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Research Article

Genetic Parameter for Growth Performance of Saburai Goat in Tanggamus District, Lampung Province, Indonesia

Sulastri Sulastri, Siswanto Siswanto, Kusuma Adhianto*

Animal Science Department, Faculty of Agriculture, University of Lampung, Jl Sumantri Brojonegoro no 1 Bandarlampung, Lampung, Indonesia, 35145.

Abstract | Saburai goat was local name crossbred Boer buck and Ettawa grade goat does. The main objectives of this study were to estimate heritability (h^2), repeatability (r), and genetic correlation (r_g) among body measurements and body weight. Survey method were used to collect data 150 progenies. Variables observed at birth, weaning and yearling were body weight (BW, WW,YW) body measurement, body height (BBH, WBH, YBH), body length (BBL, WBL, YBL), chest circumference (BCC, WCC, YCC), hip height (BHH, WHH, YHH), ear length (BEL, WEL, YEL), and ear width (BEW, WEW, YEW). The result indicated that h^2 for performance at birth that was lowest were BEW (0.07±0.02) and the highest were BHH (0.14±0.05), at weaning that was lowest were WEW (0.07±0.01), the highest were WCC (0.17±0.00) and WHH (0.17±0.00), at yearling that were lowest were YEL (0.09±0,01) and YEW (0,09±0,02), the highest were YHH (0,19±0,06). Repeatability at birth that was lowest were BEL (0.10±0.02), the highest were BBH(0.16±0.01) and BHH(0.16±0.03), at weaning that was lowest were WEL (0.12±0.02) and WEW (0.12 ±0.04), the highest were WBL (0.19±0.03), at yearling that was lowest were YEW (0.14±0.03), the highest were YBH (0.22±0.09) and YBL (0.22±0.08). Genetic correlation at birth that was lowest were between BBW and BEW (0.08±0.01), the highest between BBW and BCC (0.14±0.07), r_g at weaning that was lowest were between WBW and WEW(0.10±0.03), the highest were between WBW and WCC (0.21±0.08), r_g at yearling that was lowest were between YBW and YEW (0.08±0.01), the highest between YBW and YBL (0.19±0.08), between YBW and YCC (0.19±0.07), between YBW and YHH (0.19±0.09). It could be concluded that body measurement can be used as selection criteria to increase body weight.

Keywords | Saburai goat, Heritability, Repeatability, Genetic correlation, Body measurement

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***Correspondence** | Kusuma Adhianto, Animal Science Department, Faculty of Agriculture, University of Lampung, Jl Sumantri Brojonegoro no 1 Bandarlampung, Lampung, Indonesia, 35145; **Email**: kusuma.adhianto@fp.unila.ac.id
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INTRODUCTION

Goats are widely spread in Lampung Province due to its function as animal importance, subsistence, economic and social livelihoods. EGG was one of some goat breed at Lampung however its growth performance were low (yearling weight not more than 40 kg). Grading up program between Boer buck and EGG goat to create goat which was high growth performance. Since the program was begun in 2002 until now the improvement of growth performance of Saburai was not high as prediction (Sulastri and Adhianto, 2016).

Saburai goat was crossbred between Boer buck and Ettawa grade goat (EGG) does. Saburai does would be crossed to Boer buck to result Saburai goat in the grading up program of Boer buck and EGG does. The grading up program was conducted to create Boer grade goat (Saburai goat). Saburai goat will be improved at Tanggamus regency, Lampung Province Indonesia as meat goat. Some Boer buck was introduced to Lampung for conducting the program. The success of introducing specialized breeds depends also on high survival rates that are essential for replacement of old stock, effectiveness of selection, reduction of costs and increased productive performance.

In the grading up program, Saburai does should be selected before being crossed to Boer buck to obtain growth performance of Saburai grade goat which was high and over than its parents. Up to now, no selection for the Saburai does, therefore yearling weight of Saburai grade goat had not obtain more than 40 kg. Export market just received goats from Indonesia which has yearling weight more than 40 kg (Shipley and Shipley, 2005).

Weight body at certain age were important components influencing the profitability of goat and important objectives in selection strategies. Selection would be success when genetic variance of traits were medium up to high; Estimates of heritability for growth traits related to growth are needed to develop a proper selection program. Birth weight, weaning weight and yearling weight were undoubtedly the most important traits in goat production (Devendra and Burns, 1994).

Body weight at certain age associated each other due to genetic correlation in that traits. Selection in one traits would improve the other traits correlated genetically. Nevertheless, genetic correlation could predict the improvement the other traits (Falconer and Mackay, 1996). Therefore, The main objectives of this study were to estimate (heritability (h^2), repeatability (r), and genetic correlation (r_g) among body measurements and body weight. The information would be useful to determine criteria of selection for improvement growth traits of Saburai goats.

MATERIALS AND METHODS

Data Collection and Statistical Analysis

The study was conducted from January to August 2017. Recording of Saburai growth traits raised at the Saburai Goat Breeding Village Centre at Dadapan village, Sumberrejo subdistrict, Tanggamus regency(5.3027° S, 104.5655° E), Lampung province were used as materials in this research. Survey method were conducted to collect data of growth traits obtained from recording of growth traits. The growth traits observed were body weight and body measurements. Data of body weight included in this research were birth weight (BW), weaning weight (WW), yearling weight (YW). Data of body measurements observed consisted of body length (BL), body height (BH), chest depth (CD), chest width (CW), hip height (HH), ear length (EL), ear width (EW) at birth (B), weaning (W), yearling (Y). Recording for growth traits and body measurements of 150 progeny of 9 bucks were collected to estimate heritability value and genetic parameters by one way lay out method.

Analysis Data

Correcting Data: Data of BW were corrected on sex of individuals, WW on sex, age of dam, and weaning time (days), YW on sex and weaning. The formulas to correct data of BW, WW, and YW as follows (Sulastri, 2014).

BW= (BWA)(CFS)

$$WW = BW + \left(\frac{WWA - BW}{TWW}(90)\right)(CFS)(CFAD)$$

$$YW = \left(\frac{YWA - W}{TYW - TWW}\right)(275)(CFS)$$

Explaination:

BW	=Birth weight corrected
BWA	=Birth weight actual
CFS	=Correction factor for sex
WW	=Weaning weight corrected
WWA	=Weaning weight actual
TWW	=Time to get weaning weight (days)
CFAD	=Correction factor for age of dam
YW	=Yearling weight corrected
YWA	=Yearling weight actual
TYW	=Time toget yearling weight actual

Correction factor for sex (CFS) was obtained as follows:

$CFS = \frac{\overline{X_M}}{\overline{X_F}}$ ($\overline{X_M}$ =average of male goat BW, $\overline{X_F}$ = average of female goats BW). The CFS were used to calculate BW of female goats.

Heritability Estimation

Data corrected had been analyzed to estimate heritability parameter by analyses for variance of one way lay out method. Mathematic model of the analysis as recommended by Becker (1992), $Y_k = \mu + \alpha_i + e_k$ (Y_{ik}=*mean*, α_i =effect of bucks i^{th}, e_{ik} =genetic and environment deviation affect individual in buck group. Analysis of variance presented in Table 1.

Heritability value were calculated by formula:

$$h_s^2 = \frac{4\sigma_s^2}{4\sigma_s^2 + 4\sigma_w^2}$$

Standard error were calculated by formula:

$$S.E(h_s^2) = 4\sqrt{\frac{2(1-t)^2(1+(k-1)t)^2}{k(k-1)(s-1)}}$$

t =intraclass correlation

$$t = \frac{\sigma_s^2}{\sigma_s^2 + \sigma_w^2}$$

Table 1: Analyse of variance to estimate heritability

Source of variance	Degree of freedom	Sum of square	Mean square	Component of variance
Between bucks	s-1	SS_S	MS_S	$\sigma_w^2 + k\sigma_s^2$
Between progeny within bucks	n.-s	SS_W	MS_W	σ_w^2

Explanation:

s= number of bucks; n_i = number of progeny in bucks; i^{th}= number of does mated to bucks i^{th}; k =coeffisien= n_i; n. =number of individual; σ_s^2 =component of variance between bucks; σ_w^2 =component of variance between individuals within bucks

Repeatability Estimation

Data corrected had been analysed repeatability by intraclass correlation methof recommended by Becker (1992). The mathematic model were $Y_{km}=\mu+\alpha_k+e_{km}$ (μ is the common mean, αk is the effect of the k-th individual and ekm is the environmental deviation of m-th measurement within an individual. All effects are random, normal, and independent with expactations equal to zero in Table 2. Repeatability was estimated by formula as follows:

$$R = \frac{\sigma_W^2}{\sigma_W^2 + \sigma_E^2}$$

Standard error of R is the square root of sampling variance of the intraclass correlation, R as recommended by Becker (1992):

The formula of sum of square (SS) were :

$$SS_W = \sum_k \frac{Y_k^2}{m_k} - C$$

$$SS_E = \sum_k \sum_m Y_{km}^2 - \sum_k \frac{Y_k^2}{m_k}$$

The formula of Mean Square were :

$$MS_W = SS_W / (n-1)$$
$$MS_E = SS_E / n(m-1)$$

Component of variance and formula of repeatability (r) were :

$$\hat{\sigma}_E^2 = MS_E$$

$$r = \frac{\hat{\sigma}_W^2}{\hat{\sigma}_W^2 + \hat{\sigma}_E^2}$$

$$\hat{\sigma}_W^2 = (MS_W - MS_E) / k_1$$

The formula of standar error for repeatality (r) :

$$S.E.(r) = \sqrt{\frac{2(1-R)^2[1+(k_1-1)R]^2}{k_1(k_1-1)(N-1)}}$$

Table 2: Analyse of variance to estimate repeatality

Source	d.f.	SS	MS	Component of variance
Between individuals	N-1	SS_W	MS_W	$\sigma_E^2 + k_1\sigma_W^2$
Between measurements , within individuals	N(M-1)	SS_E	MS_E	σ_E^2

N=number of individuals (number of does); M=number of measurements per individual (per doe); equal number for each individual; k_1=M

$$\sigma_E^2 = MS_E$$

$$\sigma_W^2 = \frac{MS_W - MS_E}{k_1}$$

If the number of measurements per doe were anequal, k_1 was computed by formula as follows:

$$k_1 = \frac{1}{N-1}\left(M - \frac{\sum M_i^2}{M}\right)$$

Genetic Correlation

Data corrected had been analyzed to estimate genetic correlation by analyses of covariance of one way lay out method parameter . Mathematic model of the analysis as recommended by Becker (1992), $Y_k = \mu + \alpha_i + e_k$ (Y_{ik}=*mean*, α_i =effect of bucks i^{th}, e_k =genetic and environment deviation affect individual in buck group. Analysis of covariance presented in Table 3.

The formula of genetic correlation (r_G) were:

$$r_G = \frac{4cov_s}{\sqrt{(4\sigma_{s(x)}^2)(4\sigma_{s(y)}^2)}}$$

$$k = \frac{1}{s-1}\left(n_{..} - \frac{\Sigma n_i^2}{n_{..}}\right)$$

n..=total number of individual
The formula of standard error (S.E.) for genetic correlation (r_G) was:

$$S.E(r_G) = \sqrt{var(r_G)}$$

Table 3: Analyses covariance to estimate genetic correlation

Source of variance	Degree of freedom	Sum of cross product	Mean of cross product	Component of covariance
Between bucks	s-1	SCP_s	MCP_s	Cov_w+kcov_s
Between progeny within bucks	n-s	SCP_w	MCP_w	Cov_w

Explanation:
Cov_s= component of covariance between traits correlated with bucks; Cov_w= component of covariance between traits of individual within bucks

Table 4: Coefficient for genetic correlation in one way lay out method

Korelasi	Koefisien		
	L	A	B
r_G	K	1	1
r_E	K	3	k+3
r_P	K	3	k+3

Explaination:
r_G = genetic correlation; r_E = environment correlation; r_P = phenotypic correlations

RESULTS AND DISCUSSION

from the results of the study found that the genetic parameters will increase, in accordance with the development of age

Heritability for Growth Traits

Result of this research indicated that heritability growth traits at birth, weaning, and yearling were mediumup to high except EL_0, EW_0 and EL_{12}that were low. Heritability EL_3, EW_3, and EW_{12} were medium (Table 1) . Heritability were classified low and medium when thevalue 0,00 up to 0,10 and>0,10 up to 0,20, respectively (Hardjosubroto, 1994). Ear length and ear width were not effective to be improved by selection however important as qualitative character of breed. One character of Saburai were ear length and ear width from EGG although not as high as EGG.

Heritability of growth traits at birth were medium however not more than that at weaning and yearling. Variance of genetic for growth trait at birth were low due to selection process internally began fertilization, growth process as foetus up to be born as kid. Besides that, selection to improve growth traits at birth implicated to dystocia. Heritability of growth traits at birth generally low (Hardjosubroto, 1994) due to the traits were determined not only by genetic potential but also by maternal and environmental factors (Mandal et al., 2006).

Heritability for BW_0in this research were lower than that was resulted in Saburai goats at Campang village, Gisting subdistrict, Tanggamus regency, 0.80±0.40 in BW_0 (Beyleto et al., 2012). Some results of research about heritability varied depend on genetic variance of population, method of estimation, and breed. Heritability of BW_0 in Boerka goat (Boer buck><Kacang doe) 0.23±0.15 and in Boerka (Kacang buck><Boer doe) 0.09±0.14 (Elieser, 2012), 0.34 in Boer goat (Els, 1999), 0.19±0.08 for BW_0, 0.14±0.07 for BL_0, 0.24±0.89 for BH_0, 0.25±0.10 for CG_0in Boer goats (Zhang et al., 2008), 0.17±0.07 for BW_0 in Boer goats (Zhang et al., 2009), 0.178±0.044 for BW_0 in Adelaide Boer (Niekerk et al., 1996).

In Black Bengal goats, heritability for BW_0, BW_3 and BW_{12}were 0.05, 0.28, 0.18 (Faruque et al., 2010), although there were different in heritability BW_{12}. Heritability of three breed in one population (Saanen, Bornova, Saanen><Killis goat) for BW0 were 0.43±0.11 (Kosum et al., 2004), 0.20 in Sicilian Girgentana goat (Portolano et al., 2002), 0.80 in Emirati goat (Al Shorepy et al., 2002),

Heritability of weaning and yearling traits (except ear length and ear width) were effective to improve growth traits. Weaning traits and yearling traits could be used as criteria of selection to determine replacement stock. However, that criteria was not as accurate as yearling weight because in weaning weight still included maternal effect (Mandal et al., 2006) and in yearling weight didn't so. The maternal genetic effect seems to do not affect the late growth (Zhang et al., 2009).

Heritability for BW_3 resulted in this research (0,24±0,08) were similarly with the other research for the same traits, 0.30±0.17 in Saburai goats, 0.18±0.20 in Boerka crossbred between Kacang buck><Boer doe, 0.24±0.17 in Boerka crossbred between Boer buck><Kacang doe, 0.30±0.17 in Saburai goat (Beyleto et al., 2010), 0.051±0.079 in Boer goats (Kosum et al., 2004), 0.60 in Boer goats (Els, 1999),0.22±0.08 in Boer goat (Zhang et al., 2009)., 0.28 in Black Bengal goats (Faruque et al., 2010). 0.19 in West African Dwarf goats (Ayizanga, 2009)

Heritability for BW_{12}in this research 0.29±0.17 that was differ with heritability for BW_{300}(0.10±0.08) in Boer goats (Zhang et al., 2009), 0.80±0.40 in Saburai goat (Beyleto et al., 2010), 0.38±0.34 in Boerka crossbred between Kacang buck and Boer doe, 0.31±0.21 in Boeka crossbred between Boer buck and Kacang doe (Elieser, 2012), 0.21±0.25±0.22 in West African Dwarf goats (Ayizanga, 2009)

Repeatability for Growth Traits

Repeatability for growth traits were medium up to high except EW_0 (0,10±0,03) that was low, that indicated most of variance of phenotypic for those traits due to variance of genetic and variance of permanent environment. This research was similar with the other research, Repeatability for birth weight and weaning weights of Teddy goat were 0.2089 ± 0.0315 and 0.1381 ± 0.0315, respectively. The moderate estimates indicate that selection on the basis of first record will be effective to improve birth weight. But the low estimates for weaning weight indicate that selection should be based on multiple records (Tahir et al., 1994).

Repeatability for growth traits of Saburai goat at Campang village, Gisting subdistrict, Tanggamus regency, Lampung Province was high. Repeatability of BW_0, BW_3, and BW_{12} estimated by intraclass correlation method were 0.80±0.22, 0.70±0.33, 0.30±0.10, respectively and by interclass correlation were 0.42±0.07, 0.32±0.08, 0.30±0.08, respectively (Beyleto et al., 2010), that of Boer goats were 0.17±0.07, 0.22±0.08, 0.10±0.08, respectively (Zhang et al., 2009), for BW_0 and BW_3 of Boerka goats by interclass correlation method were 0.29±0.14 and 0.25±0.21, of Boer goats were 0.48±0.16 and 0.45±0.20, of Kacang goat were 0.44±0.002 and 0.30±0.01 (Elieser, 2012). Repeatability of performance that was medium up to high indicated that that of progeny of does selected could be predicted higher than their does (Falconer and Mackay, 1996).

Genetic Correlation

Result of this research indicated that genetic correlation between BW_0 and body measurements at birth, between, BW_3 and body measurements at weaning, between BW_{12} and body measurements at yearling, among BW_0, BW_3, and BW_{12} were positive and ranges medium up to high, except between BW_0 and EL_0 (0.10±0.00), BW_0 and EW_0(0.09±0.00). That result mean that selection to improve BW could be done using body measurements as criteria of selection. Besides that, selection to improve BW_{12} could be done using BW_0 and BW_3 as criteria of selection.

In crossbred (F1) between Boer and local Indonesian goat, the genetic correlation value between weaning weight and body length was 0.81 ± 0.4 (high positive), weaning weight and chest girth was 0.47 ± 0.77 (moderate positive) and weaning weight and wither height was 0.14 ± 0.55 (low positive). It was concluded that weaning weight has strong genetic relation with body length, which means that selection based on body length would give correlated response to weaning weight (Rosahastuti, 2008).

Genetic correlation between BW_0 and BW_{12}, BW_3 and BW_{12} of Saburai goats at Campang village, Gisting sundistrict, Tanggamus regency, Lampung Province were 0,50±0,04, 0,44±0,08, 0,21±0,03, respectively (Beyleto et al., 2010). Genetic correlation for BW_3 and BW_6, BW_3 and BW_{12}, and BW_6 and $BW_{12}$of Boerka crossbred (Boer bucks><Kacang does) were 0.64±0.29, 0.23±0.28, 0.70±0.26, respectively (Elieser, 2012).

CONCLUSION

In conclusion, improvement for growth traits of Saburai goats was properly conducted by mass selection and body measurement could be used as criteria for selection to improve body weight.

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AUTHORS CONTRIBUTION

Sulastri: Animal work, sample collection, and manuscript preparation.
Siswanto: Sample collection, serum biochemical parameters analysis, and manuscript preparation.
Kusuma Adhianto: Designing the experiment, animal work, manuscript preparation, and publishing the article "corresponding author".

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