Multibreed single-step genomic evaluation model for Finnish beef cattle

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Interbull 2023, Aug. 26, 2023
Starting point of the project

• Existing **Single breed (SB)** evaluation models for **Angus, Charolais, Hereford, Limousin, and Simmental**.

• Separate evaluations for **slaughter, growth, and calving** -trait groups within breed.

• Same **model effects** in all **breeds**.

• **Breed specific variance components.**

• No genomic information were used in the existing evaluation

• No observations from F1 crosses can be used

• Evaluation of breed crosses not optimal
Traits and evaluations, **three trait groups:**

<table>
<thead>
<tr>
<th>Trait</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calving ease</td>
</tr>
<tr>
<td>Birth weight</td>
</tr>
<tr>
<td>Weaning weight (day 200)</td>
</tr>
<tr>
<td>Yearling weight</td>
</tr>
<tr>
<td>Slaughter weight</td>
</tr>
<tr>
<td>EUROP quality class</td>
</tr>
<tr>
<td>EUROP fat class</td>
</tr>
</tbody>
</table>

**1) Calving ease evaluation**

**2) Growth evaluation**

**Source**
- Herd
- Slaughter house
Multibreed Single-Step Model was built in two steps

Multibreed pedigree BLUP (PBLUP) evaluation model

• Single breed models used as base.
• Unknown parent groups (UPG) in the pedigree.

Multibreed ssGBLUP Metafounder (MF) evaluation model

• Multibreed PBLUP model as base.
• Genomic relationships within and across breeds were included.
• UPG groups replaced by metafounders (Matti Taskinen’s presentation)
• Residual polygenic proportion 30 %.

Development goals for MB evaluation model

• All animals included, also pedigree, genotypes, and observations of the F1 crosses.
• Logical differences between breeds in breeding values.
• High correlation within breed on EBVs between Multi- and Single Breed evaluations for purebred animals.
• Breed proportions of main breeds estimated for each animal
• For each animal, specific variance components based on individual's breed proportions were applied.
Changes compared to SB model

- Observations from F1 animals were included.
- Model of heterosis effects.
- Full Finnish pedigree instead of limited “beef pedigree” from routine evaluation.
  - Breed proportions of 5 main breeds and "other breeds" estimated from pedigree and rounded to closest quarter (25%).
    - SB model used sire’s breed as a breed of offspring.
- More accurate inbreeding coefficients, UPG (and MF) definitions include breed.
- Breed interaction in fixed effects.
Heterosis and recombination in the models

Heterosis

• **Total heterosis** (of the 7 breeds in the evaluation) and **heterosis coefficients** for the most common 10 breed crosses included in the model, 11 parameters for each trait.

Recombination

• After examining different alternatives we decided to include only the **total recombination loss** in to the model, i.e., 1 effect for each trait.

For all three evaluations, heterosis and recombination is modelled in the same way.
### Number of animals with observations and genotyped animals by breed

<table>
<thead>
<tr>
<th>Breed</th>
<th>Animals with at least one observation</th>
<th>Genotyped, n</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aberdeen Angus</td>
<td>59,973</td>
<td>3,796</td>
</tr>
<tr>
<td>Charolais</td>
<td>70,601</td>
<td>3,212</td>
</tr>
<tr>
<td>Hereford</td>
<td>108,865</td>
<td>3,917</td>
</tr>
<tr>
<td>Limousin</td>
<td>63,876</td>
<td>2,061</td>
</tr>
<tr>
<td>Simmental</td>
<td>37,227</td>
<td>2,363</td>
</tr>
<tr>
<td>OTHER/CROSS</td>
<td>206,019</td>
<td>2,145</td>
</tr>
<tr>
<td><strong>TOTAL</strong></td>
<td><strong>546,561</strong></td>
<td><strong>17,494</strong></td>
</tr>
</tbody>
</table>
Results

- **GEBVs** and standardised **indices** compared between breeds.
- **Reliabilities** ($R^2$) of GEBVs and EBVs compared between PBLUP and ssGBLUP for genotyped and non-genotyped animals.
- Validation results of MB PBLUP model and MB ssGBLUP model.

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Trends of GEBVs and indices for weight traits
Model $R^2$ for genotyped animals in PBLUP and ssGBLUP
Model $R^2$ for NON -genotyped animals in PBLUP and ssGBLUP
Validation

• For the validation results for 1 year data cut is presented.

• All observations of a validation animal were removed from the reduced data, if animal had at least one observation in data cut window.
  • I.e. if a slaughter weight was to be removed, also birth, weaning, and yearling weights were removed, even they were observed outside of the cut window.
  • => No own observations in reduced data.

• Validations separately for traditional EBV and single step models:
  • Full (G)EBV vs reduced (G)EBV, (Legarra-Reverter)
  • Full data YD vs reduced data (G)EBV. (cross validation)

• Results for bulls and cows together
Validations: correlations and accuracy, 1 year data cut, genotyped animals, PBLUP and ssGBLUP compared

<table>
<thead>
<tr>
<th>Breed</th>
<th>Birth weight</th>
<th>200-d weight</th>
<th>365-d weight</th>
<th>Slaughter weight</th>
<th>Europ carcass quality</th>
<th>Europ carcass fat</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>e bv</td>
<td>g bv</td>
<td>%</td>
<td>e bv</td>
<td>g bv</td>
<td>%</td>
</tr>
<tr>
<td>AAN</td>
<td>1103</td>
<td>0,70</td>
<td>0,82</td>
<td>17</td>
<td>1133</td>
<td>0,69</td>
</tr>
<tr>
<td>CHA</td>
<td>687</td>
<td>0,63</td>
<td>0,77</td>
<td>22</td>
<td>700</td>
<td>0,78</td>
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<tr>
<td>HER</td>
<td>937</td>
<td>0,74</td>
<td>0,88</td>
<td>19</td>
<td>844</td>
<td>0,66</td>
</tr>
<tr>
<td>LIM</td>
<td>297</td>
<td>0,70</td>
<td>0,80</td>
<td>14</td>
<td>297</td>
<td>0,54</td>
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<tr>
<td>SIM</td>
<td>647</td>
<td>0,83</td>
<td>0,89</td>
<td>7</td>
<td>647</td>
<td>0,78</td>
</tr>
</tbody>
</table>

Legarra-Reverter correlation of BV between full and reduced data, 1-year cut

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<tbody>
<tr>
<td>AAN</td>
<td>1103</td>
<td>0,35</td>
<td>0,39</td>
<td>11</td>
<td>633</td>
<td>0,38</td>
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<tr>
<td>CHA</td>
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<td>0,26</td>
<td>0,32</td>
<td>23</td>
<td>389</td>
<td>0,32</td>
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<tr>
<td>HER</td>
<td>937</td>
<td>0,39</td>
<td>0,51</td>
<td>31</td>
<td>646</td>
<td>0,27</td>
</tr>
<tr>
<td>LIM</td>
<td>292</td>
<td>0,28</td>
<td>0,33</td>
<td>18</td>
<td>142</td>
<td>0,1</td>
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<tr>
<td>SIM</td>
<td>643</td>
<td>0,47</td>
<td>0,49</td>
<td>4</td>
<td>304</td>
<td>0,35</td>
</tr>
</tbody>
</table>

Cross-validation correlation between full data YD and reduced data BV, 1-year cut
Conclusions and implementation

Reliabilities for genotyped animals clearly higher compared to non-genotyped.

• ssGBLUP model gave mainly the same or better validation results than PBLUP model.

• Also MF ssGBLUP slightly better than UPG ssGBLUP.

First official multi-breed ssGBLUP evaluations were published March 2023

• Published indices were standardized within breed.
References
