

Effect of Heterogeneous Variance by Sex and Genotypes by Sex Interaction on EBVs of Postweaning Daily Gain of Angus Calves

T. Oikawa*, K. Hammond¹ and B. Tier

Animal Genetics and Breeding Unit², University of New England, Armidale, NSW 2351, Australia

ABSTRACT : Angus postweaning daily gain (PWDG) was analyzed to investigate effects of the heterogeneous variance and the genotypes by sex interaction on prediction of EBVs with data sets of various environmental levels. A whole data (16,239 records) was divided into six data sets according to averages of the best linear unbiased estimator (BLUE) of herd environment. The results comparing prediction models showed that single-trait model is adequate for most of the data sets except for the data set of poor environment for both of the bulls and the heifers where the heterogeneity of variance and the genotypes by sex interaction exists. In the prediction with the data set of the low environment level, the bull's EBVs by the single-trait models had high product moment correlations with male EBVs of the bulls by the multitrait model. Whereas the heifer's EBVs had moderate correlations with female EBVs by the multitrait model. This moderate correlation seems to be resulted by the heterogeneity of variance and low heritability of the heifer's PWDG. The prediction models with heterogeneity of variance had little effect on the prediction of EBVs for the data sets with moderate to high genetic correlations. (*Asian-Aus. J. Anim. Sci. 1999, Vol. 12, No. 6 : 850-853*)

Key Words : Breeding Value, Sex, Genotype by Sex Interaction, Growth, Beef Cattle

INTRODUCTION

The heterogeneity of variance between sexes and genotypes by sex interaction were found for postweaning daily gain of Australian Angus cattle in a separate study (Oikawa et al., unpublished). If the heterogeneity of variance is important, it should be properly applied to the prediction model. The national genetic evaluation of Simmental cattle in the U.S. takes into account the heterogeneity of variance by sexes and percentage of Simmental in prediction model (Lee and Pollak, 1997). The improvement in accuracy of predicting EBVs is expected by application of the heterogeneity of variance. In this study, the prediction models was compared among single-trait models (with heterogeneity of variance) and a multitrait model to investigate the effect of the heterogeneity of variance and the genotype by sex interaction on prediction of animal's EBV and to find the most appropriate prediction model for field data analysis.

MATERIAL AND METHODS

Data studied were the same as our estimation study for the variance components; the Group Breed Plan data set from 1972 to 1989. The total number of records was 16,239 after editing the data. The trait analyzed was postweaning daily gain (PWDG, kg). The data were divided into six data sets by three

environment levels; high, medium and low in each sex according to the average BLUEs of the cohorts. Pairs of herd levels for each sex are as follows;

1. HH : High in both bulls and heifers
2. HM : High in bulls and medium in heifers
3. MH : Medium in bulls and high in heifers
4. MM : Medium in both bulls and heifers
5. ML : Medium in bulls and low in heifers
6. LL : Low in both bulls and heifers

Estimated breeding values (EBVs) were obtained for each animal and compared among four models; three single-trait models and a multitrait model. The multitrait model was the same as the estimation model for the (co)variance components in our estimation study, where PWDG in each sex were treated as a separate trait.

The single-trait models were as follows;

1. MO-1: A single-trait model without heterogeneous variance by sex
2. MO-2: A model with heterogeneous residual variance by sex
3. MO-3: A model with heterogeneity of variance in both additive genetic and residual variance. But the genetic correlation among the performance in the two sexes is assumed to be unity

MO-3 is the similar model used by Boldman and Freeman (1990) for dairy production data. Computational procedures for MO-2 and MO-3 were those reported by Gianola (1986).

The model for MO-1 is:

* Address reprint request to T. Oikawa. Faculty of Agriculture, Okayama Univ., Okayama 700-8530, Japan.

¹ Animal Production & Health Division, FAO, Rome, Italy.

² AGBU is a joint unit of the NSW Department of Agriculture and Fisheries and the University.

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$$y_{ij} = \text{hysmg}_i + a_j + e_{ij}$$

where:

- y_{ij} = PWDG of animal j in herd-year-season-sex-management group i ;
 hysmg_i = fixed effect of herd-year-season-sex-management group i ;
 a_j = random additive genetic effect of animal j ;
 e_{ij} = random residual of animal j in herd-year-season-sex-management group i .

In matrix notation, the model would be

$$y = Xb + Za + e,$$

where y is a vector of observations, b is a vector of the fixed effect, X is an incidence matrix relating elements of b to elements of y , a is a vector of random additive genetic effects, Z is a known incidence matrix relating the elements of a to y , and e is the vector of residual effects.

Then

$$E \begin{bmatrix} Y \\ a \\ e \end{bmatrix} = E \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix},$$

$$\text{Var}(a) = A\sigma_a^2,$$

$$\text{Var}(e) = \Pi\sigma_e^2,$$

where A is the numerator relationship matrix among animals, σ_a^2 and σ_e^2 are additive genetic variance and residual variance, respectively.

The residual variance matrix for MO-2 is:

$$\text{Var}(e) = \begin{bmatrix} \sigma_{eM}^2 & 0 \\ 0 & \sigma_{eF}^2 \end{bmatrix} \# I$$

where " $\#$ " is the Kronecker product operation of matrix, σ_{eM}^2 and σ_{eF}^2 are residual variance of male and female animals, respectively.

The residual variance of MO-3 is the same as of MO-2, and the additive genetic variance matrix is:

$$\text{Var}(a) = \begin{bmatrix} \sigma_{aM}^2 & \sigma_{aMF} \\ \sigma_{aMF} & \sigma_{aF}^2 \end{bmatrix} \# A$$

where σ_{aM}^2 , σ_{aF}^2 and σ_{aMF} ($=\sigma_{aFM}$) are additive genetic variance of PWDG in female, male and additive genetic covariance between male and female, respectively.

The variance components for the prediction were estimated in a separate study. Mixed model equations were constructed using sparse matrix techniques (Tier and Smith, 1989).

Correlations of animals' EBVs were compared for four categories of animals; bulls with and without progeny, heifers with and without progeny. The numbers of animals in each category are presented in table 1. Product moment correlations were calculated for all animals. In HH data, the correlations were calculated with the MO-3 EBVs instead of the average of the male EBVs and the female EBVs.

Table 1. Number of animals in the data sets

Data ^a	Bull		Heifer	
	Parent	Non-parent	Parent	Non-parent
HH	31	1,218	245	1,207
HM	21	819	234	876
MH	9	918	318	1,273
MM	14	731	84	782
ML	12	641	141	696
LL	18	1,170	402	1,430

^a H, M and L refer to high, medium and low environment level. The first letter indicates the bull's level, and the second letter indicates the heifer's level (e.g. HM is high in the bull and medium in the heifer.).

RESULTS AND DISCUSSION

Table 2 presents product moment correlations among EBVs by the multitrait model; female (F), male (M) and average (A) EBVs. The correlations of M-A or F-A were higher than the correlations of M-F. Thus the average EBVs are good compromise compared

Table 2. Product moment correlations (%) between the male EBVs and the female EBVs (M-F), the male EBVs and the average EBVs (M-A) and the female EBVs and the average EBVs (F-A)

Data ^a	Bull						Heifer					
	Parent			Non-parent			Parent			Non-parent		
	M-F	M-A	F-A	M-F	M-A	F-A	M-F	M-A	F-A	M-F	M-A	F-A
HM	83	98	92	92	99	96	81	96	95	91	97	98
MH	33	93	66	76	97	90	84	95	96	82	94	96
MM	86	92	99	89	94	99	94	96	100	94	98	100
ML	88	97	97	71	95	90	74	92	94	81	93	97
LL	28	99	41	-43	99	-31	-42	90	3	-32	86	20

^a H, M and L refer to high, medium and low environment level. The first letter indicates the bull's level, and the second letter indicates the heifer's level.

with the separate EBVs. The negative correlations in LL suggest environmental effect large enough to cause the interaction. The correlations of M-A in the bulls tended to be higher than the correlations in the heifers. It was a reasonable result because records of the bulls were used in the male EBVs. The M-F correlations were very low in LL because of the low genetic correlation (Oikawa et al., unpublished). The low correlations were also estimated for the bulls of MH and the animals of ML. No consistent difference was observed between the parental and the non-parental animals.

Table 3 presents correlations between the sex-specific EBVs by the multitrait model and the EBVs by the single-trait models. The correlations between the male EBVs and the EBVs by the single-trait models in the heifers were lower than those in the bulls, and were very low in LL. The difference among the single-trait models was small.

The correlations between the female EBVs and the EBVs by the single-trait models in the bulls were lower than those in the heifers. The low correlations were estimated between the female EBVs and the EBVs by the single-trait models in the bulls of LL and MH. The correlations between the male EBVs and the EBVs by the single-trait models in the bulls were high in LL. Compared between the single-trait models, the correlations of MO-3 were slightly higher than

MO-1 and MO-2.

If the genetic correlation is unity as in HH, the single-trait model is a correct model. If the heterogeneity of variance is large between the heifers and the bulls, MO-3 is theoretically the best model. But the results showed that the difference among the single-trait models was small. The heterogeneous variance applied to MO-2 and MO-3 has little effect on the prediction of EBVs. On the other hand, the low genetic correlation between the sex specific traits had a large effect on the prediction of EBVs.

Tilsch et al. (1989) reported a significant sire by sex interaction for fattening performance and quantified the effect of the interaction on response to selection by simulation. Their result showed that the genetic progress was 50% less than the potential response in females if the interaction was ignored. For this data set, the genotype by sex interaction was suggested to exist in LL by the result of our estimation study. Thus the result agreed with the result, but reduction in accuracy of the prediction caused by the interaction seems to be less than their report.

For the other data sets including the data sets with moderately low genetic correlations, the product moment correlations between the male EBVs and the single-trait EBVs in the bulls and the correlations between female EBVs and the single-trait EBVs in the heifers were high. When the genetic correlation is very

Table 3. Product moment correlations (%) between EBVs of the multi-trait model (male, female and average) and EBVs of the three single trait models (MO-1, MO-2 and MO-3)

Data ^a	Bull						Heifer					
	Parent			Non-parent			Parent			Non-parent		
	MO-1	MO-2	MO-3	MO-1	MO-2	MO-3	MO-1	MO-2	MO-3	MO-1	MO-2	MO-3
Male EBVs												
HM	97	97	98	99	99	99	89	89	91	94	94	94
MH	97	90	92	99	96	97	93	88	89	92	87	88
MM	96	97	92	95	98	95	97	97	95	98	98	98
ML	98	96	96	96	96	97	92	84	85	94	88	89
LL	97	95	98	98	97	98	10	2	24	6	0	20
Female EBVs												
HM	93	94	92	96	96	96	98	99	98	99	99	99
MH	53	70	68	83	90	88	97	99	99	98	99	99
MM	75	94	99	77	92	99	91	98	100	95	99	100
ML	96	97	97	86	86	85	93	98	98	95	98	98
LL	41	44	42	-29	-26	-30	81	84	75	86	88	83
Average EBVs												
HH	99	100	-	99	100	-	99	100	-	99	100	-
HM	100	99	100	100	100	100	98	98	99	99	99	99
MH	98	100	100	98	100	100	99	98	99	100	98	99
MM	83	97	100	84	96	100	93	99	100	96	100	100
ML	100	100	100	100	99	99	99	99	99	99	99	99
LL	98	97	99	99	99	99	50	43	63	52	47	65

^a H, M and L refer to high, medium and low environment level. The first letter indicates the bull's level, and the second letter indicates the heifer's level.

low such as in LL, the single-trait EBVs for the heifers were different from the EBVs by the multitrait model. Thus except for the prediction in LL, reliable EBVs can be predicted by the single-trait model for most of the data sets. Even with the low genetic correlation in LL, the EBVs of the bulls can be predicted with high accuracy by the single-trait model, however, in the heifers, the female EBVs by single-trait model were less accurate.

The low genetic correlation and the large heterogeneity of phenotypic variance of the heifer's PWDG in LL may lower the accuracy of predicting the heifer's EBVs. But a single-trait model seems to be appropriate in most of the situations even if the genetic correlation is moderately low. Multitrait evaluation may be justifiable only under the situations of the genotypes by sex interaction and large heterogeneity of variance which is likely to occur in poor environment.

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