Optimizing design of small-sized nucleus dairy cattle breeding programs with minimal recording

Kariuki C.M.\textsuperscript{1,2}, H. Komen\textsuperscript{1}, A.K. Kahi\textsuperscript{3}, J.A.M. van Arendonk\textsuperscript{1}

\textsuperscript{1}Wageningen University, Animal Breeding and Genomics Centre, The Netherlands
\textsuperscript{2}Chuka University, Department of Animal Sciences, Kenya
\textsuperscript{3}Egerton University, Department of Animal Sciences, Kenya
Acknowledgements

Netherlands Organization for International Cooperation in Higher Education (NUFFIC)
Introduction

- Current genetic improvement in developing countries is through semen importation

- GxE between regions estimated to be 0.49 (Ojango and Pollot, 2002)
Environment specific breeding programs

- Alternative approach: environment-specific breeding programs

- Limitation – minimal and erratic pedigree and performance recording at farm level (Wasike et al., 2011)

- Negatively impacts genetic evaluation of selection candidates
Objective

- Small-sized nucleus dairy cattle breeding program?
- What selection strategy to adopt?
  - Response to selection
  - Accuracy
- We ignored inbreeding for this study
Materials and Methods

- Deterministically simulated a nucleus program

Nucleus

- 100 elite dams
  - 45 daughters born annually
    - Dams selected
  - 45 sons born annually
    - Sires selected

Commercial cow population

- 10 active sires
  - 45 sons born annually
    - Sires selected

Recorded cows

Two levels: 2,500 and 5,000

Extra information for evaluation

Non-recorded cows

SelAction (Rutten et al., 2004)
## Materials and Methods

### Selection strategies

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DP</td>
<td>Phenotypes of nucleus dams</td>
</tr>
<tr>
<td>PT</td>
<td>Progeny testing</td>
</tr>
<tr>
<td>GS</td>
<td>Genomic selection</td>
</tr>
<tr>
<td>GS+DP</td>
<td>Genomic + nucleus dams</td>
</tr>
<tr>
<td>GS+PT</td>
<td>Genomic + progeny testing</td>
</tr>
</tbody>
</table>
Materials and Methods

- GS was implemented by mimicking a correlated trait with $h^2 = 1$ and genetic and phenotypic correlations were calculated following Dekkers (2007)

- Selected for a single trait – total merit trait

- Truncation selection with 8 age-classes
Results – response to selection ($\Delta R$)

- Response for the basic DP scheme in genetic standard deviation ($\sigma_g$)

<table>
<thead>
<tr>
<th>Number of CRC</th>
<th>Scheme 2,500</th>
<th>Scheme 5,000</th>
<th>$L$ (years)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DP</td>
<td>0.042</td>
<td>0.047</td>
<td>4.2</td>
</tr>
</tbody>
</table>

- For comparison alternative selection strategies were benchmarked against basic DP scheme and presented as a percentage
# Results – response to selection ($\Delta R$)

<table>
<thead>
<tr>
<th>Scheme</th>
<th>Number of CRC</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2,500</td>
<td>5,000</td>
<td>L (years)</td>
<td></td>
</tr>
<tr>
<td>PT</td>
<td>13.5</td>
<td>27.0</td>
<td>6.2</td>
<td></td>
</tr>
<tr>
<td>GS</td>
<td>24.3</td>
<td>70.3</td>
<td>3.0</td>
<td></td>
</tr>
<tr>
<td>GS+DP</td>
<td>24.3</td>
<td>43.2</td>
<td>4.2</td>
<td></td>
</tr>
<tr>
<td>GS+PT</td>
<td>16.2</td>
<td>29.7</td>
<td>6.2</td>
<td></td>
</tr>
</tbody>
</table>

Extra response as percentage of the response in DP schemes

- For these results the pedigree is assumed to be known accurately
## Results – accuracy ($r_I$)

<table>
<thead>
<tr>
<th>Scheme</th>
<th>2,500</th>
<th>5,000</th>
</tr>
</thead>
<tbody>
<tr>
<td>PT</td>
<td>0.62</td>
<td>0.73</td>
</tr>
<tr>
<td>GS</td>
<td>0.21</td>
<td>0.30</td>
</tr>
<tr>
<td>GS+DP</td>
<td>0.33</td>
<td>0.39</td>
</tr>
<tr>
<td>GS+PT</td>
<td>0.64</td>
<td>0.74</td>
</tr>
</tbody>
</table>
Conclusions

- Feasibility exists for creating genetic gains through nucleus programs with minimal performance recording

- GS will have the highest responses

- Lower accuracies in GS will be offset by the higher annual responses
Thank you for your attention!

charles.kariuki@wur.nl