Songklanakarin J. Sci. Technol.
35 (1), 1-10, Jan. - Feb. 2013

SONGKLANAKARIN JOURNAL OF SCIENCE AND TECHNOLOGY
http://www.sjst.psu.ac.th

Original Article

Estimation of genetic parameters and genetic trends for weight and body measurements at birth in sheep populations in Thailand

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Received 8 March 2012; Accepted 19 November 2012

Abstract

The main objective of this study was to estimate the genetic parameters and genetic trends for birth weight (BW), heart girth (HG), and body length (BL) at birth of sheep populations in Thailand. Data were collected during 1998 to 2011 from four livestock research and testing stations. Fixed effect testing showed that sex, herd, contemporary group and breed group greatly influenced on the investigated traits ($P<0.05$). The log likelihood ratio test showed that all traits significantly affected by maternal additive genetic effect as well as covariance between animal effects. Estimated direct heritabilities from multivariate analysis of the model for BW, HG and BL were 0.32, 0.52 and 0.54, while estimated maternal heritabilities were 0.23, 0.14 and 0.14, respectively. Positive correlations were found among direct additive genetic (0.29 to 0.97), maternal additive genetic (0.23 to 0.95), and phenotype (0.18 to 0.96). Direct-maternal correlations within traits (-0.68 for BW, -0.92 for HG and -0.89 for BL) and between traits (-0.89 to -0.08) were antagonistic effect. Direct additive genetic trends for BW, HG and BL in the second period (2005 to 2011) were significantly increased (0.02 kg/year, 0.89 and 0.73 cm/year) while maternal additive genetic trends characteristically depicted significantly decreased (-0.01 kg/year, -0.92 and -0.72 cm/year).

Keywords: sheep, birth weight, body measurement at birth, genetic parameters and genetic trends

1. Introduction

In the past decade, sheep production in Thailand did not play a crucial role in sustaining agricultural production. Live lambs in meat, wool and dual purpose types were imported from US, Africa, and other parts of the world as an alternative agricultural enterprise by the Department of Livestock Development, Thailand. However, sheep was not a popular animal in comparison to other livestock animals, such as cattle, swine and poultry. In 2005, Queen Sirikit of Thailand needed to improve the wool sheep quality for hand-woven production with the purpose of increasing income for Thai farmers. Consequently, wool sheep breeding was improved to develop wool in higher quality and quantity (Anothaisinthawee, 2005). At the present time, not only wool sheep but also meat sheep such as Dorper and Santa Inès were important for consumer especially Thai Muslims. The number of sheep has increased in last decade. In 2010, there were 51,735 heads, mostly raised by small farmer villages for income support, and 6,191 farmers who domesticated sheep in Thailand. Moreover, the demand of mutton was slightly increased in every year (DLD, 2010). Unfortunately, sheep breeding would not achieve a maximum genetic progress because of limitations in lamb numbers, inappropriate farm management, and data collection. The dataset for this study was received from four livestock research and testing stations in Thailand, which are the main stations for lamb raising, and which have complete pedigree information and birth

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performance records. Birth weight (BW), heart girth (HG), and body length (BL) are primarily and routinely used as conventional methods to collect relevant data of the herds. These traits are controlled by polygene as random effect, including direct and maternal additive genetic effects, and are affected by feeding and management as well as environmental factors concerning farm conditions, which can affect both lamb and its dam. Knowledge of genetic variations and correlations among traits are required for both the design of effective sheep breeding programs and the accurate prediction of genetic progress. Nevertheless, research on genetic parameters of economically important traits of sheep populations in tropical climate is poorly developed. The existence of purebred and crossbred animals in sheep population in Thailand is in need of an in-depth study. Moreover, estimation of genetic parameters and genetic trends are important to test the breeding scheme efficiencies and to provide genetic information for development of selection programs in the future. Thus, the objectives of this study were to determine factors affecting BW, HG, and BL, and to estimate (co)variance components, genetic parameters, and genetic trends for the traits.

2. Materials and Methods

2.1 Data

Data were obtained from DLD which is a center for recruiting lamb production dataset from four livestock research and testing stations in Thailand, Chaiyaphum Provincial Livestock Station (CPS), Mae Hong Sorn Research Station (MHS), Nakhon Sawan Livestock Station (NSS), and Thepa Livestock Station (TPS). Locations of the herds and lamb breeds within herds are represented in Table 1. The population consisted of purebred and several types of crossbred sheep that were selected as parent stock of the next generation. The climate in southern Thailand including the TPS station was classified into two seasons, rainy season from November to March and summer from April to October. The other parts of Thailand with the stations CPS, MHS and NSS have three seasons, such as summer from mid February to April, rainy season from May to October and winter from November to February. The records were validated by checking their pedigrees. Incorrect data of those animals born after their offspring and having proper sex records were deleted in the analysis. Animals were born from 1998 to 2011. Details of the data structure for sheep population are summarized in Table 2. Raw data comprised 3,004 records for BW and 1,875 for HG and BL. Unfortunately, these four herds have a few weaning weight records.

2.2 Farm management

Principles and strategies of farm management system in four herds showed similar conditions and the unimportant managements in each farm could be unclassified. Each herd consisted of the similarities and differences in meat and wool sheep. Lambs were born all year round and were raised together with their parents until weaning; lambs were weaned at about three months of age. Young ewes were mated for the first time at approximately 18 months. The breeding goal in dam line was to produce more than a lamb/dam/year. Sires and dams remained in the breeding herds for three and five years, respectively. Sires in each herd could be used across years but they could irregularly mate with dams across herds. During the natural breeding season, extended ewes were detected in estrus using teaser rams that were mated to fertile rams at the rate of 20 to 25 ewes per ram at CPS, MHS, and TPS. Only NSS had the rate of 30 ewes per ram. The sheep had access to graze pasture during the day. Not only natural pasture but also plicatulum (*Paspalum plicatulum*), ruzi grass (*Brachiaria ruziziensis*) and para grass (*Brachiaria mutica*) were cultivated for feeding at TPS. Both ruzi and para grass were used to feed sheep at CPS and MHS. However, only pangola grass (*Digitaria eriantha*) was used for forage at NSS. Sheep were supplemented with concentrated diet

Table 1. Locations and breeds of lamb of investigated herds in Thailand.

Herd	Location	Breeds of lambs[a]
Chaiyaphum Provincial Livestock Station (CPS)	North-eastern Thailand (15° 55’N and 102° 16’E)	B, MN, DP, K and their crossbreds
Mae Hong Sorn Research Station (MHS)	Northern Thailand (19° 18’N and 97° 58’E)	B, DP, CR, DS, TN and their crossbreds
Nakhon Sawan Livestock Station (NSS)	Central Thailand (15° 33’N and 100° 42’E)	S, K and DP
Thepa Livestock Station (TPS)	Southern Thailand (6° 49’N and 100° 57’E)	BB, TN and their crossbred

[a] B=Bond, MN=Merino, DP=Dorper, K=Katahdin, CR=Corriedale, DS=Dorset, TN=Thai native, S=Santa Inês and BB=Barbados Blackbelly

Table 2. Details of data structure at four livestock research and testing stations.

	[a]CPS	MHS	NSS	TPS	Total
Research period	2000-2007	1998-2010	2002-2011	2007-2011	1998-2011
No. of sire	28	37	34	8	107
No. of dam	202	490	274	79	1,045
No. of animal become sire and dam	85	354	57	10	506
No. of male lambs	275	845	222	89	1,431
No. of female lambs	260	942	266	105	1,573
No. records of BW[b]	535	1,787	488	194	3,004
No. records of HG	535	658	488	194	1,875
No. records of BL	535	658	488	194	1,875

[a] See for Table 1 [b]BW=birth weight, HG=heart girth and BL=body length at birth

containing 16% crude protein, about 1 to 1.5% of their body weights. The concentrated diet was composed of local gains, modified-rice straw, molasses, vitamins, and minerals. Drinking water and mineral blocks were fed *ad libitum*. Sheep were confined in large pen during the night. All animals had serum testing annually against brucellosis, paratuberculosis and melidosis at the onset of their puberty and were treated twice a year against internal parasites with albendazole and/or fenbendazole. Moreover, young ewes and rams were routinely vaccinated against foot and mouth disease (FMD) twice a year. Live weights and body measurements were taken at birth. Weight was taken at birth using a weighing scale. The HG was measured using tape by taking body circumference immediately posterior to the front leg. Measured also by tape, the BL was considered to be the distance between point of shoulder (lateral tuberosity of the humerus) and pinbone (tuber ishii). All body dimensions were taken when the animal was standing naturally with head raised and body weight on all four feet.

2.3 Statistical analyses

Preliminary weight and body measurements at birth were analyzed using the Generalized Linear Model (GLM) procedure of the R program, version 2.11.1 (R program, 2010) to identify non-genetic factors to be included in the final model. The fixed effects were sex, herd, contemporary group, and breed group, except interactions among them because some interactions were inappropriate for the dataset and some interactions were non-significant effects from preliminary analysis. Birth type was excluded in the model because 85% of dataset was single lambs and preliminary analysis could not significantly detect in this effect. The statistical model for the determination of BW, HG, and BL was given by:

$$y_{ijklm} = \mu + S_i + H_j + CG_k + BG_l + e_{ijklm} \quad (1)$$

where y_{ijklm} is the individual performance for each trait, μ is the overall means, S_i, H_j, CG_k and BG_l are the fixed effects of sex (i = male and female), herd (j = CPS, MHS, NSS and TPS), contemporary groups (k = 1, 2, …, 148), and breed groups (l = 1, 2, …, 29) respectively, and e_{ijklm} is the random residual effect (e_{ijklm}~NID $(0,\sigma^2_e)$).

2.4 Model fitting, estimation of (co) variance and genetic trends

A single trait animal model was fitted to the data including all pedigree information. Direct additive genetic, maternal additive genetic or maternal permanent environmental effects were taken into account by including appropriate random effects into the model of analysis. Allowing and ignoring for genetic covariance between direct and maternal additive genetic effects yield up to six different analyses for each trait. The statistical models were as follows:

Model 1: $y = Xb + Z_a a + e$
Model 2: $y = Xb + Z_a a + Z_{pe} pe + e$
Model 3: $y = Xb + Z_a a + Z_m m + e$ with $\text{cov}(a,m) = 0$
Model 4: $y = Xb + Z_a a + Z_m m + e$ with $\text{cov}(a,m) \neq 0$
Model 5: $y = Xb + Z_a a + Z_m m + Z_{pe} pe + e$ with $\text{cov}(a,m) = 0$
Model 6: $y = Xb + Z_a a + Z_m m + Z_{pe} pe + e$ with $\text{cov}(a,m) \neq 0$

The X, Z_a, Z_m and Z_{pe} were design matrices relating records of fixed, direct additive, maternal additive and maternal permanent environmental effects, respectively. The symbols β, a, m, pe, and e were the vectors of fixed, direct additive, maternal additive genetic and maternal permanent environmental effects, and residual effects for each individual, respectively. The assumptions of the complete model were assumed as follows:

$$E[y] = [X\beta], \quad V\begin{bmatrix} a \\ m \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2_a & A\sigma_{a,m} & 0 & 0 \\ A\sigma_{a,m} & A\sigma^2_m & 0 & 0 \\ 0 & 0 & I\sigma^2_{pe} & 0 \\ 0 & 0 & 0 & I\sigma^2_e \end{bmatrix} \quad (2)$$

The direct additive genetic, maternal additive genetic and maternal permanent environmental effects and residual effects were normal distributed with mean zero and variance $V(a) = A\sigma^2_a$, $V(m) = A\sigma^2_m$, $V(pe) = I\,\sigma^2_{pe}$ and $V(e) = I\,\sigma^2_e$ where I was identity matrix of order equal to the number of records. The σ^2_a, σ^2_m, σ^2_{pe} and σ^2_e were direct additive genetic, maternal additive genetic, maternal permanent environmental and residual variances, respectively. The A represented a numerator relationship matrix that obtained from pedigree structure. Finally, σ_{am} was the covariance between direct and maternal additive genetic effects. Each trait was analyzed by univariate animal model in order to select the best fit model. Variance and covariance components were estimated by the average information restricted maximum likelihood (AI-REML) and fitting an animal model throughout using ASREML (Gilmour *et al.*, 2002). Model with different random components were compared using the log likelihood ratio test (LRT), calculated as twice the difference between the logL of each model. The LRT was given by $D = 2\log(l_{R2}/l_{R1}) = 2[\log(l_{R2})-\log(l_{R1})]$, where l_{R1}=log-likelihood of restricted model and l_{R2}=log likelihood of the more general model. To declare the significance of differences, the likelihood ratio test was tested against the chi-square distribution with degrees of freedom being the difference in number of variance and covariance components in the models. If $2\Delta\log L$ values were not significantly different ($P>0.05$), the model with fewest number of variance would then be chosen (Gilmour *et al.*, 2002). The best fit model was applied for multivariate analysis in order to estimate genetic parameters, genetic and phenotypic correlations and genetic trends. The genetic parameters and genetic correlation were defined by Falconer and Mackay (1996). Estimated breeding values (EBV) in both direct and maternal additive genetic effects from multivariate analysis were computed as a weighted sum of breed group coefficients. Linear regressions of EBV_a and EBV_m yearly means were computed by R program.

3. Results and Discussion

3.1 Fixed effect testing and least square analysis for BW, HG and BL

The number of sheep in Thailand in the last decade not declined, moreover the quantity for mutton import increased from 2004 to 2010 (DLD, 2010). On the other hand, productive and reproductive data are incomplete records because sheep production was characterized as a non-traditional choice of agricultural activity. Data correction has been neglected by small farmer's agribusinesses but has been done in government research stations. The investigated traits such as BW, HG, and BL were routinely recorded for pre- and post- weaning growth improvement. This study provides basic information and a way to promote complete accurate data recording for a breeding scheme in order to support a high demand of mutton for Halal food. Table 3 shows the preliminary weight and body measurement analysis indicating that sex, herd, and breed group as fixed effects that have a significant impact on BW, HG, and BL. Moreover, contemporary group as year-month of birth was a significantly fixed effect. Some interactions such as sex*herd, and sex*breed group had a non-significant effect for only BW, while sex*contemporary group had a slightly significant effect (P=0.048 for BW and P=0.05 for HG and BL). Interaction of breed group*contemporary group, herd*breed group, herd*contemporary group and interaction among three and four main fixed effects were assumed to be ignore in this study because the data structure was not appropriate analyzed and some subclasses of these interaction fixed effects disappeared. Significances of sex and breed group for BW, HG, and BL were similar to the results obtained by Akkahart and Sukwong (2009) and Wiriyasombat *et al.* (2003) who studied factors affecting on body weight and measurements in Thai sheep population. Moreover, Behzadi *et al.* (2007), Oke and Ogbonnaya (2011) and Savar-Sofla *et al.* (2011) reported that fixed effects such as sex, location of raising, lambing year, and birth type have a significant influence on BW. This basic information indicated that weight and body measurement at birth of lambs in different of these significant fixed effects had dissimilar phenotypic performance. The significant influences of environmental effects on weight and body measurement at birth in this study could be explained in part by the differences in years-month such as environment, feeding and grazing resources, male and female endocrine system, inadequate availability of nutrients during pregnancy, competition for milk between lambs, maternal effects, and maternal ability of dam at different ages. Overall means and standard deviations were 3.59±0.73 kg for BW, 33.16±3.83 cm for HG, and 31.02±3.49 cm for BL. The mean of BW in this study was lower than that of Hanford *et al.* (2006), Oliveira Lobo *et al.* (2009) and Selvaggi *et al.* (2011) who reported means of BW in Polypay sheep (4.05±0.78 kg), Brazilian meat sheep (3.84±0.86 kg) and Gentile di Puglia lambs (3.85±0.16 kg). The range mean of BW in Ghezel and Moghani sheep in Iran was 4.18±0.83 to 4.61±0.79 kg (Baneh *et al.*, 2010; Bayeriyar *et al.*, 2011; Savar-Sofla *et al.*, 2011). However, Bosso *et al.* (2007) and El-Awady (2011) reported that the mean of BW in West African Dwarf, Djallonke and Barki sheep (1.57±0.36, 2.01±0.48 and 3.23±0.33 kg, respectively) was lower than that of this study. An in-depth study of least square analysis in effects of sex, herd and breed groups indicated that male lambs were heavier in BW, higher in HG and longer in BL than female lambs. The result of high BW of male lambs was agreed with the results from Wiriyasombat *et al.* (2003), Behzadi *et al.* (2007), Akkahart and Sukwong (2009), Oke and Ogbonnaya (2011), and Savar-Sofla *et al.* (2011). The research from Wiriyasombat *et al.* (2003) reported no significant effect of sex for HG and BL at TPS in Thailand. The effect of herd that could be assumed feeding and management was significantly different in all traits. In fact, not only climate, such as temperature and humidity might impact the conditions of animal livelihood, but also available roughage in dry season might be given as per unavailability in each region. MHS had the

Table 3. Fixed effect testing and least square means± standard error of sex, herd and breed group for BW, HG, and BL.

	No.	BW	HG	BL
Sex		**	*	*
Male	1,431	3.41±0.04^{a}	32.92±0.15^{a}	31.08±0.14^{a}
Female	1,573	3.30±0.04^{b}	32.63±0.74^{b}	31.17±0.12^{a}
Herd[a]		*	**	*
CPS		3.15±0.55^{a}	32.50±2.93^{a}	30.32±2.14^{a}
MHS		3.79±0.71^{b}	34.26±3.54^{b}	32.26±3.75^{a}
NSS		3.30±0.64^{c}	34.26±3.12^{b}	29.58±2.72^{b}
TPS		3.21±0.38^{a}	30.08±2.19^{c}	31.19±2.12^{a}
Breed group[b]		**	**	**
B	140	3.62±0.05^{a}	33.21±0.38^{a}	31.63±0.37^{a}
BB	23	3.14±0.17^{b}	31.87±0.88^{b}	29.08±0.88^{b}
CR	251	3.53±0.04^{c}	33.22±0.28^{a}	31.25±0.28^{a}
DP	98	3.42±0.07^{c}	32.88±0.36^{ab}	30.81±0.36^{ab}
DS	81	3.40±0.07^{c}	33.16±0.68^{a}	32.09±0.68^{a}
KD	92	3.39±0.04^{c}	32.48±1.57^{ab}	30.53±0.35^{ab}
SI	116	3.66±0.03^{a}	33.93±0.77^{a}	32.88±0.95^{a}
TN	101	3.03±0.06^{d}	30.21±0.32^{b}	29.22±0.32^{b}
1/4 B x 3/4 CR	42	3.21±0.10^{b}	32.63±2.26^{ab}	29.24±2.25^{b}
1/2 B x 1/2 CR	100	3.55±0.06^{c}	32.16±0.46^{ab}	30.80±0.46^{ab}
1/2 B x 1/2 DS	304	3.43±0.04^{c}	32.83±0.29^{ab}	31.32±0.29^{a}
1/2 B x 1/2 MN	38	3.49±0.10^{c}	33.01±0.52^{ab}	30.92±0.52^{ab}
1/2 B x 1/2 TN	253	2.96±0.04^{d}	32.55±0.43^{ab}	29.12±0.43^{b}
1/2 DP x 1/2 TN	72	3.45±0.07^{c}	32.38±1.41^{ab}	31.94±0.64^{a}
1/2 SI x 1/2 KD	44	3.68±0.06^{a}	34.17±1.05^{a}	31.75±0.54^{a}
3/4 B x 1/4 CR	286	3.32±0.04^{c}	33.57±0.35^{a}	31.99±0.35^{a}
3/4 B x 1/4 MN	64	3.16±0.07^{b}	32.07±0.40^{ab}	31.80±0.39^{a}
3/4 BB x 1/4 TN	66	3.12±0.07^{b}	30.55±0.39^{b}	28.97±0.39^{b}
3/4 CR x 1/4 DS	166	3.32±0.05^{c}	32.10±0.44^{ab}	30.78±0.44^{ab}
3/4 SI x 1/4 KD	65	3.63±0.04^{a}	34.05±1.12^{a}	32.35±0.24^{a}
1/2 DP x 1/2 MN	26	3.51±0.12^{c}	33.87±0.64^{a}	29.92±0.64^{ab}
3/4 DP x 1/4 MN	126	3.43±0.06^{c}	33.40±0.28^{a}	29.75±0.28^{ab}
7/8 B x 1/8 MN	29	3.26±0.12^{b}	32.23±0.59^{ab}	31.96±0.59^{a}
7/8 BB x 1/8 TN	63	3.06±0.08^{d}	30.35±0.40^{b}	29.21±0.40^{b}
7/8 DP x 1/8 KD	165	3.21±0.05^{b}	32.72±0.25^{ab}	29.78±0.25^{ab}
1/2 B x 1/4 DS x 1/4 TN	41	3.43±0.10^{c}	34.02±1.01^{a}	32.18±1.00^{a}
1/2 B x 1/4 CR x 1/4 DS	45	3.34±0.09^{c}	34.28±1.21^{a}	31.96±1.20^{a}
1/2 B x 1/4 DS x 1/4 DP	49	2.98±0.11^{d}	33.16±0.92^{a}	29.38±0.92^{ab}
1/2DP x 1/4SI x 1/4 TN	58	3.51±0.10^{c}	34.52±0.99^{a}	31.58±1.85^{a}

BW=birth weight; HG=heart girth and BL=body length at birth; [a] See for Table 1 and the numbers of lamb were shown in Table 2; [b] Details for breeds of lambs were shown in Table 1; * and ** significantly different at $P<0.05$ and $P<0.01$; ^{a}, ^{b}, ^{c} and ^{d} within the same column within treatment values marked with different letter are significantly different at $P<0.05$.

heaviest weight of lambs but CPS and TPS had the lowest BW of lambs. MHS and NSS had the highest HG but only TPS had the lowest HG. MHS had the longest BL when compared with others. Also, MHS tended to have the heaviest weight and largest body when compared with the other research stations. Moreover, other fixed effects such as birth type and age of dam were influenced on BW (Hanford *et al.*, 2006, Akkahart and Sukwong, 2009, Selvaggi *et al.*, 2011). Effect of birth type in this study might be influenced on the investigated traits, if the dataset is expanding. However, the majority of this dataset was single lambs and preliminary analysis showed non-significant effect. Ages of dam from four research stations were not recorded. Breed group was divided into 29 groups consisting of purebred, 2- and 3-breed crosses. Purebred lambs (B and SI) and crossbred lams (1/2 SI x 1/2 KD and 3/4 SI x 1/4 KD) had the highest BW, while TN, 7/8 BB x 1/8 TN and 1/2 B x 1/4 DS x 1/4 DP animals had the lowest BW. This indicated that B and SI were suitable breeds to be used for genetic improvement for BW. Length of HG of all breed groups was similar, with the exception of BB and TN purebreds and 2-crossbreds of BB and TN or these two breeds with other breeds (1/2 DP x 1/2 TN, 3/4 BB x 1/4 TN and 7/8 BB x 1/8 TN). It indicated that the characteristic of BB was not a good body measurement, but it was well adaptation and high prolific (Fahmy, 1996). Santa Inès purebred, tended to be highest BL when compared with all breed groups. Animal with 3/4 BB x 1/4 TN tended to have the lowest BL. Breed group comparisons between BB and TN for investigated traits were disaccording to Wiriyasombat *et al.* (2003) who reported that BW of BB (2.6 kg) was significantly lower than TN (2.8 kg), but HG and BL of BB (30.2 and 30.8 cm) were significantly higher than TN (31.2 and 31.9 cm). The results of this study were also similar to those of Akkahart and Sukwong (2009), reporting that purebred of DP lambs was found heavier in BW, higher in HG and longer in BL than 7/8 DP x 1/8 KD (P<0.05). However, extremely high BW, HG and BL should be concerned for breeding plan in the future because the lambs would be susceptible to dystocia.

3.2 Model comparison from univariate analysis

Univariate analysis of six different models for BW, HG and BL showed that the profile of changes in estimates of (co)variance components tended to be different. Log L values of all different models are represented in Table 4. It can be shown that allowing for direct and maternal additive covariance (Model 4) for BW significantly increased logL when compared with other models. However, the full model (Model 6) for HG and BL had the highest logL. Fortunately, it was not significantly different with Model 4 and Model 5. Also, Model 4 was the best fit model for the investigated traits because logL of this model for BW was as a maximum value. Moreover, it was not significantly different and less complicated when compared with Model 5 and Model 6 for HG and BL. This model ignoring a maternal permanent environmental effect, direct heritabilities for BW, HG, and BL were moderate (0.31, 0.22, and 0.33). Maternal heritability for BW was moderate (0.22) but maternal heriatbilities for HG and BL were low (0.15 and 0.11) (result not shown). It indicated that the breeders could select the best sires and dams for the traits from variation of direct additive genetic effect while only BW had more variation with characteristics for good mothering genetic ability than the others. The both direct heritabilities were in ranged with Boujenane and Kerfal (1990) and Selvaggi *et al.* (2011) for BW. Direct and maternal heritabilities for HG and BL were higher than Mandal *et al.* (2008) in Muzaffarnagari sheep in India. In addition, the model provided corresponding estimates of direct-maternal additive correlations to be moderate to slightly high and negative values (-0.60 for BW, -0.41 for HG and -0.48 for BL). It was disaccording to Savar-Sofla *et al.* (2011) who reported positive direct-maternal additive genetic correlation for BW (0.59). However, the negative direct-maternal additive genetic correlation for BW was similar to the result by Tosh and Kemp (1994). The direct-maternal additive genetic correlations for HG and BL from univariate analysis in the same model had rarely compared with other publications. The information or prior values from the results of the univariate analysis for BW, HG and BL were those applied for the multivariate analysis.

Table 4. logL values of six models for BW, HG, and BL.

Model	Traits		
	BW	HG	BL
1	-100.19^{a}	-2961.91^{a}	-3007.96^{a}
2	-82.77^{b}	-2959.47^{b}	-3005.77^{b}
3	-79.98^{c}	-2958.21^{c}	-3004.93^{b}
4	-70.95^{d}	-2955.47^{d}	-3002.47^{c}
5	-78.85^{c}	-2956.04^{d}	-3002.87^{c}
6	-77.01^{c}	-2656.47^{d}	-3001.98^{c}

BW=birth weight; HG=heart girth and BL=body length at birth; ^{a}, ^{b}, ^{c} and ^{d} within the same column marked with different letter are significantly different at P<0.05.

3.3 Genetic parameters from multivariate analysis

Direct and maternal heritabilities and correlations of direct additive genetic, maternal additive genetic and phenotype among traits are represented in Table 5. Estimated direct heritabilities for BW, HG, and BL from multivariate analysis were considerably moderate (0.32, 0.52, and 0.54, respec-

Table 5. Direct heritabilities (in diagonal and bold number), maternal heritabilities (in the parenthesis of diagonal), direct additive genetic correlations (upper diagonal), maternal additive genetic correlations (in the parenthesis of upper diagonal and italic number) and phenotypic correlations (lower diagonal) among for BW, HG, and BL.

	BW	HG	BL
BW	**0.32±0.06** (0.23±0.02)	0.29±0.12 (*0.30±0.12*)	0.26±0.11 (*0.23±0.13*)
HG	0.21±0.04	**0.52±0.04** (0.14±0.02)	0.97±0.01 (*0.95±0.01*)
BL	0.18±0.04	0.96±0.01	**0.54±0.04** (0.14±0.02)

BW=birth weight, HG=heart girth, BL=body length at birth tively) and estimated maternal heritabilities for these traits were moderate only BW (0.23) and low for HG and BL (0.14 and 0.14, respectively). Trends of the results from multivariate analysis were according to univariate analysis in this study. Moderate in direct heritabilities of the investigated traits and in the maternal genetic ability for only BW indicated that the populations had moderate variations in direct additive genetic effect for all traits and in good characteristics of mothering genetic abilities for only BW. This result indicated that estimated direct heritabilities were higher than maternal heritabilities. It implied that the genetic improvement programs should consider these traits as direct additive genetic effect since they had more influence of phenotypic characteristics than maternal additive genetic effects. In general, direct heritabilities tended to be higher than maternal heritabilities for early growth traits (Hassen *et al.*, 2003). The range of direct heritabilities estimates for BW from multivariate analysis in the literature varies substantially from 0.04 in Kermani and Romanov breeds (Maria *et al.*, 1993; Rashidi *et al.*, 2008) to 0.46 in Menz breed (Gizaw *et al.*, 2007). These direct heritabilities of BW, HG, and BL in the present study is within the range reported by other in recent researches (Tosh and Kemp, 1994; Snyman *et al.*, 1995; Larsgard and Olesen, 1998; Bromley *et al.*, 2000; Matika *et al.*, 2001; Abegaz *et al.*, 2005; Hanford *et al.*, 2005; Oliveira Lobo *et al.*, 2009; Selvaggi *et al.*, 2011). The direct heritabilities for HG and BL in the present study were higher than Mandal *et al.* (2008) who reported that direct heritabilities for both traits were 0.14 and 0.14. Maternal heritability for BW in this present study was ranged to Tosh and Kemp (1994), Sousa *et al.* (1999) and El-Awady (2011) who reported that maternal heritabilities were ranged from 0.10 to 0.31 but it was higher than Hall *et al.* (1995) in dual purpose crossbred breed (0.08). Meyer *et al.* (1994) and Tosh and Kemp (1994) supported that differences in the maternal additive genetic effects among breeds have been attributed to variations in milk production. It would be influenced on weaning weight and sequential weight. These maternal heritabilities of HG and BL in present study were similar to Mandal *et al.* (2008) who reported that low maternal heritabilities for both traits (0.15 and 0.13). It was suggested that maternal additive genetic effect was of lower importance for these traits. The relatively low productivity and poor nutritional environment resulted in lambs not expressing their genetic potential (Mandal *et al.*, 2008). Both heritabilities for investigated traits from multivariate analysis were higher than univariate analysis because direct-maternal additive genetic correlations among traits and correlations of both genetic and phenotype were taken into account in multivariate analysis. The direct additive genetic, maternal additive genetic and phenotypic correlations between BW and two traits of body measurements at birth (HG and BL) were low to moderate and positive. The correlations between body measurement traits were strongly high and positive (0.97, 0.95 and 0.96, respectively). The results implied that the BW could be improved by selection high HG and BL. Many publications reported that the positive and high genetic correlations between BW and weaning weight or yearling weight (Hanford *et al.*, 2006; Bosso *et al.*, 2007; Savar-Sofla *et al.*, 2011; El-Awady, 2011). It indicated that BW may be a candidate trait for growth improvement. However, it will be better, if real data is utilized. Also, collecting data of animal performance and honest recording data would be a fundamental for sheep improvement in order to increase productivity and eventually the economic efficiency of the herds.

The direct-maternal additive genetic correlations within traits were -0.68±0.07 for BW, -0.92±0.03 for HG, and -0.89±0.03 for BL. It implied that selection of animals for high direct additive genetic values could also get low maternal ability. In fact, if the producers selected these traits by considering only direct additive genetic effect, they would have inferior maternal performance of ewes. These antagonistic correlations were consistent with Tosh and Kemp (1994), Sousa *et al.* (1999), Hassen *et al.* (2003), Sarmento *et al.* (2006) and Oliveira Lobo (2009) who reported direct-maternal additive genetic correlations for BW were -0.15 and -0.56. Moreover, direct BW-maternal HG and direct HG–maternal BW were -0.35±0.14 and -0.12±0.09; direct BW-maternal BL and direct BL-maternal BW were -0.26±0.14 and -0.08±0.01; direct HG-maternal BL and direct BL-maternal HG were -0.89±0.04 and -0.85±0.04. These results implied that further selection of direct additive genetic effect for a trait may be declined in maternal ability for the other traits. As a result, the breeders should consider these within and between traits of antagonistic relationship for selection parent stock in order to improve the genetic progress in the herd.

3.4 Direct and maternal additive genetic trends

The evaluation of genetic trend gives an indication of breed direction as well as the rate of genetic improvement since the application program (Bosso *et al.*, 2007). The direct and maternal additive genetic trends in this study for BW, HG and BL had irregular fluctuation. These results could be interpreted in two periods, 1998 to 2004 and 2005 to 2011. The direct and maternal genetic trends from these periods are represented in Table 6. The direct genetic trends in the first period showed a highly significant increase for BW (0.02 kg/year) and a highly significant decrease for HG (-0.33 cm/year) and BL (-0.22 cm/year), but they were significantly increased in the second period (0.02 kg/year for BW, 0.89 cm/year for HG, and 0.73 cm/year for BL). One possible reason showed that sheep production in the first period needs to increase size of herds while selection program would be developed in the second period. The maternal genetic trends in the first period had a highly significant increase for BW and HG (0.04 kg/year and 0.11 cm/year) but a non-significant decrease for BL. In contrast to the second period, the investigated traits had a highly significant decrease of maternal genetic trends (-0.01 kg/year for BW, -0.92 cm/year for HG, and -0.72 cm for BL). It indicated that selection criteria in the second period would consider only direct additive genetic effect. In fact, if the breeders selected these traits by consi-

Table 6. Direct and maternal genetic trends of two periods for BW, HG, and BL.

	Periods	
	1998-2004	2005-2011
EBV$_a$ of BW (kg/year)	0.02±0.004**	0.02±0.004**
EBV$_m$ of BW (kg/year)	0.04±0.002**	-0.01±0.004**
EBV$_a$ of HG (cm/year)	-0.33±0.070**	0.89±0.130**
EBV$_m$ of HG (cm/year)	0.11±0.040*	-0.92±0.050**
EBV$_a$ of BL (cm/year)	-0.22±0.070**	0.73±0.130**
EBV$_m$ of BL (cm/year)	-0.03±0.040^{ns}	-0.72±0.060**

BW=birth weight; HG=heart girth and BL=body length at birth; ^{ns}, * and ** represented that the period was not significantly increase or decrease, significant increase ($P<0.05$), and highly significant increase ($P<0.01$).

dering only direct additive genetic effect, they would have inferior maternal behavior especially effects of the uterine environment and extra-chromosomal inheritance. The direct additive genetic trend of BW in this study was similar to Van Wyk *et al.* (1993), Duguma (2001), Mokhtari and Rashidi (2010) and Mohammadi and Sadeghi (2011) who reported that an annual increase in this trait of 0.02 kg/year. In contrast, Hanford *et al.* (2005) and Gizaw *et al.* (2007) reported that direct additive genetic trends for BW in Rambouillet sheep and multibreed sheep were 1.00 and 0.04 kg/year. Moreover, maternal additive genetic trend in the first period for BW was similar to Mohammadi and Sadeghi (2011), 0.03 kg/year in Zel sheep but it was higher than Farokhad *et al.* (2011), 0.02 kg/year in Arman sheep. Thus, to substantially increase the genetic trends of sheep production in Thailand, obvious breeding objectives, optimized breeding plans, suitable selection criteria and accuracy of data collecting should be concerned because this information would be used in genetic evaluation program in order to achieve the maximum genetic trends under environmental conditions in Thailand.

4. Conclusions

This study concluded that sex, herd, contemporary group and breed group had obviously an influence on the investigated traits. Male lambs were larger and longer than female lambs ($P<0.05$). Weight and body measurements at birth in the herd of MHS tended to be better than the others. However, the HG of lambs at MHS was similar to NSS and the BL of lambs at MHS was similar to CPS. Purebred lambs (B and SI) and crossbred lambs (1/2 SI x 1/2 KD and 3/4 SI x 1/4 KD) had the highest BW but TN, 7/8 BB x 1/8 TN and 1/2 B x 1/4 DS x 1/4 DP animals had the lowest BW. The HG of 1/2 DP x 1/4 SI x 1/4 TN tended to be highest while TN tended to be lowest. Purebred of SI tended to be the highest BL when compared with total breed groups. Animals with 3/4 BB x 1/4 TN tended to have the lowest BL. The best fit models of univariate analysis for BW, HG, and BL were animal models with maternal additive genetic effect and accounting covariances between these both additive genetic effects. The results from multivariate analysis with the model has shown the moderate direct heritabilities (0.32 for BW, 0.52 for HG and 0.54 for BL) and low to slightly moderate maternal heritabilities (0.23 for BW, 0.14 for HG and 0.14 for BL). Correlations of direct additive genetic, maternal additive genetic and phenotype between BW and body measurement (HG and BL) were slightly moderate and positive (0.18 to 0.30). These correlations between HG and BL were positive and high values (0.95 to 0.97). Direct-maternal additive genetic correlations within traits (-0.92 to -0.68) and between traits (-0.89 to -0.08) of investigated traits were negative. Direct additive genetic trends in both periods for BW were significantly increased (0.02 and 0.02 kg/year). Maternal additive genetic trends for BW were significantly increased in the first period (0.04 kg/year) but it was significantly decrease in the second period (-0.01 kg/year). Direct additive genetic trends for HG and BL in the second period were significant increase (0.89 and 0.73 cm/year) but maternal additive genetic trends were significant decrease (-0.92 and -0.72 cm/year).

Acknowledgements

The authors thanks the Department of Livestock Development for providing dataset. Finally, we would like to acknowledge the Commission of Higher Education of Thailand for supporting the grant for this study.

References

Abegaz, S., Van Wyk, J.B. and Olivier J.J. 2005. Model comparisons and genetic and environmental parameter estimates of growth and the Kleiber ratio in Horro sheep. South African Journal of Animal Science. 35, 30-40.

Akkahart, K., and Sukwong, C. 2009. Factors affecting on growth performance of Dorper x Katahdin crossbred sheep. Available at: http://www.dld.go.th/research-AHD/research/Webpage/Research_Sheep_1.html [June 21, 2011] (in Thai).

Anothaisinthawee, S. 2005. Wool characteristics and economic return of wool raising. Progress report from Department of Livestock and Development, Thailand. 10 pp (in Thai).

Baneh, H., Hafezian, S.H., Rashidi, A., Gholizadeh, M. and Rahimi, G. 2010. Estimation of genetic parameters of body weight traits in Ghezel sheep. Asian-Australasian Journal of Animal Science. 53, 149-153.

Bayeriyar M., Farahani, A.H.K. and Shahrbabak, H.M. 2011. Estimation of genetic parameters for economic important traits in Moghani Iranian sheep. African Journal of Biotechnology. 10, 14678-14683.

Behzadi, M.R.B., Shahroudi, F.E. and Van Vleck, L.D. 2007. Estimates of genetic parameters for growth traits in

Kermani sheep. Journal of Animal Breeding and Genetics. 124, 296-301.

Bosso, N.A., Cisse, M.F., van der Waaij, E.H., Fall, A. and van Arendonk, J.A.M. 2007. Genetic and phenotypic parameters of body weight in West African Dwarf goat and Djallonke sheep. Small Ruminant Research. 67, 271-278.

Boujenane I. and Kerfal, M. 1990. Estimates of genetic and phenotypic parameters for growth traits of D'man lambs. Animal Production. 51, 173-178.

Bromley, C.M., Snowder, G.D. and Van Vleck, L.D. 2000. Genetic parameters among eight prolificacy and wool traits of Columbia, Polypay, Rambouillet and Targhee sheep. Journal of Animal Science. 78, 846-858.

Department of Livestock and Development. 2010. Available at: http://www.dld.go.th/ict/th/index.php?option [July 21, 2011] (in Thai).

Duguma, G. 2001. A genetic study of early growth traits and ewe productivity in Merino sheep. M.Sc. Thesis. University of Stellenbosch, Republic of South Africa.

El-Awady, H.G. 2011. Different animal models for estimating genetic parameters of Barki sheep in Egypt. Journal of American Science. 7, 882-887.

Fahmy, M.H. 1996. Prolific sheep. CAB international, Wallingford, UK. pp. 150-350.

Falconer, D.S. and Mackay, T.F.C. 1996. Introduction to quantitative genetics. 4th ed. Longman House, Jarlow, England, U.K. pp 122-143.

Farokhad, M.L., Roshanfekr, H., Amiri, S., Mohammadi, K. and Mirzadeh, K. 2011. Genetic trends estimation for some of the growth traits in Arman sheep. Journal of Animal Veterinary Advances. 10, 1801-1803.

Gilmour, A.R., Cullis, B.R. and Welham S.J. 2002. ASREML Reference Manual. NSW Agriculture, Orange, Australia. pp. 1-210.

Gizaw, S., Lemma, S., Komen, H. and Johan, A. M. 2007. Estimates of genetic parameters and genetic trends for live weight and fleece traits in Menz sheep. Small Ruminant Research. 70, 145-153.

Hall D.G., Fogarty, N.M. and Gilmour, A.R. 1995. Performance of crossbred progeny of Trangie Fertility Merino and Booroola Merino rams and Poll Dorset ewes. I. Lamb birth weight, survival and growth. Australian Journal of Experimental Agriculture. 35, 1069-1074.

Hanford, K.J., Van Vleck, L.D. and Snowder, G.D. 2005. Estimates of genetic parameters and genetic change for reproduction weight and wool characteristics of Rambouillet sheep. Small Ruminant Research. 57, 175-186.

Hanford, K.J., Van Vleck, L.D. and Snowder, G.D. 2006. Estimates of genetic parameters and genetic trend for reproduction, weight and wool characteristics of Polypay sheep. Livestock Production Science. 102, 72-82.

Hassen, Y., Fuerst-Waltl, B. and SÖlkner, J. 2003. Genetic parameter estimates for birth weight, weaning weight and average daily gain in pure and crossbred sheep in Ethiopia. Journal of Animal Science. 120, 29-38.

Larsgard, A.G. and Olesen, I. 1998. Genetic parameters for direct and maternal effects on weight and ultrasounic muscle and fat depth of lambs. Livestock Production Science. 55, 273-278.

Mandal, A., Roy, R. and Rout, P. K. 2008. Direct and maternal effects for body measurements at birth and weaning in Muzaffarnagari sheep of India. Small Ruminant Research. 75, 123-127.

Maria, G.A., Boldman, K.G. and Van Vleck, L.D. 1993. Estimates of variance due to direct and maternal effects for growth traits of Romanov sheep. Journal of Animal Science. 71, 845-849.

Matika, O., van Wyk, J.B., Eramus, G.J. and R.L. Baker. 2001. Phenotypic and genetic relationships between lamb and ewe traits for the Sabi sheep of Zimbabwe. South African Journal of Animal Science. 31, 215-222.

Meyer, K., Carrick, M.J. and Donnelly, B.J.P. 1994. Genetic parameters for milk production of Australian beef cows and weaning of their calves. Journal of Animal Science. 72, 1155-1165.

Mohammadi, H. and Sadeghi, M. 2011. Estimates of genetic and phenotypic trends for body weight traits of Zel sheep obtained by univariate and multivariate animal model analysis. Journal of Animal Science. 89, 531-532.

Mokhtari, M.S. and Rashidi, A. 2010. Genetic trends estimation for body weight of Kermani sheep at different ages using multivariate animal models. Small Ruminant Research. 88, 23-26.

Oke, U.K. and Ogbonnaya, E.O. 2011. Application of physical body traits in the assessment of breed and performance of WAD sheep in a humid tropical environment. Available at: http://www.lrrd.org/lrrd23/2/oke23024.htm. [July 21, 2011].

Oliveira Lobo, A.M.B., Braga Lobo, R.N., Paiva, S.R., de Oliveria, S.M.P. and Faco, O. 2009. Genetic parameters for growth, reproductive and maternal traits in a multibreed meat sheep population. Genetic Molecular Biology journal. 32, 761-770.

Rashidi, A., Mokhtari, M.S., Safi Jahanshahi, A. and Mohammad Abadi, M.R. 2008. Genetic parameter estimates of pre-weaning growth traits in Kermani sheep. Small Ruminant Research. 74, 165-171.

R program. 2010. R program version 2.11.1. Institute for Statistics and Mathematics, GNU General Public License. 213 pp.

Sarmento, J.L.R., Torres, R.A., Sousa, W.H., Pereira, C.S., Lopes, P.S. and Breda, F.C. 2006. Estimação de parâmetos genèticos paracaracterísticas de crescimento de ovinos Santa Inês utilizando modelos uni e multicaracterística. Brazilian Journal of Veterinary Research and Animal Science. 58, 581-589 (Abstract in English).

Savar-Sofla, S., Nejati-Javaremi, A., Abbasi, M.A., Vaez-Torshizi, R. and Chamani, M. 2011. Investigation on direct and maternal effects on growth traits and the Kleiber ratio in Moghani sheep. World Applied Sciences Journal. 14, 1313-1319.

Selvaggi, M., Pinto, F., Pesce Delfino, A.R., Vicenti, A. and Dario, C. 2011. Phenotypic and genetic parameters of pre-weaning growth traits in *Gentile di Puglia* lambs. World Academy of Science, Engineering and Technology. 78, 476-478.

Snyman, M.A., Erasmus, G.J., Van Wyk, J.B. and Olivier, J.J. 1995. Direct and maternal (co)variance components and heritability estimates for body weight at different ages and fleece traits in Afrino sheep. Livestock Production Science. 44, 229-235.

Sousa W.H., Pereira, C.S., Bergmann, A.G. and Silva, F.L.R. 1999. Estimativas de components de (co)variiânica e herdabilidade direta e maternal de pesos corporais em ovinos da raça Santa Inês. Brazilian Journal of Animal Science. 28, 1252-1262 (Abstract in English).

Tosh, J.J. and Kemp, R.A. 1994. Estimation of variance components for lamb weights in three sheep population. Journal of Animal Science. 72, 1184-1190.

Van Wyk, J.B., Eramus, G.J. and Kostantinov, K.V. 1993. Genetic and environmental trends of early growth traits in the Elsenburg Dorper sheep stud. South African Journal of Animal Science. 23, 85-87.

Wiriyasombat, C., Sukrach, P., Kochapakdee, S. and Saithanoo, S. 2003. Body weight and body measurements at birth and at weaning of long-tail sheep and their crosses with Barbados Blackbelly sheep at Thepa Livestock Breeding Station. Proceeding of the 1st academic seminar on Animal Science held at Faculty of Natural Resources, Prince of Songkla University, Songkla, Thailand, 2003. 289-395.