Genotype by Country Interaction for Birth and Weaning Weights for Shorthorn Cattle in Australia and the United States

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ABSTRACT

Birth (BW) and weaning weights (WW) of Shorthorn beef cattle used to study the genotype by country (G×C) interactions between Australia (AU) and the United States (US). Data were collected depending on the connectedness on genetic links of common sires. The edited data consisted of numbers of sire, dam and calf of 2,013, 19,784 and 42,963 in AU and 4,797, 38,648 and 95,849 in the US, respectively. After that, sets of data were combined together and corresponding traits from different countries were treated as different traits. Therefore, a bivariate animal model including maternal genetic and permanent environment effects was used to study the interactions. No covariance due to maternal permanent environmental and environmental effects {cov(pe1,pe2) and cov(e1,e2) = 0} was assumed. Estimates of (co)variance components have been done by restricted maximum likelihood. Variance component estimates of the same trait across countries were slightly different. Direct and maternal genetic correlations (in parentheses) between corresponding traits were 0.93 (0.93) and 0.78 (0.86) for BW and WW, respectively. This implied that a joint BW genetic evaluation could be conducted using a model that treated the information as a single population. For WW, sires across AU and the US needed evaluation to consider carefully the G×C interactions.

Key words: G×E interaction - Genetic evaluation - Shorthorn

INTRODUCTION

Across country evaluation of sires in beef cattle is becoming a challenge of interest, because of the globalization that the product can distribute from the source of origin to others as well as the genetic material of animal. The widespread exchange of genetic material through import/export of live animals, semen, and embryos has created strong genetic links between countries (1). However, the usefulness of across country genetic evaluation sire are hampered by the genotype and environment (G×E) interactions. This interaction becomes very important if individuals of a particular population are to be reared under different conditions. If there is no interaction then the best genotype in one environment will be the best of all. But if there is much

interaction then particular genotypes must be sought for particular environments (2). This indicates that pooled data from many sources for joint analysis need to be concerned very much with the G×E interactions. For models to study the G×E interaction, Bertrand et al (3) suggested that genetic effects of the dam should also be accounted for, in addition to the direct additive growth trait. Many researchers have studied G×E interactions for BW or/and WW in beef cattle by using animal models that include maternal genetic and permanent environment effects (1,3,4,5,6). These studies found a small interactions between countries of study and suggested combining data sets for analysis as a single population. Hyde et al (7) found G×E interaction for BW and WW for Charolais cattle between Australia-New Zealand and Canada-United States stressing the need to consider carefully the interaction. The evidence of G×E interactions can be used to design genetic evaluation among countries. Therefore, the objective of this study was to investigate the important of genotype by country interactions for BW and WW for Shorthorn beef cattle across the US and AU evaluation.

MATERIALS AND METHODS

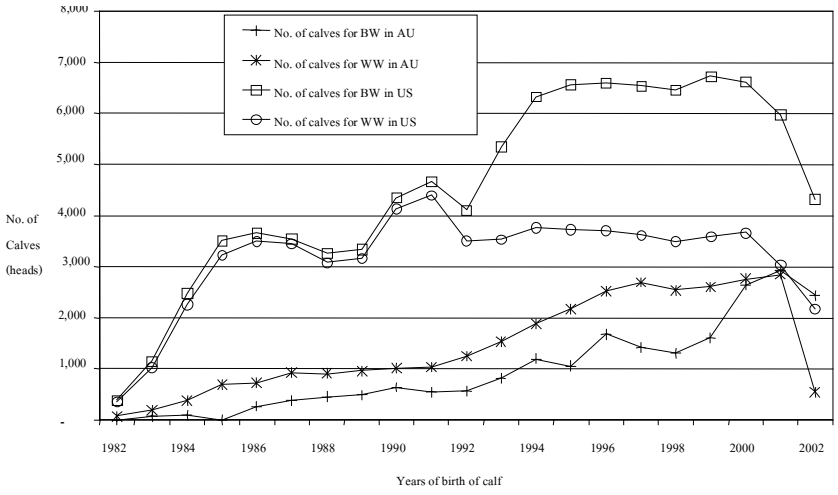
Data

Birth (BW) and weaning (WW) weights of Shorthorn beef cattle in Australia (AU) and the United States (US) were used to study the genotype by country (G×C) interaction. Data were recorded by seedstock breeders in both countries and managed for both populations with the BREEDPLAN recording system developed and serviced by the Agricultural Business Research Institute (ABRI), the University of New England. There are 123 common sires, which were used for artificial insemination (AI) in both countries. After the data were edited, it consisted of 39 common sires. Therefore, the data were collected from a whole herd that had dispersed the genetic materials of those common sires. The edited data before combination consisted of 2,013, 19,784 and 42,963 in AU and 4,797, 38,648 and 95,849 in the US for numbers of sire, dam, and calf, respectively. Hence, the combined dataset consisted of 6,771 sires, 58,432 dams, and 138,812 calves. For more details, the data structure and characteristics of each country are presented in **Table 1** and **Figure 1**. Records for calves born reached back as far as 1978 for US and 1980 for AU, but the years less than and equal to 1982 were combined together and defined as 1982 and showed the number of calves born by year shown in **Figure 1a**. Age groups of dams were grouped every 62 days from 600 days. The last group combined all residual dams whose age was more than or equal to 3,638 days and yielded 50 age groups of dam in both countries **(Figure 1b)**. Sib sizes of dam ranged between 1 to 15 progenies as shown in **Figure 1c**. The numbers of calf within each month are shown in **Figure 1d**. This indicated the impact of seasonal breeding where calves were born mostly in spring in both countries.

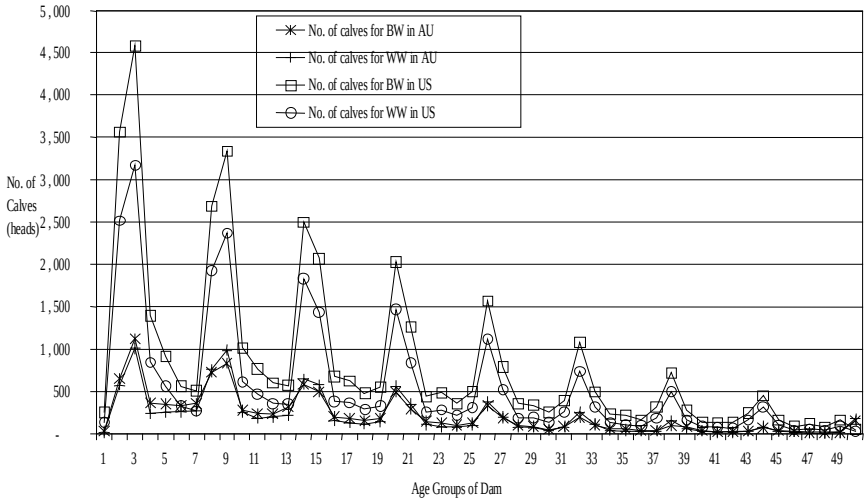
Table 1. Data structures and descriptive statistics.

Traits [1]	Australia		United States	
	BW	WW	BW	WW
No. of calves with records	20,471	30,164	95,849	66,328
No. of sires	933	1,779	4,797	3,594
No. of common sires	39	39	39	39
No. of dams	9,326	16,522	38,648	29,024
No. of contemporary groups	3,536	9,617	15,695	23,091
Weight (kg) $\bar{x}$: Mean ±SD	39.88±5.93	252.92±55.68	39.85±5.36	249.22±44.89
Age of calves $\bar{x}$: Mean ±SD	-	215.80±40.45	-	201.21±28.06

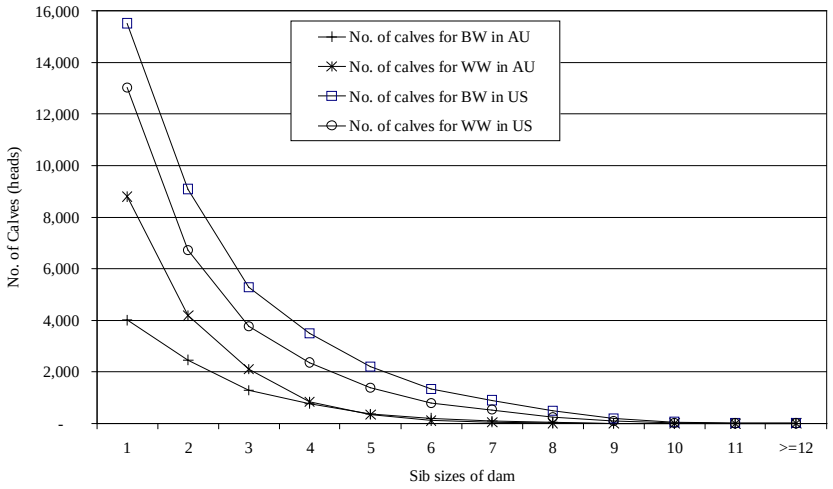
[1] BW = birth weight, WW = weaning weight



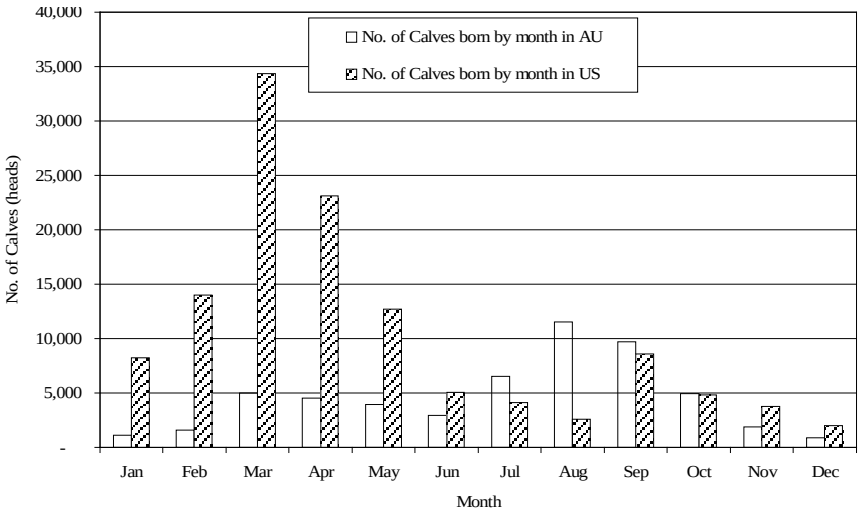
(a)


No. of calves for BW in AU
No. of calves for WW in AU
No. of calves for BW in US
No. of calves for WW in US
No. of Calves (heads)
Age Groups of Dam

(b)


No. of calves for BW in AU
No. of calves for WW in AU
No. of calves for BW in US
No. of calves for WW in US
No. of Calves (heads)
Sib sizes of dam

(c)



(d)

Figure 1. Numbers of calf born (a) by years of birth of calf, (b) by age groups of dam, (c) by sib sizes of dam, and (d) by month.

Model and Analysis

Estimates of (co)variance components and genetic parameters were obtained by restricted maximum likelihood (REML). All calculations were performed using ASReml (8). The fixed effects fitted included contemporary groups (CG), which were concatenated by herd, years of birth of calf, seasons, management groups, and sex of calf. Sex of calf was defined as male and female for BW and defined as bull, heifer, and steer for WW analyses. Age of dam was grouped every 62 days from 600 days, and yielded 50 groups in each country. Age of calf at weighting was fitted as a linear covariable and nested within sex for WW analysis. Random effects were direct additive (a), maternal additive genetics (m) and maternal permanent environmental (pe) effects. Direct-maternal additive genetics covariances were allowed all combinations into the model. The corresponding traits in each country were treated as different traits. Therefore, corresponding traits between both countries assumed no covariance due to maternal permanent environmental and environmental effects {cov (pe1,pe2 and cov (e_1,e_2) = 0} and assumed no covariance between additive genetics and maternal permanent environment effect. The matrix notation was as follows;

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & M_1 & 0 \\ 0 & Z_2 & 0 & M_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where y_1 and $y_2$were the vectors of observations; b_1 and b_2 were the vectors of fixed effects; a_1 and a_2 were the vectors of random direct genetic effects; m_1 and m_2 were the vectors of random maternal genetic effects; pe_1 and pe_2 were the vectors of random

maternal permanent environmental effects; e_1 and e_2 were the vectors of random residual effects; X_1, X_2, Z_1, Z_2, M_1, M_2, W_1 and W_2 were design matrices relating the observations to the respective fixed and random direct, maternal genetics and maternal permanent environmental effects, respectively. The subscripts 1 and 2 were defined according to AU and the US. The random effects in the model had null means and the covariance structure was assumed to be as follows;

$$\text{var}\begin{bmatrix} a_1 \\ a_2 \\ m_1 \\ m_2 \end{bmatrix} = \begin{bmatrix} \sigma^2_{a1} & \sigma_{a1a2} & \sigma_{a1m1} & \sigma_{a1m2} \\ \sigma_{a1a2} & \sigma^2_{a2} & \sigma_{a2m1} & \sigma_{a2m2} \\ \sigma_{a1m1} & \sigma_{a2m1} & \sigma^2_{m1} & \sigma_{m1m2} \\ \sigma_{a1m2} & \sigma_{a2m2} & \sigma_{m1m2} & \sigma^2_{m2} \end{bmatrix} \otimes A$$

$$\text{var}\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} = \begin{bmatrix} I\sigma^2_{pe1} & 0 \\ 0 & I\sigma^2_{pe2} \end{bmatrix}; \qquad \text{var}\begin{bmatrix} e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} I\sigma^2_{e1} & 0 \\ 0 & I\sigma^2_{e2} \end{bmatrix}$$

where σ^2_{a1}, σ^2_{a2} were the direct genetic variances; σ^2_{m1}, σ^2_{m2} were the maternal genetic variances; σ_{a1m1}, σ_{a1m2}, σ_{a2m1}, σ_{a2m2} were the direct-maternal genetic covariances; σ_{a1a2}, σ_{m1m2} were the direct and maternal genetic covariances; σ^2_{pe1}, σ^2_{pe2} were the maternal permanent environmental variances; σ^2_{e1}, σ^2_{e2} were the residual variances; I was the identity matrix; A was the numerator relationship matrix; and $\otimes$ was the direct product.

The genetic parameters were derived from the method of Meyer (1) and de Mattos et al (4,5). Product-moment and Spearman rank correlations were used to further examine ranking changes of common sires breeding values for additive direct (EBV_d) and for maternal genetics (EBV_m) among the environments.

RESULTS AND DISCUSSION

Fixed Effects Estimates

Estimated values for the fixed effect of age groups of dam for both traits of the young dam in AU tended to be higher than in the US. However, the solution patterns were similar between both countries for both traits **(Figure 2)**, which seem to fit with a second degree polynomial. Hence, ages of dam could be fitted as a linear and quadratic form of polynomial into the model as the studied by Meyer (1). Regression coefficients for covariance of ages of calf at weighting within sex were similar between both countries. The coefficients for bull, heifer, and steer were 0.93±0.02, 0.82±0.02 and 0.77±0.05 in AU and 0.92±0.01, 0.85±0.01 and 0.76±0.01 in the US respectively. Those coefficients were nearly the same as Meyer (1), but sex was defined as male and female.

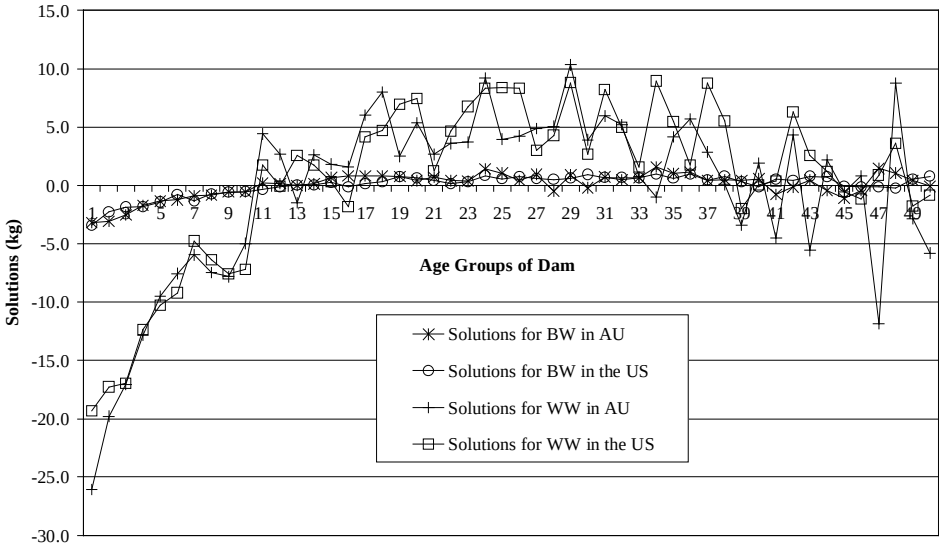


Figure 2. Plotted the solutions of age groups of dam.

(Co)variance Components Estimates

Estimates of (co)variance components are presented in **Table 2**. The direct (σ_a^2) and maternal genetics variances (σ_m^2) for BW in AU were 29.42 and 169.8% higher than in the US respectively. The estimates of maternal permanent environmental variance (σ_{pe}^2) and environmental variance (σ_e^2) in AU were 53.9 and 78.0% of the US respectively. However, the estimates of phenotypic variance (σ_P^2) were not different between both countries. The estimates of σ_a^2 and σ_m^2 for WW in AU were 78.6 and 89.7% of the US while the estimate of σ_{pe}^2 in AU was 12.5% higher than the US. The estimate of σ_e^2 in AU was 74.7% of the US. Therefore, the estimate of σ_P^2 in AU was 81.2% of the US. Those (co)variance components showed remarkable agreement within the range of previous studies reported for BW or/and WW of beef cattle (1,5,9,10,11,12).

Genetic Parameters Estimates

Estimates of genetic parameters are presented in **Table 3**. The estimate of direct heritability (h^2), maternal heritability (m^2) for BW in AU were 26.0 and 183.3% higher than in the US. The estimates of both parameters were higher than previously reported using univariate analysis by Kuha et al (10) except the estimate of maternal permanent environmental variance as a proportion of phenotypic variance (c^2), which was similar. However, after the total heritability (h_T^2) was estimated, the result was not different from the previous study reported by Kuha et al (10). The estimates of m^2, h_T^2

and c^2 for WW in both countries were nearly the same as previous reported by Kuha et al (10) except the estimate of h^2 which is higher in this study.

Table 2. Estimates of (co)variance components of corresponding traits between both countries.

Traits	Birth Weight		Weaning Weight	
(Co)variance components[1]	AU	US	AU	US
σ^2_a	11.92	9.21	237.38	301.91
σ_{a1a2}	9.73		209.74	
σ^2_m	3.13	1.16	96.71	107.78
σ_{m1m2}	1.78		87.43	
σ_{a1m1}	-3.21		-85.96	
σ_{a2m2}	-1.75		-107.27	
σ_{a1m2}	-1.79		-114.95	
σ_{a2m1}	-3.65		-26.61	
σ^2_{pe}	0.27	1.13	84.59	75.20
σ^2_e	6.87	8.81	301.22	403.01
σ^2_p	18.99	18.57	633.90	780.90
log likelihood	-196,759.23		-291,579.42	

[1] σ^2_a = direct genetic variance; σ^2_m = maternal genetic variance; σ_{a1a2} = direct genetic covariance between countries 1 and 2; σ_{m1m2} = maternal genetic covariance between countries 1 and 2; σ_{am} = direct-maternal genetics covariances; σ_{a1m2}, σ_{a2m1} = direct-maternal genetics covariances between countries 1 or 2 and countries 2 or 1 respectively; σ^2_e = environmental variance; σ^2_p = phenotypic variance; and subscript 1 and 2 were Australia (AU) and the United States (US), respectively.

To study the genetics correlation, Van Vleck and Cundiff (12) concluded that there is no genotype by sex if the estimate of genetic correlation ≥ 0.85. In addition, many researchers concluded that no genotype by environment or by country or by production environment interactions if genetic correlation ≥ 0.80 (1,4,6,13). From this study, the estimates of direct (r_a) and maternal genetics correlations (r_m, in parentheses) between both countries for BW and WW were 0.93 (0.93) and 0.78 (0.86), respectively. This indicates that genetic correlations for BW were not significantly different from unity. On the other hand, the genotype by country (G×C) interactions are not present for BW between AU and the US Shorthorn. For WW, the estimate of r_a between AU and the US showed significant difference from unity while r_m was seeming different. This implies that WW in two countries might be influenced by the different genes, and some changes in the ranking of animals on estimated breeding values (EBV) occurs between countries.

Breeding Value Estimates

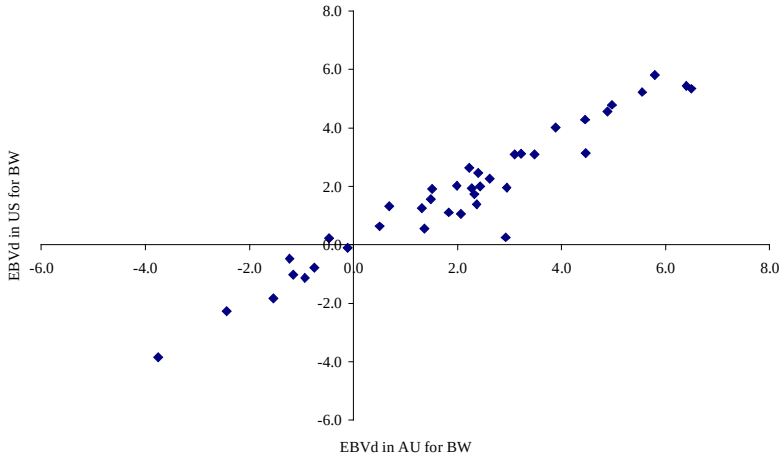
The average (± standard deviation) of estimate breeding values for direct (EBV_d) and maternal (EBV_m, in parentheses) genetic correlations of common sires in

AU and the US were 2.04±2.43 (-0.76±1.27) and 1.76±2.25 (-0.44±0.72) for BW, and 9.46±8.51 (-1.24±6.18) and 11.03±9.72 (-4.68±5.90) for WW, respectively. Product moment and spearman rank correlations (in parentheses) for EBV_d and EBV_m were 0.97 (0.94) and 0.97 (0.95) for BW, and 0.76 (0.71) and 0.85 (0.88) for WW respectively. The correlations are confirmed in **Figure 3** below.

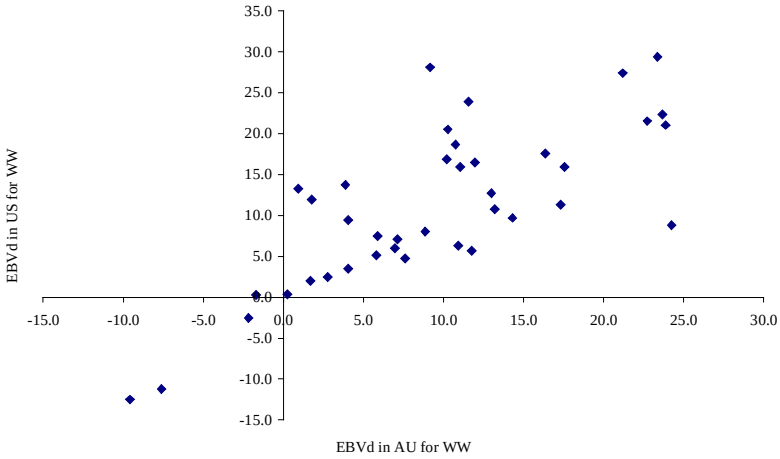
Table 3. Estimates of genetic parameters of corresponding traits between both countries.

Traits / Parameters[1]	Birth Weight		Weaning Weight	
	AU	US	AU	US
h^2	0.63	0.50	0.37	0.39
m^2	0.17	0.06	0.15	0.14
h_T^2	0.46	0.39	0.25	0.25
c^2	0.01	0.06	0.13	0.10
r_a	0.93		0.78	
r_m	0.93		0.86	
r_{a1m1}, r_{a2m2}	-0.52	-0.53	-0.57	-0.59
r_{a1m2}, r_{a2m1}	-0.48	-0.68	-0.91	-0.16

* h^2 = direct heritability; m^2 = maternal heritability; h_T^2 = total heritability; c^2 = maternal permanent environmental variance as a proportion of phenotypic variance; r_a = direct genetic correlation; r_m = maternal genetic correlation; r_{am} = direct-maternal genetic correlation; and r_{a1m2}, r_{a2m1} = direct-maternal genetics correlations between countries 1 or 2 and countries 2 or 1, respectively; and subscript 1 and 2 were Australia (AU) and the United States (US), respectively.



(a)


35.0
30.0
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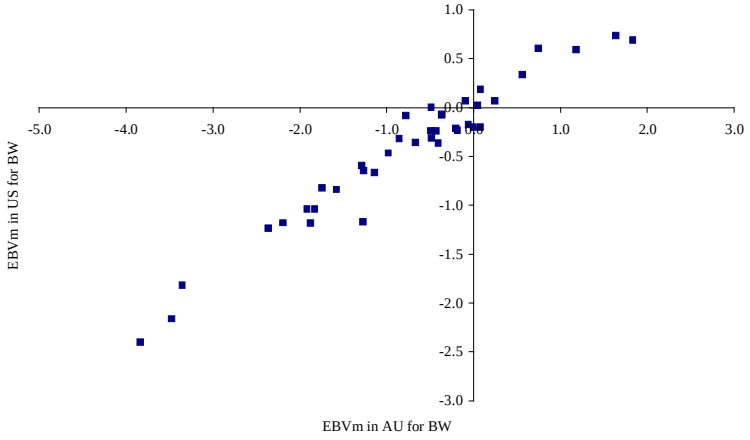
EBVd in US for WW
EBVd in AU for WW

(b)


1.0
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-4.0
-3.0
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2.0
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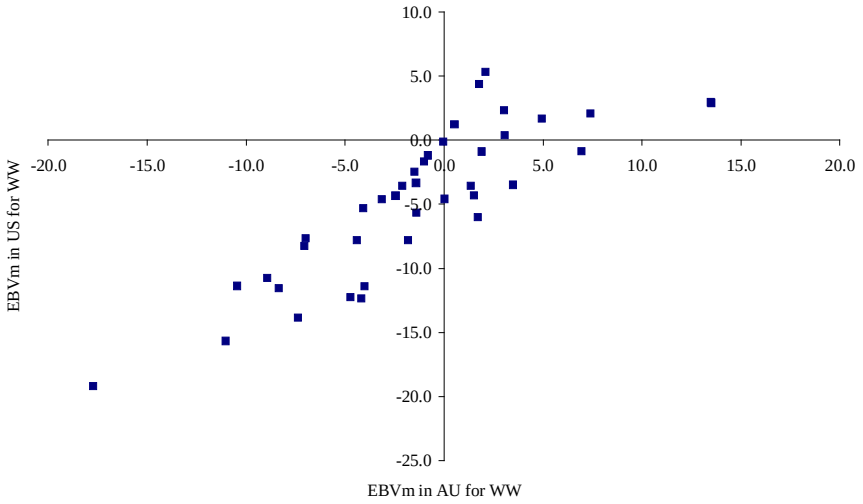
EBVm in US for BW
EBVm in AU for BW

(c)



(d)

Figure 3. Plotted the estimates breeding value of common sires for direct (a,b) and maternal (c,d), for birth weight (a,c) and weaning weight (b,d).

CONCLUSIONS

Direct and maternal genetic correlations (in parentheses) estimates between corresponding traits were 0.93 (0.93) and 0.78 (0.86) for BW and WW, respectively. The results indicated that genotype by country interaction was not affecting for birth weights of Shorthorn beef cattle between both countries. This implied that a joint BW genetic evaluation could be conducted in a model that treated the information as a single population. For WW, jointing sire across AU and the US genetic evaluation needed to consider carefully the G×C interactions, and adjustment factors for each country be need necessary.

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บทคัดย่อ

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ปฏิกิริยาระหว่างพันธุกรรม-ประเทศสำหรับน้ำหนักแรกเกิดและหย่านมของโคพันธุ์ชอร์ทฮอร์นระหว่างประเทศออสเตรเลียและสหรัฐอเมริกา

ลักษณะน้ำหนักแรกเกิดและหย่านมของโคเนื้อพันธุ์ชอร์ทฮอร์นในประเทศออสเตรเลียและสหรัฐอเมริกาถูกนำมาใช้ในการศึกษาปฏิกิริยาระหว่างพันธุกรรม-ประเทศระหว่างประเทศทั้งสอง โดยทำการคัดเลือกข้อมูลซึ่งมีความเชื่อมโยงกับพ่อที่มีลูกเกิดในทั้งสองประเทศ (common sires) ได้ข้อมูลประกอบด้วยพ่อ แม่ และลูก จำนวน 2,013 19,784 และ 42,963 ตัว ในประเทศออสเตรเลีย และ 4,797 38,648 และ 95,849 ตัว ในประเทศสหรัฐอเมริกา ตามลำดับ ลักษณะเดียวกันซึ่งมีแหล่งที่มาจากต่างประเทศกันถูกกำหนดให้เป็นลักษณะที่ต่างกัน ทำการวิเคราะห์ข้อมูลแบบทีละสองลักษณะด้วยโมเดลตัวสัตว์ที่ประกอบด้วยอิทธิพลพันธุกรรมทางตรง อิทธิพลพันธุกรรมและสภาพแวดล้อมถาวรของแม่ โครงสร้างข้อมูลจะไม่มีโควาเรียนซ์กันในอิทธิพลระหว่างสภาพแวดล้อมถาวรของแม่ และสภาพแวดล้อมระหว่างประเทศทั้งสอง กำหนดให้ไม่มีและมีโควาเรียนซ์กันระหว่างอิทธิพลเนื่องจากพันธุกรรมทางตรงกับพันธุกรรมของแม่ตามการวิเคราะห์ที่ 1 และ 2 ตามลำดับ ประมาณองค์ประกอบความแปรปรวนด้วยวิธี restricted maximum likelihood และทดสอบความแตกต่างด้วยวิธี likelihood ratio พบว่า การวิเคราะห์ที่ 2 เหมาะสมกว่าการวิเคราะห์ที่ 1 ค่าองค์ประกอบความแปรปรวนจากทั้งสองประเทศในลักษณะเดียวกันจะต่างกันเพียงเล็กน้อย สหสัมพันธ์พันธุกรรมทางตรงและพันธุกรรมของแม่ (ในวงเล็บ) ระหว่างประเทศทั้งสองจากโมเดลที่ดีที่สุดสำหรับน้ำหนักแรกเกิดและหย่านม เท่ากับ 0.93 (0.93) และ 0.78 (0.86) ตามลำดับ นั่นคือ ลักษณะน้ำหนักแรกเกิดสามารถประเมินค่าทางพันธุกรรมร่วมกันระหว่างประเทศทั้งสองเสมือนเป็นประชากรเดียวกันได้ แต่ทั้งสองประเทศจักต้องคำนึงถึงปฏิกิริยาดังกล่าวเมื่อต้องประเมินค่าทางพันธุกรรมร่วมกันในลักษณะน้ำหนักหย่านม

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