THESIS APPROVAL

GRADUATE SCHOOL, KASETSART UNIVERSITY

Master of Science (Tropical Agriculture)

DEGREE

Tropical Agriculture	Agriculture
FIELD	**FACULTY**

TITLE: Genetic Parameters for Pre-weaning Growth and Some Body Measurement Traits of Crossbred Cattle among Thai Native, Brahman and Charolais (and /or Kamphaengsaen) Breed in Thailand

NAME: Mr. Tamirat Tessema Teklemichael

THIS THESIS HAS BEEN ACCEPTED BY

THESIS ADVISOR

(Assistant Professor Panwadee Sopannarath, Ph.D.)

THESIS CO-ADVISOR

(Associate Professor Sornthep Tumwasorn, Ph.D.)

GRADUATE COMMITTEE CHAIRMAN

(Associate Professor Yingyong Paisooksantivatana, Ph.D.)

APPROVED BY THE GRADUATE SCHOOL ON

DEAN

(Associate Professor Gunjana Theeragool, D.Agr.)

THESIS

GENETIC PARAMETERS FOR PRE-WEANING GROWTH AND SOME BODY MEASUREMENT TRAITS OF CROSSBRED CATTLE AMONG THAI NATIVE, BRAHMAN AND CHAROLAIS (AND/OR KAMPHAENGSAEN) BREED IN THAILAND

TAMIRAT TESSEMA TEKLEMICHAEL

A Thesis Submitted in Partial Fulfillment of
the Requirements for the Degree of
Master of Science (Tropical Agriculture)
Graduate School, Kasetsart University
2012

Tamirat Tessema Teklemichael 2012: Genetic Parameters for Pre-weaning Growth and Some Body Measurement Traits of Crossbred Cattle among Thai Native, Brahman and Charolais (and/or Kamphaengsaen) Breed in Thailand. Master of Science (Tropical Agriculture), Major Field: Tropical Agriculture, Faculty of Agriculture. Thesis Advisor: Assistant Professor Panwadee Sopannarath, Ph.D. 61 pages.

Genetic parameters for birth and weaning weights and some body measurement traits in crossbred beef cattle among Thai Native (N), Brahman (B) and Charolais (C) raised in central part of Thailand were estimated using MTDFREML. Single trait, bivariate and multiple trait models were employed to estimate the direct heritability (h^2) of birth weight (BWT), weaning weight (WWT), weaning hip height (WHH) and weaning body length (WBL), maternal heritability (m^2) and fraction of variance due to maternal permanent environmental effect (c^2) for BWT and WWT, and direct genetic correlation between all traits by fitting contemporary groups (CG) and sex as fixed effect and weaning age (WAGE) for WWT, WHH and WBL, breed fraction of B and C as covariate. Estimates of h^2 ranged from 0.46 to 0.51, 0.43 to 0.70, 0.87 to 0.97 and 0.45 to 0.50 for BWT, WWT, WHH and WBL, respectively. The estimate of m^2 and c^2 were 0 and 0.01 for BWT, 0 to 0.18 and 0.19 for WWT, respectively. The direct additive genetic correlations between traits ranged from 0.48 to 0.97. Single, bivariate and multiple trait animal models fitting only additive effect was fitted the data better than the alternative models used to analyze the data set. Further research is needed due to the problems associated with the estimation of maternal components. Any attempt of considering the result of this study for breeding program of the studied population could lead to an accelerated genetic improvement.

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Student's signature Thesis Advisor's signature

ACKNOWLEDGMENT

First and foremost I thank God; the loving father, for his indispensable gift and providence throughout my life.

My first gratitude will go to my advisor Assistant Professor Dr. Panwadee Sopannarath. I would like to gratefully and sincerely thank and pay homage for her guidance. Her mentorship was paramount in providing a well rounded experience. Under her guidance I successfully overcame many difficulties and learned a lot. Her unflinching courage and conviction will always inspire me, and I hope to continue to work with her marvelous thoughts. I am also extremely indebted to my co-advisor Associate Professor Sornthep Tumwasorn for providing me invaluable experience and knowledge. I am thankful to him for picking me up as a student at the decisive stage of my MSc study. It is just a privilege to be his student and I wish him a long and joyful life. I would also like to thank the external examiner Assoc. Prof. Dr. Monchai Duangjinda.

I owe a great deal of appreciation and gratitude and heartfelt thank to all KU professors those in the department of animal science for their knowledge and assistance in helping me to grow as an independent thinker. I would also like to express my gratitude to Rural Capacity Building Project (RCBP) of the ministry of agriculture and rural development of Ethiopia, Oromia Agricultural Research Institute (OARI) and Yabello pastoral and dry land agriculture research center (YPDRC) for giving me the chance to pursue my MSc study and supported me financially.

It is also a privilege to express my deep sense of gratitude for my mother Mrs. Mulu, father Mr. Tessema, brothers and sisters. I simply wish them a long lasting success and joy. I would also like to express my gratefulness to all Thai and Ethiopian friends those who gave me good advice, support and friendship during my stay at Kasetsart University (KU).

Tamirat Tessema
October 2012

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LIST OF ABBREVIATION

A = Numerator relationship matrix

B = Brahman

BWT = Birth weight

C = Charolais

c^2 = Fraction of variance due to maternal permanent environmental effect

CG = Contemporary group

cm = Centimeter

e^2 = Fraction of variance due to random residual effect

h^2 = Heritability

I = Identity matrix

m^2 = Maternal heritability

r_{am} = Direct-maternal genetic correlation

N = Thai Native

WBL = Weaning body length

WHH = Weaning hip height

WWT = Weaning weight

σ_a^2 = Direct genetic variance

σ_{am} = Direct-maternal genetic covariance

σ_c^2 = Maternal permanent environmental variance

σ_e^2 = Random residual variance

σ_m^2 = Maternal genetic variance

σ_p^2 = Phenotypic variance

GENETIC PARAMETERS FOR PRE-WEANING GROWTH AND SOME BODY MEASUREMENT TRAITS OF CROSSBRED CATTLE AMONG THAI NATIVE, BRAHMAN AND CHAROLAIS (AND/OR KAMPHAENGSAEN) BREED IN THAILAND

INTRODUCTION

Cattle farming has been widely practiced in Thailand before the existing situation was changed and predominantly the cattle population of the country is exclusively used for beef production due to boosted mechanization over the past years. As it is reported by DLD (2008) the number of beef cattle in the country is estimated to be around 9 millions which comprise around 4.9 millions in the North Eastern region. The country undergoes considerable activities to improve the potential of Native cattle using crossbreeding technique as a major tool. To get succeed this objective many potential beef breeds such as Brahman and Charolais have been imported from western countries (Chauychuwong *et al.*, 1997). The emerging increased crossbred cattle population is the outcome of imported high potential exotic beef breeds to the country.

Tumwasorn *et al.* (1982) reported the trend of crossbred beef cattle population and explained as their number is tremendously increasing from time to time. Now a day, one-third of the cattle population of the country is found to be crossbred (Waritthitham *et al.*, 2010). Kamphaengsaen breed is one of the beef breed which is derived from 25% Thai Native, 25% Brahman and 50% Charolais through cross breeding system (Tumwasorn *et al.*, 1993). Introduction of the newly developed breed is an ongoing activity which already started centralizing on the surrounding farmers.

Sopannarath *et al.* (2003) explained as regular evaluation of performance would be beneficial in order to assure and increase the efficiency of beef production as a sustained business firm. Likewise, several livestock breeders stated as precise estimate of genetic parameters are required for designing and implementing of well-organized genetic improvement program (Wasike *et al.*, 2006). Having the awareness of genetic information such as heritability and genetic correlations of a particular cattle breed is essential to carry out efficient breeding scheme (Correa *et al*., 2006). Because, those information are very crucial if, determining selection methods and forecasting genetic merits for the considered population is required (Cardoso *et al*., 2004). Moreover, knowing the genetic relationships between mature size and rate of maturity with that of early growth has a paramount importance to plan breeding program for beef cattle (Meyer, 1995). Furthermore, genetic evaluation is helpful if genetic and non-genetic parameters for each cattle breed population are estimated (Cepon *et al*., 2008).

Additionally, several literatures made clear as body measurements of beef cattle can be employed for a number of uses such as prediction of growth rate, to determine nutritional requirements, to find out body condition and conformation (Wilson *et al.*, 1997). As a result, breeders frequently consider linear body measurements to execute strategies for the genetic improvement of beef cattle (Jenkins *et al*., 1991).

Previous estimates of genetic parameters have been found variable based up on utilized models (Kaps *et al*., 1999) and the nature of a particular data set and the type of trait considered for the study (Rumph *et al*., 2002). Consequently, having performed analysis using different models will help to identify the best models that fit to a particular data which intern desperately helpful up on deciding the right breeding decision. Moreover, Waritthitham *et al.* (2010) explained there is limited genetic parameter information in regard to some important traits on the performance of crossbred beef cattle population in Thailand. Therefore, there is a need to act upon estimating genetic information on growth and linear body measurement characteristics of the crossbred cattle in the country.

OBJECTIVES

1. To estimate variance components and genetic parameters for pre-weaning growth of crossbred cattle among Thai Native, Brahman and Charolais (and/or Kamphaengsaen) breeds in Thailand.

2. To estimate the genetic correlation between pre-weaning growth and some body measurement traits in the beef cattle population.

LITERATURE REVIEW

Zebu breed is the predominant cattle found in larger proportion in tropical areas. This breed thrives well under the stringent environments of tropical areas. Adaptation to the warm climate, resistance to diseases and low feed in the tropics are few worth mentioning among others (McDowell, 1972). Contrarily, growth performance and beef type traits of Zebu breed were reported to be relatively very low (Ozluturk *et al.*, 2006; Waritthitham *et al.*, 2010). These traits can be improved through crossbreeding technique that is extensively used to improve the productivity of beef cattle. Crossbreeding helps maximize the desirable outcomes of heterosis effects and utilization of disparity between breeds for the best possible genetic merit and performance under a range of environmental conditions (Brandt *et.al.* 2010). However, crossbreeding as a prerequisite requires knowledge of genetic parameters and distinction among breed which will help decide to selecting individual animals for crossbreeding based on their favorable futures to be used as parents of next generation. Performance evaluation is a common practice and a corner stone for a sustained beef production improvement (Sopannarath *et. al.*, 2003). Thus, the purpose of beef cattle evaluation is to identify the best performing animals that are suitable for a given environment. Ultimately, selection decision will be made for predetermined objectives based on breeding values predictions performed on all animals available as breeding stock prior to selection.

However, the presence of genetic resentment between animal effects which broadly varies among breeds causes complications on the prediction of the total genetic worth (Robinson, 1996b). Birth weight and weaning weight are determined by animals’ own additive merit and the ability of the dam in providing adequate maternity at prenatal and postnatal stage that ensure the normal subsequent development and growth rate of her calf (Meyer, 1992; Robinson, 1996a). Subsequently, the maternal component is subdivided in to maternal additive genetic effect and maternal permanent environmental effect (Sopannarath, 2002).

Genetic parameters are the bases for improvement of breeding programs. Yet substantial dissimilarity exists in the literature up on estimates of direct and maternal effects and their variance and covariance components (Meyer, 1992). Methods of estimation, statistical models, experimental data resources or field data, breeds and production systems, assortative mating or previous selection are some of the factors that are reported to affect the estimates of (co)variance components and genetic parameters (Shi *et. al.*, 1993).

Factors affecting genetic parameter estimates of growth traits

Models: In the genetic improvement of livestock, animal breeders employ a number of models to estimate or predict different parameters. Models might differ based on the data set, type and number of trait considered in a particular study (Table 1). Meyer (1992) illustrated the different characteristic of different models and the disparity of results obtained between various models for a particular data set. Similarly, Sopannarath *et al.* (2003) reported a noticeable result difference between models utilized to fit a particular data set in the study of weaning weight parameters, estimation of direct and maternal effects and their correlation. These authors reported reduction of the estimated values by up to 58% to 64% when adding maternal permanent environmental effects on some models. Having noticed variation in fitting models, Meyer *et al.* (1993) justified that fitting both dams' genetic and permanent environmental effect was considered the best model for weaning weight than the alternative models used.

Table 1 Variance components and genetic parameters for birth weight (BWT) and weaning weight (WWT) of beef cattle.

Models[1]	Variance components[2]						Genetic parameters[3]				LogL[4]
	σ_a^2	σ_m^2	σ_{am}	σ_c^2	σ_e^2	σ_p^2	h^2	m^2	r_{am}	c^2	
---BWT---											
Model 1	10.54	-	-	-	8.24	18.78	0.56	-	-	-	-42.76
Model 2	9.24	-	-	1.86	7.63	18.52	0.49	-	-	0.10	-12.48
Model 3	7.28	2.63	-	-	8.16	18.52	0.39	0.14	-	-	-4.18
Model 4	7.61	1.55	0.13	0.94	8.30	18.37	0.41	0.08	0.05	0.04	0.00
---WWT---											
Model 1	223.00	-	-	204.50	648.40	871.30	0.27	-	-	-	-236.90
Model 2	86.50	-	-	251.50	527.70	865.80	0.10	-	-	0.29	-15.14
Model 3	66.20	328.20	-	-	561.80	956.30	0.07	0.34	-	-	-67.55
Model 4	120.40	115.50	-69.20	201.30	505.60	873.60	0.14	0.13	-0.59	0.23	0.00

[1] Model 1 = simple animal model; Model 2 = model with permanent environmental effects due to dam and assumed no correlation with all other effects in the model; Model 3 = model with all maternal effects to the genotype of the dam, fitted the maternal genetic effect as a second random effect for each animal with the same covariance structure as the direct additive genetic effects and assumed $r_{am} = 0$ and Model 4 = model included maternal a permanent environmental and a genetic material effect with $r_{am} \neq 0$.

[2] σ_a^2 =direct genetic variance; σ_m^2 = maternal genetic variance; σ_{am} = direct-maternal genetic covariance; σ_c^2 = permanent environmental variance; σ_e^2 = random residual variance; σ_p^2 = phenotypic variance

[3] h^2 = direct heritability; m^2 = maternal heritability; r_{am} = direct-maternal genetic correlation; c^2 = fraction of variance due to maternal permanent environmental effect

[4] LogL = log likelihood expressed as deviation from model with the highest value.

Source: Meyer (1992)

In addition, Rumph *et al.* (2002) explained as there is difference between models in accommodating information of different genetic and variance estimates. Furthermore, some models may cause inflation on estimating genetic parameters. This can be easily realized from varied genetic parameters and variance estimates obtained from different models for birth and weaning weights (Meyer *et al.,* 1993). Thus, model that accommodate more information is assumed to be relatively efficient than models which accommodate less information.

Breed Group: Bourdon (2000) explained as genetic parameters are not fixed, they do vary from population to population and from environment to environment. Genetic parameter estimates for growth traits were found different from one type of breed to the other type. As a result, the estimate obtained by using the data from a particular group of beef cattle is specific to that particular population (Falconer and Mackay, 1996). Genetic parameter estimates made by Meyer (1992) clearly stated the variation of parametric estimates among breeds by confirming direct heritability (h^2) estimates of 0.41 ± 0.04 and 0.36 ± 0.05; maternal heritability (m^2) of 0.08 ± 0.02 and 0.07 ± 0.03 and direct-maternal genetic correlation (r_{am}) of 0.01 ± 0.04 and 0.05 ± 0.03 for birth weight in Hereford and Angus beef breed, respectively. Under the same study the parametric variation across breeds of weaning weight was explored and the results were 0.14 ± 0.03, 0.20 ± 0.05 and 0.58 ± 0.11 (h^2); 0.13 ± 0.03, 0.14 ± 0.04, and 0.36 ± 0.08 (m^2) and -0.08 ± 0.03, 0.04 ± 0.04 and -0.36 ± 0.08 (r_{am}) for Hereford, Angus and Zebu crossbred beef cattle, respectively.

Paternal Environment Interaction: Sopannarath (2003) explained that, when there is variation among progeny groups, interaction of sire and herd occurs implying that the genetic correlations along with expressions of the same genotype in different herds are found to have lesser amount of unification. Variation up on interaction is due to varied variances between herds. Olson *et al.* (1991) made clear that weight traits would significantly influenced by the effects of interaction of locations and breed groups. Bertrand and Benyshek (1987) confirmed as paternal environmental interactions such as sire × herd and sire × contemporary group are vital and predicting genetic values of sires for weaning weight should consider these factors.

Maternal Influence: Sopannarath (2003) confirmed that consideration of maternal genetic and environmental effects in the process of estimating parameters for weaning weight in Hereford beef cattle would be associated with the reduction of those effects. Also, Diop *et al.* (1999) explained that dam effects known to be one of the factors that influence growth traits of beef cattle. Maternal effect which usually greatly concurred with the direct genetic effect of calves, regularly affects pre-weaning growth trait (Gutierrez *et. al.,* 1997). Based on literatures reviewed, Cucco *et al*. (2010) explained estimates of m^2 for pre-weaning growth traits increases as a result of substantial influence of the dam until 18 months of age. As a result, Taheri and Reza (2009) confirmed that there was antipathy between direct and maternal effects, and described that paying no attention to maternal effects during genetic parameter estimation for growth traits leads to overestimation of direct genetic effects.

Direct and maternal heritabilities for growth traits

Improvement of growth performance in beef cattle related to meat output for a given production system is very important (Eler *et. al.,* 1995). Knowledge of genetic parameters is crucial in planning suitable breeding program and at early growth of beef cattle genetic parameters. Estimate of h^2 would be very vital for genetic evaluation of performance traits (Dodenhoff *et. al.,* 1999). The estimates for all parameters are specific to a population and time (Waldron *et al.,* 1993).

Bennett and Gregory (1996) estimated the direct and maternal heritabilityies for composite beef cattle breeds in U.S. Meat Animal Research Center. The composite beef cattle breeds were called as MARC I (1/4 Braunvieh, 1/4 Charolais, 1/4 Limousin, vAngus, and vHereford), MARC II (1/4 Gelbvieh, 1/4 Simmental, 1/4 Angus, and 1/4 Hereford), and MARC III (1/4 Pinzgauer, 1/4 Red Poll, 1/4 Angus, and 1/4 Hereford) and estimates of h^2 were 0.56, 0.54, and 0.54 for birth weight and 0.40, 0.36 and 0.34 for weaning weight respectively and in the mean time m^2 were 0.72, 0.71 and 0.67 for birth weight and 0.54, 0.42 and 0.48 for weaning weight consequently. Recently, Jeanmas (2008) reported estimates of h^2 for birth and weaning weights were 0.21, 0.23 and estimates of m^2 were 0.18, 0.08 respectively in crossbred beef cattle among Thai Native, Brahman and Charolais under Kamphaengsaen beef breeding program in Thailand. Ahunu *et al.* (1997) performed a study on Ndama and West African Shorthorn crossbred cattle at University of Ghana Agricultural Research Station, Kpong and reported estimates of h^2 0.45 ± 0.08 for birth weight and 0.38 ± 0.18 and 0.32 ± 0.15 estimates of h^2 and m^2 for weaning weight, respectively. Similarly, in the study carried at National Cattle Breeding Station Belmont in Central Queensland, Australia on a composite beef breed (Belmont Red cattle), Burrow (2001) found that the estimates of h^2 and m^2 were found to be 0.57 and 0.17 for birth weight and 0.18 and 0.34 for weaning weight, respectively.

Moreover, Bertrand and Benyshek (1987) performed genetic parameter estimation of Brangus beef cattle breed utilizing the data obtained from the International Brangus Breeders Association and estimates of h^2 and m^2 ranged from 0.25 to 0.28 and 0.13 to 0.20 for birth weight and weaning weight, respectively. Additionally, the study made by Schoeman *et al.* (2000) in South Africa on a synthetic beef cattle population, the estimates of h^2 were 0.66 and 0.53 and estimates of m^2 were 0.22 and 0.36 for birth weight and weaning weight, respectively. When the situation is analyzed based on the literatures reviewed, while some of the estimates are found in agreement with each other, contradictions of some others is also certainly observed (Table 2).

Nelsen *et al.* (1986) carried out a research at U.S. Department of Agriculture and Montana Agriculture Experiment station on using paternal half sib procedures and reported estimates of h^2 0.45 for heart girth, 0.24 and 0.49 at 403 and 490 days of age for hip height in Hereford herd. Likewise, Maiwashe *et al.* (2002) reported estimates of h^2 0.18±0.05 and 0.27±0.05 for body length using single trait and multiple trait analysis respectively. Moreover, Hass *et al.* (2007) reported estimates of h^2 0.38 ± 0.02, 0.35 ± 0.02 and 0.36 ± 0.02 for heart girth in Holstein, Brown Swiss and Red and White breed, respectively.

Table 2 Genetic parameter estimates for birth weight (BWT) and weaning weight (WWT) in different beef cattle populations

Breed	Country	Parameters			Source
		h^2	m^2	r_{am}	
---BWT---					
Multibreed_1	Thailand	0.28	0.08	- 0.31	Supakorn *et al.* (2005)
Multibreed_2	Canada	0.51	0.09	0.17	Tosh *et al.* (1999)
Belmont red	Australia	0.57	0.18	- 0.25	Burrow (2001)
Composite	Botswana	0.65	0.22	-0.93	Tawah *et al.* (1993)
Multibreed_3	South Africa	0.72	0.14	-0.40	Skrypzeck *et al.* (2000)
Multibreed_4	Ethiopia	0.14	0.07	0.47	Demeke *et al*. (2003)
Synthetic breeds	South Africa	0.66	0.22	- 0.32	Schoeman *et al*. (2000)
Zebu-Cross	Australia	0.61	0.11	0.01	Mackinnon *et al.* (1991)
---WWT---					
Multibreed_1	Thailand	0.37	0.04	- 0.28	Supakorn *et al.* (2005)
Composite	Botswana	0.29	0.27	-0.39	Tawah *et al.* (1993)
Belmont red	Australia	0.17	0.34	-0.19	Burrow (2001)
Multibreed_2	Canada	0.33	0.11	- 0.13	Tosh *et al.*(1999)
Multibreed_4	Ethiopia	0.07	0.03	0.07	Demeke *et al*. (2003)
Synthetic breeds	South Africa	0.53	0.36	- 0.53	Schoeman *et al*. (2000)
Multibreed_3	South Africa	0.53	0.21	- 0.65	Skrypzeck *et al.* (2000)
Zebu-Cross	Australia	0.20	0.32	0.00	Mackinnon *et al.* (1991)

h^2 = direct heritability, m^2 = maternal heritability and r_{am} = direct - maternal genetic correlation

Multibreed_1 = Thai Native, Brahman and Charolais

Multibreed_2 = Angus, Hereford, Shorthorn, Charolais, Simmental and Limousin

Multibreed_3 = Afrikaner, Bonsmara, Brahman, Brown Swiss, Charolais, Hereford, Holstein, S.A. Angus, Simmental and South Devon and

Multibreed_4 = Boran, Barca, Horro, Friesian, Jersey and Simmental

Direct - maternal genetic correlation

The genetic correlation between direct and maternal effects (r_{am}) was identified to be affected by sires and dams, owing to either larger genetic variance or confounding environmental effects and when the models used was unable to account the fixed effects that matters a particular trait **(**Vergara *et al*., 2009)**.** This implies presence of great variation between estimation (Table 3). As there is antagonistic correlation between direct and maternal genetic effects (Supakorn *et al*., 2005), in the contrary positive correlation between the same parameters was reported by Elzo *et al*. (1998)**.** Based on these information while the negative correlation worsen maternal ability for selection made based on direct additive genetic effects, the positive one will encourage the potential of conducting joint selection at a time.

Accordingly, Supakorn *et al.* (2005) estimated r_{am} values of -0.31 and -0.28 for birth and weaning weights, respectively for multibreed population in Thailand. Similarly, research carried out in Spain by El-Saied *et al.* (2006) on Charolais beef breed found relatively elevated antipathy between r_{am} for birth and weaning weights which were -0.87 ± 0.05 and -0.67 ± 0.03, respectively. Tosh *et al.* (1999) reported relatively smaller negative (-0.13) estimate of r_{am} for multibreed population of beef cattle in Canada. Sarmiento and Garcia (2007) reported estimated r_{am} values of -0.37 ± 0.01 and -0.34 ± 0.13 for birth and weaning weights, respectively in Romosinuano beef breed. These results were in agreement with the estimates reported by Supakorn *et al.* (2005) for Kamphaengsaen beef breed. In the contrary, Raphaka and Dzama (2010) found positive estimates of genetic correlation between direct and maternal effects of 0.20 ± 0.17 and 0.88 ± 0.21 for birth and weaning weight, respectively. This is substantial for weaning weight with different magnitude and direction compared to the earlier literatures findings.

Factors affecting genetic parameter estimates of measurement traits

Magnabosco *et al.* (2002) illustrated that herd, year-season of birth, sex, age of the animal and feed management influenced the genetic values of linear body measurements of a particular breed. Under the same study, estimates of h^2 for various linear body measurement traits of Brahman breed ranged from medium to high heritability estimates 0.32 for body length and 0.57 for hip width. Moreover, the estimates of correlation between body measurements traits justified to have high genetic correlation. Riley *et al.* (2007) confirmed that the values of some linear body measurements would vary based on body condition throughout the feeding period of a particular animal. Choy *et al.* (2002) also reported that results of genetic parameter estimates for linear body measurement traits might not be analogous from model to model (Table 3).

Table 3 The difference of models on heritability (h^2) and repeatability (r) estimates for mature weight (MW), hip height (HH) and condition score (CS).

Models	Parameters	Traits		
		MW	HH	CS
Model 1	h^2	0.83 ± 0.03	0.83 ± 0.02	0.43 ± 0.05
Model 2	h^2	0.84 ± 0.03	0.84 ± 0.02	-
Model 3	h^2	0.40 ± 0.10	0.62 ± 0.09	0.11 ± 0.05
	r	0.77 ± 0.03	0.81 ± 0.03	0.38 ± 0.04
Model 4	h^2	0.54 ± 0.11	0.65 ± 0.09	-
	r	0.80 ± 0.03	0.81 ± 0.03	-

Model 1 = simple repeated-measure animal model, Model 2 = simple repeated-measure animal model with regression on CS, Model 3 = repeated-measure animal model with permanent environmental effect and Model 4 = repeated-measure animal model with permanent environmental effect and regression on CS.

Source: Choy *et al.* (2002)

Meyer and Graser (1999) stated a model allowing for non-zero co-variances between direct and maternal genetic effects fitted the data better than a model assuming no correlation for all pelvic measurement traits of interest in that particular study. This indicated that the estimates of genetic parameters are dependent up on efficiency of the model accommodating a number of factors that can affect parametric estimation for traits of interest.

Genetic parameter estimation of measurement traits

In a study targeted at identifying factors affecting the size of three years old beef cows, Brown and Franks (1964) reported heritability estimates of 0.69 ± 0.18 and 0.48 ± 0.21 for weaning hip height and weaning body length, respectively. Likewise, Price and Wiltbank (1978) found the association of some linear type traits related to dystocia in heifers for crossbreed and found heritability estimates of 0.35 and 0.42 for body length and hip width, respectively. Based on the mentioned estimates it was found that the measurement traits had higher h^2 than birth weight. On the other hand, Nugent and Notter (1991) identified heritability estimates of 0.24 ± 0.10 and 0.16 ± 0.10 for weaning hip height and weaning body length, respectively. The estimates were relatively lower for the trait as compared to the earlier literatures on heritability estimate particularly of weaning body length.

MATERIALS AND METHODS

Data source and animal management

Data used in this study were obtained from Kamphaengsaen Buffalo and Beef Production Research and Development Center (BPRDC) and 14 large and small scale commercial farms of animals born in the year 2003 to 2012 (Table 4). The study area was classified into three calving seasons; cold (November to February), hot (March to June) and rainy (July to October). Gras hay and total mixed ration (TMR) prepared from different feed source such as leucaena *(Leucaena leucocephala)* and hedge lucerne (*Desmanthus virgatus)* and rice straw were identified as feed source in beef farms. Moreover, water and mineral block salt was provided as *ad libitum* to beef cattle population in the considered farms.

Actual birth and weaning weights were collected in the years 2003 and 2012 and body measurement traits namely weaning hip height and weaning body length were carried out by coinciding the date of weaning with the time of taking body measurements in the years 2010 and 2011. For all traits, measurements were taken at the event where the animals squarely positioned on all their four feet with their head at upright state (Figure 1).

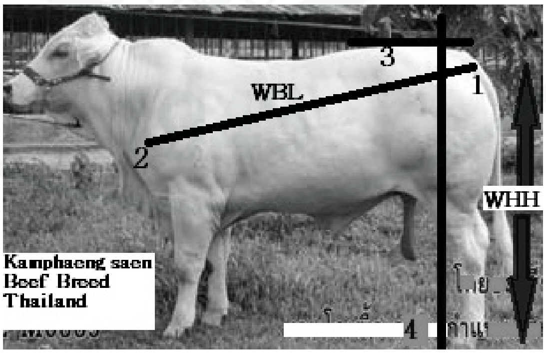

Figure 1 Points of reference for taking weaning hip height (WHH), weaning body length (WBL), pin bone (1), point of shoulder (2), point on the spine (3) and ground (4).

After checking and correcting the collected data set, the structure and descriptive statistics of the interest population was produced (Tables 4 and 5). Contemporary groups (CG) were formed by grouping two or more animals born in the same herd, year and season. After once the contemporary groups established, connectedness was examined using common sires between contemporary groups. Only contemporary groups with at least two sires and two performance records were used in the analysis. Grouping is performed to minimize anything that is different in the environment. Improper contemporary grouping can lead to biased and inaccurate comparison (Bourdon, 2000).

Table 4 Pedigree structures of crossbred beef cattle among Thai Native (N), Brahman (B) and Charolais (C) for pre-weaning growth and measurement traits.

Item[1]	Traits[2]			
	BWT	WWT	WHH	WBL
Number of animals in pedigree	1,915	1,915	1,915	1,915
Number of animals with records	1,050	587	222	222
Number of sires	179	120	66	66
Number of dams	648	405	190	190
Number of dams with own and progeny records	37	12	0	0
No. of CG[2]	45	35	12	12

[1] CG = contemporary group

[2] BWT = birth weight; WWT = weaning weight; WHH = weaning hip height WBL = weaning body length

The breed fractions of Thai Native (N), Brahman (B) and Charolais (C) were found to vary from 0 to 0.63, 0 to 75 and 0 to 0.75, respectively (Table 5). After some early and late age animals removed from the data set then age ranges for all weaning traits varied from 141 to 265 days.

Table 5 Descriptive statistics for birth weight (BWT) weaning weight (WWT), weaning hip height (WHH) and body length (WBL).

Traits[1]	Factors[2]	n	Mean	SD	Min.	Max.	CV (%)
BWT (kg)		1,050	29.65	6.39	17.00	46.00	21.57
	N		0.28	0.10	0.00	1.00	36.79
	B		0.27	0.10	0.00	0.75	36.03
	C		0.44	0.16	0.00	0.75	35.21
WWT (kg)		587	159.09	37.08	95.00	257.00	23.31
	WAGE (days)		218.97	28.17	141.00	265.00	12.87
	N		0.28	0.09	0.09	0.75	33.42
	B		0.27	0.09	0.00	0.75	31.16
	C		0.46	0.14	0.00	0.75	31.15
WHH (cm)		222	101.48	7.75	79.00	120.00	7.63
	WAGE (days)		210.40	25.75	147.00	264.00	12.24
	N		0.26	0.07	0.13	0.63	27.21
	B		0.25	0.05	0.13	0.50	19.50
	C		0.50	0.09	0.00	0.75	18.06
WBL (cm)		222	94.71	9.87	70.00	150.00	10.42
	WAGE (days)		210.43	25.80	147.00	264.00	12.26
	N		0.26	0.07	0.13	0.63	27.18
	B		0.25	0.05	0.13	0.50	19.50
	C		0.50	0.09	0.00	0.75	18.06

[1] BWT = birth weight; WWT = weaning weight; WHH = weaning hip height; WBL= body length

[2] WAGE = weaning age; N = Thai Native; B = Brahman; C = Charolais breed fractions

Statistical analysis

PROC GLM procedure of SAS (2003) was used in order to estimate the importance of fixed effects (contemporary group, sex, weaning age, Brahman and Charolais breed fractions) on values of dependent variables namely birth weight, weaning weight, weaning hip height and weaning body length. The model was as follow:

$$y_{ijk} = \mu + CG_i + S_j + \beta_1(A_{ijk} - \overline{A}) + \beta_2(B_{ijk} + \overline{B}) + \beta_3(C_{ijk} + \overline{C}) + e_{ijk}$$

Where,

y_{ijk} = the traits measured on the ijk^th^ animal;

μ = the overall means of the population;

CG_i = the fixed effect associated with the i^th^ contemporary group,

S_j = the fixed effects of j^th^ animal sex;

β_1 = regression coefficient of continuous independent variable of age at weaning A_{ijk} (this effect was not considered for BWT)

β_2 and β_3 = regression coefficients of continuous independent variables of Brahman (B_{ijk}) and Charolais (C_{ijk}) breed fractions which deviated from Thai Native

e_{ijk} = random residual NID $(0, \sigma_e^2)$

Models for estimation of genetic parameters

Mixed model equation (MME) was used to attain the best linear unbiased estimator (BLUE) of fixed effects and best linear unbiased predictor (BLUP) for the random effects. Variance components were estimated using multiple trait derivatives free restricted maximum likelihood derived from Boldman *et al*. (1993). The program was restarted until the -2logL values to the 10^{-9} decimal did not change (global minimum of -2logL likelihood). At the beginning, single trait analysis was done then bivariate and multiple trait analysis was followed utilizing the results from the single trait analysis as starting values. Six different models were used for birth and weaning weights and only simple animal model was applied for weaning hip height and weaning body length. Single trait animal models are:

Model 1 Simple animal model

$$y = Xb + Za + e$$

Model 2 and 3 Direct and maternal genetic effect (with $r_{am} = 0$ and $r_{am} \neq 0$) models

$$y = Xb + Za + Mm + e$$

Model 4 Direct genetic and maternal permanent environmental effect model

$$y = Xb + Za + Wc + e$$

Model 5 and 6 Direct and maternal genetic effect (with $r_{am} = 0$ and $r_{am} \neq 0$) and maternal permanent environmental effect models

$$y = Xb + Za + Mm + Wc + e$$

Where: y is a $N \times 1$ vector of records, b denotes the vector of fixed effects, X is incidence matrix that associates b with y; a is the vector of breeding value for direct genetic effects, Z is incidence matrix that associates a with y; m is vector of breeding value for maternal genetic effects, M is the matrix that associates m with y; c is maternal permanent environmental effects, W is incidence matrix that associates c with y; and e is the vector of random residual effects.

For relatively the most complex model the assumption of first and second moments can be presented:

$$E\begin{bmatrix} y \\ a \\ m \\ c \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

$$\mathrm{var}\begin{bmatrix} a \\ m \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_{Nc}\sigma_c^2 & 0 \\ 0 & 0 & 0 & I_N\sigma_e^2 \end{bmatrix}$$

Where: A is the numerator relationship matrix; σ_a^2 is direct genetic variance; σ_m^2 is maternal genetic variance; σ_c^2 is maternal permanent environmental variance; N is number of records; N_c is number of maternal permanent environment; I is identity matrix of appropriate order and σ_e^2 is random residual variance.

Finally, the results of variance components were used to estimate genetic parameters. The equations are:

Direct heritability:

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2}$$

Maternal heritability:

$$m^2 = \frac{\sigma_m^2}{\sigma_p^2}$$

Direct-maternal genetic correlation:

$$r_{am} = \frac{\sigma_{am}}{\sigma_a \sigma_m}$$

Proportion of variance due to maternal permanent environmental effect:

$$c^2 = \frac{\sigma_c^2}{\sigma_p^2}$$

Proportion of variance due to random residual effect:

$$e^2 = \frac{\sigma_e^2}{\sigma_p^2}$$

Phenotypic variance:

$$\sigma_p^2 = \sigma_a^2 + \sigma_m^2 + \sigma_{am} + \sigma_c^2 + \sigma_e^2$$

Where: σ_a^2 is the direct genetic variance; σ_m^2 is maternal genetic variance, σ_{am} is direct-maternal genetic covariance, σ_c^2 is maternal permanent environmental variance; σ_e^2 is random residual variance, σ_p^2 is total phenotypic variance

For birth and weaning weights, single animal models were compared using log likelihood function. In order to identify the appropriate model, the difference between the -2logL for pairs of models were tested using the chi-square (χ^2) distribution with degrees of freedom being the difference in number of parameters in the models (Boldman *et al*., 1993). After the single animal models that fitted the data set was identified, bivariate and multiple trait animal models were carried out from the results of single trait analysis.

Bivariate animal model (two trait simple animal model) is:

$$\begin{pmatrix} y_i \\ y_j \end{pmatrix} = \begin{pmatrix} X_i & 0 \\ 0 & X_j \end{pmatrix} + \begin{pmatrix} b_i \\ b_j \end{pmatrix} + \begin{pmatrix} Z_i & 0 \\ 0 & Z_j \end{pmatrix} + \begin{pmatrix} a_i \\ a_j \end{pmatrix} + \begin{pmatrix} e_i \\ e_j \end{pmatrix}$$

The assumption of first and second moments for bivariate animal model can be presented:

$$E\begin{pmatrix} y_i \\ y_j \end{pmatrix} = \begin{pmatrix} X_i & 0 \\ 0 & X_j \end{pmatrix} + \begin{pmatrix} b_i \\ b_j \end{pmatrix}$$

$$V(a) = G = G_0 \otimes A$$

Where:

$$G_0 = \begin{pmatrix} \sigma^2_{a_i} & \sigma_{a_{ij}} \\ \sigma_{a_{ij}} & \sigma^2_{a_j} \end{pmatrix}$$

$$V(e) = R = R_0 \otimes I$$

Where:

$$R_0 = \begin{pmatrix} \sigma^2_{e_i} & \sigma_{e_{ij}} \\ \sigma_{e_{ij}} & \sigma^2_{e_j} \end{pmatrix}$$

Where: The terms in the model are defined as in analysis for single trait models, with i and j refers to traits (birth weight, weaning weight, weaning hip height and weaning body length) that involved in bivariate analysis

Multiple trait animal model is:

$$\begin{pmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \end{pmatrix} = \begin{pmatrix} X_1 & 0 & 0 & 0 \\ 0 & X_2 & 0 & 0 \\ 0 & 0 & X_3 & 0 \\ 0 & 0 & 0 & X_4 \end{pmatrix} \begin{pmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \end{pmatrix} + \begin{pmatrix} Z_1 & 0 & 0 & 0 \\ 0 & Z_2 & 0 & 0 \\ 0 & 0 & Z_3 & 0 \\ 0 & 0 & 0 & Z_4 \end{pmatrix} \begin{pmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \end{pmatrix}$$

Where: Subscripts 1, 2, 3 and 4 represent birth weight, weaning weight, weaning hip height and weaning body length, respectively.

The assumption of first and second moments for multiple trait animal model can be presented:

$$E\begin{pmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \end{pmatrix} = \begin{pmatrix} X_1 & 0 & 0 & 0 \\ 0 & X_2 & 0 & 0 \\ 0 & 0 & X_3 & 0 \\ 0 & 0 & 0 & X_4 \end{pmatrix} \begin{pmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \end{pmatrix}$$

The $V(a) = G = G_0 \otimes A$ where:

$$G_0 = \begin{pmatrix} \sigma^2_{a1} & \sigma_{a12} & \sigma_{a13} & \sigma_{a14} \\ \sigma_{a12} & \sigma^2_{a2} & \sigma_{a23} & \sigma_{a24} \\ \sigma_{a13} & \sigma_{a23} & \sigma^2_{a3} & \sigma_{a34} \\ \sigma_{a14} & \sigma_{a24} & \sigma_{a24} & \sigma^2_{a4} \end{pmatrix}$$

The $V(e) = R = R_0 \otimes I$ where:

$$R_0 = \begin{pmatrix} \sigma^2_{e1} & \sigma_{e12} & \sigma_{e13} & \sigma_{e14} \\ \sigma_{e12} & \sigma^2_{e2} & \sigma_{e23} & \sigma_{e24} \\ \sigma_{e13} & \sigma_{e23} & \sigma^2_{e3} & \sigma_{e34} \\ \sigma_{e14} & \sigma_{e24} & \sigma_{e34} & \sigma^2_{e4} \end{pmatrix}$$

The results of variance components from both bivariate and multiple trait analysis were used to estimate genetic parameters. The equations are:

Direct genetic correlation between traits is

$$r_{a_{ij}} = \frac{\sigma_{a_{ij}}}{\sigma_{a_i}\sigma_{a_j}}$$

Random residual correlation between traits is:

$$r_{e_{ij}} = \frac{\sigma_{e_{ij}}}{\sigma_{e_i}\sigma_{e_j}}$$

The terms in the models are defined as in single trait animal model but with $\sigma_{a_{ij}}$ as the direct genetic covariance between trait i and trait j and $\sigma_{e_{ij}}$ is random residual covariance between trait i and trait j

RESULTS AND DISCUSSION

Results

Factors affecting pre-weaning growth and body measurement traits

The influence of contemporary groups, sex, weaning age and Brahman and Charolais breed fractions on pre-weaning growth and body measurement traits are given in Table 6. Effect of contemporary groups was found significant (*P*<0.01) for all considered traits. Male calves were 1.25 and 5.74 kg heavier (*P*<0.05) at birth and weaning, respectively than female. However, effects of sex were not significant for weaning hip height and weaning body length. Weaning age affected significantly on weaning weight, weaning hip height and weaning body length (*P*<0.01). The effects of Brahman and Charolais breed fractions on birth weight and weaning weight were significant (*P*<0.01) while weaning hip height (*P*<0.01) and weaning body length (*P*<0.05) were affected by Charolais breed fraction only.

Table 6 Effect of contemporary group (CG), least squares means of sex and linear regression coefficients of Brahman and Charolais breed fraction effects.

Item[1]		BWT (kg)	WWT(kg)	WHH(cm)	WBL(cm)
	CG	**	**	**	**
Sex	Male	30.56 ± 0.33^a	162.98 ± 2.49^a	102.23 ± 0.74	95.50 ± 0.98
	Female	29.31 ± 0.35^b	157.25 ± 2.52^b	101.75 ± 0.77	93.83 ± 1.03
β_1		-	0.36 ± 0.06**	0.10 ± 0.02**	0.11 ± 0.03**
β_2		22.57 ± 2.74**	133.45 ± 27.35**	-0.83 ± 10.82^{NS}	10.85 ± 14.37^{NS}
β_3		22.62 ± 1.68**	93.64 ± 15.74**	11.78 ± 5.95**	20.83 ± 7.91*

** (P<0.01), * (P<0.05), ^{NS} (non significant)

^{a,b} least square means for sex with different superscripts are different (P<0.05)

[1] BWT = birth weight (BWT), WWT = weaning weight, WHH = weaning hip height and WBL = weaning body length

[2] β_1, β_2 and β_3 = linear regression coefficients of age at weaning and measurements, Brahman and Charolais breed fractions

Estimation of (co) variance components and genetic parameters from single trait animal models

Birth weight and Weaning weight

The estimates of variance components and genetic parameters for birth weight are presented in Table 7. Since the likelihood estimate did not converge when the direct-maternal correlation was fitted into the Models, the results from Model 3 and 6 were not presented. From the Models without r_{am} (Models 1, 2, 4 and 5), σ_p^2 and h^2 for birth weight were found to be 28.51 to 28.57 kg^2 and 0.46 to 0.48. The σ_m^2 for Models 2 and 5 and σ_c^2 for Model 4 were closer to 0. Heritability estimates (> 0.40) were found across all the considered models except Models 3 and 6. From log likelihood ratio test, Model 1 was the best and simplest model than Models 4 and 5. The variance components and genetic parameter estimates for weaning weight are given in Table 8. Since the likelihood estimate did not converge when the direct-maternal correlation was fitted into the Models, the results from Model 3 and 6 were not presented. From the Models without r_{am} (Models 1, 2, 4 and 5), σ_p^2 and h^2 for weaning weight were found to be 989.94 to 1,007.88 kg^2 and 0.64 to 0.43. The σ_m^2 for Models 2 and 5 were ranged from 0.00 to 0.18 and σ_c^2 for Models 4 and 5 were closer to 0.19. From log likelihood ratio test, Model 1 was the best and simplest model than both Model 4 and 5. Fitting of σ_m^2 and σ_c^2 did not improve the model for both birth and weaning weights.

Weaning hip height and weaning body length

The estimates of variance components and genetic parameters for weaning hip height and weaning body length are presented in Table 9. The σ_p^2 and h^2 for weaning hip height and weaning body length found to be 35.44 and 61.27 cm^2, respectively. Heritability estimates for weaning hip height and weaning body length were 0.87 and 0.45 respectively.

Table 7 Estimates of (co) variance components and genetic parameters for birth weight (BWT).

Items[1]	Model 1	Model 2	Model 4	Model 5
Variance components[2]				
σ_a^2	13.75	13.74	13.17	13.15
σ_m^2	-	0.00	-	0.00
σ_{am}	-	-	-	-
σ_c^2	-	-	0.37	0.37
σ_e^2	14.83	14.83	14.97	14.99
σ_p^2	28.57	28.57	28.52	28.51
Parameters[3]				
h^2	0.48 ± 0.10	0.48 ± 0.13	0.46 ± 0.12	0.46 ± 0.13
m^2	-	0.00 ± 0.06	-	0.00 ± 0.23
r_{am}	-	-	-	-
c^2	-	-	0.01 ± 0.06	0.01 ± 0.22
e^2	0.52 ± 0.10	0.52 ± 0.10	0.53 ± 0.10	0.53 ± 0.10
–2 logL	0.00	0.00	119.95	119.95

[1] Model 1 = simple animal model; Model 2 = direct and maternal model (with $r_{am} = 0$); Model 4 = direct genetic and maternal permanent environmental effect; Model 5 = direct and maternal genetic permanent environmental effect (with $r_{am} = 0$). Model 3 = Model 2 (with $r_{am} \neq 0$); Model 5 = Model 6 with $r_{am} \neq 0$.

[2] σ_a^2 = direct genetic variance; σ_m^2 = maternal genetic variance; σ_{am} = direct-genetic covariance; σ_c^2 = maternal permanent environmental variance; σ_e^2 = random residual variance; σ_p^2 = phenotypic variance

[3] h^2 = direct heritability; m^2 = maternal heritability; r_{am} = direct-maternal genetic correlation; c^2 = fraction of variance due to maternal permanent environmental effect; e^2 = fraction of variance due to random residual effect

[*] Models compared in reference to Model 1

Table 8 Estimates of (co) variance components and genetic parameters for weaning weight (WWT).

Items[1]	Model 1	Model 2	Model 4	Model 5
Variance components[2]	-----------------------------	kg^2	------------------------------	
σ_a^2	647.57	437.23	429.54	429.30
σ_m^2	-	176.92	-	0.00
σ_{am}	-	-	-	-
σ_c^2	-	-	190.53	190.99
σ_e^2	330.31	377.46	369.88	369.95
σ_p^2	1,007.88	991.61	989.94	990.23
Parameters[3]				
h^2	0.64 ± 0.15	0.44 ± 0.17	0.43 ± 0.16	0.43 ± 0.17
m^2	-	0.18 ± 0.10	-	0.00 ± 0.41
r_{am}	-	-	-	-
c^2	-	-	0.19 ± 0.09	0.19 ± 0.41
e^2	0.36 ± 0.15	0.38 ± 0.13	0.37 ± 0.13	0.37 ± 0.10
–2 logL	0.00	-2.67	-3.51	-3.52

[1] Model 1= simple animal model; Model 2 = direct and maternal model (with $r_{am} = 0$); Model 4= direct genetic and maternal permanent environmental effect; Model 5= direct and maternal genetic permanent environmental effect (with $r_{am} = 0$). Model 3 =Model 2 with $r_{am} \neq 0$; Model 5 = Model 6 with $r_{am} \neq 0$.

[2] σ_a^2 = direct genetic variance; σ_m^2 = maternal genetic variance; σ_{am} = direct-genetic covariance; σ_c^2 = maternal permanent environmental variance; σ_e^2 = random residual variance; σ_p^2 = phenotypic variance

[3] h^2 = direct heritability; m^2 = maternal heritability; r_{am} = direct-maternal genetic correlation; c^2 = fraction of variance due to maternal permanent environmental effect; e^2 = fraction of variance due to random residual effect

[*] Models compared in reference to Model 1

Table 9 Estimates of (co) variance components and genetic parameters for weaning hip height (WHH) and weaning body length (WBL).

Traits	Variance components (cm^2)[1]			Genetic parameters[2]	
	σ_a^2	σ_e^2	σ_p^2	h^2	e^2
WHH	30.80	4.64	35.44	0.87 ± 0.30	0.13 ± 0.31
WBL	27.71	33.55	61.27	0.45 ± 0.26	0.55 ± 0.26

[1] σ_a^2 = direct additive genetic variance; σ_e^2 = random residual variance; σ_p^2 = phenotypic variance

[2] h^2 = direct heritability; e^2 = fraction of variance due to random residual effect

Estimation of (co) variance components and genetic parameters from bivariate analysis

Estimates of variance components from bivariate analysis performed involving two particular traits at a time are presented in Table 10. In addition, covariance component estimates and the resulting correlations from bivariate analysis for traits involved in pair wise run are given in Table 11. In general, the outcomes of estimates obtained from different pair wisely fitted trait in bivariate model were closer to the result obtained from single trait analysis. The fluctuations in the partitioning of the total variance were not high apparently leading to closer parameters estimates, particularly birth weight. Moreover, the direct genetic covariance and the resulting correlation between all traits were positive. However, the estimates of residual covariance were found negative except between weaning weight and weaning body length resulting to a negative residual correlation between traits.

Table 10 Estimates of variances and genetic parameters for birth weight (BWT), weaning weight (WWT), weaning hip height (WHH) and weaning body length (WBL) from bivariate model.

Item		Variance components[1]			Genetic parameters[2]	
		σ_a^2	σ_e^2	σ_p^2	h^2	e^2
		----------------------kg^2----------------------				
BWT	+WWT	14.25	14.39	28.64	0.50	0.50
	+WHH	13.59	14.92	28.52	0.48	0.52
	+WBL	13.65	14.87	28.52	0.48	0.52
	Average	13.83	14.73	28.56	0.49	0.51
		----------------------kg^2----------------------				
WWT	+BWT	761.61	272.93	1,034.54	0.74	0.26
	+WHH	673.06	342.98	1,016.04	0.66	0.34
	+WBL	729.25	299.15	1,028.37	0.71	0.33
	Average	721.31	305.02	1,026.31	0.70	0.30
		----------------------cm^2---------------------				
WHH	+BWT	36.08	0.02	36.10	1.00*	0.00
	+WWT	31.85	3.43	35.29	0.90	0.10
	+WBL	33.00	2.61	35.61	0.93	0.07
	Average	33.64	2.02	35.67	0.94	0.06
		----------------------cm^2----------------------				
WBL	+BWT	30.95	31.21	62.15	0.50	0.50
	+WWT	28.15	32.88	61.03	0.46	0.54
	+WHH	36.96	25.14	62.10	0.60	0.40
	Average	32.02	29.74	61.76	0.50	0.50

[1] σ_a^2 = direct additive genetic variance; σ_e^2 = random residual variance; σ_p^2 = phenotypic variance

[2] h^2 = direct heritability; e^2 = fraction of variance due to random residual effect
*close to 1.

Table 11 Estimates of covariances and correlations from bivariate analysis of birth weight (BWT), weaning weight (WWT) and weaning hip height (WHH) and body length (WBL).

Trait 1 Trait 2	BWT WWT	BWT WHH	BWT WBL	WWT WHH	WWT WBL	WHH WBL
$\sigma_{a\,ij}$	97.31	11.17	14.73	89.19	111. 85	33.88
$r_{a\,ij}$	0.93	0.50	0.72	0.61	0.78	0.97
$\sigma_{e\,ij}$	-24.91	-0.58	-5.44	-17.19	-0.36	-4.62
$r_{e\,ij}$	-0.40	-1.00*	-0.20	-0.50	0.00*	-0.57

$^1\sigma_{a\,ij}$ = direct genetic covariance; $\sigma_{e\,ij}$ = random residual covariance; $r_{a\,ij}$ = direct genetic correlation between traits i and j; $r_{e\,ij}$ = random residual correlation between traits i and j.

*close to -1 or 0

Estimation of (co) variance components and genetic parameters from multiple trait analysis

Estimates of variance components and genetic parameters from multiple trait analysis for the interest traits are presented in Table 12. Estimates of variance components were closer to estimates found from the single trait and bivariate analysis. However, the estimates were closer to single trait analysis more than bivariate analysis. On the other hand, the patterns of direct genetic and residual variances were coincided in terms of direction but the magnitude obtained from single, bivariate and multiple trait analysis were almost similar resulting to closer estimates of direct genetic and random residual effects.

Table 12 Estimates of (co) variance components and genetic parameters from multiple trait analysis for birth weight (BWT), weaning weight (WWT), weaning hip height (WHH) and weaning body length (WBL).

Item	BWT	WWT	WHH	WBL
(Co) variance components[1]	(kg)	(kg)	(cm)	(cm)
BWT (kg)	13.17	90.72	10.32	12.78
	15.13			
WWT (kg)	-20.66	720.66	90.70	92.69
		304.02		
WHH (cm)	-0.04	-15.39	34.38	30.86
			0.95	
WBL (cm)	-3.36	18.92	-2.36	30.40
				30.34
Parameters[2]				
BWT	0.47	0.93	0.48	0.64
	0.53			
WWT	-0.30	0.70	0.58	0.63
		0.30		
WHH	-0.01	-0.91	0.97	0.95
			0.03	
WBL	-0.16	0.20	-0.44	0.50
				0.50

[1] Diagonal: direct genetic variance (line 1) and random residual variance (line 2)

[1] Above diagonals: additive genetic covariances

[1] Below diagonals: random residual covariances

[2] Diagonals: heritability (line 1) fraction of variance due to residual effect (line 2)

[2] Above diagonals: direct genetic correlations

[2] Below diagonals: random residual correlations

Discussions

Factors affecting pre-weaning growth and some measurement traits

The effect of contemporary groups which was established as a combination of herd-year- season was very important (*P*<0.01) for all traits (Table 6). The significant effect of contemporary groups could be attributed to seasonal variations in terms of quality and quantity feed availability and management differences across herd and years. Correspondingly, the result identified in this study was found in agreement with several studies performed in respect to the subject matter. Accordingly, Afolayan *et al*. (2002) revealed the situation as calves that were born in two distinct years and sub grouped under different contemporary groups did not showed similar performance. The calves born in previous years possessed heavier weight, longer height and length than the one born three years later. Likewise, Goyache *et al*. (2003) explained that weaning weight was largely dependent on the age at weaning which is one criterion to let a particular calf grouped in a particular contemporary group.

Least square mean of sex are presented in Table 6. Male calves were heavier (*P*<0.05) than females at birth (1.25 ± 0.33 kg) and weaning (5.74 ± 2.68 kg). Even though, the male calves possessed somewhat, longer weaning hip height and body length, it was found not significantly difference as response to sex of a particular calf. This study was in agreement with several literature findings (Ebangi, *et al*., 2002 and Crews, 2006) revealed the significantly difference of growth trait between bulls and heifers. Moreover, the result reported by Anderson and Willham (1978) confirmed that bulls were significantly heavier than heifers at weaning. On the other hand, Riley *et al*. (2007) reported that males had greater weaning hip height than females. The general consensus regarding sex of calves was, female calves are always lighter and smaller than male calves with the certainty that the gap would increase as calves grew older and older (Gilbert *et al*., 1993)

The regression coefficient of weaning weight on weaning age was identified positive (0.36 ± 0.06 kg/day) and highly significant (*P*<0.01*;* Table 6). The result found in the current study was in accordance with findings of Minyard and Dinkel (1965) a highly significant effect of age on weaning weight indicating the linear regression of weight on age within ranch-year-month subclasses was 0.55 kg/day. Similarly, Johnson and Dinkel (1951) indicated growth rate of calves raised under similar situation was nearly linear from birth to approximately 5 months of age and, thereafter, it was found increased at a decreasing rate. The significance of weaning age on weaning hip height and weaning body length identified in this study was coincided with literature findings. An early weaning calf had lower weaning weight and shorter weaning hip height (Riley *et al*., 2007). Similarly, Gilbert *et al*. (1993) revealed that age of the animal influenced measurements traits such as body length and heart girth indicating that their value increases with the augmentation of age.

Regression estimates of birth weight (22.57 ± 2.74 kg) and weaning weight (133.45 ± 27.35 kg) on Brahman breed fraction showed a highly significant difference (*P*<0.01). However, the regression coefficient of weaning hip height and weaning body length on Brahman breed fraction was positive and did not significantly different when compared to pure Thai Native beef cattle. The effect of Charolais breed fraction on birth weight and weaning weight were 22.62 ± 1.68 and 93.64 ± 15.74 kg heavier at birth and weaning than Thai Native, respectively. Moreover, Charolais breed fraction effect on weaning hip height and weaning body length were significant at *P*<0.05 and P<0.01 resulting Charolais breed was 11.78 ± 5.95 and 19.46 ± 7.14 cm longer than Thai Native at weaning hip height and weaning body length, respectively. The result found in this study was consistent with estimates reported by Sopanarath *et al.* (2005) significantly higher birth and weaning weights in favor of Brahman breed fraction was recognized. Moreover, Franke *et al*. (2001) reported as the breed fraction effects of different beef breed including Brahman and Charolais breed fractions were significantly affected birth and weaning weights of beef cattle. Similarly, Gilbert *et al*. (1993) reported as measurement trait such as hip height was significantly influenced by breed type of an animal. This could be attributed complementarities of genes from the parental breeds (Brahman, Charolais and Thai Native). The significant effects regarding Brahman and Charolais breed fractions on the traits studied was a good indication that genotype plays an important role in the growth performance and skeletal development of the current population.

(Co) variance components and genetic parameters from single trait analysis

Birth weight

Estimates of σ_a^2 for birth weight was consistently higher across all the models used. Widely varied results have been reported for different type of beef breed in different areas. The current result of σ_a^2 for crossbred beef cattle was consistent with the results 14.31 kg^2 reported by Meyer *et al*. (1993) for birth weight of Australian Charolais cattle using animal model and 16.7 kg^2 reported by Shelby *et al.* (1963) for Hereford top cross steers. However, the current result was not coincided with several studies reported for different type of beef breed. Accordingly, Jeanmas *et al*. (2008) reported estimates of σ_a^2 (5.11 kg^2) for crossbred beef cattle among Thai Native, Brahman and Charolais. Waldron *et al.* (1993) reported estimates of σ_a^2 3.5 to 8.4 kg^2 fitting four different models for Angus and Hereford beef breed herds. Estimates of σ_a^2 using simple additive animal model were 7.77 ± 0.91 for Angus and 10.02 ± 1.11 for Hereford beef cattle (Birchmeier *et al*., 2002).

Several literatures have been mentioned in higher values of σ_a^2 and strong antagonistic interactions between direct and maternal genetic effects considered as possible reasons for rising of both the direct and maternal additive genetic variances (Robinson, 1996a; Meyer, 1992). Nelsen *et al.* (1984) explained that the type of mating system can be a determinant factor that could influence the prediction of genetic parameters as a result of changed variance components. Changing age slicing from 15 to 60 days did not affected significantly the variance of birth weight rather influenced the effectiveness of data for evaluation at the animal and sire levels (Johnston *et al.,* 2007). The higher direct genetic variance observed in the current study could be as a result of inability to partition σ^2_m and σ^2_c from σ^2_a from which might related to the smaller number of dams with its own and progeny performance record.

Estimates of σ^2_m for birth weight are presented in Table 7. The importance of estimating σ^2_m for birth and weaning weights were boldly stated in several situations. The estimate identified in the current population was not consistent with the mentioned report. The observed variation may be due to the fact that the different data source used as long as the estimation of maternal effects reported as it is exclusively dependent on structure of pedigree relationships (Maniatis and Pollott, 2003).

The presence of genetic antagonism between direct and maternal effects and was frequently revealed by enormous literature reports. However, there were some indicatives that the estimates of this component can also be positive (0.2 to 1.0 (Waldron *et al*., 1993). In the contrary, estimate of σ_am was negative as reported by Supakorn *et al.* (2005) from bivariate model. It was confirmed that the negative association between direct and maternal is not favorable of each other (Eler *et al.*, 1994).

Intaratham *et al.* (2008) reported the estimate of σ^2_c 0.21 for Thai Native beef cattle population indicting that the importance of dams variation for birth weight should not be overlooked. Similarly, Eler *et al.* (1995) and Meyer *et al.* (1993) reported the estimates of σ^2_c can reach up to of 0.3 and 1.71 kg^2 for Australian multibreed beef cattle and Nelore beef cattle respectively. However, the result obtained in this study was not coincided with the mentioned reports for the other type of beef breed. The low estimate with larger standard error identified for the current population might be due to the structure of the pedigree in the current population. Different literature reports noted that, measuring the importance of maternal components is not an easy task and requires well organized data set with promising dam to offspring ratio and relatively extended generation (Maniatis *et al.,* 2003; Clement *et al.,* 2001).

The estimate of σ_p^2 (23.59 to 28.51 kg^2) found for birth weight in this study was in accordance with several literature reports revealed for beef cattle population. Accordingly, the estimated σ_p^2 values of 24.32 kg^2 (Jeanmas *et al*., 2008) from single animal model for crossbred beef cattle among Thai Native, Brahman and Charolais were within similar range when compared with the results obtained using the corresponding models in this study. However, the estimate of σ_p^2 (14.31 kg^2) for birth weight of Australian Charolais cattle using animal model was found by far smaller than the estimate identified in the current study (Meyer *et al.*, 1993). Overall, the residual effect could be one of the main reasons for such large variation of the mentioned component.

Several literatures reported remarkably varied estimates of h^2 ranging from 0.23 to 0.72 (Meyer, 1992; Waldron *et al.*, 1993, Shelby *et al.*, 1955). The current result was consistent with some of literature estimates revealed for different type beef breed. Accordingly, 0.46 to 0.54 for three composite beef breed derived from different pure breed beef cattle (Bennett and Gregory, 1996); 0.37 to 0.57 for Australian multibreed beef cattle (Meyer *et al*., 1993) 0.39 for Asturiana de los Valles beef cattle (Gutierrez *et al*., 2007) were comparable with the current results. In the contrary, estimates of h^2 in *Bos indicus* cross *Bos taurus* beef cattle ranged from 0.21 to 0.28 for crossbred beef cattle among Thai Native, Brahman and Charolais (Supakorn *et al.*, 2005; Jeanmas *et al*., 2008); from 0.31 to 0.34 for Angus (Meyer 1994; Waldron *et al*., 1993) and 0.31 for French Limousine beef cattle breed (Shi *et al*., 1993) were lower than the current estimate. Moreover, Tosh *et al*. (1999) and Skrypzeck *et al.* (2000) reported high range estimates (0.51; 0.71) for multibreed population of beef cattle in Canada and South Africa, respectively.

Weaning weight

Several literatures indicated a wide range of estimates regarding to variance component estimation of weaning weight for beef cattle. Estimate σ_a^2 found in this study using single trait animal models were relatively higher when compared with the estimates of 155.40 kg ^{2} (Jeanmas *et al*., 2008) reported for crossbred beef cattle among Thai Native, Brahman and Charolais. Meyer *et al.* (1993) was reported smaller estimate that ranged from 97.3 to 177.7 kg^2 for Australian beef breed using different models. Using sire model relatively lower estimate of σ_a^2 values of 50.36 and 158.50 kg^2 reported by Johnson *et al.* (1992) for Angus and Hereford breed respectively

Cow's provision of environment for its offspring to survive and grow is an important phenomenon. Accordingly, several studies regarding σ_m^2 and σ_c^2 performed and varied results were reported. The results 59.2 (σ_m^2) and 74.0 kg^2 (σ_c^2) revealed by Jeanmas *et al*. (2008) for crossbred beef cattle among Thai Native, Brahman and Charolais in Thailand were smaller than the estimate of current study obtained from Model 2. Moreover, the report 112.46 (σ_m^2) and 166.66 kg^2 (σ_c^2) by Sopannarath *et al.* (2003) for Hereford and 169.40 (σ_m^2) and 106.79 kg^2 (σ_c^2) by Robinson (1996a) for Angus beef cattle population indicated that these components were vital for weaning weight and were close to the present study.

The estimate of σ_p^2 value identified in this study was not coincided with the result 740.00 kg^2 reported by Jeanmas *et al*. (2008) involving direct, maternal and permanent maternal environmental components in the animal model. However, the estimates of current study were found closer range with the result 897.47 kg^2 reported by Supakorn *et al*. (2005) using bivariate animal model. The larger σ_p^2 in this study could be due to inability to identify fixed and additional random effects in the models. For this reason, the estimate of σ_p^2 reported by Meyer *et al.* (1993) 784.9 to 829.7 kg^2

and Iwaisaki *et al.* (2005) 690.8 kg^2 could be good examples. In the contrary, larger σ_p^2 values in Asturiana de los Valles beef breed estimated using multiple trait animal model and a random regression model were 761, 1,274 and 1,328 and 775, 1,203 kg^2 and 1,551 kg^2 for early weaning (between 90 to 180 days), standard weaning (between 180 to 240 days) and late weaning (between 240 to 345 days) respectively (Menendez-Buxadera *et al*., 2008).

Estimate of h^2 were found greater than the estimated h^2 results 0.23 (Jeanmas *et al*., 2008) and 0.37 (Supakorn *et al*., 2005) for crossbred beef cattle in Thailand. Prayaga *et al.*, (2008) reported relatively moderate estimates of h^2 (0.17 to 0.23). However, reasonably comparable estimates of h^2 value 0.48 (Sopannarath *et al.*, 2003) and 0.45 (Meyer *et al.*, 1993; Dodenhoff *et al*., 1998) were reported for different beef cattle herds. In fixing and omitting certain fixed effects to models, Meyer (1997) identified as the estimate of h^2 for weaning weight was fluctuated form 0.15 to 0.39.

The results for m^2 and c^2 obtained by fitting maternal components in single trait models was in contrast to the findings of Jeanmas *et al*. (2008) 0.08 (m^2) and 0.10 (c^2) for single trait analysis of weaning weight in crossbred beef Similarly, the result reported by Supakorn *et al*. (2005) also confirmed that the mentioned effects were important and need to be accounted if genetic improvement in crossbred cattle of Thailand is required. Several studies strongly recommend the importance of considering m^2 and c^2 components particularly for weaning weight in beef cattle. Estimates of m^2 and c^2 were reported to be 0.13 and 0.12 (Iwaisaki *et al.*, 2005); 0.05 to 0.25 and 0.11 to 0.26 (Prayaga *et al.*, 2008) for different type beef breed, respectively. Bertrand and Benyshek, (1987) and Dodenhoff *et al*. (1999) reported estimates of m^2 0.05 and 0.07, respectively. The importance of c^2 for Hereford beef herd was reported to be 0.11 to 0.17 (Sopannarath *et al.*, 2003). The variation and the magnitude could possibly indicate how much m^2 and c^2 effects are important for weaning weight of beef cattle. Even though the magnitude of the current result was coincided with the mentioned literature results and tied with larger standard error, log likelihood ratio test confirmed the environment provided to a particular calf by its own dam was not important source of variation in the current population.

The relatively higher estimates obtained from the current study could be the result of some reasons that are responsible for inflated values as mentioned from several previous literature outputs. Accordingly, large sampling correlations between parameters (Meyer, 1997), inappropriate model and inflated negative correlation between direct genetic and maternal components (Gutierrez *et al*., 1997), unaccounted environmental differences within contemporary groups (Chen *et al*., 2008) or misidentification of the animals (Lee and Pollack, 1997) were mentioned to be the basis of inflated estimations. Moreover, Robinson (1996a) noted a possible confounding effect between environmental and genetic effects linked to sire resulting in an overestimation of the additive genetic variance.

Likelihood ratios were tested as a deviation from simple animal model (Model 1) in order to choose among estimates coming from different models of single trait analysis for birth and weaning weights. However, there was no any significant differences between models used in response to fitting maternal effects in the direct effect model. Accordingly, direct genetic model was identified the most appropriate model for both birth and weaning weights. However, model which considered maternal and maternal permanent environmental effects frequently reported appropriate to use for genetic parameters estimation of pre-weaning growth traits particularly weaning weight. Nunez-Dominguez *et al*. (1993) suggested that traits such as birth and weaning weights of calves are influenced by the maternal environment, which is in part due to the genetic makeup of the cow.

Weaning hip height and weaning body length

The estimated σ_a^2 values identified for weaning hip height in this study was found high and not coincided with estimated σ_a^2 values 14.00 to 17.55 cm^2 for matured hip height reported by Choy *et al.* (2002). However, estimated σ_p^2 values reported under the mentioned study (27.34 cm^2) were close to the current study. The difference indicated that hip height at maturity is less affected by environmental variance than the weaning hip height. The average estimate of σ_a^2 (13.9 cm^2) revealed by Rodriguez-Almeida *et al.* (1995) was relatively smaller one. Moreover, the estimate of σ_a^2 for 18 months hip height was 19.6 (Vargas *et al*., 1998) and 27.43 cm^2 (Vargas *et al*., 2000) in Brahman beef breed. The estimates of σ_a^2 (5.71 cm^2) and σ_p^2 (12.17 cm^2) reported by Boligon *et al*. (2011) for weaning hip height involving direct, maternal genetic and maternal permanent environmental effects in Nellore cattle might be considered as lower estimates for this trait.

Moreover the estimate of current study for weaning body length was not corresponded to literature reports for this trait. Accordingly, the estimate of σ_a^2 (11.15 cm^2) and σ_p^2 (34.65 cm^2) reported by Magnabosco *et al.* (2002) for Brahman beef breed was found in different range particularly for additive variance. The smaller σ_a^2 could be a result of intensive selection applied in the population. Bogdanovic (2012), reported that the estimates of σ_a^2 and σ_p^2 could decrease in response to time through identifying estimates of different magnitude at 4 months of age and after 8 months later for the mentioned component for weaning body length.

Numerous literatures revealed that most of body measurement traits have moderate to high h^2 estimates (Gilbert *et al*., 1993). The estimates found in this study were regarded as higher one indicating genetic progress can be made if h^2 was not overestimated by confounding with maternal genetic and maternal permanent environmental effects. Afolayan *et al*. (2007) reported relatively moderate estimate of h^2 0.42 ± 0.06 and 0.25 ± 0.08 for body height and length respectively. Consequently, the estimates of h^2 found in this study for weaning hip height and weaning body length were consistent with previously reported research outcomes such as 0.73 and 0.87 for weaning hip height and hip height at 18 months of age

(Vargas *et al*., 2000) and 0.71 ± 0.05 for mature height (Nephawe *et al*., 2004). Moreover, literatures reports indicated that estimate of h^2 could be changed from time to time within the same population. Accordingly, the h^2 estimates for weaning hip height and weaning body length were 0.43 ± 0.13 and 0.25 ± 0.10 at weaning and 0.58 ± 0.21 and 0.38 ± 12 after 168 days later at post weaning gain test date (Gilbert *et al*., 1993).

Estimates of (co)variance components and genetic parameters from bivariate and multiple trait analysis

Estimates of (co)variance and genetic parameters obtained from single, bivariate and multiple trait analysis were close to each other. Birth weight was the most consistent trait across the models (single, bivariate and multiple trait models) with no significant change was observed throughout. However, weaning weight was found fluctuated across the models to some level. This result was found consistent with the estimates of h^2 (0.28) reported by Woodward *et al.* (1992) and Meyer *et al.* (1993) also reported estimates of h^2 (0.43, 0.43 to 0.46 and 0.43 to 0.45) for birth weight from single, bivariate and multiple trait analysis, respectively. Nevertheless, the estimates of h^2 mentioned for weaning weight were not consistent with the stated outers. The inconsistency of estimates between the mentioned report and the current result particularly for weaning weight could be the number of random effects fitted to the models.

Weaning hip height had higher heritability (h^2 = 0.94 to 0.97) than weaning body length (h^2 = 0.45 to 0.50). Although the magnitude varies, Gilbert *et al*. (1993) also reported high estimates of h^2 for weaning hip height (0.43) than weaning body length (0.25). Probably this might have been attributed to breed type and age among others. Accordingly, Brown and Franks (1964), Neville *et al*. (1978) and Choy *et al*., (1996) reported estimates of h^2 ranging from 0.54 to 0.75 for cow height of different age in Angus, Hereford and crossbred beef cattle. The estimate of h^2 0.36 to 0.39 and 0.42 to 0.54 for weaning hip height from bivariate model reported by Meyer (1995) were less than the current analysis. The estimate h^2 (0.65) reported for weaning hip height by Vargas *et al.* (2000) was close to the present study. The estimates of h^2 for weaning hip height (0.28) and weaning body length (0.22) were not similar with the estimates of the same traits at yearling, 0.33 and 0.14, respectively (Marle-Koster *et al.,* 2000).

Genetic correlation between pre-weaning and growth traits

The estimates of direct genetic correlation from bivariate and multiple trait analysis are shown in Tables 10 and 12. All traits were found correlated positively. Direct genetic correlations between the considered traits were higher indicating some genes are affecting these traits in similar manner. The genetic correlation between birth and weaning weights was 0.93 in the current population. The estimate identified for birth and weaning weights in the current study was found consistent with the estimate 0.93 reported by Supakorn *et al.* (2005) and Jeanmas *et al*. (2008) for Thai Native, Brahman and Charolais crossbred beef cattle in Thailand. Meyer *et al.* (1993) reported high estimate of direct genetic correlation (0.66 to 0.71) between birth and weaning weights. In contrast, the estimate of direct genetic correlation between birth and weaning weights (0.33) reported by Marle-Koster *et al.* (2000) did not coincide with the current study. The association between birth and weaning weights plus consistency among literature reports suggests that the association between growth traits is more than a part-whole relationship.

The genetic correlation between birth weight and weaning hip height in the current study was moderate. The current result was consistent with the estimate 0.50 reported by Bennett and Gregory (2001) for pure breed and composite beef cattle population. Boligon *et al*. (2011) revealed lower (0.12 ± 0.03) genetic correlation between birth weight and weaning hip height. However, the current estimate was in contrast with the reported result. On the other hand, Sawanon *et al.* (2011) identified that the linear regression of birth weight on body length was positive indicating that heavier birth weight was associated with larger body length in crossbred male beef cattle among Thai Native, Brahman and Charolais.

The genetic correlation between weaning weight and weaning hip height was higher indicating growth characteristics in crossbred beef cattle among Thai Native, Brahman and Charolais cattle seems to be favorably related to hip height. Most literature reports were relatively consistent ranging from 0.65 to 0.76 (Vargas *et al.,* 2000; Bennett and Gregory, 2001; Pereira *et al.,* 2008; Zerbino *et al.,* 1983; Carabano *et al.,* 2004). The high direct genetic correlation obtained in the current study pointed out that hip height can indicate the condition of calf's weaning weight. However, the estimate of the direct genetic correlation for the mentioned trait clearly indicated as favorable for one another.

Genetic correlations (0.95) between pairs of body measurements at weaning were comparable with the estimate (0.93) observed within growth and was higher than the one identified between growth and body measurement traits**.** The current result was consistent with research report (0.71 ± 0.14) revealed by Gilbert *et al.* (1993) for Hereford and Angus bulls. The high correlation of direct additive genetic effects between measurement traits suggests boundless potential for improving simultaneously both traits in the current population.

The result found in this study was coincided with results revealed by some studies regarding to genetic correlations of traits for numerous beef breeds around the world. Consequently, Supakorn *et al*. (2005) reported a very higher (0.93) direct additive genetic correlation in crossbred beef cattle in Thailand. Likewise, Vargas *et al.* (2000) reported relatively higher phenotypic correlation (0.54) between weaning hip height and weaning weight. Gilbert *et al*. (1993) reported moderate (0.37) direct genetic correlation between weaning weight and weaning body length.

CONCLUSION AND RECOMMENDATION

The results of this study could be concluded that the effects of contemporary group, sex, age at weaning and breed fraction of animal should be accounted as fixed effects in genetic model. The estimates of h^2 for birth and weaning weights, weaning hip height and weaning body length were high in single, bivariate and multiple trait animal models. It was suggested that methods of selection would provide genetic progress in the population. However, the estimates were allied with relatively high standard error the result should be used in cautions. The estimates of h^2 for those traits might be overestimated because of unable to partition the maternal genetic and maternal permanent environmental effects from this data structure. Accordingly, the influence of maternal components should be verified using larger and well structured data set in the future. High genetic correlations between traits were recognized. There should be some genes that influence the interested traits alike. Selection simultaneously for those characters in the population was possible. Therefore, information of one could be used to make decision about the other when there was no information to use or can be used as supplements when information was available for all traits. Utilizing the information of genetic association would result to long term breeding program and could be very crucial for small scale farms where weight performance records were not always easy due to lack of equipments.

Further research considering larger data sets with high number of dam with its own and its progeny records and several progeny per dam would be beneficial to solve the problems associated with the estimation of maternal components and understand in detail in the population.

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CURRICULUM VITAE

NAME : Mr Tamirat Tessema Teklemichael

BIRTH DATE : May 09, 1984

BIRTH PLACE : Akaki (Addis Ababa), Ethiopia

EDUCATION :

YEAR	**INISTITUTE**	**DEGREE/DIPILOMA**
2006	Haramaya University	B.Sc. (Animal Science)

POSITION/TITLE : Junior Researcher

WORK PLACE : Yabello Pastoral and Dry Land Agriculture Reseaserch Center, Yabello, Ethiopia

SCHOLARSHIP : Rural Capacity Building Project 2008–2012, Ministry of Agriculture, Ethiopia