

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 ♂ x 5000 ♀ for 10 generations
- 60K SNP assuming 600 QTL
- 5 replicates
 - 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 ♂ and ♀, respectively, for mating
 - 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 ♂ and ♀, respectively, for mating
- True breeding values (TBV) = $b_0 + b_1 \times (G)EBV$
(G)EBV with no phenotypes and with genotypes in generations 9 and 10
 $b_0 > 0.0 \Rightarrow$ overestimation; $b_0 < 0.0 \Rightarrow$ underestimation
 $b_1 < 1.0 \Rightarrow$ inflation; $b_1 > 1.0 \Rightarrow$ deflation

Linear type traits in US Holsteins

- Data for the national genetic evaluation in August 2014 from *Holstein Association USA Inc. (Brattleboro, Vermont, USA)*.
10M records for 10M animals
60K SNP markers for 570K genotyped animals
- Daughter Yield Deviation (DYD) in 2014 = $b_0 + b_1 \times (G)EBV$ in 2010

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

Single-step genomic mixed model

$$\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \mathbf{H}^{-1}\boldsymbol{\alpha} \end{bmatrix} \begin{bmatrix} \mathbf{b} \\ \mathbf{a} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{bmatrix}$$

$$\mathbf{H}^{-1} = \begin{bmatrix} \mathbf{A}^{11} & \mathbf{A}^{12} \\ (\mathbf{A}^{12})' & \mathbf{A}^{22} \end{bmatrix} + \begin{bmatrix} 0 & 0 \\ 0 & (\mathbf{G}^{-1} - \omega\mathbf{A}_{22}^{-1}) \end{bmatrix}$$

Results

Simulation

Bulls: regression coefficient (b_1) on TBV = $b_0 + b_1 \times (G)EBV$

Sire's generation	Inbreeding in A		No inbreeding in A		No dams	
	EBV	GEBV	EBV	GEBV	EBV	GEBV
BLUP selection with genotypes in the last 4 generations						
All	-	0.96	-	0.83	-	0.94
10	-	0.80	-	0.64	-	0.78
9	0.98	0.79	0.92	0.65	-	0.75
8	0.98	0.76	0.96	0.62	0.93	0.63
No selection with genotypes in the last 4 generations						
All	-	0.88	1.03	0.88	-	0.85
10	-	0.87	1.08	0.86	-	0.89
9	1.02	0.83	1.03	0.83	0.96	0.84
8	1.00	0.89	1.01	0.88	1.00	0.87
BLUP selection with genotypes in all generations						
All	-	1.00	-	0.98	-	0.95
10	-	0.83	-	0.68	-	0.84
9	0.98	0.78	0.96	0.64	-	0.78
8	1.00	0.81	1.00	0.66	0.99	0.79

Cows: regression coefficient (b_1) on TBV = $b_0 + b_1 \times (G)EBV$

Cow's generation	Inbreeding in A		No inbreeding in A		No dams	
	EBV	GEBV	EBV	GEBV	EBV	GEBV
BLUP selection using genotypes in the last 4 generations						
All	-	1.00	-	0.89	-	0.99
10	-	0.96	-	0.84	-	0.94
9	1.04	0.95	1.01	0.83	-	0.93
8	1.00	0.81	0.98	0.66	0.94	0.70
No selection using genotypes in the last 4 generations						
All	1.02	0.97	1.02	0.96	-	0.94
10	1.03	1.00	1.04	0.98	-	0.99
9	1.04	1.01	1.06	1.00	1.01	1.00
8	1.01	0.92	1.03	0.91	0.99	0.90
BLUP selection using genotypes in all generations						
All	-	1.01	-	1.00	-	0.96
10	-	0.97	-	0.84	-	0.98
9	0.99	0.96	0.98	0.84	-	0.96
8	0.99	0.89	0.97	0.70	0.93	0.84

Linear type traits in US Holsteins

Bulls: regression coefficient (b_1) on DYD = $b_0 + b_1 \times (G)EBV$ sorted by genetic progress (GP)

Trait	Genetic progress	PA	No inbreeding	Inbreeding In A	Inbreeding UPG	V(a)=0.5	w=0.9
Rear udder height	2.39	0.70	0.74	0.79	0.82	0.85	0.92
Rear udder width	2.25	0.71	0.75	0.81	0.83	0.89	0.93
Fore udder attachment	2.08	0.68	0.78	0.83	0.87	0.91	0.98
Udder depth	1.61	0.72	0.86	0.87	0.94	0.96	1.05
Foot angle	1.43	0.72	0.74	0.80	0.86	0.87	0.98
Rear legs rear view	1.40	0.59	0.69	0.78	0.81	0.81	0.94
Feet & legs score	1.26	0.53	0.59	0.67	0.69	1.05	0.79
Udder cleft	1.24	0.87	0.82	0.84	0.93	0.98	1.06
Teat placement	1.09	0.82	0.85	0.87	0.94	0.93	1.05
Stature	1.06	0.79	0.84	0.86	0.91	0.95	0.99
R teat placement	1.05	0.92	0.89	0.96	1.00	0.99	1.13
Dairy form	0.96	0.78	0.85	0.87	0.93	1.00	1.01
Rump width	0.82	0.81	0.84	0.87	0.93	0.96	1.04
Strength	0.45	0.81	0.86	0.88	0.94	0.96	1.06
Body depth	0.43	0.79	0.83	0.86	0.90	0.93	0.99
Teat length	-0.34	0.80	0.85	0.88	0.93	1.00	1.04
Rear legs side view	-0.14	0.85	0.82	0.86	0.93	0.98	1.08
Rump angle	0.05	0.74	0.89	0.92	0.98	0.98	1.08
Mean	1.01	0.76	0.81	0.85	0.90	0.94	1.01
Correlation with GP	GP	-0.44	-0.47	-0.46	-0.49	-0.55	-0.50

Conclusions

- Selection = more genetic progress => more inflation in genomic predictions
- Inconsistency between A and G => more inflation
- To reduce the inflation:
 - 1)include inbreeding in A
 - 2)use smaller additive genetic variances or re-estimate variance components
 - 3)use accurate pedigree information
 - 4)adjust the weight ($\omega < 1.0$) on \mathbf{A}_{22}^{-1}

References

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