Estimation of Additive, Non Additive Gene Effects and Genetic Parameters on Pre-Weaning Growth Traits in Meat Goats in Southern Thailand

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Abstract

A total of 791 animals involved in Thai Native (T), Boer (B), Saanen (S) and their crosses were studied. Fixed effects of sex, birth type, breed group and year-season of birth were found to significantly affect birth weight (BW), weaning weight (WW) and average daily gain (ADG) ($P < 0.05$). Two statistical models were analyzed in this study. The first model showed that the B breed had higher BW and the S breed had highest WW and ADG than the others ($P < 0.05$). The T breed had the lowest BW, WW and ADG ($P < 0.05$) among all breeds and breed crosses. Direct additive and maternal breed effects of B and S breeds from Model 2 had significantly positive values ($P < 0.05$). It indicated that the B and S purebreds had heavier body weights than the T breed. Direct heterosis, maternal heterosis and recombination effects were not significant. The heterosis estimates of crossbreeding between S and T purebreds tended to yield heavier weaned kids ($P > 0.05$). Estimated direct and maternal heritabilities were found to be 0.25 and 0.08 for BW, 0.38 and 0.11 for WW and 0.35 and 0.12 for ADG. The direct genetic, maternal genetic and phenotypic correlations among pre-weaning traits were positive with moderate to high values (0.30 to 0.89). The findings provided basic information that farmers and breeders could utilize for an appropriate approach to crossbreeding and monitoring the genetic potential in this herd.

Keywords: Additive gene effect, genetic parameters, meat goats, non additive gene effect, pre-weaning growth traits

Introduction

Meat goat production in Thailand is characterized as a non-traditional alternative agricultural enterprise and characterized as an emerging class of livestock offering Thai farmers for on-farm income. Major determinants of profitability in the meat goat enterprise are growth traits. The benefit of crossbreeding goats is an improvement of performance on the economically important traits. Current producers had tried to take advantage of the benefit on growth traits by utilizing crossbreeding programs to improve growth and milk yield. Additive and non additive gene effects are major concerns and need to be estimated prior to developing crossbreeding and selection programs. The heterosis effect has been reported to be higher in these traits and found to range between low to moderate values for heritability. This made ruminant animals an ideal candidate to be improved through the use of crossbreeding [1]. An implementation of any crossbreeding system should significantly yield higher growth performance. The efficiency of various crossbreeding systems was determined by differences among breed effects relative to magnitudes of heterosis and recombination effects [2]. Moreover, estimation of the genetic

parameters for birth weight, weaning weight and average daily gain should consider direct and maternal effects for monitoring genetic potential in the population.

This population consists of purebred and crossbred goats with resulting crossbreds selected as parents for the next generation. In addition, characteristics of this population had similarities with farm village and commercial goat production. A high proportion of goats are found in southern Thailand. In Thailand, some investigators such as [3-6] reported pre-weaning weight and pre-weaning growth rate raised by small farmers in villages and at university farms. It is important to carry out further in depth studies on the genetic effects on the goat population under village tropical environmental and climatic conditions. Therefore, the main objectives of this study were to estimate genetic effects of direct breed, maternal breed, heterosis and recombination effects and genetic parameters in the goat population in order to monitor the genetic potential in this herd.

Materials and methods

Data were collected from a commercial goat farm in southern Thailand. Pre-weaning growth traits were obtained from purebreds and crossbreds of Thai Native (T), Boer (B) and Saanen (S) goats. The erroneous data of those animals born after their offspring and without proper sex records were not included in the analysis. Animals born from the years 2005 until 2008 were included in the study. Raw data comprised 791 records for birth weight (BW), weaning weight (WW) and average daily gain (ADG). The 1/2B1/2T, 1/2T1/2S, 1/2S1/2T and 1/2B1/4S1/4T crossbreds were included in this analysis because the several types of two- and three- crossbred groups had extremely low frequency in the data set. Crossbreds between sire of T and dam of S and vice versa were grouped because of non significant difference on pre-weaning growth traits from preliminary analysis. Crossbreds between B and S

were not observed in this herd. In this herd the number of 2 breed crosses (43.62 %) was higher than purebred (32.36 %) and 3 breed group (24.02 %). The number of S purebred was found to be the lowest in the population.

The management system in the herd was that kids born all year round were raised together with their parent until weaning. The age at weaning weight averaged 150 days. Kidding seasons were classified into 2 seasons as summer (December to March) and rainy season (April to November). These seasons were considered and tested for significant difference in relative humidity, temperature and quantity of rain fall in each month in accordance with [7]. Animals of all breed groups were raised under the same management conditions. The pens were 150 square meters in size and the number of goats kept within a pen were approximately 100 heads per pen. A male was penned with 50 females. Natural mating was used for mating in this herd. Does were mated throughout the year. The meat goats had access to a grazing pasture during the day through rotational grazing. Animals were fed with meal concentrate (20 % crude protein) approximately 1.5 to 2 % of their body weight while drinking water was fed *ad libitum*. The meat goats were confined in large pens during the night. All animals in the herd were treated against internal parasites 3 times a year. Young does were routinely checked and vaccinated against bacterial (*Brucella abortus*) infection annually at the onset of their puberty.

Data were analyzed using the generalized linear model (GLM) procedure reported in [8]. Two types of models were used for all growth traits. The 1st model included only the fixed effects of sex, birth type, breed group and year-season of birth as a contemporary group. This model was used primarily to determine genetic and non-genetic factors contributing to kid growth performance. Interaction effects were mostly negligible in preliminary analyses because of non significances.

The first statistical model for determination of BW, WW and ADG was:

$$y_{ijklm} = \mu + Sex_i + BT_j + BG_k + CG_l + e_{ijklm}$$

The terms in the models were:

y_{ijklm} = individual performance for each trait

μ = the overall mean

Sex_i = the ith fixed effect of sex (i = male and female)

BT_j = the jth fixed effect of types of birth (j = single, twin and triplet)

BG_k = the fixed effect of breed group (k = T, B, S, 1/2B1/2T, 1/2S1/2T and 1/2B1/4S1/4T)

CG_l = the fixed effect of contemporary group (year-season of birth) (l = 1, 2, …, 7)

e_{ijklm} = random residual effect ($e_{ijklmn} \sim NID (0, \sigma^2_e)$)

A 2nd model was a partly multiple regression model that were used to partition the kid genetic group effect into direct breed (g^I), maternal breed (g^m), direct heterosis (h^d), maternal heterosis (h^m) and recombination effect (r^d). The coefficients for all effects were produced as described by [9] and are given in **Table 1**.

$$y_{ijkl} = \mu + b_1 g^I B + b_2 g^I S + b_3 g^m B + b_4 g^m S + b_5 h^d + b_6 h^m + b_7 r^d + Sex_i + BT_j + CG_k + e_{ijkl}$$

The definition of y_{ijkl}, μ, Sex_i, BT_j, CG_k and e_{ijkl} are as defined in the first model. The b_1 and b_2 coefficients are for average direct breed effects due to Boer and Saanen breeds, respectively; $g^I B$ and $g^I S$ are the percentage of genes of the lth kid contributed by Boer and Saanen breeds, respectively; b_3 and b_4 are coefficients for average maternal breed effects, due to Boer and Saanen breeds, respectively; $g^m B$ and $g^m S$ are the percentage of genes in the dam of the lth kid contributed by Boer and Saanen breeds, respectively; b_5, b_6 and b_7 are coefficients for direct heterosis, maternal heterosis and recombination effects; h^d is the theoretical percentage of direct heterosis of the lth kid, h^m is the theoretical percentage of maternal heterosis from dam of the lth kid and r^d is the theoretical percentage of recombination loss of the lth kid. The

coefficients for direct breed, maternal, direct heterosis, maternal heterosis and recombination effects add to unity resulting in a singular matrix in the multiple regression model. Hence, Boer and Saanen direct genetic and maternal breed effects were estimated as deviations from Thai Native. As an example, the coefficients actually filled in the analysis for 1/2B1/4S1/4T kids correspond to 0.5, 0.25, 0, 0.5, 1, 1 and 0.25 for $g^I B$, $g^I S$, $g^M B$, $g^M S$, h^d, h^m and r^d, respectively. In analyzing the data, epistasis loss, linkage and nonlinear genetic effects were assumed to be negligible. The phenotypic values of crossbreds were divided by an average of least square means of appropriate purebreds by calculating heterosis values. However, orthogonal comparisons of breed differences and pairs of least square means between male and female and pair in each breed group were analyzed by option contrast of the R program.

Restricted maximum likelihood estimates of heritabilities and genetic, maternal and phenotypic correlations among BW, WW and ADG were obtained using ASREML [10]. Genetic parameters were estimated using multivariate analyses. Fixed effects were sex, birth type, breed group and contemporary group as same as Model 1. Direct additive, maternal genetic and residual effects were set as random effects into the multivariate animal model but no direct-maternal genetic

covariance was allowed. Nevertheless, the maternal permanent environmental effect was close to zero from the preliminary univariate analysis. The information or prior values for estimation of (co)variance in multivariate analysis values were those from univariate analysis in the same data set.

Results and discussion

Description of data

Means for BW, WW and ADG in this population were found to be 2.73 ± 0.54, 14.71 ± 2.11 kg and 0.08 ± 0.01 kg/day respectively. An average of body weight of Thai indigenous kids at weaned age was only 6.80 kg and those of Thai indigenous and crossbred kids under improved farm conditions were 9.16 and 11.15 kg, respectively [11]. In the Thai village, the management of the reproduction system is poorly managed. Bucks and does are kept together without controlled mating which led to inbreeding in the herd. Moreover, farmers do not durance their goats and feed them with poor quality food and not enough roughage. Under improved farm conditions BW, WW and ADG of kids were higher due to better management, feed and feeding [4].

Table 2 shows all of the fixed effects were significant (P < 0.05) for pre-weaning growth traits. The effects of sex, types of birth and year-season of birth from model 2 were closed by significant testing from model 1. A significant sex effect was found only for BW as shown in [12,13]. This agrees with reports by [5,6] who reported that sex, types of birth and breed groups influenced the pre-weaning growth traits of meat goats in Thailand. The result shows that single kids were heavier (P < 0.05) than twin and triplet kids for BW, WW and ADG. It indicated that single kids were heavier and grew faster than other groups because of efficiency of milk yield and milking ability. This present result agrees well with [6,12,14-15] for Thai Native goat, common African goat, the Damascus goat and Mali goat, respectively.

Table 1 Genetic groups of kids with additive and non additive genetic effects and coefficients of the mixing relating genetic group means of kids with crossbreeding parameters.

Genetic group			Means	Coefficients of the matrix								
				g^I			g^M			Non additive genetic effect		
Kid	Sire	Dam		T	B	S	T	B	S	h^d	h^m	r^d
T	T	T	1	1	0	0	1	0	0	0	0	0
B	B	B	1	0	1	0	0	1	0	0	0	0
S	S	S	1	0	0	1	0	0	1	0	0	0
1/2B1/2T	B	T	1	0	0.5	0	1	0	0	1	0	0
1/2T1/2S	T	S	1	0	0	0.5	0	0	1	1	0	0
1/2S1/2T	S	T	1	0	0	0.5	1	0	0	1	0	0
1/2B1/4S1/4T	B	1/2T1/2S	1	0	0.5	0.25	0	0	0.5	1	1	0.25

T = Thai Native, B = Boer, S = Saanen, g^I = direct breed effect, g^m = maternal breed effect, h^d = direct heterosis effect, h^m = maternal heterosis effect and r^d = direct recombination effect.

Table 2 P-values (Significant testing) of fixed effects from a simple model and estimates for additive and non additive genetic effects from a multiple regression model.

Breed	BW (kg)	WW (kg)	ADG (kg/day)
A simple model			
Sex	0.0081	0.0048	0.0057
Birth type	< 0.0001	0.0126	0.0216
Breed group	0.0154	0.0123	0.0224
Year-season of birth	0.0222	0.0412	0.0023
Multiple regression model			
$g^I B$	1.54 ± 0.32**	4.18 ± 2.26**	0.040 ± 0.01**
$g^I S$	1.12 ± 0.90*	2.41 ± 0.78**	0.030 ± 0.01*
$g^m B$	1.45 ± 0.33**	2.52 ± 1.23**	0.060 ± 0.01**
$g^m S$	1.18 ± 0.70*	1.78 ± 0.80*	0.040 ± 0.01*
h^d	0.14 ± 0.10	0.31 ± 0.77	0.001 ± 0.001
h^m	0.19 ± 0.24	0.50 ± 0.38	0.008 ± 0.001
r^d	0.25 ± 0.16	0.55 ± 0.48	0.016 ± 0.004

See footnotes in **Table 1** for description abbreviations
BW= Birth weight, WW = Weaning weight and ADG = Average daily gain
Significantly different at * P < 0.05 and ** P < 0.01

Table 3 Least square means and standard errors among breed groups for pre-weaning growth traits.

Breed[1]	n	BW (kg)	WW (kg)	ADG (kg/day)
Overall means ± SD	791	2.73 ± 0.54	14.71 ± 2.11	0.08 ± 0.01
T	134	2.07 ± 0.31[a]	9.50 ± 2.12[a]	0.03 ± 0.01[a]
B	63	3.26 ± 0.50[b]	15.82 ± 2.13[b]	0.07 ± 0.01[b]
S	59	2.89 ± 0.46[c]	18.03 ± 2.12[c]	0.10 ± 0.01[c]
2-breed cross				
1/2B1/2T	125	2.45 ± 0.40[c]	12.55 ± 2.10[a]	0.06 ± 0.01[b]
1/2S1/2T	220	2.43 ± 0.51[c]	16.57 ± 2.11[b]	0.09 ± 0.01[c]
3-breed cross				
1/2B1/4S1/4T	190	3.04 ± 0.23[bc]	16.80 ± 2.08[b]	0.08 ± 0.01[bc]

SD = standard deviation
[1]See footnotes in **Table 1** and **2** for description abbreviations of traits and breeds
[a, b] and [c] within the same column values marked with the different letter are significantly different at * P < 0.05 and ** P < 0.01

Table 4 Least square means differences between sex and standard error for growth traits.

Breed[1]	BW (kg)	WW (kg)	ADG (kg/day)
	Bucks-does	Bucks-does	Bucks-does
T	0.04 ± 0.02*	1.19 ± 0.40*	0.01 ± 0.003*
B	0.15 ± 0.08*	0.59 ± 0.12*	0.01 ± 0.002*
S	1.17 ± 0.13*	5.80 ± 0.61*	0.03 ± 0.001*
2-breed cross			
1/2B1/2T	0.24 ± 0.11	1.93 ± 0.22	0.02 ± 0.010
1/2S1/2T	0.59 ± 0.14*	3.99 ± 0.87*	0.01 ± 0.001*
3-breed cross			
1/2B1/4S1/4T	0.23 ± 0.03	3.91 ± 0.91*	0.02 ± 0.005

[1]See footnotes in **Table 1** and **2** for description abbreviations of traits and breeds
Significantly different at * $P < 0.05$ and ** $P < 0.01$

Least square means and standard errors among breed groups for BW, WW and ADG are presented in **Table 3**. Purebred goats of B had higher BW and S breed had higher WW and ADG than other purebred groups ($P < 0.05$). T breed was found to have the lowest growth performance. Likewise, [5,16-17] reported that growth rate of Boer, Angora and crossbred with Boer or Angora goats was better than indigenous purebred ($P < 0.05$). BW of 1/2B1/2T and 1/2S1/2T were found to be similar but the WW and ADG of 1/2S1/2T crossbred were higher than the 1/2B1/2T crossbred. The result indicates that the B or S breed could improve the BW from the T breed. The S breed could improve WW and ADG for two crossbred animals because crossbred kids received a good mothering ability, milking ability and more milk yield from the Saanen breed. The milk quality of Saanen was better than Nubian and Toggenburg in Taiwan [18]. Therefore, utilization of Saanen as an alternative breed could improve WW and ADG in this population. The ADG of the 1/2S1/2T crossbred was better than the S and T purebreds. It indicated that there was a heterosis effect for this crossbred. The pre-weaning growth traits of the 3 breed crosses were similar to those of B and S purebreds and 2 types of 2 breed cross for BW, WW and ADG. This result suggests that 1/2B1/4S1/4T is not an appropriate choice to produce 3 breed crosses in goat breeding programs.

Significant sex difference between male and female goats of whole population led an in-dept study among breed groups. **Table 4** represents least square means of pre-weaning growth traits differences between male and female goats for 6 breed groups in this data set. Least square means differences between bucks and does were positive within breed groups. It indicated that bucks were significantly heavier than does, except for the 1/2B1/2T breed for all growth traits and the 1/2B1/4S1/4T breed for BW and ADG. The result agreed well with [19] who stated that sex differences increased with growth rate indicating that male kids were more responsive to improvements in the environment.

Additive breed differences and heterosis effects for growth performance

The multiple regression model in **Table 2** shows estimates of direct breed, maternal breed, direct heterosis, maternal heterosis and recombination effects. Direct breed and maternal breed effects of B and S breeds were significantly positive on growth performance. Direct heterosis, maternal heterosis and recombination effects were not significant. The lack of a heterosis effect on the growth performance in this crossbred data set suggests crossbreeding is unfavourable. In contrast, [20,21] reported that the crossbreeding parameter showed significant and negative influence on paternal heterosis on weight at birth. Crossbreds between Saudi Aradi and Damascus were associated with significant direct heterosis in the majority of growth [22].

The result in our study revealed additive breed differences of 3 purebreds and heterosis effects that are represented in **Table 5**. Additive breed differences between T-B and T-S were negative values on pre-weaning growth traits ($P < 0.05$). It indicated that growth performance of Thai Native breed animals was lower than Boer and Saanen breeds. Additive breed difference estimated between B-S was positive on BW but WW and ADG were found to be negative ($P < 0.05$). It indicated that the producer could improve growth performance especially WW and ADG by Saanen breeds as dam lines in order to develop genetic progress on these growth traits in the Thai goat herd.

Heterosis values tended to increase for all growth traits of 1/2S1/2T crossbred which is in agreement with [23] using British Saanen, Boer x British Saanen and Anglo-Nubian male kids reported that kids of the British Saanen breed were heavier at 8 wk and at slaughter than Boer x British Saanen. In Egypt, [20] using Alpine and Rove breed and Alpine x Rove cross revealed that estimates of heterosis for body weights ranged from 7 to 27 %. In another study, [24] with Black Bengal, Barbari and Anglo-Nubian kids and Barbari x Black Bengal found that estimates of heterosis were −11, 10 and −1 % for body weights at birth, 6 and 12 months of age, respectively. Unfortunately, heterosis estimates for the 1/2B1/2T crossbred gave antagonistic values and the 3 breed cross (1/2B1/4S1/4T) was close to 0 on BW, WW and ADG. This non additive effect may differ substantially in a different data set. Thus, a larger data set would be needed to clarify the role of both heterosis and recombination effect for these growth traits in goat population in Thailand.

Heritability, direct genetic, maternal genetic and phenotypic correlations

The heritability estimates for pre-weaning growth traits suggested that a substantial improvement could be achieved by selection. **Table 6** represents REML estimates of direct heritability on the diagonal, maternal heritability in parentheses on the diagonal, genetic correlations above the diagonal, maternal genetic correlation in parentheses of above the diagonal and phenotypic correlation below the diagonal. Direct heritability estimates involving all traits were moderate values (0.25 for BW, 0.38 for WW and 0.35 for ADG). Maternal heritability estimates were low (0.08 for BW, 0.11 for WW and 0.12 for ADG). Low maternal heritability values indicate that does in this goat population had low variation for good mothering genetic ability. Similar estimates in the Black Bengal goats and Angora goats in Iraq and Emirati were reported by [13,25-26]. A higher estimate of direct heritability (0.68) was reported for Common African and Alpine crossbred kids [12]. This finding probably contradicts that of other researchers because of the selection criteria, farm management and model for analysis.

Estimates of genetic correlations (**Table 6**) were moderate and positive between BW and WW (0.45) and between BW and ADG (0.52) while it was high and similar positive between WW and ADG (0.89). Maternal correlations were high and positive between BW and WW (0.66), between BW and ADG (0.52) and WW and ADG (0.74). It indicates that selection for heavier WW or high ADG in this herd could result in increases in BW. The emphasis should be on increasing WW and ADG without increasing BW. The positive genetic correlation between BW and body weight at weaning agrees with [27,28] who reported positive genetic correlations between weight and subsequent weight (0.60 to 0.92) in sheep. Phenotypic correlations had the same trend as genotypic correlations. It shows that phenotypic correlations among pre-weaning growth traits were positive and moderate to high (0.34 to 0.79).

Table 5 Additive breed differences, direct heterosis values and standard error for growth traits.

Breed[1]	BW (kg)	WW (kg)	ADG (kg/day)
Additive			
T-B	-1.52 ± 0.17**	-4.36 ± 3.76**	-0.03 ± 0.02**
T-S	-1.10 ± 0.66*	-2.47 ± 3.46*	-0.02 ± 0.03**
B-S	0.96 ± 0.75*	-2.68 ± 2.83*	-0.03 ± 0.02*
General Heterosis			
2-breed cross			
(1/2B1/2T) - ((B + T)/2)	-0.20 ± 0.38	-1.03 ± 4.25	0.02 ± 0.02
(1/2S1/2T)* - ((T + S)/2)	0.68 ± 0.04	3.75 ± 2.58	0.03 ± 0.03
3-breed cross			
(1/2B1/4S1/4T)) - ((B + (1/2S1/2T))/2)	0.20 ± 0.35	0.55 ± 0.50	-0.01 ± 0.01

[1]See footnotes in **Table 1** and **2** for description abbreviations of traits and breeds
*1/2T1/2S and 1/2S1/2T breed groups were included

Table 6 Estimates of direct heritabilities (diagonal), maternal heritabilities (in parentheses of the diagonal), direct genetic correlations (above the diagonal), maternal genetic correlation (in parentheses of above the diagonal) and phenotypic correlations (below the diagonal) among growth birth weight (BW), weaning weight (WW) and average daily gain (ADG).

	BW	WW	ADG
BW	0.25 ± 0.05	0.45 ± 0.19	0.30 ± 0.10
	(0.08 ± 0.03)	(0.66 ± 0.20)	(0.52 ± 0.19)
WW	0.50 ± 0.16	0.38 ± 0.05	0.89 ± 0.01
		(0.11 ± 0.05)	(0.74 ± 0.28)
ADG	0.34 ± 0.06	0.79 ± 0.01	0.35 ± 0.05
			(0.12 ± 0.04)

Conclusions

The fixed effects of sex, birth type, breed group and year-season of birth had a significant difference on pre-weaning growth traits. The B breed was found to be high in BW and the S breed was found to be high in WW and ADG whereas the T breed had the lowest BW, WW and ADG.

Direct breed and maternal breed effects of B and S deviated from T and showed significant positive values (P < 0.05). However, direct heterosis, maternal heterosis and recombination effects were not significant. Additive breed different estimates between T-B and T-S were found to be negative for BW, WW and ADG (P < 0.05). It showed that the growth performance of B and S was higher than T. Heterosis estimates of 1/2S1/2T crossbred were positive for pre-weaning growth traits. It was concluded that breed fraction

of S should be considered in crossbreeding program in order to increase economic efficiency. However, producers and breeders should consider direct additive and maternal genetic effects because they could be heritable to the next generation. Less heterosis estimates of 3 crossbred and 1/2B1/2T cross bred were found in this small population.

There were moderate direct heritability and low maternal heritability estimates of all traits obtained in this study. Genetic correlations among pre-weaning growth traits were moderate and positive except between WW and ADG. Maternal correlations were high and positive which means that continual selection on maternal effects to increase BW would result in a correlated respond in WW and ADG.

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