

## HETEROGENEOUS VARIANCES BY SEX AND SIRE BREED IN 200- AND 365-d WEIGHTS OF CALVES FROM HEREFORD AND ANGUS DAMS

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### SUMMARY

Calculation of EPD's from crossbreeding programs may be biased if heterogeneity of variance exists and is not accounted for. Records of weaning and yearling weights of  $F_1$  calves sired by bulls of 22 breeds evaluated in a top cross experiment were used to investigate the nature of heterogeneity of variance caused by sex and sire breed on these traits. Variances were different ( $P < .02$ ) in scale but not as fractions of the phenotypic variance ( $P > .10$ ) according to sex and sire breed subclasses. Adjustments for differences in scale of phenotypic variances are recommended.

### INTRODUCTION

Procedures for using EPD's in crossbreeding programs for beef cattle (Notter, 1989; Cundiff, 1994) and for predicting EPD's for crossbred animals (Arnold et al., 1992; Arnold and Golden, 1994) have been presented. Garrick et al. (1989) showed that heterogeneity of variances can exist in beef cattle according to breed composition and sex, which could result in reranking of animals to be selected if no adjustments are applied (Garrick et al., 1989; Núñez-Domínguez et al., 1994), with the result that genetic progress could be reduced (Vinson, 1987).

The objective of this study was to investigate the nature of heterogeneity of variance caused by sex and sire breed in 200- (WW) and 365-d (YW) weights of calves from Hereford (H) and Angus (A) dams sired by bulls of 22 breeds.

### MATERIALS AND METHODS

Records of progeny from 673 and 672 sires for WW and YW, respectively, from 22 of the breeds that have been evaluated in the Germ Plasm Evaluation Program at the Roman L. Hruska U.S. Meat Animal Research Center (MARC), Clay Center, NE, were used. All calves were out of Hereford or Angus dams. Weaning ( $n=7829$ ) and yearling ( $n=7367$ ) weights were preadjusted to 200 and 365 d of age, respectively.

Because few records were available ( $<330$ ) for some of the sire breeds, a sample of data for seven sire breeds with most of the records (4440 and 4164, for WW and YW, respectively) was used to investigate heterogeneity of variance due to sire breed subclasses (H, A, Charolais, Limousin, Simmental, Gelbvieh and Pinzgauer). Three multivariate sire and dam models with records of animals of the four combinations of sex (male, female) and breed of dam (H,A) considered different traits and differing in variance-covariance structure were fitted: model 1), all (co)variances were assumed to be the same for all sire breeds; model 2), all (co)variances as fractions of phenotypic variance ( $\sigma_p^2$ ) were assumed to be the same for all sire breeds, but  $\sigma_p^2$  was assumed to be different for each sire breed; and model 3), all (co)variances were assumed to be different for each sire breed, except that (co)variances corresponding to dam effects were estimated in common for all sire breeds. Model 3 was considered because within a sire breed only a few cows had more than one progeny,

but the number of cows with more than one progeny with records was large enough to estimate the dam component when putting data together for all sire breeds. The three models included fixed effects due to genetic group of sire, birth year of calf and age of dam both within sire breed, and heterosis as a covariate (0=purebred, 1=crossbred). According to likelihood ratio tests (Dobson, 1990), (co)variances differed ( $P < .001$ ) in scale, but not as fractions of phenotypic variance ( $P > .10$ ) by sire breed subclass.

Thus, to examine heterogeneity of variance due to sex all data corresponding to the 22 sire breeds was used. Three models were used. For model 4), measurements on both sexes were considered to be the same trait, and only measurements by breed of dam (H,A) were treated as different traits. Sex was fitted as a fixed effect. For model 5), each combination of sex (male, female) and breed of dam (H,A) was considered as a different trait, except that variance components as fractions of  $\sigma_p^2$  were assumed to be the same for both sexes within each breed of dam, with correlations between sexes assumed to be unity. Phenotypic variances were assumed to be different. For model 6), measurements for each sex-breed of dam combination were treated as different traits with different variances and correlations different from unity. For these three models, fixed effects were the same as for the first three models, but heterosis effects for *Bos taurus* x *Bos taurus* and for *Bos indicus* x *Bos taurus* crosses were fitted as separate covariates. Likelihood ratio tests (Dobson, 1990) were used to compare models.

## RESULTS

Table 1 shows the values of the likelihood ratio tests obtained from comparing the different models. Variances differed ( $P < .02$ ) in scale, but not as fractions of the phenotypic variance ( $P > .10$ ) by sire breed and sex subclasses for both WW and YW.

Table 1. Likelihood ratio tests (LRT) of comparisons between models [1], [2] and [3], and between models [4], [5] and [6] used to analyze 200-d and 365-d weights

Models for comparison	Ho:	df	200-d weight		365-d weight	
			LRT	P	LRT	pa
[2] vs [3]	Fractions of $\sigma_p^2$ : equal for all breeds	60	27.6	.9999	39.6	.9809
[1] vs [2]	Scales: equal for all breeds	24	57.7	.0001	42.7	.0109
[5] vs [6]	Fractions of $\sigma_p^2$ : equal for both sexes	9	3.2	.9558	4.0	.9114
[4] vs [5]	Scales: equal for both sexes	4	77.0	.0000	223.7	.0000

$$^a p = P(\chi^2 > \text{LRT} \mid \text{Ho is true})$$

A combined estimate of  $\sigma_p^2$  was obtained from the sample data set for the seven sire breeds and both sexes together, but with measurements from different breeds of dam considered different

traits, using model 4. Then, ratios of phenotypic standard deviations with respect to specific phenotypic standard deviations for each sire breed-sex-dam breed combination obtained by fitting model 3 were calculated and are shown in Table 2. In general, phenotypic standard deviations for males were larger than for females, and also, were larger for the heavier breeds (Charolais, Gelbvieh and Pinzgauer) than for the other four breeds, with more accentuated differences for YW than for WW.

Table 2. Pooled estimate of the phenotypic standard deviation ( $\sigma_p$ ) from analysis of seven breeds and both sexes within each breed of dam (H,A) divided by estimates of  $\sigma_p$  for each sire breed-sex-dam breed combination for 200-d and 365-d weights

Sire breed	200-d weight				365-d weight			
	H dams		A dams		H dams		A dams	
	Male	Female	Male	Female	Male	Female	Male	Female
Hereford	1.00	1.04	1.02	1.10	.97	1.09	.95	1.20
Angus	1.07	1.01	.96	1.23	1.05	1.14	.94	1.22
Charolais	.88	1.03	.89	.89	.84	1.14	.84	1.20
Gelbvieh	.89	.88	1.04	1.09	.87	.95	1.00	1.34
Pinzgauer	.81	1.05	.97	1.05	.79	1.28	.84	1.06
Simmental	1.09	1.15	.89	1.12	1.02	1.09	.90	1.24
Limousin	1.08	1.37	.93	1.04	1.02	1.58	.99	1.30

Pooled estimates of (co)variance components over 22 breeds of sires, obtained with model 6, are in Table 3. Estimated variances as fractions of  $\sigma_p^2$  were similar for males and females. From estimates for sire components, estimated heritabilities were .20 and .28 for WW of both male and female calves from H and A dams, respectively. For YW, estimates of heritabilities were .44 and .52 for males and .40 and .56 for females from H and A dams, respectively. Most of correlation estimates between sire effects on male and female calves from H and A dams were close to unity, with the lowest correlation estimates between sire effects on male calves from H dams and female calves from A dams (.84 and .86 for WW and YW, respectively). Correlation estimates of approximately unity were obtained in all cases for dam effects on weights of male and female calves.

#### DISCUSSION

Direct additive genetic variances as proportions of  $\sigma_p^2$  for WW and YW appear to be similar for different breeds of beef cattle of the *Bos taurus* type. These results agree with heritability estimates that are being used for National Cattle Evaluations in the U.S. (Personal communications, Drs. E. J. Pollak and J. K. Bertrand). However, this assumption may not be adequate for variance components due to maternal genetic and permanent environmental effects, which could not be investigated in the present study.

As indicated by correlation estimates, expression of sire additive genetic effects may not be different on male and female calves from Hereford or Angus cows. If true, this result would eliminate the need to treat them as different traits, which, in turn, simplifies the model and reduces the number of parameters to be estimated. The results suggest adjustments are needed for differences in scale of phenotypic variances according to sire breed and sex subclasses when calculating EPD's from crossbred data.

Table 3. Pooled estimates over breeds of sire, for variances as fractions of the phenotypic variance ( $\sigma_p^2$ ) for sire (dam) effects (diagonal), and correlations between sire (below diagonal) and dam (above diagonal) effects on expression of 200- and 365-d weights of male (M) and female (F) calves out of Hereford (H) and Angus (A) dams.

Trait	Dam breed-Sex	H-M	H-F	A-M	A-F	$\sigma_p^2$ <sup>a</sup>
200-d weight	H-M	.05(.45)	1.00	—	—	2667
	H-F	.95	.05(.39)	—	—	2278
	A-M	.91	.99	.07(.34)	1.00	2376
	A-F	.84	.96	.99	.07(.35)	1972
365-d weight	H-M	.11(.27)	1.00	—	—	6255
	H-F	.93	.10(.28)	—	—	4209
	A-M	.94	.97	.13(.22)	1.00	6131
	A-F	.86	.97	.88	.14(.23)	3833

<sup>a</sup>Phenotypic variance given in lb<sup>2</sup>.

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