Genomics selection in livestock

ILRI – ICARDA Perspectives

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Benefits of genomic selection

- Benefits of genomic selections have well been demonstrated in developed countries
  - Reduced generation interval
  - Accuracies of above 70% have been reported for young genomic proven bulls
  - Higher rates of genetic gains

- Genomic systems in developed countries are characterised
  - With large reference populations
  - Collaboration among countries
  - Well defined phenotypes and mostly within pure breeds
Trajectories for the livestock sector* and opportunities for genomics selection

• **Rapid inclusive growth systems**
  ✓ developing sustainable food systems that deliver key animal-source nutrients to the poor
  ✓ facilitating a structural transition in the livestock sector of developing countries.
  ✓ transition is from many smallholders keeping livestock in low-productive systems to eventually fewer households raising more productive animals. **Productivity traits - Adaptive traits.**

• **High growth systems with externalities**
  ✓ dynamic markets, IT, investment capital, infrastructure and skilled human resources
  ✓ fast-changing small-scale livestock systems. **NOT OUR CLIENTS**

• **Fragile growth systems**
  ✓ productivity is severely limited by remoteness, harsh climates or environments,
  ✓ emphasis will be to enhance the important roles of livestock in the resilience of people and communities to environmental variability.
  ✓ **Productivity traits - Adaptive traits.**

The largest dairy herd in the world (Al Karj – Kingdom of Saudi Arabia)

Almarai Dairy Farms

High growth with externality

Sustainability ....
Rapid inclusive growth systems
Fragile growth systems

E.g. Pastoral systems

Maximize Adaptive diversity
Genomic selection in livestock systems: no one-size-fit

- **High growth** → Classical GS
- **Strong growth** → Innovatives GS approaches
- **Fragile growth**
Opportunities offered by genomics in small holder systems

- Quick wins from genotypic data includes
  - Reduces the need for accurate pedigree recording as genomic relationship can easily be computed
  - Parentage discovery using SNP data
  - Usage to determine the breed composition of cross-bred animals in the absence of pedigree.
  - Gives the opportunity to match different genotypes & management system

- Using DGEA small holder data -- 1038 cows HD genotypes
  - Successfully determined the breed composition of the animals using admixture analysis
  - Computed G matrix and undertake genomic predictions: GBLUP, SNP-BLUP and BayesC & BayesCpi
# Classification of cows by breed composition

<table>
<thead>
<tr>
<th>Dairy%</th>
<th>Breedtype</th>
<th>Dairy% by Breedtype</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (0-20%)</td>
<td>Zebu</td>
<td>6</td>
</tr>
<tr>
<td>2 (0.33-35%)</td>
<td>Mixed + Zebu</td>
<td>6</td>
</tr>
<tr>
<td>3 (36-60%)</td>
<td>Ayr/Gue/Jer</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>Fri</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>Mixed + Zebu</td>
<td>6</td>
</tr>
<tr>
<td>4 (61-87.5%)</td>
<td>Ayr</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>Fri</td>
<td>2</td>
</tr>
<tr>
<td>4</td>
<td>Ayr/Fri</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>Gue/Fri</td>
<td>4</td>
</tr>
<tr>
<td>4</td>
<td>Ayr/Gue/Fri</td>
<td>5</td>
</tr>
<tr>
<td>4</td>
<td>Mixed + Zebu</td>
<td>6</td>
</tr>
<tr>
<td>5 (&gt;87.5%)</td>
<td>Ayr</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>Fri</td>
<td>2</td>
</tr>
<tr>
<td>5</td>
<td>Ayr/Fri</td>
<td>3</td>
</tr>
<tr>
<td>5</td>
<td>Gue/Fri</td>
<td>4</td>
</tr>
<tr>
<td>5</td>
<td>Gue/Fri/Ayr</td>
<td>5</td>
</tr>
</tbody>
</table>


Accuracy of prediction

Zebu + Mixed crosses: 32%

Cows with 61-87.5% dairy: 35%

Cows with >87.5% dairy: 41%
Projects with major genomic initiatives

- The Africa Dairy Genetic Gain (ADGG) project in Ethiopia & Tanzania
  - Development of a small and cheaper chip to determine breed composition and parentage discovery
  - Certification of young bulls on the basis of breed composition and genomic profile
Opportunities

• Availability of data offers opportunities to GWAS and positive signatures of selection to identify regions of genome associated with productivity and adaptability.

• Usage of gene editing in addition to genomic selection increase frequency of alleles for adaptability (Jenko et al, 2015).

• Genomic data gives for better understanding of genetic diversity in the fragile growth sector and how to select for it.
Regional and International Collaborations (dairy sector)

- Across regional genomics might be necessary for application of genomics for small holder farmers
  - Only third of the 20,000 bulls in the reference pop for the German genomic system are home proven.
  - In the UK, less than one third of 22,000 bulls in the reference pop are domestic bulls
  - Possibly most exotics sires used in crossing breeding are similar across regions or countries
  - Policies that promote easy flow of data across country boundaries while maintaining data security and ownership will be needed
Regional and International Collaborations (dairy sector)

- Need to collaborate with developed countries where some of the sires of these cows could have been genotyped
  - Parentage discovery & determine breed composition
  - Genotype by environmental interaction if enough data
Conclusions

• Genomics offers quick wins in small holder systems through use of genomic relationship matrix and parentage discovery

• Given smaller data structure, well adapted methodologies both in terms of developing relevant chips and analytics tools will be needed

• Collaboration on across country or regional basis will be needed to ensure adequate data and best sires can be used across regions

• Strong national partnership with be needed to deliver the impact of better genetics resulting from genomics

• Genotyping of cross bred animals offers possibilities for further optimize cross breeding systems