**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 (Sulas-tri 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**

\[
BW = \left( \frac{BWA - BW}{TWW} \right) (90) (CFS) (CFAD)
\]

**WW**

\[
WW = \left( \frac{YWA - W}{TYW - TWW} \right) (275) (CFS)
\]

### Explanation:

- **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 to get yearling weight actual

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

\[
CFS = \frac{X_M}{X_F} (X_M = \text{average of male goat BW}, X_F = \text{average of female goats BW})
\]

**Heritability Estimation**

Data corrected had been analyzed to estimate heritability parameter by analyses for variance of one way lay out method. Mathemetic model of the analysis as recommended by Becker (1992), \( Y_k = i + \alpha_i + \epsilon_k \) (\( Y_a = \text{mean}, \alpha_i = \text{effect of bucks}^{th} , \epsilon_k = \text{genetic and environment devia-} \text{tion affect individual} \text{ in buck group. Analysis of variance presented in Table 1.} \)

**Heritability value** were calculated by formula:

\[
h^2 = \frac{46_s^2}{46_s^2 + 46_a^2}
\]

**Standard error** were calculated by formula:

\[
\text{S.E}(h^2) = \sqrt{\frac{2(1-t^2)}{k(k-1)(s-t)}}
\]

\( t = \text{intraclass correlation} \)
Table 1: Analyse of variance to estimate heritability

<table>
<thead>
<tr>
<th>Source of variance</th>
<th>Degree of freedom</th>
<th>Sum of square</th>
<th>Mean square</th>
<th>Component of variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between bucks</td>
<td>s-1</td>
<td>SSₙ</td>
<td>MSₙ</td>
<td>σₛ² + kσₘ²</td>
</tr>
<tr>
<td>Between progeny within bucks</td>
<td>n.-s</td>
<td>SSₘ</td>
<td>MSₘ</td>
<td>σₘ²</td>
</tr>
</tbody>
</table>

Explanation:

s = number of bucks; nᵢ = number of progeny in bucks; iⁿᵢ = number of does mated to bucks iⁿ; k = coefficient nᵢ, n. = number of individuals; σₛ² = component of variance between bucks; σₘ² = component of variance between individuals within bucks

Repeatability Estimation

Data corrected had been analysed repeatability by intraclass correlation method recommended by Becker (1992). The mathematic model were Yᵢkm = μ + αᵢ + eᵢkm (µ is the common mean, αᵢ is the effect of the k-th individual and eᵢkm is the environmental deviation of m-th measurement within an individual. All effects are random, normal, and independent with expectations equal to zero in Table 2. Repeatability was estimated by formula as follows:

R = \frac{σₘ²}{σₘ² + σₑ²}

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

S.E. (R) = \sqrt{\frac{2(1-R²)(1+k-1)R²}{k(k-1)(N-1)}}

Table 2: Analyse of variance to estimate repeatability

<table>
<thead>
<tr>
<th>Source of variance</th>
<th>d.f.</th>
<th>SS</th>
<th>MS</th>
<th>Component of variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between individuals</td>
<td>N-1</td>
<td>SSW</td>
<td>MSW</td>
<td>σₑ² + kσₘ²</td>
</tr>
<tr>
<td>Between measurements, within individuals</td>
<td>N(M-1)</td>
<td>SSE</td>
<td>MSE</td>
<td>σₑ²</td>
</tr>
</tbody>
</table>

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

σₑ² = MSₑ

σₘ² = \frac{MSₘ - MSₑ}{kᵢ}

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

kᵢ = \frac{1}{N-1}(M - \sum \frac{mᵢ}{M})

Genetic Correlation

Data corrected had been analyzed to estimate genetic correlation by analyses of covariance of one way lay out method parameter. Mathematical model of the analysis as recommended by Becker (1992), \( Yᵢk = i + αᵢ + eᵢk \) (\( Yᵢk = \) mean, αᵢ = effect of bucks iⁿ, eᵢk = genetic and environment deviation affect individual in buck group. Analysis of covariance presented in Table 3.

The formula of genetic correlation (rₘᵢ) were:

\[ rₘᵢ = \frac{4 cov_a}{\sqrt{(\hat{σ}_a²)(\hat{σ}_e²)}} \]
The formula of standard error (S.E.) for genetic correlation ($r_G$) was:

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

Table 3: Analyses covariance to estimate genetic correlation

<table>
<thead>
<tr>
<th>Source of variance</th>
<th>Degree of freedom</th>
<th>Sum of cross product</th>
<th>Mean of cross product</th>
<th>Component of covariance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between bucks</td>
<td>s-1</td>
<td>SCP&lt;sub&gt;s&lt;/sub&gt;</td>
<td>MCP&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Cov&lt;sub&gt;s&lt;/sub+w+kCov&lt;sub&gt;s&lt;/sub&gt;</td>
</tr>
<tr>
<td>Between progeny within bucks</td>
<td>n-s</td>
<td>SCP&lt;sub&gt;n&lt;/sub&gt;</td>
<td>MCP&lt;sub&gt;n&lt;/sub&gt;</td>
<td>Cov&lt;sub&gt;n&lt;/sub&gt;</td>
</tr>
</tbody>
</table>

Explanation:
- Cov<sub>s</sub> = component of covariance between traits correlated with bucks
- Cov<sub>n</sub> = component of covariance between traits of individual within bucks

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

<table>
<thead>
<tr>
<th>Korelasi</th>
<th>Koefisien</th>
</tr>
</thead>
<tbody>
<tr>
<td>$r_G$</td>
<td>L A B</td>
</tr>
</tbody>
</table>

| $r_G$    | K 1 1     |
| $r_E$    | K 3 k+3   |
| $r_P$    | K 3 k+3   |

Explanation:
- $r_G$ = genetic correlation
- $r_E$ = environment correlation
- $r_P$ = phenotypic correlations

RESULTS AND DISCUSSION

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 (Hardjosubrato, 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<sub>0</sub> in this research were lower than that was resulted in Saburai goats at Campang village, Gisting subdistrict, Tanggamus regency, 0.80±0.40 in BW<sub>0</sub> (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<sub>0</sub> 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<sub>0</sub>, 0.14±0.07 for BW<sub>12</sub>, 0.24±0.89 for BW<sub>1</sub>, 0.25±0.10 for CG in Boer goats (Zhang et al., 2008), 0.17±0.07 for BW<sub>0</sub> in Boer goats (Zhang et al., 2009), 0.178±0.044 for BW<sub>0</sub> in Adelaide Boer (Niekerk et al., 1996).

Heritability for BW<sub>3</sub> 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<sub>12</sub> in this research 0.29±0.17 was
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 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 subdistrict, 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_0 and BW_6, BW_3 and BW_6, and BW_9 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”.

REFERENCES