Crossbred Reference Can Improve Response To Genomic Selection

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BACKGROUND

- Most of the animals used in livestock production systems are crossbreds

- Limitations
  - Selection is in purebred nucleus lines or breeds that are housed in high-health environments
  - Genetic differences
BACKGROUND

- Genomic selection

- Training on crossbreds
  - Collection of crossbred P and G
  - SNP effects might be breed specific

- Training on pure lines
  - Environmental differences between purebreds and crossbred animals
  - G×E
OBJECTIVE

- To compare crossbred response by variety of training populations

- To investigate the benefits of distinguishing two types of heterozygotes in crossbreds
SIMULATION STEPS

Generations

0
1000
2000
2001
2300
2308

Populations

N=1000
N=1000
N=100

Breed A
Breed B

A
F_{1}
B

AARHUS UNIVERSITY
SIMULATION STEPS

Generations

1

5

A

A_F

A_M

A_1

A_4

A_F

A_M

AB_1

B

B_F

B_M

B_1

B_4

B_F

B_M

AB_5
### SIMULATION PARAMETERS

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of chromosomes</td>
<td>1</td>
</tr>
<tr>
<td>Genome size</td>
<td>100 cM</td>
</tr>
<tr>
<td>Number of markers</td>
<td>1000</td>
</tr>
<tr>
<td>Number of QTL</td>
<td>100</td>
</tr>
<tr>
<td>Additive effects for QTL</td>
<td>Gamma</td>
</tr>
<tr>
<td>Dominance degrees ($h_i$)</td>
<td>Normal</td>
</tr>
<tr>
<td>Dominance effects for QTL</td>
<td>$d_i = h_i \cdot</td>
</tr>
<tr>
<td>Heritability</td>
<td>0.4 (0.3, 0.1)</td>
</tr>
</tbody>
</table>
# SCENARIOS

<table>
<thead>
<tr>
<th>Scenarios</th>
<th>Training</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sc. 1</td>
<td>Separate (A, B)</td>
</tr>
<tr>
<td>Sc. 2</td>
<td>Combined (A+B)</td>
</tr>
<tr>
<td>Sc. 3</td>
<td>Crossbreds (F₁)</td>
</tr>
<tr>
<td>Sc. 4</td>
<td>Crossbreds (F₁)</td>
</tr>
<tr>
<td>Sc. 5</td>
<td>Crossbreds (F₁)</td>
</tr>
<tr>
<td>Sc. 6</td>
<td>Crossbreds (F₁)</td>
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</tbody>
</table>

AA-Aa-aa
AA-Aa-aA-aa
CORRELATION OF PHASE

![Graph showing correlation of phase vs marker distance in cM]
CUMULATIVE RESPONSE TO SELECTION IN CROSSBREDS

Phenotypic Mean

- Sc.1 Separate
- Sc.2 Combined
- Sc.3 Cross_P1
- Sc.4 Cross_P2
- Sc.5 Cross_PG1
- Sc.6 Cross_PG2

Generation

1 2 3 4 5
HETEROSES

CP=BA+H

Sc.1 Separate
Sc.2 Combined
Sc.3 Cross_P1
Sc.4 Cross_P2
Sc.5 Cross_PG1
Sc.6 Cross_PG2
CONCLUSION

• Training on crossbred progeny gives higher response to selection than training on pure lines

• Distinguishing two types of heterozygotes would increase response to selection

• If correlation of phase between two breeds is low, joining breeds won’t help

Thank YOU!
\[ E(r) = r_0^2 (1 - c)^2T \]

- \( r_0^2 \) is LD in the common ancestral population
- \( c \) is the recombination rate between markers
- \( T \) is the time since breed divergence in generations
### Selection criteria

**GEBVP**: Genomic Estimated Breeding value for PUREBRED  
**GEBVC**: Genomic Estimated Breeding value for CROSSBRED

<table>
<thead>
<tr>
<th>A₁A₂</th>
<th>Breed A</th>
<th>Breed B</th>
<th></th>
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</thead>
<tbody>
<tr>
<td></td>
<td>pₐqₐ</td>
<td>pₐqₐ</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>A₁A₁</th>
<th>pₐ×a+qₐ×d</th>
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<th></th>
</tr>
</thead>
</table>

- **Breed A**
  - A₁A₁ × A₁A₁  
  - A₁A₂ × A₂A₂
  - pₐ(A₁A₁) or qₐ(A₁A₂)

- **Breed B**
  - A₁A₁ × A₁A₁  
  - A₁A₂ × A₂A₂
  - pᵦ(A₁A₁) or qᵦ(A₁A₂)
Results

LD

Average $r^2 = 0.43$ Breed A
0.42 Breed B
PREDICTION ACCURACY

Accuracy of selection in Breed A

Accuracy of selection in Breed B

Sc.1 Separate
Sc.2 Combined
Sc.3 Cross_P1
Sc.4 Cross_P2
Sc.5 Cross_PG1
Sc.6 Cross_PG2