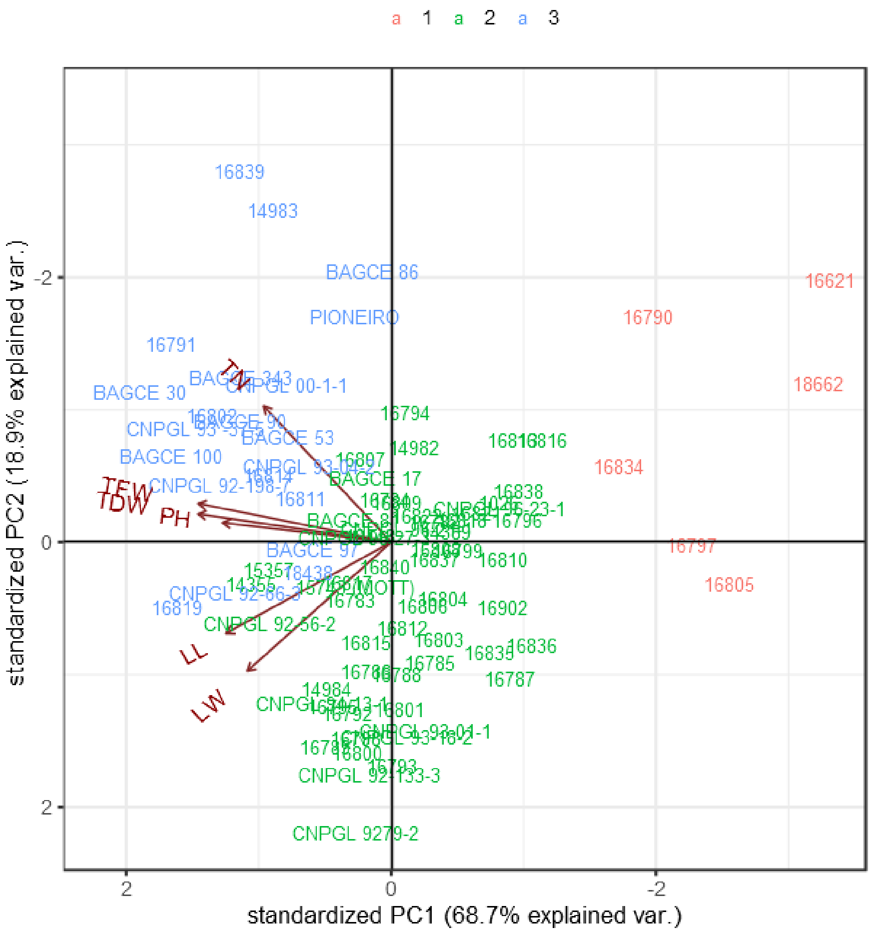
| **Marker Density (SNPs)** | **Traits** | |
|---|---|---|
| | IVOMD% | ME (MJ/kg) |
| **200** | 0.36 | 0.42 |
| **500** | 0.42 | 0.43 |
| **1000** | 0.43 | 0.45 |
| **3000** | 0.44 | 0.46 |
| **100000** | 0.45 | 0.46 |

Vinayan, M.T., Seetharam, K., Babu, R. *et al.* Genome wide association study and genomic prediction for stover quality traits in tropical maize (*Zea mays* L.). *Sci Rep* **11,** 686 (2021). https://doi.org/10.1038/s41598-020-80118-2

# Genomic selection in tropical forage grasses

**e.g. Napier grass**

- Five times more biomass than natural pastures
- Increased yield when intercropped with legumes and irrigated
- GWAS/Marker Assisted Selection under development
    - Agronomic performance and nutritional qualities



PCA biplot of 84 accession showing yield traits

# The challenge of reliable systems for data collection

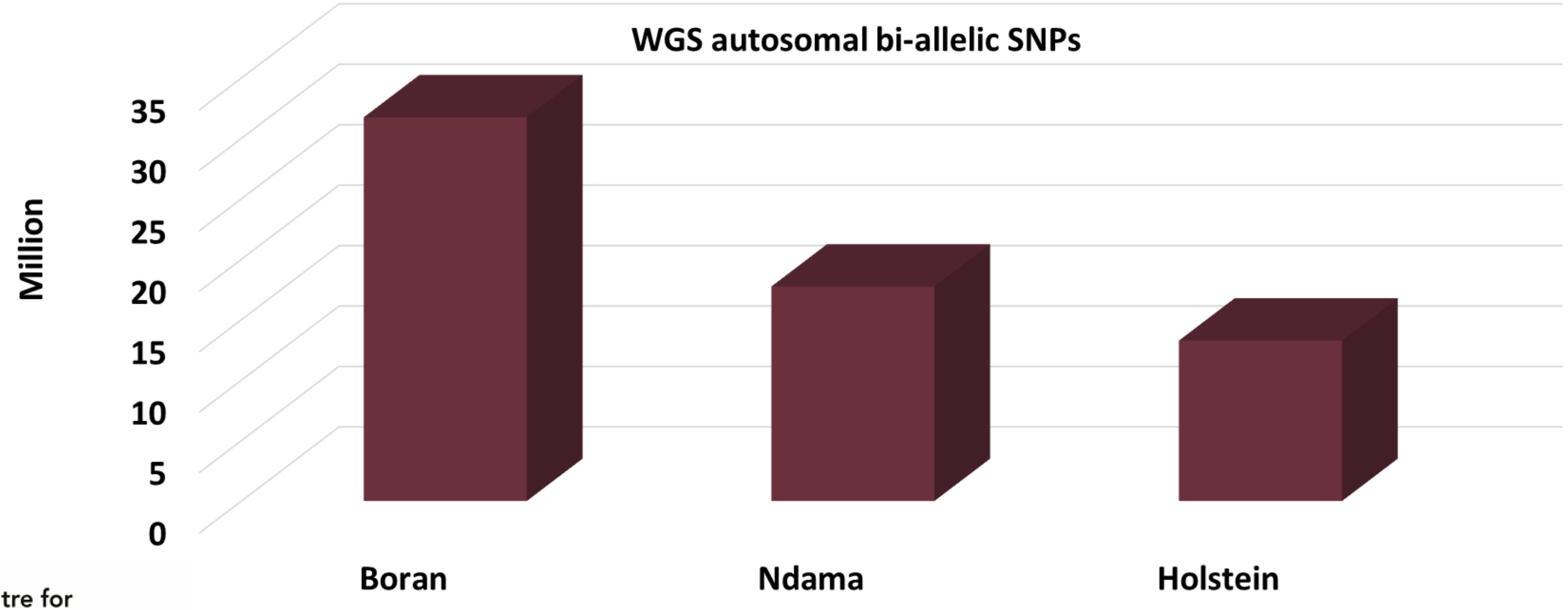
- “In the age of the genotype [genomics], phenotype is king”- Mike Coffey
- Several digital tool being pioneered
  - ODK on Tablet and smart phone : ADGG & ICow
  - Farmer-based systems – suitable for USSD phones
  - Multi-component software, on dedicated “data loggers” and mobile phones - BAIF-India
  - AniCloud and AniCapture – CBBP (offline data capture)
- Sensors to capture novel phenotypes on fertility (Muasa et al, 2019)

# Genetic parameters and accuracy of prediction using part-lactation data

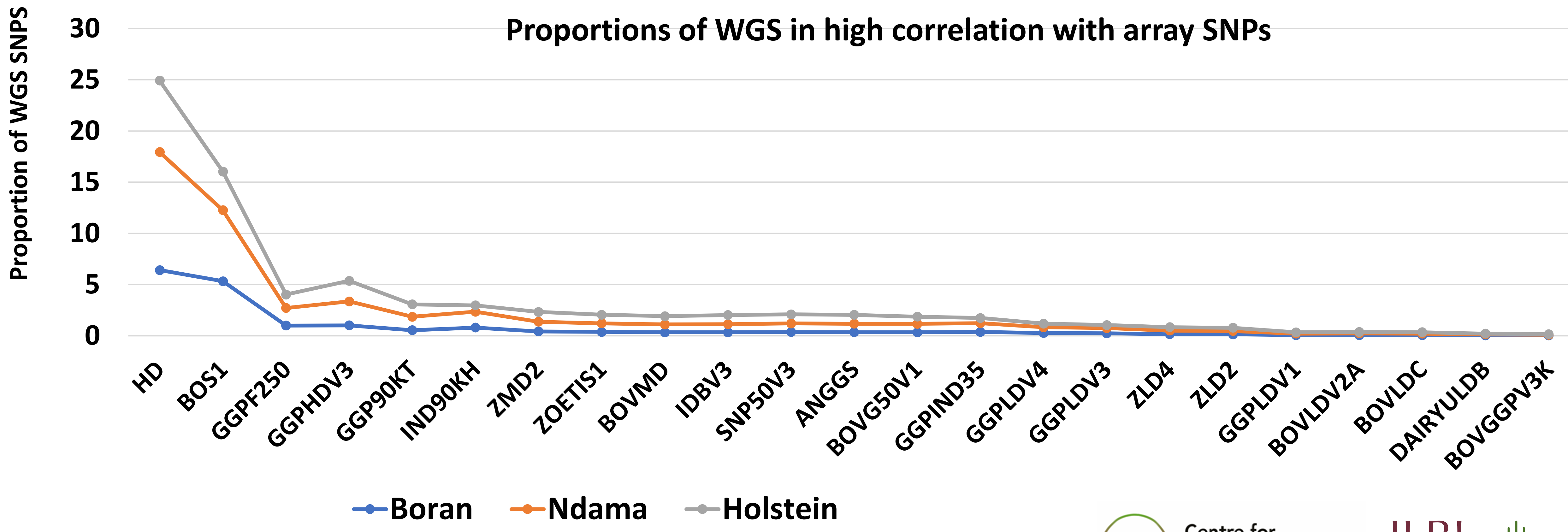
| | 100 DIM | 200 DIM | 300 DIM | 400 DIM | 500 DIM |
|---|---|---|---|---|---|
| **N** | 4400 | 8886 | 13177 | 17005 | 19599 |
| **Heritability** | 0.19±0.05 | 0.17±0.04 | 0.16±0.04 | 0.14±0.03 | 0.11±0.03 |
| | | | | | |
| | Rank correlations of gEBVs with those from 500 DIM | | | | |
| **All Bulls (702)** | 0.87 | 0.93 | 0.97 | 0.99 | |
| **Top 20%** | 0.30 | 0.61 | 0.75 | 0.79 | |
| | | | | | |
| | Genetic prediction of 276 young animals born after 2014 with records excluded | | | | |
| **Accuracy** | 0.44 | 0.52 | 0.54 | 0.57 | 0.58 |
| **Regression** | 0.83 | 0.95 | 0.97 | 1.04 | 1.06 |

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

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



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



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# Cost efficiency of genomics

- Currently, most genotyped animals are females
  - an outcome of development projects
  - Breed societies in some cases in Brazil
  - Lack of major drivers AI and breeding companies and breed societies
  - Most cases, samples sent abroad for genotyping
- Approaches needed to increase cost efficiency for wide application of genomics

# Cost efficiency of genomics

- One stop shop with modern breeding technologies and marker service laboratory , data management and analyses.
- Bundled genomic services to individual farmers and farmer organizations : determination of parentage, breed composition, genomic selection and mating services

# Cost efficiency of genomics

- Cost efficiency increases when genomics is combined with reproductive technologies.
  - Use of sexed semen of genomically proven young bulls
  - Beef cattle : use of IVF, with embryos from genotyped donors gave 79% higher genetic gain (Carvalheiro, 2014 )

# Deliverance of Improved genetics from genomics

- AI uptake still low and widespread use of local bulls
- Therefore, genomic prediction must be extended to local bulls - ADGG
- Improvement in AI services
- Work with the countries NAIC, breed societies and farmer organization.
- Understanding the breeding structure—CBBP for small ruminants and exploiting that

# Conclusions

- Genomics offers quick wins for developing countries:  genomic prediction, parentage discovery reducing need for accurate pedigree.

- Offers opportunity for across country or regional collaboration; this  will be needed to ensure adequate data and  best sires can be used across regions
- In general, genotypic data offers opportunities to model underling genetics for resilience traits

# Conclusions

- Bundled genomic services in combination with reproductive technologies will needed to improve cost-efficiency and widespread application of GS
- Of great importance is an efficient delivery mechanism needs to be in place for the superior genetics

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*More productive and profitable dairy cows*

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iCow

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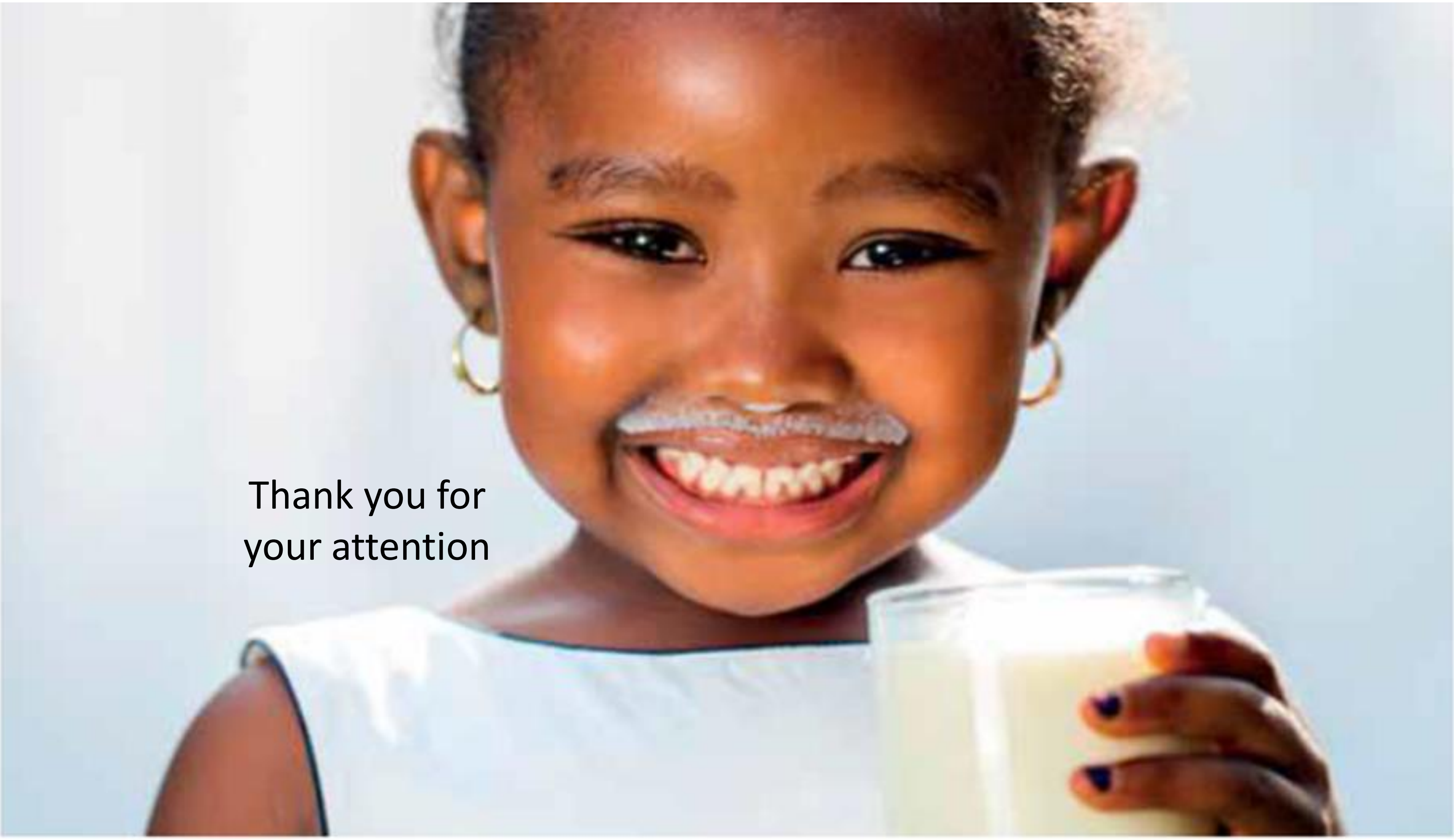

Thank you for
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