

ESTIMATES OF VARIANCES DUE TO SIRE \times HERD EFFECTS FOR WEIGHTS OF HEREFORD CATTLE

Karin Meyer

Animal Genetics and Breeding Unit¹, University of New England, Armidale, NSW 2351

SUMMARY

Estimating variances due sire \times herd effects requires a large number of sires to be represented in multiple herds, otherwise too much variation between animals is 'picked up' as variance due to sire \times herd effects, and heritability estimates are biased downwards. Such bias can be avoided by using only records for progeny of multiple-herd use sires to estimate the additive genetic variance. Estimates of variance components and genetic parameters from analyses of weights of Hereford cattle are presented for herds with high, medium and low proportions of sires used across multiple herds. Results from analyses estimating separate genetic variances for progeny of single and multiple herd sires, estimating a joint genetic variance for all animals, and ignoring sire \times herd effects are compared.

Keywords : Sire \times herd effects, variance components, weight, beef cattle

INTRODUCTION

Genetic evaluation schemes for beef cattle, such as BREEDPLAN, routinely fit sire \times herd (S \times H) interactions as random effects in the model of analysis (Graser *et al.*, 1999). This allows for covariances between progeny of a sire in a given herd, which causes them to have records more similar than expected from their genetic relationships. A problem in genetic evaluation of beef cattle is the accurate definition of contemporary groups. Usually this requires recording of paddocks or management groups. If cows remain in similar groups to those at mating, weaning weights of calves by a given bull tend to show more resemblance than genetically determined, due to group or paddock effects. If group codes are then not recorded, estimates of genetic differences between animals are likely to be biased by unrecognised, systematic group effects. Fitting random S \times H effects can reduce such bias. To estimate variances due to S \times H effects, we need records on progeny of sires used in multiple herds, i.e. bulls used via artificial insemination (AI). If sires and herds are confounded, as for most natural service sires, we cannot partition the variance between sires into its components due to additive genetic and S \times H effects. For most field data, however, a large proportion of records pertains to progeny of single herd sires. Disregarding the latter and using only records of progeny of AI sires would result in markedly fewer records and poor data structure. This paper shows how bias in estimates of genetic variances can be avoided by using only the variation between progeny of multiple herd sires, while still utilising all data to estimate fixed and other random effects in the model of analysis, for weights of Hereford cattle.

MATERIAL AND METHODS

Data. Records for birth (BW), weaning (WW), yearling (YW) and final (FW) weight for Australian Hereford and Polled Hereford cattle were extracted from the National Beef Recording Scheme data base. Ages at recording allowed were 80 to 300 days for WW, 301 to 500 days for YW, and 501 to 700 days for FW. After basic editing, subsets of the data were formed according to the proportion of AI usage. Firstly, herds with high, medium and low proportions of animals which were progeny

¹AGBU is a joint venture of NSW Agriculture and UNE

Table 1. Characteristics of the data structure

AI level	Birth Weight			Weaning Weight			Yearling Weight			Final Weight	
	low	medium	high	low	medium	high	low	medium	high	low	high
No. records	34679	32838	37265	62758	70651	58119	49693	54709	38563	42639	42194
... AI (%)	16.7	30.2	55.3	19.0	35.4	55.2	18.1	34.2	56.7	28.9	59.2
No. animals ^A	60467	57651	71089	101124	106440	95040	88103	95611	73514	85271	81467
... "T1" ^B (%)	52.2	60.2	76.6	49.8	57.1	72.6	50.4	62.4	77.3	64.4	78.9
Mean (kg)	37.5	37.6	37.9	224.3	225.5	236.0	331.7	343.4	364.0	465.9	491.2
SD (kg)	5.8	5.6	5.3	52.8	54.7	55.5	76.6	82.6	88.1	108.6	119.9
No. herds	65	75	119	85	73	101	91	90	100	110	112
No. CG ^C	3056	3263	3698	6262	6506	5418	3805	4020	3311	3536	3345
No. S×H ^D	2074	2107	2569	3291	3967	3548	3275	3883	3242	3857	3668
... for AI sires	384	600	1227	758	1243	1690	750	1196	1555	1071	1721
No. sires ^E	1834	1732	1763	2805	3182	2440	2780	3123	2208	3170	2547
... AI (%)	144	225	421	272	458	582	255	436	521	384	600
No. dams ^E	16570	15312	20966	27147	29145	27265	23458	26244	21237	23295	23851

^Aincluding parents without records, ^Bsee text, ^Ccontemporary groups, ^Dsire × herd effects, ^Ewith progeny in the data

of AI sires were identified. Records were then extracted for each set of herds, eliminating any herds which, in the subset, did not have progeny of AI sires any longer, and records in contemporary group subclasses of size less than 3. Two loops through the pedigree were performed to obtain additional pedigree information. Characteristics of the data structure are summarised in Table 1.

Modelling heterogeneous genetic variances. Let \mathbf{a} be the vector of additive genetic effects for all animals in a mixed model, with \mathbf{A} the numerator relationship and σ_A^2 the additive genetic variance, i.e. $V(\mathbf{a}) = \sigma_A^2 \mathbf{A}$. Consider the Cholesky factorisation $\mathbf{A} = \mathbf{L}\mathbf{D}\mathbf{L}'$, with \mathbf{L} a lower triangular matrix and \mathbf{D} a diagonal matrix. This can be extended to model heterogeneous genetic variances, as described by Visscher and Thompson (1992). Assume we have g groups of animals with different genetic variance, and let \mathbf{a} , \mathbf{L} and \mathbf{D} be partitioned accordingly. For $g = 2$,

$$\mathbf{A} = \begin{pmatrix} \mathbf{L}_{11} & \mathbf{0} \\ \mathbf{L}_{21} & \mathbf{L}_{22} \end{pmatrix} \begin{pmatrix} \mathbf{D}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{D}_2 \end{pmatrix} \begin{pmatrix} \mathbf{L}'_{11} & \mathbf{L}'_{21} \\ \mathbf{0} & \mathbf{L}'_{22} \end{pmatrix} = \mathbf{A}_1 + \mathbf{A}_2 \quad (1)$$

$$\text{with } \mathbf{A}_1 = \begin{pmatrix} \mathbf{L}_{11}\mathbf{D}_1\mathbf{L}'_{11} & \mathbf{L}_{11}\mathbf{D}_1\mathbf{L}'_{21} \\ \mathbf{L}_{21}\mathbf{D}_1\mathbf{L}'_{11} & \mathbf{L}_{21}\mathbf{D}_1\mathbf{L}'_{21} \end{pmatrix} \quad \mathbf{A}_2 = \begin{pmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{L}_{22}\mathbf{D}_2\mathbf{L}'_{22} \end{pmatrix} \quad (2)$$

$$\text{and } V(\mathbf{a}) = \sum_{i=1}^g \sigma_{A_i}^2 \mathbf{A}_i = \sigma_{A_1}^2 \mathbf{A}_1 + \sigma_{A_2}^2 \mathbf{A}_2 \quad (3)$$

Analyses. Estimates of variance components were obtained by restricted maximum likelihood. Fixed effects fitted included contemporary groups (CG), defined as herd-sex-management group-date of weighing subclasses (month of weighing for BW), a birth type effect, and the so-called "heifer factor", i.e. an age of dam class (heifer ≤ 28 , cows > 28 months). Dam age was fitted as a linear and quadratic covariable, and age at weighing as a linear covariable (except for BW), nested within sex. Random effects were direct genetic, maternal genetic, maternal permanent environmental and S×H effects. Three

analyses were carried out for each data set. Analyses A distinguished between animals which were progeny of multiple herd (“T1”) and single herd (“T2”) sires, and estimated different genetic variances for the two groups. Parents without records were considered to be “T1”. Only estimates of σ_{A1}^2 were used in calculating phenotypic variances and estimates of the direct heritability, as estimates of σ_{A2}^2 were expected to be biased. Analyses B estimated a single σ_A^2 using information from all animals, and analyses C omitted S×H effects from the analysis, estimating a single σ_A^2 .

RESULTS AND DISCUSSION

Estimates of variance components and genetic parameters are summarised in Table 2. Analyses A yielded consistently higher estimates of σ_{A1}^2 and h^2 than B, suggesting that \hat{h}^2 from analyses B were biased downwards due to S×H effects ‘picking up’ part of the variance between animals due to confounding of sires and herds. As expected, the discrepancy in estimates tended to increase with decreasing proportion of AI progeny, especially for WW and YW. Conversely, estimates of h^2 from analyses C were generally highest, indicating that estimates were biased upwards when S×H effects were not taken into account. Estimates of the proportion of variance due to S×H effects (s^2) ranged from 2 to almost 7%, and were on average only slightly higher for analyses B than A. Values for s^2 were highest for BW. Estimates of σ_{A2}^2 for two of the three data sets for BW were only somewhat smaller than estimates of σ_{A1}^2 (analyses A), suggesting that this trait was least affected by problems of mispartitioning of the between animal variances. Estimates of σ_{A2}^2 for WW and YW were close to zero (except for medium AI use for YW), indicating a data structure which allowed almost all variation between progeny of single herd sires to be interpreted as variance due to S×H effects. Estimates of σ_{A2}^2 for FW were considerably less affected, presumably because animals are likely to be regrouped at some time after weaning which would reduce the association between sire progeny groups and CG.

Estimates of maternal genetic variances and maternal heritabilities (m^2) showed some tendency for estimates to be highest for analyses C and smallest for analyses A. However, differences were small and no particular trend was expected. Similarly, the proportion of variance due to maternal, permanent environmental effects (c^2) differed little between analyses. Residual variances were consistently lowest for analyses C. Except for BW in herds with low AI use, analyses A yielded a significant increase in log likelihood for all data sets. In all cases log likelihoods for analyses B were substantially higher than for analyses C, i.e. estimates of s^2 were significantly different from zero.

CONCLUSIONS

Analyses highlighted problems of the data structure inherent for field records for beef cattle for analyses fitting a S×H effect. It was shown that a model utilising only the variation between progeny of multiple herd sires to estimate genetic variances yielded higher estimates than conventional analyses considering all animals. This was attributed to estimates from the latter being biased as too much variation was ‘picked up’ by S×H effects, for single herd sires or if sire progeny groups and contemporary groups were confounded. On the whole, estimates of genetic parameters were similar to those from comparable studies. Estimates of c^2 for WW ranged from 20 to 26%, emphasizing the importance of maternal effects for Hereford cattle, while h^2 values for WW ranged from 11 to 15%, which is somewhat lower than reported for most other breeds.

REFERENCES

- Graser, H.-U., Johnston, D. J. and Tier, B. (1999) *Proc. Ass. Advan. Anim. Breed. Genet.* **13**:197–198.
 Visscher, P. M. and Thompson, R. (1992) *Anim. Sci.* **55**:315–320.

Table 2. Estimates of variance components^A (kg²) and genetic parameters^B for analyses fitting separate genetic variances for progeny of multiple- and single-herd sires (A), a single genetic variance (B) and omitting sire × herd effects (C), together with corresponding log likelihood (log \mathcal{L}).

	Model	σ_{A1}^2	σ_{A2}^2	σ_M^2	σ_S^2	σ_C^2	σ_E^2	σ_P^2	h^2	m^2	s^2	c^2	log \mathcal{L}	
BW	low	A	7.10	6.82	1.26	0.85	0.76	8.72	18.69	0.380	0.068	0.045	0.041	0
		B	6.98		1.26	0.86	0.77	8.67	18.54	0.377	0.068	0.046	0.042	-0.2
		C	8.03		1.39		0.67	8.28	18.36	0.437	0.076		0.037	-36.3
	medium	A	7.31	6.16	1.15	0.78	0.67	8.33	18.25	0.401	0.063	0.043	0.037	0
		B	6.87		1.17	0.82	0.68	8.17	17.71	0.388	0.066	0.046	0.038	-3.5
		C	7.84		1.27		0.59	7.83	17.53	0.447	0.073		0.034	-39.3
	high	A	5.41	1.82	0.98	1.07	0.38	10.00	17.85	0.303	0.055	0.060	0.022	0
		B	4.75		1.03	1.11	0.43	9.52	16.84	0.282	0.061	0.066	0.026	-39.5
		C	5.77		1.21		0.31	9.21	16.50	0.350	0.073		0.019	-128.8
WW	low	A	76.2	0.0	51.2	25.4	165.7	361.8	680.4	0.112	0.075	0.037	0.244	0
		B	48.3		55.0	22.4	165.7	346.7	638.2	0.076	0.086	0.035	0.260	-40.5
		C	92.6		51.6		164.4	328.7	637.3	0.145	0.081		0.258	-114.7
	medium	A	106.6	0.0	68.8	12.8	145.6	384.5	718.3	0.148	0.096	0.018	0.203	0
		B	67.6		70.1	16.1	146.8	371.2	671.9	0.101	0.104	0.024	0.219	-82.6
		C	96.8		72.1		144.7	359.7	673.3	0.144	0.107		0.215	-135.9
	high	A	82.8	0.7	67.9	17.8	170.5	381.2	719.4	0.115	0.093	0.025	0.237	0
		B	70.2		69.3	18.3	171.4	368.2	697.3	0.101	0.099	0.026	0.246	-26.2
		C	101.1		70.9		169.1	356.4	697.5	0.145	0.102		0.243	-69.2
YW	low	A	224.0	0.0	37.4	38.0	126.2	633.3	1058.9	0.212	0.035	0.036	0.119	0
		B	159.9		37.3	41.6	128.8	576.3	944.1	0.169	0.040	0.044	0.137	-73.8
		C	221.3		46.2		121.0	551.9	940.4	0.235	0.049		0.129	-143.7
	medium	A	198.1	55.0	53.0	30.3	113.2	687.8	1082.3	0.183	0.049	0.028	0.105	0
		B	176.0		52.9	32.4	112.5	653.6	1027.4	0.171	0.052	0.032	0.110	-24.2
		C	227.2		55.4		108.2	634.5	1025.2	0.222	0.054		0.106	-73.4
	high	A	236.8	0.0	46.4	45.1	147.9	746.8	1223.1	0.194	0.038	0.037	0.121	0
		B	192.1		49.7	47.2	150.2	719.1	1158.4	0.166	0.043	0.041	0.130	-46.4
		C	254.8		55.8		144.1	697.9	1152.5	0.221	0.048		0.125	-91.9
FW	low	A	384.0	250.3	45.8	46.0	67.4	838.9	1382.1	0.278	0.033	0.033	0.049	0
		B	354.0		47.2	48.1	67.6	808.6	1325.5	0.267	0.036	0.036	0.051	-9.2
		C	407.4		52.7		60.8	794.3	1315.1	0.310	0.040		0.046	-50.4
	high	A	352.5	139.3	67.7	43.4	83.8	1016.7	1564.0	0.225	0.043	0.028	0.054	0
		B	321.2		70.2	45.8	84.0	990.2	1511.4	0.213	0.046	0.030	0.055	-17.6
		C	379.9		75.7		77.3	972.7	1505.6	0.252	0.050		0.051	-50.9

^A σ_{A1}^2 and σ_{A2}^2 : direct additive genetic for “T1” and “T2” animals, resp., σ_M^2 : maternal, additive genetic, σ_S^2 : due to sire × herd effects, σ_C^2 : maternal, permanent environmental, σ_E^2 : residual, and σ_P^2 : phenotypic, ^B h^2 and m^2 : direct and maternal heritability, s^2 and c^2 proportion of variance due to sire × herd effects and maternal, permanent environmental effects