Introduction

- With no daughter’s record, why genomic (G) EBV for young genotyped bulls biased?
- Several possibilities: selection, missing pedigree, inaccurate pedigree, inaccurate genetic parameters, ... creating inconsistency between pedigree-base (A) and genomic (G) relationships?

Objectives

Investigate what causes bias or inflation in GEBV for young genotyped animals in dairy cattle

Materials and Methods

Simulation

- 50 × 5000 for 10 generations
- 60K SNP assuming 600 QTL
- 5 replicates
  - A) 20K genotyped animals in the last 4 generations
  - 30K phenotypes in all 10 generations
  - 40K animals in pedigree
  - Average inbreeding coefficient = 6.1%
  - top 10% and 50% in EBV from A and G, respectively, for mating
  - B) The same population structure as in A) with random selection average inbreeding coefficient = 1.4%
  - 50K genotyped animals and 30K phenotypes in all 10 generations
  - 55K animals in pedigree
  - Average inbreeding coefficient = 5.9%
  - top 10% and 50% in EBV from A and G, respectively, for mating
  - True breeding values (TBV) = b0 + b1 x GEBV (GEBV) with no phenotypes and with genotypes in generations 9 and 10
    - b0 > 0.0 → overestimation
    - b0 < 0.0 → underestimation
    - b1 < 0.0 → inflation
    - b1 > 1.0 → deflation

Linear type traits in US Holsteins

- Data for the national genetic evaluation in August 2014 from Holstein Association USA Inc. (Brattleboro, Vermont, USA).
- 100K records for 10K animals
- 60K SNP markers for 570K genotyped animals
- Daughter Yield Deviation (DYD) in 2014 = b0 + b1 x GEBV in 2010

(G)EBV for young genotypes bulls with no phenotypes in 2010

Single-step genomic mixed model

$$\begin{bmatrix} X'X & X'Z & \mu' \end{bmatrix} \begin{bmatrix} \beta \\ \rho \\ \delta \end{bmatrix} = \begin{bmatrix} Y' \end{bmatrix}$$

$$H^{-1} = \begin{bmatrix} \mu^{-1} & 0 \\ 0 & (\mu^{-1} - \omega A)^{-1} \end{bmatrix}$$

Results

Simulation

Bulls: regression coefficient (b0) on TBV = b0 + b1 x (G)EBV

<table>
<thead>
<tr>
<th>Sire’s generation</th>
<th>Inbreeding in A</th>
<th>No inbreeding in A</th>
<th>No dams</th>
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<tbody>
<tr>
<td>EBV GEBV</td>
<td>EBV GEBV</td>
<td>EBV GEBV</td>
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<td>BLUP selection with genotypes in the last 4 generations</td>
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<tr>
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<tr>
<td>BLUP selection with genotypes in all generations</td>
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<tr>
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<tr>
<td>8 1.00 0.81</td>
<td>1.00 0.66</td>
<td>0.99 0.79</td>
<td></td>
</tr>
</tbody>
</table>

Conclusions

- Selection = more genetic progress -> more inflation in genotypic predictions
- Inconsistency between A and G = more inflation
- To reduce the inflation:
  - 1true inbreeding in A
  - 2use smaller additive genetic variances or re-estimate variance components
  - 3use accurate pedigree information
  - 4adjust the weight (w<1.0) on A22

References