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

<table>
<thead>
<tr>
<th>Trait</th>
<th>Model</th>
<th>Heritability</th>
<th>Variance due to Pe</th>
<th>Variance due to herd</th>
<th>Phenotypic Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk Yield</td>
<td>FRM</td>
<td>GBLUP</td>
<td>0.12±0.03</td>
<td>0.10±0.03</td>
<td>0.23±0.02</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ssGBLUP</td>
<td>0.12±0.03</td>
<td>0.12±0.03</td>
<td>0.22±0.02</td>
</tr>
<tr>
<td></td>
<td>RRM</td>
<td>GBLUP</td>
<td>0.22</td>
<td>0.14</td>
<td>0.21</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ssGBLUP</td>
<td>0.24</td>
<td>0.15</td>
<td>0.21</td>
</tr>
<tr>
<td>Body Weight</td>
<td>FRM</td>
<td>GBLUP</td>
<td>0.24±04</td>
<td>0.20±0.04</td>
<td>0.22±0.03</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ssGBLUP</td>
<td>0.22±04</td>
<td>0.22±04</td>
<td>0.26±03</td>
</tr>
</tbody>
</table>
Forward validation results for daily milk yield (kg) and body weight (kg)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Method</th>
<th>Correlation</th>
<th>Regression</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield</td>
<td>FRM-GBLUP</td>
<td>0.57</td>
<td>1.1</td>
</tr>
<tr>
<td></td>
<td>FRM-ssGBLUP</td>
<td>0.59</td>
<td>1.0</td>
</tr>
<tr>
<td></td>
<td>RRM-GBLUP</td>
<td>0.55</td>
<td>1.0</td>
</tr>
<tr>
<td></td>
<td>RRM-ssGBLUP</td>
<td>0.53</td>
<td>0.92</td>
</tr>
<tr>
<td>Body weight</td>
<td>FRM-GBLUP</td>
<td>0.83</td>
<td>1.0</td>
</tr>
<tr>
<td></td>
<td>FRM-ssGBLUP</td>
<td>0.77</td>
<td>1.1</td>
</tr>
</tbody>
</table>
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
Some limiting data infrastructure: The application of 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
Some limiting data infrastructure: The application of 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)
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.
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
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.

<table>
<thead>
<tr>
<th>Marker Density (SNPs)</th>
<th>Traits</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>IVOMD%</td>
</tr>
<tr>
<td>200</td>
<td>0.36</td>
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<tr>
<td>500</td>
<td>0.42</td>
</tr>
<tr>
<td>1000</td>
<td>0.43</td>
</tr>
<tr>
<td>3000</td>
<td>0.44</td>
</tr>
<tr>
<td>100000</td>
<td>0.45</td>
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</tbody>
</table>

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
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

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

![Bar chart showing WGS autosomal bi-allelic SNPs for Boran, Ndama, and Holstein breeds.]
Assessment of the 23 commercial Bovine SNP arrays in 3 cattle breeds

Proportions of WGS in high correlation with array SNPs

Proportion of WGS SNPS

Boran  Ndama  Holstein
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 need 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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Dairy Farmers & Farmer organizations
Thank you for your attention

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