

ORIGINAL ARTICLES

**(Co)variance Components for Birth and Weaning Weights of Shorthorn
Beef Cattle in Australia and the United States**

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ABSTRACT

(Co)variance components and genetic parameters for birth (BW) and weaning weights (WW) of Shorthorn beef cattle in Australia (AU) and the United States (US) were estimated using Restricted Maximum Likelihood. Five different uni- and bivariate models were used to fit both traits within each country. In Model 1, only a direct genetic effect (a) was fitted. In Models 2 and 3, a maternal genetic effect (m) was added. A genetic covariance between direct-maternal effects [$cov(a, m)$] was ignored (model 2) or included (model 3). Models 4 and 5 both m and maternal permanent environment effects (pe), were allowed from model 1, and assumed $cov(a, m)$ in the same manner as model 2 and 3, respectively. When ignoring m effect, the direct heritability estimates were inflated and differed markedly from other models. The likelihood ratio test showed that model 5 was the best fit for both traits in the US while models 2 and 4 were the fittest for BW and WW in AU, respectively. The estimates of direct, maternal, total heritabilities, and maternal permanent environment variance of the full model in AU and in the US (in parentheses) were 0.46 (0.48), 0.09 (0.05), 0.42 (0.42) and 0.00 (0.06) for BW, and 0.23 (0.32), 0.16 (0.09), 0.24 (0.26) and 0.13 (0.10) for WW, respectively. After m and pe were fitted, the estimate of total heritability decreased slightly for BW in both countries and for WW in AU, but decreased re-markedly for WW in the US. Estimate of direct-maternal genetic correlation was moderately negative and tended to be more negative after pe was fitted for both traits in the US. The parameters estimates using bivariate analysis were not different to the results from univariate analysis. This analysis yielded additive and maternal genetics correlations between BW and WW. These estimates were positive and medium to high correlation, which were higher in AU than in the US. Correlation of estimated breeding values for direct additive and maternal genetics between the full model and others were high and close to unity. The differences of some parameters between both countries indicate that joint genetic evaluation might require genotype by environment interaction to be considered.

Key words : Genetic parameters - Growth traits - Likelihood ratio test - Shorthorn

INTRODUCTION

Birth (BW) and weaning weights (WW) are economically important growth traits in beef cattle, which should be included as selection criteria in breeding programs. BW of a calf and its early growth rate till weaning are determined not only by its own genetic potential, but also by the maternal environment that the dam provides. The expression of maternal effects is sex-limited and occurs late in life of the female and lags by one generation (1). The relative importance of additive (direct) genetic, maternal (indirect) genetic and maternal permanent environmental effects for growth should be considered when beef producers formulate breeding plans (2). For optimal experimental designs, Thompson (3) suggested that in the presence of maternal effects sampling variances of estimates of the direct heritability were roughly three to five times as large as when there were direct effects only. In most studies, only additive genetic components have been considered. Some distinguished between genetic and permanent environmental effects due to the dam while others ignored the latter. Koch (4) emphasized the possibility of a negative direct-maternal genetic covariance, if not modelled, to bias the estimates of the direct and maternal genetics variances. Most studies, such as Meyer (2), Ferriera et al (5) and de Mattos et al (6) found that those effects reduced the bias of the estimate of direct heritability. Nowadays, researchers can use advanced models and more sophisticated statistics procedures to estimate variance components and genetic values. Results from different statistical models can be compared to determine their strength and weaknesses and to determine whether simpler computational models may be adequate. The objective of this research was to estimate (co)variance components and parameters of direct, maternal genetics and maternal permanent environment effects using different statistical models for BW and WW in Shorthorn beef cattle population from Australia (AU) and the United States (US).

MATERIALS AND METHODS

1. Description of the Data

The edited data were composed of 21,896 and 39,900 records of Shorthorn beef cattle in Australian and 115,261 and 77,789 records in the United States birth and weaning weights respectively. Data were recorded by seed-stock breeders in both countries and managed for both populations with the BREEDPLAN recording system developed and service by the Agricultural Business Research Institute (ABRI), the University of New England. Characteristics of data structure and some descriptive statistics are shown in **Table 1**.

2. Models

2.1 Univariate Analysis

A single trait animal model was fitted to the data for each trait including all pedigree information. The maternal genetic and maternal permanent environmental effects were taken into account by including appropriate random effects into the model of analysis. Ignoring and allowing for genetic covariances between direct and maternal

effects which yielded 5 different models for each trait and country. The statistical models were as follows;

$$\begin{array}{ll}
 \text{Model 1:} & y = \mathbf{m} + \text{fixed} + a + e \\
 \text{Model 2:} & y = \mathbf{m} + \text{fixed} + a + m + e & \text{with } \text{cov}(a,m) = 0 \\
 \text{Model 3:} & y = \mathbf{m} + \text{fixed} + a + m + e & \text{with } \text{cov}(a,m) = \mathbf{1} \ 0 \\
 \text{Model 4:} & y = \mathbf{m} + \text{fixed} + a + m + pe + e & \text{with } \text{cov}(a,m) = 0 \\
 \text{Model 5:} & y = \mathbf{m} + \text{fixed} + a + m + pe + e & \text{with } \text{cov}(a,m) = \mathbf{1} \ 0
 \end{array}$$

Fixed effects consisted of contemporary groups (CG), which concatenated herds, years of birth of calves, seasons, management groups and sex of calves. For BW analysis, sex was defined as male and female, and was defined as bull, heifer and steer for WW analysis. The other fixed effect was age group of the dam, with a group every 62 days starting from 600 day ages. The last group combined all older dams together; this resulted in 59 and 50 groups for AU and the US, respectively. For WW analysis, ages of calf was fitted as covariate nested within sex of the calf. The first model, model 1, was a simple animal model with animal additive genetic effects (a) as the only random effect. Model 2 attributed all maternal effects to the genotype of the dam, by fitting maternal genetics effects (m) as a second random effect and assumed that direct and maternal genetic effect were uncorrelated ($\text{cov}(a,m) = 0$). Model 3 was attributed the same as Model 2, but allowed a covariance between them. Model 4 and 5 included maternal genetic and a maternal permanent environmental effects ignoring and accounting for a genetic correlation between direct and maternal genetics effect in the same manner as model 2 and 3, respectively. The first and the second moments of the model were assumed as follows;

$$E \begin{bmatrix} y \\ a \\ m \\ pe \\ e \end{bmatrix} = \begin{bmatrix} X\beta \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} ; \quad \text{Var} \begin{bmatrix} a \\ m \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

where σ_a^2 was direct additive genetic variance; σ_m^2 was additive maternal genetic variance; σ_{am} was additive genetic covariance between direct and maternal; σ_{pe}^2 was variance due to maternal permanent environmental effects; σ_e^2 was residual error variance; A and I were numerator relationship and identity matrices, respectively.

2.2 Bivariate Analysis

BW and WW were analyzed jointly using the model as described in univariate analysis previously. The full model was affected by direct, maternal genetic and maternal permanent environment effects. The definition of each element is similar to the univariate model previously presented, and 1, 2 were used to refer to BW and WW, respectively. The assumptions were,

Table 1. Characteristics of data structure and some descriptive statistics.

Traits ¹	Australia		The United States	
	BW	WW	BW	WW
No. of records	21,896	39,900	115,261	77,789
No. of animals	53,588	53,588	115,261	115,261
No. of sires	1,025	2,376	5,717	4,168
No. of dams	10,053	22,185	46,749	34,382
No. of CG ²	6,075	12,259	20,977	29,675
Weight (kg); $\bar{x} \pm SD$	39.93 \pm 5.96	253.43 \pm 57.69	39.72 \pm 5.36	248.34 \pm 44.98
Age of calves(days); $\bar{X} \pm SD$	-	217.25 \pm 40.53	-	201.27 \pm 28.38
Age of dams (days); $\bar{X} \pm SD$	1,497.22 \pm 713.19	1,535.16 \pm 725.79	1,513.62 \pm 23.66	1,496.25 \pm 714.30

¹ BW = birth weight; WW = weaning weight

² CG = Contemporary groups

$$\text{var} \begin{bmatrix} u_1 \\ u_2 \\ m_1 \\ m_2 \\ pe_1 \\ pe_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a1}^2 & A\sigma_{a1a2} & A\sigma_{a1m1} & A\sigma_{a1m2} & 0 & 0 & 0 & 0 \\ A\sigma_{a1a2} & A\sigma_{a2}^2 & A\sigma_{a2m1} & A\sigma_{a2m2} & 0 & 0 & 0 & 0 \\ A\sigma_{a1m2} & A\sigma_{a2m1} & A\sigma_{m1}^2 & A\sigma_{m1m2} & 0 & 0 & 0 & 0 \\ A\sigma_{a1m2} & A\sigma_{a2m2} & A\sigma_{m1m2} & A\sigma_{m2}^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_{pe1}^2 & I\sigma_{pe1pe2} & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_{pe1pe2} & I\sigma_{pe2}^2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & I\sigma_{e1}^2 & \sigma_{e1e2} \\ 0 & 0 & 0 & 0 & 0 & 0 & I\sigma_{e1e2} & I\sigma_{e2}^2 \end{bmatrix}$$

3. Estimation of (co)Variance Components and Genetic Parameters

Estimates of (co)variance components were obtained by the average information restricted maximum likelihood (AI-REML) using ASReML (7). The method involves maximizing the likelihood function ($\log L$) given the data. Each model was restarted using the resulting estimates of the previous parameters as new priors, until changes in the likelihood function value was zero, to ensure that a global rather than a local maximum likelihood had been reached. The genetic parameters, genetic correlation (r_{am}) and total heritability ($h_{\bar{t}}^2$) defined some as Falconer and Mackay (8) or some as Willham (9). Pearson product moments and Spearman rank correlations were used to calculate the correlation between the model of study for the predicted of EBV_d and EBV_m . Comparisons of the different models for seeking the best fit were made using likelihood ratio tests (LRT). The differences between the function values for pairs of models can be tested against the chi-square distribution with degrees of freedom being the difference in number of variance or covariance components in the models (7,10).

RESULTS AND DISCUSSION

1. Univariate Analysis

Estimates of (co)variance components and genetic parameters with maximum log likelihood values for birth weight (BW) and weaning weight (WW) of Shorthorn beef in Australia and the United State are summarized in **Table 2 and 3**, respectively.

Birth Weight (BW)

From **Table 2**, the model ignoring maternal effects (Model 1) has yielded substantially higher estimates of direct additive variance (σ_a^2) and direct heritability (h^2) than for other models. Fitting maternal genetics effect (Model 2 and 3) increased $\log L$ significantly. With an estimate of the BW maternal heritability (m^2) of 6 and 9%, the estimate of h^2 was reduced by 14.5 and 4.5% for model 2 and 3, respectively in AU. While in the US, the estimates of m^2 from both models were 7 and 9%, which reduced the estimate of h^2 by 19.6 and 9.8%, respectively. After the maternal

permanent environmental (σ_e^2) was fitted into the models (model 4 and 5), the Log L values increased further for the US data. However, this did not occur in AU. Ignoring maternal permanent environment effects due to the dam tended to be picked up in estimates of direct maternal variance (σ_m^2), increasing by 0 to 6% in both countries. The estimate of direct additive variance for BW in AU was smaller than US, which was 78, 84, 92, 86.1 and 80.3% of the US value in models 1 to 5, respectively. However, it had no effect on the h^2 estimate. Estimates of m^2 in AU and the US were in similar for models ignoring maternal permanent environmental effect. After fitting this effect, the estimate of m^2 in US decreased while in AU did not change. This study found very small estimates of maternal permanent environmental variance ($c^2 = 0.0005$). This means that model 2 has the best fit model for BW trait in AU.

Estimates of the genetic covariance between direct and maternal genetics effects (σ_{am}) are medium and negative in both countries resulting in small to medium negative correlations of direct-maternal genetics (r_{am}). These tended to be more negative when the maternal permanent environment was fitted in the US (from -0.21 to -0.38). This result is different to the study in Hereford and Angus by Meyer (2), who reported r_{am} of 0.038 and 0.285 for the two breeds, respectively. However, the results agreed with Ferreira et al (5), who reported a negative r_{am} for BW in Hereford. Models including σ_{am} had slightly greater Log likelihood in AU, compared to models ignoring the effect. In the US differences in Log likelihood between model 4 and 5 were larger. Allowing for σ_{am} increases the estimates of h^2 by between 12.2 to 17.1%, and 28.6 to 66.7% for the estimate of m^2 in both countries. The results contradict the study by Meyer (2), that allowing for σ_{am} reduced estimates of both h^2 and m^2 compared to models ignoring the covariance. These indicate that the covariance between direct and maternal genetics affect the estimates of those parameters. The estimates of total heritability (h_T^2) were little different between corresponding models in both countries. This parameter tends to be smaller in the US herd for the model allowing maternal genetic and maternal permanent environmental effects.

Weaning Weight (WW)

The simple animal model (Model 1) always yielded higher estimates of σ_a^2 and h^2 than those from other models. After the maternal genetic effect was fitted, the Log likelihood values increased over those for model 1. The estimates of m^2 for WW in AU were 24 and 28%, while in the US they were 13 and 17% for models 2 and 3, respectively. The estimates of h^2 were dropped by 58.7 and by 54.3% in AU, and by 39.5 and 30.2% in the US with models 2 and 3. In models 4 and 5, where a maternal permanent environmental effect was included, the estimates of h^2 changed little, but the estimates for m^2 decreased from models 2 and 3 by 45.8 and 42.9% in AU, and by 61.5 and 47.1% in the US. This indicates that, the maternal genetic effect should be considered for WW in both countries. The estimates of total heritability (h_T^2) were slightly different between corresponding models of each country. This parameter tends to be higher in US than in AU for models allowing maternal genetic and maternal permanent environmental effects. As for BW, the estimate of h_T^2 from model 1 was the highest. The pattern of this parameter agreed with Meyer (2).

Table 2. Estimates of (co)variance components and genetic parameters for BW of Shorthorn beef cattle in Australia (AU) and the United States (US).

Parameters	Model 1		Model 2		Model 3		Model 4		Model 5	
	AU	US	AU	US	AU	US	AU	US	AU	US
σ_a^2	8.04	10.31	6.88	8.19	7.69	9.21	6.88	7.99	7.69	9.58
σ_{am}	-	-	-	-	-0.89	-0.84	-	-	-0.89	-1.15
σ_m^2	-	-	0.94	1.35	1.48	1.81	0.94	0.63	1.48	0.96
σ_c^2	-	-	-	-	-	-	0.00	0.97	0.00	1.19
σ_e^2	8.80	9.82	8.89	10.31	8.50	9.79	8.89	10.11	8.50	9.27
σ_p^2	16.84	20.13	16.71	19.85	16.77	19.96	16.71	19.70	16.77	19.84
Log L^1	5.10 ^a	68.80 ⁱ	0.80 ^b	22.80 ^j	0.00 ^b	19.10 ^j	0.80 ^b	8.10 ^k	0.00 ^b	0.00 ^l
h^2	0.48	0.51	0.41	0.41	0.46	0.46	0.41	0.41	0.46	0.48
m^2	-	-	0.06	0.07	0.09	0.09	0.06	0.03	0.09	0.05
r_{am}	-	-	-	-	-0.27	-0.21	-	-	-0.27	-0.38
c^2	-	-	-	-	-	-	0.00	0.05	0.00	0.06
h_t^2	0.48	0.51	0.44	0.45	0.47	0.44	0.44	0.42	0.42	0.42

¹ log L : log likelihood, expressed as deviation from model with highest value; and the different letters within country indicate significantly different at $\chi^2_{0.05,1}$ or $\chi^2_{0.05,2}$

The estimates of σ_a^2 in AU were 85.1, 56.6, 55.7, 60.6 and 55.8% of the US values in models 1 to 5, respectively. After the maternal genetic effect was fitted, the component of σ_a^2 in AU was much smaller than that in the US. This indicates that the estimates of m^2 in AU were higher than those of the US, which was 84.6 and 64.7% higher for models 2 and 3, respectively. When including the maternal permanent environmental effect, the estimates of m^2 in AU were 160 and 77.8% higher than those in the US for models 4 and 5 respectively. However, the component of σ_m^2 from models 2 and 3 was partitioned to the component of σ_c^2 according to models 4 and 5 for 45.8 and 42.9% in AU and 61.5 and 47.1% in the US, respectively. This indicates that, if σ_c^2 is ignored for the estimates of breeding values (EBV) for WW, then the EBV will be overestimated. The estimates of m^2 and maternal permanent environmental variance (c^2) were within the range of previous reports utilizing equivalent models, but different breeds (2,11,12,13,14).

Allowing for σ_{am} in models increased estimates of h^2 by 28.6 and 15.4%, and increased estimates of h^2 by 16.7 and 30.8% from models ignoring this in AU and the US, respectively. The estimate of r_{am} was negative in both countries -0.23 and -0.28 for model 3, and -0.25 and -0.43 for model 5 in AU and the US. This indicates that, including the maternal permanent environmental effect into the models increased the estimate of this correlation. On the other hand, the component of σ_m^2 was reduced markedly by partition of components of σ_c^2 especially in the US. The estimates from model 5 agreed with recent reports that used similar models, but in other breeds (2,6,12,13). Meyer (2) gave the reason that milk supplied from dam to her calves was limited. However, Robinson (15) found that the negative correlation between direct-maternal became from sire by herd interaction when the large proportion of sires induced into the base population. The log likelihoods for model 5 showed the best fit in the US while model 4 was fittest for the AU population. This agreed well with Meyer (2), who studied Australian Hereford, Ferreira et al (5) and de Mattos et al (6) who studied US Hereford. They concluded that the best fit models were those that included effects of both maternal genetic and permanent environment effects in addition to direct genetic effect.

2. Bivariate Analysis

The estimates of (co)variance components and genetic parameters for each trait in this analysis were similar to those from univariate analysis. Only genetic correlations from this study are presented in **Table 4**. However, this analysis accommodated much more information in genetic correlation (r_a), maternal genetic correlation (r_m), maternal permanent environmental correlation (r_c), and environment correlation (r_e) between BW and WW in each country. The estimate of r_a in AU was 30.2 to 43.2% higher than in the US. The estimate of r_c of those traits in AU was 33.3 to 65.0% higher than in the US, which this parameter estimates in AU tended to be increased, while in US was stabilized. The r_m estimate in AU was markedly higher than for the US especially when the maternal permanent environmental effect was fitted. These differences might be affected by the component of σ_c^2 estimate for BW in AU, which was small (0.0005), and affected to overestimate the estimate of r_m between both traits.

Table 3. Estimates of (co)variance components and genetic parameters for WW of Shorthorn beef cattle in Australia (AU) and the United States (US).¹

Parameters	Model 1		Model 2		Model 3		Model 4		Model 5	
	AU	US	AU	US	AU	US	AU	US	AU	US
σ_a^2	261.50	307.17	104.23	184.25	120.58	216.50	109.43	180.66	126.07	226.07
σ_{am}	-	-	-	-	-32.15	-45.61	-	-	-27.13	-50.90
σ_m^2	-	-	133.25	90.12	159.90	123.34	71.53	36.23	90.55	61.44
σ_c^2	-	-	-	-	-	-	68.90	63.80	70.37	71.55
σ_e^2	308.96	413.06	322.86	434.67	313.16	416.96	299.92	419.24	290.64	394.15
σ_p^2	570.50	720.20	560.30	709.00	561.50	711.20	549.80	699.90	550.50	702.30
Log <i>L</i>	74.40 ^a	124.40 ⁱ	11.40 ^b	35.80 ^j	10.10 ^b	30.90 ^j	1.20 ^c	8.30 ^k	0.00 ^c	0.00 ^l
h^2	0.46	0.43	0.19	0.26	0.21	0.30	0.20	0.26	0.23	0.32
m^2	-	-	0.24	0.13	0.28	0.17	0.13	0.05	0.16	0.09
r_{am}	-	-	-	-	-0.23	-0.28	-	-	-0.25	-0.43
c^2	-	-	-	-	-	-	0.13	0.09	0.13	0.10
h_T^2	0.46	0.43	0.30	0.32	0.27	0.29	0.26	0.28	0.24	0.26

¹See Table 2 for the description

Table 4. Estimates of genetic parameters for BW and WW of Shorthorn beef cattle in Australia (AU) and the United States (US) using bivariate analysis.

Parameters	Model 1		Model 2		Model 3		Model 4		Model 5	
	AU	US	AU	US	AU	US	AU	US	AU	US
h_{bw}^2	0.49	0.51	0.41	0.41	0.45	0.46	0.41	0.41	0.45	0.47
h_{ww}^2	0.46	0.43	0.18	0.26	0.20	0.29	0.19	0.26	0.21	0.30
m_{bw}^2	-	-	0.06	0.07	0.10	0.09	0.06	0.03	0.10	0.05
m_{ww}^2	-	-	0.25	0.13	0.29	0.17	0.14	0.05	0.16	0.08
c_{bw}^2	-	-	-	-	-	-	0.00	0.05	0.00	0.06
c_{ww}^2	-	-	-	-	-	-	0.13	0.09	0.13	0.10
$h_{T(bw)}^2$	0.49	0.51	0.44	0.45	0.42	0.44	0.44	0.42	0.42	0.42
$h_{T(ww)}^2$	0.46	0.43	0.30	0.32	0.27	0.30	0.26	0.29	0.24	0.26
$r_{am(bw)}$	-	-	-	-	-0.27	-0.18	-	-	-0.27	-0.34
$r_{am(ww)}$	-	-	-	-	-0.21	-0.23	-	-	-0.20	-0.35
$r_{a(bw,ww)}$	0.53	0.37	0.63	0.47	0.56	0.43	0.62	0.46	0.55	0.40
$r_{m(bw,ww)}$	-	-	0.46	0.20	0.32	0.13	0.58	0.06	0.40	-0.07
$r_{c(bw,ww)}$	-	-	-	-	-	-	0.00	0.30	0.00	0.31
$r_{e(bw,ww)}$	0.28	0.21	0.30	0.20	0.32	0.21	0.33	0.20	0.34	0.21
Log L	85.00	198.00	14.00	52.00	11.00	46.00	2.00	12.00	0.00	0.00

¹See **Table 2** for the descriptions

3. Correlations between Estimated Breeding Values

Pearson product moment and Spearman rank correlations were used to study the behavior of estimated breeding values for direct genetic (EBV_d) and maternal genetic (EBV_m) for both traits. Correlations were between estimates from the full model (model 5), which was the best fit and the estimates from other models (**Table 5**). From this table, the correlations were quite high and close to unity for both the estimates using uni- and bivariate analyses. Product moment correlations were higher every time than rank correlation. Correlations of EBV_d were always higher than the correlation between EBV_m in the same model. The correlations of EBV_d and EBV_m estimates between model 5 and model 3 was the highest, whereas those between model 5 and model 1 were the lowest. This indicates that, if reduced the computing time (cost) is required, then model 3 is the model of choice for the US population. That is, maternal permanent environment might not be necessary especially for BW analysis. The correlations from this study were similar to the study of Dodenhoff et al (12) but higher than the study of Ferreira et al (5).

CONCLUSIONS

This study has demonstrated that the best fit model for early growth traits of Shorthorn beef cattle is the full model (model 5) for birth (BW) and weaning weights (WW) in the US. In AU, model 2 is the best fit for BW while model 4 is last for WW. Model fitting only direct additive tended to overestimate the heritability (h^2). Models without maternal permanent environment tended to inflate estimate of maternal heritability (m^2) for WW. Estimates of direct and maternal effects genetics correlations between BW and WW in AU were higher than those in the US. Correlations of estimated breeding values for direct and maternal of model 5 were nearly unity with the other, and highest being model 3. The total heritability (h^2_t) was slightly decreased after maternal genetics and maternal effects permanent environmental effects were fitted for WW in AU, but decreased markedly in the US. The evidences of some differences in the estimates of genetic parameters for BW and WW between Australia and the United States invite investigation into genotype by environment (country) interactions.

Table 5. Pearson product moment (the 1st line) and Spearman rank (the 2nd line) correlations of estimates breeding values for direct genetic (EBV_d) and maternal genetic (EBV_m) for BW and WW between the estimates from model 5 and other models.

	Univariate Analysis				Bivariate Analysis			
	Model 1	Model 2	Model 3	Model 4	Model 1	Model 2	Model 3	Model 4
Australia								
EBV _d for BW	0.986	0.997	1.000	0.997	0.979	0.996	1.000	0.997
	0.969	0.986	0.996	0.986	0.970	0.992	0.999	0.993
EBV _m for BW	-	0.934	1.000	0.934	-	0.948	0.997	0.945
	-	0.913	0.999	0.913	-	0.939	0.996	0.937
EBV _d for WW	0.922	0.995	0.998	0.993	0.926	0.996	0.998	0.995
	0.901	0.991	0.996	0.987	0.913	0.993	0.995	0.991
EBV _m for WW	-	0.968	0.984	0.981	-	0.975	0.983	0.990
	-	0.960	0.983	0.972	-	0.970	0.981	0.984
The United States								
EBV _d for BW	0.979	0.996	0.999	0.996	0.980	0.996	0.998	0.997
	0.963	0.987	0.988	0.987	0.963	0.985	0.989	0.985
EBV _m for BW	-	0.809	0.906	0.859	-	0.827	0.910	0.884
	-	0.741	0.874	0.766	-	0.749	0.869	0.794
EBV _d for WW	0.929	0.989	0.998	0.986	0.932	0.992	0.997	0.990
	0.902	0.976	0.989	0.967	0.899	0.976	0.985	0.972
EBV _m for WW	-	0.826	0.913	0.878	-	0.868	0.927	0.921
	-	0.788	0.881	0.821	-	0.807	0.896	0.850

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บทคัดย่อ

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องค์ประกอบความแปรปรวน (รวม) สำหรับน้ำหนักแรกเกิดและหย่านมโคพันธุ์ฮอร์ทอร์นในประเทศออสเตรเลียและอเมริกา

ประมาณองค์ประกอบความแปรปรวนและแปรปรวนร่วม และพารามิเตอร์ทางพันธุกรรมของลักษณะน้ำหนักแรกเกิดและหย่านมของโคเนื้อพันธุ์ฮอร์ทอร์นในประเทศออสเตรเลียและสหรัฐอเมริกาโดยวิธี Restricted Maximum Likelihood วิเคราะห์ข้อมูลที่ลักษณะและที่ละสองลักษณะด้วยโมเดล 5 แบบ ประกอบด้วย โมเดล 1 เป็นโมเดลที่สนใจเฉพาะอิทธิพลสุ่มพันธุกรรมทางตรง โมเดล 2 และ 3 เพิ่มอิทธิพลสุ่มพันธุกรรมของแม่จากโมเดล 1 และกำหนดให้ไม่มีและมีความสัมพันธ์ระหว่างอิทธิพลสุ่มทั้งสอง ตามลำดับ ส่วนโมเดล 4 และ 5 เพิ่มอิทธิพลสุ่มสภาพแวดล้อมถาวรของแม่และกำหนดความสัมพันธ์เหมือนโมเดล 2 และ 3 ตามลำดับ พบว่า ค่าประมาณอัตราพันธุกรรมทางตรงของลักษณะทั้งสองจะลดลงอย่างชัดเจนหลังจากเพิ่มอิทธิพลเนื่องจากพันธุกรรมและสภาพแวดล้อมของแม่ขึ้นเป็นลำดับ ทดสอบความแตกต่างระหว่างโมเดลด้วยวิธี likelihood ratio test พบว่า ลักษณะทั้งสองในประเทศสหรัฐอเมริกาถูกอธิบายได้ดีที่สุดด้วยโมเดล 5 ส่วนน้ำหนักแรกเกิดและหย่านมในประเทศออสเตรเลียแค่โมเดล 2 และ 4 ก็อธิบายได้เพียงพอ ตามลำดับ ค่าอัตราพันธุกรรมทางตรง อัตราพันธุกรรมของแม่ อัตราพันธุกรรมรวม และวาเรียนซ์สภาพแวดล้อมของแม่จากโมเดล 5 ในน้ำหนักแรกเกิดในประเทศออสเตรเลียและสหรัฐอเมริกา (ในวงเล็บ) เท่ากับ 0.46(0.48) 0.09(0.05) 0.42(0.42) และ 0.00(0.06) ตามลำดับ น้ำหนักหย่านม เท่ากับ 0.23(0.32) 0.16(0.09) 0.24(0.26) และ 0.13(0.10) ตามลำดับ พบว่า อัตราพันธุกรรมรวมของน้ำหนักแรกเกิดจะลดลงเพียงเล็กน้อยหลังจากเพิ่มอิทธิพลสุ่มทางพันธุกรรมและสภาพแวดล้อมของแม่ และค่าดังกล่าวของน้ำหนักหย่านมจะลดลงอย่างชัดเจน พารามิเตอร์จากการวิเคราะห์ที่ละลักษณะไม่ต่างจากที่ละสองลักษณะ แต่การวิเคราะห์ที่ละสองลักษณะได้ค่าสหสัมพันธ์ระหว่างพันธุกรรมทางตรงและพันธุกรรมของแม่ระหว่างลักษณะทั้งสอง พบว่าสหสัมพันธ์ดังกล่าวเป็นแบบบวกระดับปานกลางถึงสูงโดยสหสัมพันธ์ในประเทศออสเตรเลียจะสูงกว่าในประเทศสหรัฐอเมริกา ส่วนค่าทำนายคุณค่าการผสมพันธุ์ พบว่าค่าจากโมเดล 5 มีสหสัมพันธ์เป็นบวกสูงเข้าใกล้หนึ่งกับโมเดลอื่นๆ ความแตกต่างกันในหลายๆ พารามิเตอร์ระหว่างสองประเทศ ชี้ให้เห็นว่าควรต้องศึกษาอิทธิพลของปฏิกริยาร่วมทางพันธุกรรมกับสภาพแวดล้อมก่อนทำการประเมินค่าทางพันธุกรรมร่วมกัน

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