Can genomics enable genetic evaluations for smallholder farmers?

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Kenyan Smallholders

Account for ≈ 70% of milk production

• ~3-5 acres of land.
• Mixed farming (crops, 1-5 cows)
• Low AI use.
• Weaker breeding & production infrastructure.
• Highly heterogeneous environment.

Poor penetrance of breeding practices.
Milk yields of ≈ 3 L of milk per day

Breeding hasn’t been effective in this system

Kenyan Smallholders

• Low AI use.
• Small herd size.
• Weak Connectedness
• Highly Heterogeneous environments.
• Small herd size.

Advanced Economies

• High AI.
• Large herd size.
• Strong Connectedness
• Homogeneous environments.
Estimation of Breeding Values

Phenotype = HerdID + BV + Residual

HerdID included to correct data for environment/herd.

<table>
<thead>
<tr>
<th>ID</th>
<th>HerdID</th>
<th>BV</th>
<th>Residual</th>
<th>Pheno</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td></td>
<td></td>
<td>-2.067</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td></td>
<td></td>
<td>-0.201</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td></td>
<td></td>
<td>1.435</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td></td>
<td></td>
<td>2.382</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td></td>
<td></td>
<td>-0.687</td>
</tr>
</tbody>
</table>
### PBLUP versus GBLUP

- **Currently:**
  - Herd size too small
  - Connectedness too weak.
- **Solve connectedness, the rest will follow.**
- **Genomics can strengthen connectedness by capturing shared haplotypes blocks across herds.**

<table>
<thead>
<tr>
<th>Sire 1</th>
<th>Sire 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>(S_1)</td>
<td>(S_2)</td>
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</table>

<table>
<thead>
<tr>
<th>Off. 1</th>
<th>Off. 2</th>
<th>Off. 3</th>
<th>Off. 4</th>
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<tbody>
<tr>
<td>(S_1)</td>
<td>(S_1)</td>
<td>(S_2)</td>
<td>(S_2)</td>
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<tr>
<td>(D_1)</td>
<td>(D_1)</td>
<td>(D_2)</td>
<td>(D_2)</td>
</tr>
</tbody>
</table>

**Herd 1**

**Herd 2**

---

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Aims

In small holders systems:

1) Can GBLUP separate environment and genetics?

2) Should herd be fixed or random effects?

3) Impact of connectedness?
Data Generation
BurnIn

- Effective Population Size (Ne) ≈100
- Sires per generation : 50
- Dams per generation : 500
- Population size : 1000
Recent Breeding

- Sires per generation: 50 -> 1000
- Dams per generation: 20000
- Select on TBV.

- Final generation subsets were created varying:
  - Population Size: 1000 -> 4000
  - Herd Size: 1 -> 32
Analysis

Bayesian Generalized Linear Regression (BGLR)\textsuperscript{2}

• Populations of; 1000, 2000, 4000.
• Analysed each dataset with three P/GBLUP models;
  \begin{itemize}
    \item 1. excluding herd effect,
    \item 2. herd as a fixed effect,
    \item 3. herd as a random effect.
  \end{itemize}
• 12000 Iterations, 2000 BurnIn.

Results
Effect of Method on EBV Accuracy

<table>
<thead>
<tr>
<th>Method</th>
<th>GBLUP</th>
<th>PBLUP</th>
</tr>
</thead>
<tbody>
<tr>
<td>1000</td>
<td>0.6</td>
<td>0.4</td>
</tr>
<tr>
<td>2000</td>
<td>0.7</td>
<td>0.5</td>
</tr>
<tr>
<td>4000</td>
<td>0.8</td>
<td>0.6</td>
</tr>
</tbody>
</table>
Fixed or Random

Effect of Model on EBV Accuracy

Model
- Herd Fixed
- Herd Random
- No Herd

Number of Animals Per Herd

Accuracy

1000  2000  4000
Fixed or Random - Small Herd Sizes

**Effect of Model on EBV Accuracy**

<table>
<thead>
<tr>
<th>Model</th>
<th>1000</th>
<th>2000</th>
<th>4000</th>
</tr>
</thead>
<tbody>
<tr>
<td>Herd Fixed</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Herd Random</td>
<td></td>
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</tr>
</tbody>
</table>

- **Accuracy**
- **Number of Animals Per Herd**

Graph shows the effect of different herd models on EBV accuracy with varying herd sizes.
<table>
<thead>
<tr>
<th>Population Size</th>
<th>Herd Size</th>
<th>Offspring per Sire</th>
<th>Accuracy</th>
<th>se</th>
</tr>
</thead>
<tbody>
<tr>
<td>4000</td>
<td>2</td>
<td>4</td>
<td>0.580</td>
<td>0.007</td>
</tr>
<tr>
<td></td>
<td></td>
<td>8</td>
<td>0.575</td>
<td>0.007</td>
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<td>16</td>
<td>0.588</td>
<td>0.006</td>
</tr>
<tr>
<td></td>
<td></td>
<td>40</td>
<td>0.609</td>
<td>0.005</td>
</tr>
<tr>
<td></td>
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<td>80</td>
<td>0.635</td>
<td>0.008</td>
</tr>
</tbody>
</table>
Conclusions

• GBLUP is able to separate environment and genetics and outperform PBLUP estimates.

• At low herd sizes, herd should be modelled as random.

• Increasing the number of offspring per sire used, increases the probability of shared haplotypes across herds.

• Genomic evaluations can exploit the existing architecture of smallholder farming systems.
Future Work

• Accuracy of Genomic Prediction of:
  – Sons
  – International Sires

• Impact of non-random association of sire breeding value with herd value on accuracy and bias when modelling herd as a random effect.
Acknowledgements