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Genetic Parameters for Birth Weight and Weaning Weight in Anglo-Nubian, Saanen, Thai Native and Crossbred Goats

Chittima Kantanamalakul[1], Panwadee Sopannarath[2], Monchai Duangjinda[3],
Suwit Anothaisinthawee[4] and Sornthep Tumwasorn[2*]

ABSTRACT

Genetic parameters were estimated for birth weight and weaning weight in Anglo-Nubian, Saanen, Thai native and crossbred goat populations maintained at the Yala Livestock Research and Breeding Center. Records on 2,845 kids descended from 54 bucks and 615 does from 1995 to 2005 were included in the analysis. Analyses were carried out using the DFREML algorithm and fitting four different animal models that included or ignored maternal genetic and permanent environmental effects. In Model 1 only the direct genetic effect was fitted. The maternal permanent environmental effect was added in Model 2, while the maternal genetic effect was added in Model 3. In Model 4, the maternal genetic and permanent environmental effects were included from Model 1. The genetic covariance between the direct and maternal effects was included in Models 3 and 4. The estimates of direct heritability increased when the maternal genetic effect was added with the direct and maternal covariance. The estimates of maternal heritability slightly decreased when the maternal permanent environmental effect was added to the model. The direct-maternal genetic correlation estimates were negative, whereas estimates of the maternal permanent environmental variance as a proportion of phenotypic variance were low. The likelihood ratio test showed that Model 4 was the best for birth weight and Model 3 was the best for weaning weight.

Key words: goat, genetic parameter, birth weight, weaning weight

INTRODUCTION

The economic value of a goat depends on its growth performance that can be measured and expressed as body weight at various ages. The growth before the pre-weaning age is important in a goat's production system, especially where the kids are sold at weaning, because birth weight and weaning weight are related to kid survival and postnatal development (Mukundan *et al*., 1981). In addition, rapid growth during the pre-weaning period minimized the cost of rearing and provided more profit to farmers (Malik *et al*., 1986).

The growth traits at an early age in farm animals are known to be influenced by direct and maternal effects (Meyer, 1992). The direct effect refers to the effect that an individual's own genes have on its performance. The maternal effect refers

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[1] School of Agricultural Extension and Cooperatives, Sukhothai Thammathirat Open University, Pakkred, Nonthaburi 11120, Thailand.
[2] Department of Animal Science, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand.
[3] Department of Animal Science, Faculty of Agriculture, Khon Kaen University, Khon Kaen 40002, Thailand.
[4] Department of Livestock Development, Ministry of Agriculture and Cooperatives, Phayathai Road, Bangkok 10400, Thailand.
* Corresponding author, e-mail: sornthep@ksc.th.com

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to the dam's own genotype for milking and mothering ability and the permanent effect of the environment on her maternal ability. The estimates of these components of variance are important to make informative genetic evaluations that are required for a successful, livestock genetic improvement program.

As a few attempts had already been made to use animal models to analyze the maternal influence on the early growth traits of goats in Thailand, this study was conducted to estimate genetic parameters for birth weight and weaning weight in a breeding goat herd in Yala province by fitting four different animal models including or ignoring maternal effects.

MATERIALS AND METHODS

Data

The pedigree and performance of goats were obtained from the Yala Livestock Research and Breeding Center on the east coast of the southern part of Thailand (5-7°N, 100-102°W). In 2007, Thailand's tropical monsoon climate had an average temperature, relative humidity and annual rainfall of 28.14°C, 74.89% and 2,386.10 millimeters, respectively (Yala Meteorological Station, 2008). The dataset in this study was collected from 2,845 kids that were born during 1995-2005. They were the progeny of 54 bucks and 615 does. The breeds of buck, doe and kid were Anglo-Nubian, Saanen, Thai native and crosses as shown in Table 1. The traits analyzed were birth weight and weaning weight.

Management

The replacement herd was usually recruited from within the herd and 20% of the bucks were imported from other stations and from abroad. The young males and females were performance tested from age 3 to 9 months based on body weight. They were selected based on their health status, growth (body weight) and pedigree. Selected goats remained at the center for breeding and replacement, while unselected ones were sold to farmers for meat. The young does were mated to bucks for the first time at nine months of age and produced their first kid between 15 and 18 months of age. The feed-concentrate contained approximately 16% crude protein and 2,600 kcal/kg ME on an as fed-basis. The bucks, pregnant does and replacement herd were fed concentrate at 1% of body weight once a day in the morning. The lactating does were fed twice a day (morning and evening) at 1.5% of body weight. The does were rotationally grazed from 9.00 am to 3.00 pm and were offered cut-and-carry forage in the evening. Roughage was mainly *Brachiaria decumbens*, *Paspalum plicatulum*, *Panicum maximum* and *Pennisetum purpureum.*

The mating period occurred from 3.00 pm until 9.00 am the next day, with one buck and 15 does being penned together. The gestation period in goats was around 150 days. After birth, the kids were suckled colostrums for three days, ear tagged, weighed and identified by sex, breed combination and by buck and doe group. The new born kids were fed with doe milk and milk replacer from 1 to 12 weeks of age. The kids started eating dry grasses, bush leaves, dry fodder and concentrate at four weeks. At weaning, kids were weighed and moved to another pen for performance testing.

Statistical analysis

The variance and covariance components for birth weight and weaning weight were estimated by using a derivative-free REML algorithm (Graser *et al.*, 1987). The maximum likelihood value was found by the Simplex method. The convergence criterion was considered to be reached when the variance of the function values used in the Simplex method was less than 10^{-9}. Analyses were restarted from the converged values to check that a global rather than a local maximum had been reached. When

Table 1 Breed groups and number of records.

Breed group			Number of records
Buck	Doe	Kid	
A	A	A	305
A	3/4A1/4N	7/8A1/8N	70
A	5/8A3/8N	13/16A3/16N	18
A	1/2A1/2N	3/4A1/4N	291
A	N	1/2A1/2N	114
S	S	S	26
S	3/4S1/4N	7/8S1/8N	13
N	N	N	764
N	1/4A1/2S1/4N	1/8A1/2S5/8N	44
3/4A1/4N	3/4A1/4N	3/4A1/4N	182
3/4A1/4N	5/8A3/8N	11/16A5/16N	14
3/4A1/4N	1/2A1/2N	5/8A3/8N	46
1/2A1/2N	3/4A1/4N	5/8A3/8N	19
1/2A1/2N	5/8A3/8N	9/16A7/16N	17
1/2A1/2N	1/2A1/2N	1/2A1/2N	359
3/4S1/4N	3/4S1/4N	3/4S1/4N	270
1/2S1/2N	3/4S1/4N	5/8S3/8N	18
1/2S1/2N	1/2S1/2N	1/2S1/2N	208
1/2S1/2N	1/2A1/4S1/4N	1/4A3/8S3/8N	12
1/2S1/2N	1/4A5/8S1/8N	1/8A9/16S5/16N	12
1/2A1/4S1/4N	1/2A1/4S1/4N	1/2A1/4S1/4N	24
1/4A1/2S1/4N	1/4A1/2S1/4N	1/4A1/2S1/4N	19
Total			2,845

A = Angol-Nubian, S = Saanen, N = Thai Native

estimates did not change, convergence was assumed.

Single-trait analyses were employed for each model that included fixed and random effects. Fixed factors were sex, parity, type of birth, year-season at kidding, expected breed content and expected heterozygosity. Sex was either male or female. The parity of the does was grouped into seven levels (1, 2, 3, 4, 5, 6 and ≥ 7). The type of birth was either single, twins or triplets. According to Hemsuhree (1997) and Chitprasan *et al.* (1998), four-month kidding periods were grouped into three seasons with a low rainfall season (January to April), a moderate rainfall season (May to August) and a high rainfall season (September to December). Average temperature, relative humidity and annual rainfall in the low rainfall season were 27.70 ± 0.76°C, 74.00 ± 1.78% and 50.32 ± 60.82 millimeters, respectively. The same parameters in the moderate rainfall season were 28.55 ± 0.49°C, 77.37 ± 2.79% and 99.76 ± 53.46 millimeters, respectively and in the high rainfall season were 27.22 ± 0.77°C, 77.98 ± 3.60% and 319.17 ± 207.47 millimeters, respectively. The expected breed content and heterozygosity in animals were treated as covariates. The expected breed content was expressed as a deviation from native and the expected heterozygosity was calculated as $\Sigma pb_i pd_j$, where pb_i and pb_j were the proportion of breed i in the buck and breed j in the doe, respectively (Van der Werf and De Boer, 1989; Hirooka *et al.*, 1998).

The random effects included in the model were direct genetic, maternal genetic, permanent environmental effects and the residual. The four animal models in matrix notation can be expressed as follows:

$$\text{Model 1}: \mathbf{y} = \mathbf{X_1b} + \mathbf{X_2g} + \mathbf{X_3h} + \mathbf{Za} + \mathbf{e}$$

$$\text{Model 2}: \mathbf{y} = \mathbf{X_1b} + \mathbf{X_2g} + \mathbf{X_3h} + \mathbf{Za} + \mathbf{Wc} + \mathbf{e}$$

$$\text{Model 3}: \mathbf{y} = \mathbf{X_1b} + \mathbf{X_2g} + \mathbf{X_3h} + \mathbf{Za} + \mathbf{Mm} + \mathbf{e} \quad \text{with } \mathrm{cov}(a,m) \neq 0$$

$$\text{Model 4}: \mathbf{y} = \mathbf{X_1b} + \mathbf{X_2g} + \mathbf{X_3h} + \mathbf{Za} + \mathbf{Mm} + \mathbf{Wc} + \mathbf{e} \quad \text{with } \mathrm{cov}(a,m) \neq 0$$

where y is a n x 1 vector of observations for each trait, $\mathbf{X_1}$ is an incidence matrix relating the fixed effects (**b**) to the vector of observations, $\mathbf{X_2}$ is an incidence matrix relating the vector of direct breed effects (**g**), $\mathbf{X_3}$ is an incidence matrix relating the vector of heterosis effects (**h**), **Z** is an incidence matrix relating the vector of direct genetic effects (**a**), **M** is an incidence matrix relating the vector of maternal genetic effects (**m**), **W** is an incidence matrix relating the vector of maternal permanent environmental effect (**c**) and **e** is a vector of residuals.

The first moments for all models were assumed to be:

$$E[y] = X_1b + X_2g + X_3h$$

The variance and covariance structures for random effects of the above models were assumed as follows:

$$\text{Model 1: } V\begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 \\ 0 & I_n\sigma_e^2 \end{bmatrix}$$

$$\text{Model 2: } V\begin{bmatrix} a \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I_c\sigma_c^2 & 0 \\ 0 & 0 & I_n\sigma_e^2 \end{bmatrix}$$

$$\text{Model 3: } V\begin{bmatrix} a \\ m \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 \\ 0 & 0 & I_n\sigma_e^2 \end{bmatrix}$$

$$\text{Model 4: } V\begin{bmatrix} a \\ m \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & 0 & 0 \\ A\sigma_{am} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I_c\sigma_c^2 & 0 \\ 0 & 0 & 0 & I_n\sigma_e^2 \end{bmatrix}$$

where **A** was a numerator relationship matrix, σ_a^2 was a direct genetic variance, σ_m^2 was a maternal genetic variance, σ_c^2 was a maternal permanent environmental variance, σ_e^2 was an error variance, I_c was an identity matrix with orders equal to the number of does,

and I_n was an identity matrix with orders equal to the number of records.

The estimates of parameters were derived from estimates of variance components. direct heritability (h^2), maternal heritability (m^2) and maternal permanent environmental variance as a proportion of phenotypic variance (c^2) were calculated as ratios of σ_a^2, σ_m^2 and σ_c^2 to the phenotypic variance (σ_p^2). The direct-maternal genetic correlation (r_{am}) was calculated as a ratio of σ_{am} to the product of the square root of σ_a^2 and σ_m^2 (Willham, 1972; Falconer and Mackey, 1996).

To identify the most appropriate model for each trait, the likelihood ratio test was conducted (Meyer, 1992). Likelihoods increased when additional parameters were included in the model and an effect was considered to have a significant influence when its inclusion caused a significant increase in the log likelihood compared to the model in which it was ignored. The significance was tested at the level of $P<0.05$ by comparing the difference in log likelihoods to the value of a chi-squared distribution with degrees of freedom equal to the difference in the number of variance and covariance components fitted for the two models.

RESULTS AND DISCUSSION

Descriptive statistics

The mean, standard deviation and coefficient of variation for the traits are shown in Table 2. In the data set used, 50.79% of the kids were male and 49.21% female. Single-born kids represented 44.78% of the sample, 50.92% were twins and 4.30% were triplets. The distribution by kidding season was 34.62% (low rainfall), 29.74% (moderate rainfall) and 35.64% (high rainfall).

Variance components and parameter estimates

The estimates of the variance components and parameters for each trait were obtained from the four models using the derivative-free REML algorithm and are summarized in Tables 3 and 4. The estimates of σ_p^2 for all models were from 0.21 to 0.22 and 9.04 to 9.48 kg^2 for birth weight and weaning weight, respectively. These were lower than those reported for the Boer goat by Els (1998) and Zhang *et al*. (2007). There was not much difference in the σ_p^2 values, except for Model 3 and Model 4 which added the direct-maternal genetic covariance for weaning weight, resulting in the estimates of σ_p^2 being higher than in the other models. Notter (1998) suggested that including the negative direct-maternal genetic covariance in the model would have a marginal influence on estimates of σ_p^2.

The estimates of σ_a^2 and h^2 were lowest in Model 2 (including the permanent environmental effect), while in Model 3 (including maternal genetic effect) they were similar to those in Model 4 (including all effects). Inclusion of the maternal genetic effect with a correlation between direct and maternal genetic effects yielded substantially higher estimates of σ_a^2 and h^2 than in the other models. The magnitude of h^2 at 0.50

Table 2 Mean, standard deviation (SD) and coefficient of variation (CV) for traits.

Trait	Number of records	Mean (kg)	SD (kg)	CV (%)
Birth weight	2,845	2.39	0.51	21.49
Weaning weight	2,845	11.07	3.37	30.42

Table 3 Variance components and parameter estimates for birth weight.

Parameter	Model 1	Model 2	Model 3	Model 4
σ_a^2	0.06	0.05	0.11	0.11
σ_m^2	-	-	0.06	0.05
σ_{am}	-	-	-0.07	-0.07
σ_c^2	-	0.02	-	0.012
σ_e^2	0.15	0.15	0.12	0.12
σ_p^2	0.22	0.21	0.22	0.22
h^2	0.30 (0.04)	0.22 (0.05)	0.50 (0.10)	0.50 (0.10)
m^2	-	-	0.28 (0.05)	0.23 (0.05)
r_{am}	-	-	-0.84 (0.35)	-0.93 (0.41)
c^2	-	0.08 (0.02)	-	0.05 (0.03)

σ_a^2 = direct genetic variance, σ_m^2 = maternal genetic variance, σ_{am} = direct-maternal covariance, σ_c^2 = permanent environmental variance, σ_e^2 = residual variance, σ_p^2 = phenotypic variance, h^2 = direct heritability, m^2 = maternal heritability, r_{am} = direct-maternal genetic correlation, c^2 = maternal permanent environmental variance as a proportion of phenotypic variance.
Figures in parentheses are standard errors of estimate.

(birth weight) and 0.45 (weaning weight) in Model 4 were greater than those observed by previous studies (Gerstmayr and Horst, 1995; Schoeman *et al*., 1997; Matika *et al*., 2003; Mandal *et al*., 2006) using the same model. The direct variance and heritability were larger than their corresponding maternal values (σ_m^2 and m^2) in similar results that were obtained with sheep (Snyman *et al*., 1995; Al-Shorepy, 2001). Estimates of σ_m^2 and m^2 were lowest in Model 4. The values of σ_m^2 decreased by approximately 16.67% (birth weight) and 7.52% (weaning weight) when the permanent environmental effect was added to the model (Model 3 vs Model 4). The estimates of m^2 for both traits (0.23 and 0.13) in Model 4 were similar to those observed by Hirooka *et al*. (1997) for the Malaysian local goat and crosses and by Ligda *et al*. (2000) for Chios sheep. The values of for birth weight were higher than those for weaning weight indicating that maternal effects expressed during gestation and lactation were expected to have a diminished influence on kids as their weight increased. In Models 3 and 4, all covariance and correlation estimates between direct and maternal genetic effects were high with a negative coefficient similar to the study of Maria *et al*. (1993). The negative estimates of σ_{am} and r_{am} resulted in a corresponding increase in estimates of σ_a^2 and h^2. Lewis and Beatson (1999) argued that selection to improve pre-weaning weights would be less effective if there were genetic antagonism between the direct and maternal additive effects. However, several studies in beef cattle found that estimates of direct-maternal genetic correlation may be negative not only because of genetic antagonism, but also because of other random factors such as a sire x year interaction, sire x year-season interaction and grand-maternal effects. Inclusion of any additional random factors in the model could result in a reasonable estimation of the genetic correlation between direct and maternal effects (Robinson, 1996; Lee and Pollak, 1997;

Table 4 Variance components and parameter estimates for weaning weight.

Parameter	Model 1	Model 2	Model 3	Model 4
σ_a^2	1.80	1.64	4.28	4.26
σ_m^2	-	-	1.33	1.23
σ_{am}	-	-	-2.08	-2.06
σ_c^2	-	0.15	-	0.11
σ_e^2	7.25	7.25	5.95	5.93
σ_p^2	9.06	9.04	9.48	9.47
h^2	0.20 (0.04)	0.18 (0.04)	0.45 (0.10)	0.45 (0.10)
m^2	-	-	0.14 (0.04)	0.13 (0.05)
r_{am}	-	-	-0.87 (0.50)	-0.90 (0.54)
c^2	-	0.02 (0.01)	-	0.01 (0.02)

See Table 3 for abbreviations.

Table 5 Log likelihood values obtained for each trait under the four models.[a]

Trait	Model 1	Model 2	Model 3	Model 4
Birth weight	-78.98*	-55.23*	-4.61*	0
Weaning weight	-26.24*	-24.98*	-0.35	0

Log likelihood expressed as a deviation from the highest value model.

* $P<0.05$.

Dodenhoff *et al*., 1998, 1999a, 1999b).

The estimates of σ_c^2 decreased by approximately 40% (birth weight) and 26.67% (weaning weight) when the maternal genetic effect was added to the model (Model 2 vs Model 4), indicating that some of the maternal genetic effects were then attributed to the maternal environment. The estimates of c^2 for all traits were 1 to 8% of the total phenotypic variance which were in the lower part of the range cited in Ligda *et al*. (2000) and Matika *et al*. (2003). Their estimates of the permanent environmental effects due to the dam were lower than those for maternal heritability in the present study. These results showed that there was little influence due to the environment of the doe during gestation and lactation. In addition, the maternal, permanent and environmental effects were shown to be less important than the maternal genetic effects.

The difference in log likelihood values between the models associated with fitting each additional random term is summarized in Table 5. The addition of each random term to the model for birth weight resulted in a significant ($P<0.05$) increase in the log likelihood value over Model 1 and the difference in log likelihood value between Models 1 and 4 was highest. For weaning weight, the inclusion of the maternal permanent environmental variance did not substantially increase the log likelihood value of Models 2 and 4 ($P>0.05$). Based on the likelihood ratio test, fitting both the genetic and environmental components of the dam effect (Model 4) resulted in a significantly better fit compared to other models for birth weight, whereas Model 3 which allowed for a maternal genetic effect gave the best fit for weaning weight.

CONCLUSION

The results showed that it was important to implement the correct model for estimation of the variance components and the genetic parameters for the birth weight and weaning weight of kids. The model ignoring maternal genetic effects tended to underestimate direct heritability. Negative estimates for the direct and maternal genetic covariance were observed and so would have a negative impact on the total predicted selection response. Based on the likelihood ratio test, fitting both genetic and environmental components of the dam effect resulted in a significantly better fit compared to other models for birth weight, whereas the maternal genetic effect gave the best fit for weaning weight.

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