Reduction of bias in breeding values of bull dams for conformation traits

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Introduction

Breeding values for conformation traits are estimated with a linear animal model in the Netherlands. One of the assumptions is that estimated breeding values (EBV) are unbiased. For production traits the parent average (PA) of young bulls tested in the Netherlands is on average 0.5 standard deviation higher than the EBV, caused by a significant bias in EBV of bull dams (Van Steenbergen *et al.*, 2006). Several methods were used to reduce bias and the bias was reduced with 33% at most. Preferential treatment of bull dams or cow families is often suggested as important reason for the bias in EBV. Another issue could be that a genotype x environment interaction occurs, which makes that genetic effects measured for a cow and her family can partly be affected by this interaction. Within a superior cow family the EBVs of family members could be more susceptible to bias.

The objective of this study was to investigate the impact of the extra random effect cow family on the reduction in bias of EBVs of bull dams. In this study the breeding value estimation for conformations traits was taken as a test case.

Material and methods

A statistical analysis was performed to estimate cow family variances. With these resulting variances breeding value estimations were done to validate reduction of bias in EBVs.

Statistical analysis. The following linear animal model was used for genetic analysis:

$$y_{ijklmn} = \mu + HV_i + A_j + LS_k + animal_l + cowfam_m + error_{ijklmn}$$

Where y is the dependent variable and μ is the general mean. Herd x visit (HV; classifier visits the herd to score cows for conformation), age at classification (A) and lactation stage at classification (LS) are fixed effects. Animal and cow family (cowfam) are random effects. The animal effect included a complete pedigree structure. For the cow family an alternative pedigree structure was used. Only female relationships were used to build up the pedigree setting all sires to zero. Genetic parameters were estimated using the statistical package of ASReml (Gilmour *et al.*, 2006). Heritability and cow family heritability were calculated as:

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$$h^2 = \frac{\sigma^2_A}{\sigma^2_A + \sigma^2_E + \sigma^2_{cowfam}} \quad \text{and} \quad h^2_{cowfam} = \frac{\sigma^2_{cowfam}}{\sigma^2_A + \sigma^2_E + \sigma^2_{cowfam}}$$

Edits on data were set to get an informative data set with several generations of classified heifers to analyse the cow family effect. Conformation scores of herdbook registered cows with at least 87.5% Black and White Holstein-Friesian genes were used. Herds were selected if they had at least 15 herd visits over time with on average at least 15 cows classified per visit. On average a herd was visited every 8 months. This resulted in a data set with 108,339 classifications of heifers from cow families having 3-5 generations of data, based on scores of 5,042 herd visits and cows from 10,321sires.

Breeding value estimation. In total, 4,776,770 records of heifers classified until December 2009 were available for the breeding value estimation of conformation traits. Three different breeding value estimations with an extra random effect for cow family were compared with the official breeding value estimation of January 2010.

A. The official breeding value estimation of January 2010
B. A breeding value estimation including an extra random effect for cow family
   1. The average cow family heritability from the statistical analysis was used to derive cow family variances used in the breeding value estimation. For the cow family effect the relationship matrix included only female relationships.
   2. The average cow family heritability used in B1 was tripled to derive cow family variances. For the cow family effect the relationship matrix included only female relationships.
   3. The average cow family heritability used in B1 was used to derive cow family variances. For the cow family effect the relationship matrix included female relationships for both parents.

EBVs were expressed with an average of 100 and a genetic standard deviation of 4.47 points.

Validation. Bias in bull dam proofs can be computed as the difference between PA of a young bull and EBV of this bull based on daughter performance. This bias is due to overestimation of the bull dam and not the sire (Van Steenbergen *et al.*, 2006). Bias in the PA of young bulls was computed as the comparison of Mendelian sampling (MS = PA - EBV) terms of the BVEs of one of the methods with the MS-term of the official EBV. In an unbiased situation the average MS term is zero. Validation of methods was based on EBVs of 1,331 Holstein bulls (≥87.5% Holstein-Friesian), born between 1999 and 2003, having a dam with Dutch identification number, and having a reliability of at least 75% for overall conformation. The restriction on reliability was imposed to ensure adequate accuracy of the EBV and guarantee that the effect of the dam on the EBV was minimal. The validation was performed for all conformation traits.

The correlations of the official breeding values with the breeding values estimated with each of the three methods were compared and should be close to unity for bull EBVs.

Results and discussion

Heritability estimates. Estimated genetic parameters are shown in table 1. Heritabilities are comparable with heritabilities used in the official Dutch breeding value estimation for conformation traits (CRV, 2009). The average cow family heritability is 0.05 ± 0.02. Compared with the statistical model in the official breeding value estimation it is possible to explain 5% of the phenotypic variance by including the random cow family effect.

Table 1. Genetic variance, cow family variance, residual variance, heritability (h^2) and cow family heritability (h^2_{cowfam}) for conformation traits

Trait	genetic	cow family	residual	h^2	h^2_{cowfam}
udder composite	35.49	3.49	57.71	0.367	0.036
feet and legs	14.62	4.35	73.38	0.158	0.047
stature	7.68	0.98	3.83	0.615	0.079
chest width	27.53	2.45	62.16	0.299	0.027
body depth	31.45	2.79	58.09	0.341	0.030
angularity	26.34	2.84	67.91	0.271	0.029
body condition score	33.23	3.05	57.23	0.355	0.033
rump angle	42.06	4.03	53.01	0.424	0.041
rump width	35.37	4.20	52.63	0.384	0.046
rear legs rear view	13.59	4.84	74.83	0.146	0.052
rear legs side view	14.58	3.17	87.85	0.138	0.030
foot angle	15.35	4.12	74.46	0.163	0.044
locomotion	9.24	6.60	77.63	0.099	0.071
fore udder attachment	28.81	7.11	63.53	0.290	0.071
front teat placement	42.26	3.46	52.61	0.430	0.035
teat length	36.10	9.92	49.94	0.376	0.103
udder depth	41.33	6.52	48.34	0.430	0.068
rear udder height	28.23	4.15	61.53	0.301	0.044
central ligament	23.93	5.82	63.82	0.256	0.062
rear teat placement	35.61	5.80	51.66	0.383	0.062

Validation. For the breeding value estimations B1 and B3 the average cow family heritability (0.05) was used to derive the cow family variances and for the breeding value estimation B2 0.15 was used. In Table 2 the results of reduction of bias are shown. Expressed in absolute genetic standard deviations the bias in the official run ranges from 0.01 to 0.18 standard deviation. Compared to production traits the bias for conformation traits is much smaller. Rear legs rear view, central ligament and rear teat placement have an underestimation of the PA instead of an overestimation. With breeding value estimation B1 15 out of 20 traits show a reduction in bias, with B2 16 traits and with B3 all traits have a reduction of the bias. The average reduction for the traits with a reduction in bias is 6% for B1, 11% for B2 and 14% for B3. Within birthyears reduction of bias is more extreme. However, on birthyear level bias varies more. The reduction of bias expressed in genetic standard deviations is up to 1% for B1 and up to 3% for B2 and B3 for udder composite.

The correlation between breeding value estimation A and B is higher than 0.995 for all conformation traits for all three methods and for sires with heifers scored in at least ten herds. Ranking of sires is not affected by including a random cow family effect in the breeding value estimation.

Table 2. Bias (parent average minus breeding value) in points EBV for conformation traits from the official breeding value estimation and three alternative methods (B1, B2 and B3) and the reduction in bias (% red.) compared to the official breeding value estimation.

	Official	B1 - cowfam 5%		B2 - cowfam 15%		B3 - 2 x cowfam	
Trait	PA-BV	PA-BV	% red.	PA-BV	% red.	PA-BV	% red.
udder composite	0.49	0.46	-5%	0.43	-13%	0.40	-19%
feet and legs	0.61	0.57	-5%	0.53	-12%	0.51	-16%
stature	0.82	0.76	-8%	0.70	-15%	0.70	-15%
chest width	0.36	0.34	-4%	0.35	-3%	0.30	-15%
body depth	0.39	0.39	0%	0.38	-1%	0.32	-17%
angularity	0.25	0.23	-6%	0.20	-20%	0.19	-23%
body condition score	0.05	0.04	-2%	0.08	74%	0.04	-14%
rump angle	0.05	0.06	18%	0.07	36%	0.04	-11%
rump width	0.23	0.22	-8%	0.21	-11%	0.19	-19%
rear legs rear view	0.29	0.29	1%	0.28	-1%	0.25	-11%
rear legs side view	-0.50	-0.50	-2%	-0.48	-4%	-0.47	-7%
foot angle	0.37	0.38	1%	0.38	3%	0.36	-5%
locomotion	0.51	0.50	-3%	0.48	-7%	0.45	-13%
fore udder attachment	0.41	0.40	-1%	0.39	-5%	0.34	-17%
front teat placement	0.08	0.08	8%	0.09	14%	0.06	-19%
teat length	0.19	0.18	-5%	0.18	-6%	0.18	-7%
udder depth	0.48	0.47	-2%	0.45	-6%	0.40	-16%
rear udder height	0.46	0.46	-1%	0.44	-4%	0.42	-9%
central ligament	-0.15	-0.12	-20%	-0.10	-35%	-0.12	-20%
rear teat placement	-0.19	-0.16	-16%	-0.13	-31%	-0.16	-17%

* 1 genetic SD is 4.47 points EBV

Conclusions

Cow family explains about 5% of the phenotypic variance. Including a random cow family effect in the breeding value estimation results in a reduced bias, but is limited to 23% at most for overestimated PAs. The method used in this study is the lower bound of the possible reduction of the bias because PA and EBV are from the same breeding value estimation. Therefore the dam BVEs are already adjusted for progeny information of the sire. Parent averages from historical runs should be used to estimate the bias in a more correct way.

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