Indirect genomic predictions of milk yield for crossbred dairy cattle

Why crossbreeding in dairy?

• Beef on dairy

• Maintain optimal mixed-breed composition

• Capitalize on heterosis

• Transform herd to another breed

VanRaden et al. 2020
Upgrading mating system

F1
Upgrading mating system

F2
Upgrading mating system

F3
Upgrading mating system

F4
Upgrading mating system

F5
How to evaluate crossbreds

• Breed origin of alleles (Christensen et al. 2014, Lopes et al. 2017, Esfandyari et al. 2015)
• Combine all in a single G-matrix (Lourenco et al. 2016)
• Breed proportions (VanRaden et al. 2020)
Objective

Evaluate the predictive ability and inflation of indirect genomic breeding values for crossbred animals using SNP marker effects from different reference groups, or breed proportions.
Materials and methods

• 13,880,217 milk yield measurements on 6,830,415 animals
• 19,787,413 in pedigree
• ~45k SNP markers
• Genotyped animals:

<table>
<thead>
<tr>
<th>Breed</th>
<th>Genotyped animals</th>
</tr>
</thead>
<tbody>
<tr>
<td>Holstein</td>
<td>375,487</td>
</tr>
<tr>
<td>Jersey</td>
<td>40,769</td>
</tr>
<tr>
<td>Cross</td>
<td>22,373</td>
</tr>
</tbody>
</table>

Didn’t use all of the Holstein due to computational demand
Data for genotyped animals

- **Holstein**
  - Genotyped: 89,558
  - Genotyped & Phenotyped: 15,695
- **Jersey**
  - Genotyped: 40,769
  - Genotyped & Phenotyped: 9,313
  - Validation: 2,186
- **Crossbreds**
  - Genotyped: 22,373
  - Genotyped & Phenotyped: 1,667
  - Validation: 358
Breed proportions

All crossbreds
- Jersey: 41%
- Holstein: 59%

Validation crossbreds
- Jersey: 52%
- Holstein: 48%
Evaluation

• ssGBLUP
• Algorithm for Proven and Young (APY)
• SNP effects from GEBV
• Indirect prediction (DGV) from SNP effects
• Predictive ability: Pearson correlation between adjusted y and DGV
### Scenarios to estimate SNP effects

<table>
<thead>
<tr>
<th>JERSEY</th>
<th>HOLSTEIN</th>
<th>CROSS</th>
</tr>
</thead>
<tbody>
<tr>
<td>- All Jersey</td>
<td>- All Holstein</td>
<td>- All crossbreds</td>
</tr>
<tr>
<td>- APY: random 15k</td>
<td>- APY: random 22k</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>JERSEY &amp; HOLSTEIN</th>
<th>MIX</th>
</tr>
</thead>
<tbody>
<tr>
<td>- All Jersey and Holstein</td>
<td>- All crossbreds</td>
</tr>
<tr>
<td>- APY: random 25k</td>
<td>- Random Holstein and Jersey genotypes to equal 22k each</td>
</tr>
<tr>
<td></td>
<td>- APY: random 25k</td>
</tr>
</tbody>
</table>
Jersey

SNP effects

Training

Validation

Holstein

Jersey

Cross
Training

Holstein

SNP effects

Validation

Holstein

Jersey

Cross
Cross

SNP effects

Training

Validation

Holstein

Jersey

Cross
Training

Jersey & Holstein

SNP effects

Validation

Holstein

Jersey

Cross
Training

Mix

SNP effects

Validation

Holstein

Jersey

Cross
Proportions

\[ DGV_H \times (\text{Holstein proportion}) + DGV_J \times (\text{Jersey proportion}) \]

<table>
<thead>
<tr>
<th>Animal</th>
<th>% Holstein</th>
<th>% Jersey</th>
</tr>
</thead>
<tbody>
<tr>
<td>Animal 1</td>
<td>80</td>
<td>20</td>
</tr>
<tr>
<td>Animal 2</td>
<td>40</td>
<td>60</td>
</tr>
<tr>
<td>Animal 3</td>
<td>48</td>
<td>52</td>
</tr>
<tr>
<td>Animal 4</td>
<td>75</td>
<td>25</td>
</tr>
<tr>
<td>Animal 5</td>
<td>20</td>
<td>80</td>
</tr>
<tr>
<td>Animal 6</td>
<td>42</td>
<td>58</td>
</tr>
<tr>
<td>Animal 7</td>
<td>90</td>
<td>10</td>
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</tbody>
</table>
# Predictive ability

<table>
<thead>
<tr>
<th>Breed used</th>
<th>Breed predicted</th>
<th>Predictive ability</th>
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<tbody>
<tr>
<td>Jersey</td>
<td>Holstein</td>
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<tr>
<td>Cross</td>
<td>0.24</td>
<td>0.26</td>
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<td><strong>0.45</strong></td>
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<tr>
<td>Cross</td>
<td>0.24</td>
<td>0.26</td>
<td>0.50</td>
<td></td>
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<td>0.45</td>
<td>0.47</td>
<td></td>
</tr>
<tr>
<td>Jersey &amp; Holstein</td>
<td>0.45</td>
<td>0.44</td>
<td>0.50</td>
<td></td>
</tr>
<tr>
<td>Mix</td>
<td>0.46</td>
<td>0.40</td>
<td>0.46</td>
<td></td>
</tr>
<tr>
<td>Proportions</td>
<td>-</td>
<td>-</td>
<td>0.32</td>
<td></td>
</tr>
</tbody>
</table>
Adjusted phenotype

Under-estimated (> 1.00)

Over-estimated (< 1.00)

Direct Genomic Breeding Value (DGV)
Adjusted phenotype

Inflation

Mix - 1.00

Under-estimated (> 1.00)

Over-estimated (< 1.00)

Direct Genomic Breeding Value (DGV)
Adjusted phenotype

**Under-estimated (> 1.00)**

**Over-estimated (< 1.00)**

Direct Genomic Breeding Value (DGV)
Adjusted phenotype

Inflation

Under-estimated (> 1.00)

Over-estimated (< 1.00)

Direct Genomic Breeding Value (DGV)
Adjusted phenotype

Direct Genomic Breeding Value (DGV)

- Cross - 1.17
- Mix - 1.00
- Proportions - 0.85
- Jersey & Holstein - 0.78

Under-estimated (> 1.00)

Over-estimated (< 1.00)
Adjusted phenotype

Under-estimated (> 1.00)

Over-estimated (< 1.00)

Direct Genomic Breeding Value (DGV)

- Cross - 1.17
- Mix - 1.00
- Proportions - 0.85
- Jersey & Holstein - 0.78
- Jersey - 0.65
Adjusted phenotype

Direct Genomic Breeding Value (DGV)

Inflation

Over-estimated (< 1.00)

Under-estimated (> 1.00)

Cross - 1.17
Mix - 1.00
Proportions - 0.85
Jersey & Holstein - 0.78
Jersey - 0.65
Holstein - 0.55
Conclusion

• Accounting for breed proportions is not necessary
• Using mix scenario was slightly less accurate but without inflation
• Breeding objectives are important
• Could possibly use SNP effects of the desired pure breed
• Small validation populations