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Genetic Parameters for Weaning Weight, Weaning Hip Height and Weaning Body Length of Crossbred Beef Cattle in Thailand

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ABSTRACT

Genetic parameters for weaning weight (WWT), weaning hip height (WHH) and weaning body length (WBL) of crossbred beef cattle among the Thai Native, Brahman and Charolais breeds raised in central Thailand were estimated using a derivative-free, restricted maximum likelihood algorithm. Multivariate animal models were employed to estimate the direct heritability (h^2) of WWT, WHH and WBL and to estimate the maternal heritability (m^2), the direct-maternal genetic correlation (r_{am}), and the fraction of variance due to maternal permanent environmental effect (c^2) only for WWT. The model fitted contemporary group (CG) and sex as fixed effects and weaning age and breed fractions of Brahman and Charolais as fixed covariates. Estimates of h^2 ranged from 0.54 to 0.68, 0.68 to 0.93 and 0.33 to 0.48 for WWT, WHH and WBL, respectively. The estimates of m^2, r_{am} and c^2 for WWT ranged from 0.20 to 0.23, -0.38 to -0.36 and 0.00 to 0.08, respectively. The direct genetic correlations between traits ranged from 0.59 to 0.98. The high genetic correlations between traits indicated the possibility of performing selection for WWT based on the information from WHH and WBL. A simple direct genetic effect model was determined to be appropriate for analyzing the current data set based on the likelihood ratio test but the estimates of h^2 for traits might bias upward.

Keywords: beef cattle, genetic parameter, weaning weight, weaning body measurement, Thailand

INTRODUCTION

A crossbred type of beef cattle between Thai Native, Brahman and Charolais breeds through a crossbreeding system is widely distributed in central and near central Thailand (Tumwasorn *et al.,* 1993). This breed was initially developed by Kasetsart University at the Buffalo and Beef Production Research and Development Center aiming for the complementation of breeds to achieve the best possible genetic merit of economically important traits (Sopannarath *et al.,* 2005). The crossbred cattle from among those breeds is a type of beef breed that possess some unique characters such as adaptation to a hot climate and a great potential to produce high quality meat (Nilchuen *et al.,* 2012). More often, the herds are kept under a semi-intensive grazing system, whereas the breeding bulls are managed under a regular confinement.

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The performances of pre-weaning traits are determined by both parents' additive genetic merit plus other components (Meyer, 1992; Robinson, 1996). As a result, having their parametric information will be crucial for any attempt to improve the performance of beef cattle. Abundant useful information is available in relation to pre-weaning and some weaning body measurement traits in beef cattle breeds (Meyer, 1993). However, few studies have been made to point out the genetic effects of some tropical beef breeds in Thailand especially for weaning traits (Sopannarath *et al.,* 2005). In addition, genetic parameters are unique to a particular population and may change over time in response to several factors. Moreover, knowing the genetic association between weaning weight and weaning body measurement traits will provide an alternative trait for small-scale farmers to make the right breeding decision since weight performance is not available due to the lack of weighing machines. As a result, the objective of this study was to estimate the genetic parameters in crossbred cattle among the Thai Native, Brahman and Charolais breeds for weaning weight and weaning body measurement traits.

MATERIALS AND METHODS

Data structure

Data from crossbred cattle among the Thai Native, Brahman and Charolais breeds were obtained from the Buffalo and Beef Production Research and Development Center, Thailand and 14 large- and small-scale commercial farms around the central and central fringes of Thailand. The weaning weight (WWT), weaning hip height (WHH) and weaning body length (WBL) of animals born during 2003 to 2012 with 1,178 pedigree records were collected (Table 1). The weaning age ranges for all traits varied from 203 to 266 d. Descriptive statistics for continuous variables are shown in Table 2. The calving season was classified into three seasons—cold (Nov–Feb), hot (March–Jun) and rainy (Jul–Oct). Contemporary groups (CG) were formed by grouping two or more animals born in the same herd, year and season. Only CG with at least two sires and herds with at least two records were used in the analyses.

Statistical analysis and models for estimation of genetic parameters

Preliminary analysis was performed using PROC GLM under the SAS procedure to estimate fixed effects (SAS, 2003). The fixed effects considered in this analysis included CG and sex (male and female). Moreover, the weaning age of animals and breed fractions of Brahman and Charolais were fitted in the model as covariates. (Co)variance components were estimated using the multiple trait, derivative-free, restricted maximum likelihood (MTDFREML) algorithm developed by Boldman *et al.* (1993). Suitability

Table 1 Structure of the data set from crossbred cattle among Thai Native, Brahman and Charolais breeds in the population.

Item	WWT	WHH	WBL
Number of animals in pedigree	1,915	1,915	1,915
Number of animals with records	587	222	222
Number of sires	120	66	66
Number of dams	405	190	190
Number of dams with own and progeny records	12	0	0
No. of CG	35	12	12

WWT = Weaning weight, WWH = Weaning hip height, WBL = Weaning body length, CG = contemporary group.

of the model was considered when a significant (*P* < 0.05) increase in log likelihood occurred while adding additional random effects in the model. Four different models (simple direct genetic effect, direct and maternal genetic effects, direct genetic and maternal permanent environmental effects, and direct, maternal genetic and maternal permanent environmental effects) were used for WWT. However, only a simple direct genetic effect model was used to analyze the data set of WHH and WBL. Because of the structure of the data set, maternal and maternal permanent environmental effects were not considered. These traits were collected from individuals that had their own performance records only. The most complex multivariate animal model in this study can be represented as follows:

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$

$$+ \begin{bmatrix} M_1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} m_1 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} W_1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} c_1 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}$$

Where y is the N × 1 vector of records, the subscripts 1, 2, and 3 represent WWT, WHH and WBL, respectively, b is the vector of fixed effects, a is the vector of random direct genetic effects, m is the vector of random maternal genetic effects, c is the vector of random maternal permanent environmental effects and e is the vector of random residual effects. X, Z, M and W are incidence matrices relating records to fixed, direct genetic, maternal genetic and maternal permanent environmental effects, respectively.

The assumption of the first moment is:

$$E\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix}$$

and the (co)variance matrix for genetic effects is as follows

$$G = G_0 \otimes A$$

Table 2 Descriptive statistics for weaning weight (WWT), weaning hip height (WHH) and weaning body length (WBL) traits of crossbred beef cattle.

Trait	Covariate factor	Number	Mean	SD	Minimum	Maximum
WWT (kg)		587	159.09	37.08	95.00	257.00
	WAGE (days)		218.97	28.17	141.00	265.00
	N		0.28	0.09	0.09	0.75
	B		0.27	0.09	0.00	0.75
	C		0.46	0.14	0.00	0.75
WHH (cm)		222	101.48	7.75	79.00	120.00
	WAGE (days)		210.40	25.75	147.00	264.00
	N		0.26	0.07	0.13	0.63
	B		0.25	0.05	0.13	0.50
	C		0.50	0.09	0.00	0.75
WBL (cm)		222	94.71	9.87	70.00	150.00
	WAGE (days)		210.43	25.80	147.00	264.00
	N		0.26	0.07	0.13	0.63
	B		0.25	0.05	0.13	0.50
	C		0.50	0.09	0.00	0.75

WAGE = Weaning age, N = breed fraction of Thai Native, B = breed fraction of Brahman and C= breed fraction of Charolais

$$\text{where} \quad G_0 = \begin{bmatrix} \sigma^2_{a_1} & \sigma_{a_{12}} & \sigma_{a_{13}} & \sigma_{a_1 m_1} \\ \sigma_{a_{12}} & \sigma^2_{a_2} & \sigma_{a_{23}} & \sigma_{a_2 m_1} \\ \sigma_{a_{13}} & \sigma_{a_{23}} & \sigma^2_{a_3} & \sigma_{a_3 m_1} \\ \sigma_{a_1 m_1} & \sigma_{a_2 m_1} & \sigma_{a_3 m_1} & \sigma^2_{m_1} \end{bmatrix}$$

The (co)variance matrix for permanent environmental effects is as follows:

$$C = C_0 \otimes I_c$$

$$\text{where} \quad C_0 = \begin{bmatrix} \sigma^2_{c_1} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

The (co)variance matrix for residual random error is as follows:

$$R = R_0 \otimes I$$

$$\text{where} \quad G_0 = \begin{bmatrix} \sigma^2_{e_1} & \sigma_{e_{12}} & \sigma_{e_{13}} \\ \sigma_{e_{12}} & \sigma^2_{e_2} & \sigma_{e_{23}} \\ \sigma_{e_{13}} & \sigma_{e_{23}} & \sigma^2_{e_3} \end{bmatrix}$$

and σ^2_a is the direct genetic variance, σ^2_m is the maternal genetic variance, σ_{am} is the direct and maternal genetic covariance, σ^2_c is the maternal permanent environmental variance, σ^2_e is the residual variance, A is the numerator relationship matrix and I is the identity matrix.

A mixed model equation was used to obtain the best linear unbiased estimator of fixed effects and best linear unbiased predictor of random effects. The program was restarted until the -2logL values did not change at level of 1×10^{-9} (global minimum of -2logL). At the beginning, single trait analysis was undertaken and then multiple trait analysis was accomplished using the results from the single trait analysis as starting values. Finally, the results of variance components were used to estimate genetic parameters.

Moreover, models were compared using the log likelihood ratio test method. The model having a higher value of the log likelihood, indicated a better fit model should be chosen. If there is not a significant difference between models, the model with the fewest number of parameters is the better model (Sopannarath *et al.,* 2003).

RESULTS AND DISCUSSION

Analysis of variance specified that the WWT, WHH and WBL traits were influenced ($P < 0.01$) by CG, the age at weaning and the breed fraction of Charolais. Male calves were heavier than female calves at weaning ($P < 0.01$) but male WHH and WBL values did not differ from female values. Increasing the Brahman breed fraction significantly improved WWT and increasing the Charolais breed fraction yielded higher WWT, WHH and WBL compared with Thai Native breed ($P < 0.01$). The highly significant ($P < 0.01$) effect of CG found in this study coincided with several literature results; Afolayan *et al.* (2002) reported that the calves born in two distinct years that were a subgroup of CG did not show similar trait performance. Accordingly, the calves that were born in previous years possessed larger weight, height, length and girth than ones that was born three years later. Similarly, sex significantly ($P < 0.05$) affected WWT but did not affect WHH and WBL. In contrast, Riley *et al.* (2007) found that males had greater weaning hip height than females. Female calves were always lighter and smaller than their male counterparts with the certainty that the gap would increase as calves grew older (Gilbert *et al.,* 1993).

In the current studied population, the breed fraction effects of Brahman and Charolais statistically influenced only WWT ($P < 0.01$). However, weaning body measurement traits (for example, heart girth and body length) were found to be influenced by breed types, and Hereford calves were recognized to have shorter body length and smaller heart girth than calves from the Angus beef breed (Gilbert *et al.,* 1993).

The variance components and genetic parameters are presented in Table 3. Heritability

(h^2) estimates were high for all considered traits and ranged from 0.52 to 0.68, 0.68 to 93 and 0.33 to 0.48 for WWT, WHH and WBL, respectively. On the other hand, estimates of maternal genetic effect (m^2) were in the range 0.20–0.23 for WWT in the studied population. Nevertheless, the fractions of the variance due to maternal permanent environmental effect (c^2) were close to zero (0.00–0.08).

Estimates of h^2 for WWT identified in this study were found to be in the same range reported by many authors. Meyer (1993) studied beef cattle in Australia and reported an estimate of h^2 (0.45) from a direct-maternal model ($r_{am} \neq 0$). Dodenhoff *et al.* (1998) also reported the same estimate (0.45 ± 0.07) for the estimate of WWT. On the other hand, the h^2 estimate for crossbreeds in Thailand was reported to be 0.23 ± 0.07 (Jeanmas *et al.,* 2008) which is smaller by almost half than that of the present study. However, the estimate of h^2 (0.37) revealed by Supakorn *et al.* (2005) was relatively close to the crossbreed value. The variation of estimates from applying several models has been reported frequently in the past. Sopannarath *et al.* (2003) reported that h^2 estimates of WWT vary from 0.17 ± 0.02 to 0.47 ± 0.02 by using different models.

Estimates of m^2, r_{am} and c^2 for WWT from multivariate analysis are also presented in Table 3. The identified m^2 (0.20–0.23) in the current study was found to be in agreement with several findings in the literature. The results revealed by Bertrand and Benyshek (1987) and by Dodenhoff *et al.* (1999) for Brangus and Limousin cattle (0.20 and 0.22) were in agreement with the current study. Moreover, the estimate of m^2 (0.08) reported by Jeanmas *et al.* (2008) was within the lower part of the range. An antagonistic association between the direct and maternal genetic effects of WWT was identified in the current study. The estimate of r_{am} found in the current study coincided with several studies for different beef breeds. Estimates of r_{am} can vary from highly negative to significantly positive values. Accordingly, Mattos *et al.* (2000) found negative values that ranged from -0.66 to -0.22, from -0.54 to -0.20 and from -0.57 to -0.41 from their study using samples from the USA, Canada and Uruguay, respectively. In contrast, Meyer (1992) reported positive estimates of r_{am} of 0.19 and 0.22 for Angus beef cattle in Australia. It has been mentioned by numerous studies that the permanent environmental variance due to the dam as a proportion of phenotypic variance (c^2) has a big impact on the economically important traits of beef cattle, particularly WWT (Meyer, 1992; Robinson, 1996; Sopannarath *et al.,* 2003).

Even though the magnitudes of m^2, r_{am} and c^2 for WWT identified in the current study seemed to influence the WWT of the population investigated, the log likelihood ratio tests showed that it was not significantly important in the current population. Sopannarath *et al.* (2003) revealed estimates of c^2 that ranged from 0.11 ± 0.01 to 0.17 ± 0.01 using several models. Similarly, the estimate of c^2 in crossbred beef cattle in Thailand was 0.10 ± 0.07 (Jeanmas *et al.,* 2008).

The variance component and heritability estimates from multivariate analysis for WHH and WBL traits are presented in Table 3. Numerous studies in the literature revealed that most of the weaning body measurement traits have moderate to high h^2 estimates (Gilbert *et al.,* 1993). Furthermore, Afolayan *et al.* (2007) reported relatively similar range estimates of h^2 (0.42 ± 0.10) for body height and moderate h^2 (0.25 ± 0.08) for body length. The estimates of h^2 found in the current study for WHH and WBL were inconsistent with previous research outcomes such as Vargas *et al.* (2000) who reported on h^2 for WHH (0.73) and hip height at 18 months of age (0.87) and Nephawe *et al.* (2004) who reported on h^2 (0.71 ± 0.05) for mature height. Moreover, the estimate of h^2 changes within the same population over time. Accordingly, the h^2 estimates for hip height and body length were 0.43 ± 0.13 and 0.25 ± 0.10 at weaning and 168 d later were 0.57 ± 0.16 and 0.38 ± 12 at the post weaning gain test date (Gilbert *et al.,* 1993).

Table 3 Estimates of variance components of the models studied for weaning weight, weaning hip height and body length traits and genetic parameters from multivariate analysis.

Item	Traits		
	Weaning weight (kg)	Weaning hip height (cm)	Weaning body length (cm)
Model 1(simple additive animal model)			
σ_a^2	690.99	32.80	29.43
σ_p^2	1,023.09	35.31	60.87
h^2	0.68	0.93	0.48
e^2	0.32	0.07	0.52
-2logL	6,309.24	6,309.24	6,309.24
Model 2 (direct additive and maternal model)			
σ_a^2	550.81	22.75	20.17
σ_m^2	200.90	-	-
$\sigma_{a_i m_{WWT}}$	-125.84	28.96	0.00
σ_p^2	994.83	33.23	59.01
h^2	0.55	0.68	0.34
m^2	0.20	-	-
r_{am}	-0.38	0.43	0.00
e^2	0.37	0.32	0.66
-2logL	6,305.41	6,305.41	6,305.41
Model 3 (direct additive and maternal permanent environmental model)			
σ_a^2	591.95	32.74	29.23
σ_c^2	80.34	-	-
σ_p^2	1,010.45	35.32	60.38
h^2	0.59	0.93	0.48
c^2	0.08	-	-
e^2	0.33	0.07	0.52
-2logL	6,308.63	6,308.63	6,308.63
Model 4 (direct additive, maternal and maternal permanent environmental models)			
σ_a^2	531.09	24.36	19.78
σ_m^2	230.84	-	-
$\sigma_{a_i m_{WWT}}$	-125. 89	55.62	37.53
σ_c^2	0.00	-	-
σ_p^2	990.76	33.50	59.09
h^2	0.54	0.73	0.33
m^2	0.23	-	-
$r_{a_i m_{WWT}}$	-0.36	0.74	0.56
c^2	0.00	-	-
e^2	0.36	0.27	0.67
-2logL	6,302.48	6,302.48	6,302.48

[1] σ_a^2 = direct additive genetic variance, σ_m^2 = maternal additive genetic variance, $\sigma_{a_i m_{WWT}}$ = covariance between direct additive variance of trait i (weaning weight = WWT, weaning hip height = WHH and weaning body length = WBL) and maternal genetic variance of WWT, σ_c^2 = maternal permanent environmental variance, σ_p^2 = phenotypic variance. h^2 = direct heritability, m^2 = maternal heritability, $r_{a_i m_{WWT}}$ = genetic correlation between direct additive effect of trait i (WWT, WHH and WBL) and maternal genetic effects of WWT, c^2 = fraction of variance due to permanent environmental effects, e^2 = residual effect.

Table 4 Direct genetic (above the diagonal) and phenotypic correlations (below the diagonal) between weaning weight (WWT), weaning hip height (WHH) and weaning body length (WBL) from simple direct genetic effect model.

Item	Weaning weight	Weaning hip height	Weaning body length
WWT	-	0.59	0.65
WHH	0.39	-	0.98
WBL	0.46	0.61	-

Estimates of direct genetic and phenotypic correlation between WWT, WHH and WBL for the simple direct genetic effect model are shown in Table 4. The outputs of the current study indicated that all traits are positively genetically correlated with each other. Moreover, the direct genetic correlations between WWT, WHH and WBL were higher than the corresponding phenotypic correlations. The results found in this study coincided with results revealed by several studies; Vargas *et al.* (2000) reported relatively higher phenotypic correlation (0.54) between WHH and WWT, while Gilbert *et al.* (1993) reported lower (0.37) and higher (0.75) values for the direct genetic and phenotypic correlation between WHH and WBL, respectively.

The -2logL results for the four different models used are presented in Table 3. Based on the log likelihood ratio tests, there were no statistically significant differences between the models considered. However, a relatively smaller variance was obtained from Model 4 that involved maternal and maternal permanent environmental effects for WWT. Moreover, Nuez-Dominguez *et al.* (1993) suggested that traits such as the birth weight, WWT and yearling weight of the calf are known to be influenced by the maternal permanent environment, which is due in part to the genetic makeup of the cow.

CONCLUSION AND RECOMMENDATIONS

The high h^2 estimates of the direct genetic effects for all the considered traits suggest that selection for these traits will provide an effective genetic progress in the population. This study showed that the model with only direct effects was the most appropriate. Even though the maternal genetic effect and direct-maternal correlation (m^2 and r_{am}, respectively) did not significantly influence the studied traits, the results obtained from the model with those effects seemed to be more reasonable. In addition, the high genetic correlations between traits indicated the possibility of performing selection for WWT based on the information from WHH and WBL.

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