

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

Karin Meyer

Animal Genetics and Breeding Unit<sup>1</sup>, 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 multiple herd use sires. 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 edits, subsets of the data were formed according to the proportion of AI usage. First, herds with high, medium and low proportions of animals which were progeny of AI sires were

<sup>1</sup>AGBU 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	34,679	32,838	37,265	62,758	70,651	58,119	49,693	54,709	38,563	42,639	42,194
... 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 <sup>A</sup>	60,467	57,651	71,089	101,124	106,440	95,040	88,103	95,611	73,514	85,271	81,467
... "T1" (%)	52.2	60.2	76.6	49.8	57.1	72.6	50.4	62.4	77.3	64.4	78.9
Mean (kg)	37.46	37.60	37.95	224.3	225.5	236.0	331.7	343.4	364.0	465.9	491.2
SD (kg)	5.78	5.62	5.25	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 <sup>B</sup>	3056	3263	3698	6262	6506	5418	3805	4020	3311	3536	3345
No. S×H <sup>C</sup>	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 <sup>D</sup>	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 <sup>D</sup>	16,570	15,312	20,966	27,147	29,145	27,265	23,458	26,244	21,237	23,295	23,851

<sup>A</sup>including parents without records, <sup>B</sup>contemporary groups, <sup>C</sup>sire × herd effects, <sup>D</sup>with progeny in the data

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  $\sigma_A^2$  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  $\leq 28$ , 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  $\sigma_{A1}^2$  were used in calculating phenotypic variances and estimates of the direct heritability, as estimates of  $\sigma_{A2}^2$  were expected to be biased. Analyses B estimated a single  $\sigma_A^2$  using information from all animals, and analyses C omitted S×H effects from the analysis, estimating a single  $\sigma_A^2$ .

## RESULTS AND DISCUSSION

Estimates of variance components and genetic parameters are summarised in Table 2. Analyses A were yielded consistently higher estimates of  $\sigma_{A1}^2$  and  $h^2$  than B, suggesting that  $h^2$  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  $\sigma_{A2}^2$  for two of the three data sets for BW were only somewhat smaller than estimates of  $\sigma_{A1}^2$  (analyses A), suggesting that this trait was least affected by problems of mispartitioning of the between animal variances. Estimates of  $\sigma_{A2}^2$  for WW and YW were close to zero (except for medium AI se 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  $\sigma_{A2}^2$  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<sup>A</sup> (kg<sup>2</sup>) and genetic parameters<sup>B</sup> 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	$\sigma_{A1}^2$	$\sigma_{A2}^2$	$\sigma_M^2$	$\sigma_S^2$	$\sigma_C^2$	$\sigma_E^2$	$\sigma_P^2$	$h^2$	$m^2$	$s^2$	$c^2$	log $\mathcal{L}$	
BW	20–40	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
	40–60	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
	60 +	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	30–45	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
	45–60	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
	60 +	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	20–40	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
	40–60	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
	60 +	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	25–50	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
	50 +	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

<sup>A</sup> $\sigma_{A1}^2$  and  $\sigma_{A2}^2$  : direct additive genetic for “T1” and “T2” animals, resp.,  $\sigma_M^2$  : maternal, additive genetic,  $\sigma_S^2$  : due to sire × herd effects,  $\sigma_C^2$  : maternal, permanent environmental,  $\sigma_E^2$  : residual, and  $\sigma_P^2$  : phenotypic, <sup>B</sup> $h^2$  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