Phenotypic and Genetic Correlations of Growth Traits in Bali Cattle Breeding Population

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Abstract. This study aimed to estimate phenotypic and genetic correlations of growth traits as selection criteria in Bali cattle test center populations at Pulukan Breeding Center Denpasar, Bali. In total 160 records were obtained from calves which born between 2013 until 2016. Data collected were birth weight (BW), weaning weight (WW), yearling weight (YW), mature weight (MW) and pedigree. Data were then standardized to weaning weight at 205 days (WW₂₀⁵), yearling weight at 365 days (YW₃₆⁵) and mature weight at 730 days (MW₇₃⁰). The data obtained were then analyzed using univariate and bivariate animal models with Restricted Maximum Likelihood (REML) method. Heritability values (h²) were 0.43 ± 0.12, 0.22 ± 0.12, 0.39 ± 0.15, 0.63 ± 0.18 for BW, WW₂₀⁵, YW₃₆⁵ and MW₇₃⁰ respectively. Phenotypic correlations among variables were vary from low to medium; which were 0.16 for BW - WW₂₀⁵, 0.11 for BW - YW₃₆⁵, 0.34 for BW - MW₇₃⁰, 0.61 for WW₂₀⁵ - YW₃₆⁵, 0.25 for WW₂₀⁵ - MW₇₃⁰ and 0.31 for YW₃₆⁵ x MW₇₃⁰. However, the genetic correlation among growth traits were considerably high: BW - WW₂₀⁵ 0.53, BW - YW₃₆⁵ 0.76, BW - MW₇₃⁰ 0.47, WW₂₀⁵ - YW₃₆⁵ 0.70, WW₂₀⁵ - MW₇₃⁰ 0.48, YW₃₆⁵ - MW₇₃⁰ 0.64. Heritability of Bali cattle growth traits are categorized as moderate to high, thus selection on these traits are potential to obtain genetic improvement in the population. Phenotypic correlations among traits were considerably low, whereas the genetic correlations spanned between medium to high. These findings implied that other than genetic, improving the farm environment and management could also affect the growth performance of Bali cattle.

Keywords: bali Cattle, growth traits, heritability, phenotypic and genetic correlation

1. Introduction
Bali cattle is one of native Indonesian cattle, adapted well to the tropical environment, and able to growth under low feed quality. This cattle having a potential to be developed into meat producer through genetic selection or crossbreeding program [1,2]. Improving growth traits and or its productivity became an effort in the livestock production system [3] by doing selection of desirable traits for meat production. In the selection process, generally know heritability, phenotypic and genetic correlation to describe the ability specific trait to be improved. For example, genetic correlation can be used to describe the ability of meat production [4].
Phenotypic correlation measuring the strength of relationship between one to other performance traits [5]. Meanwhile genetic correlation related to the relationship between trait in genetic way. In cattle growth trait, for example, birth weight positively correlated in moderate degree with weaning weight, yearling weight and mature weight. Therefore, selection for one or in combination of these traits can result in an increase of correlated trait(s) [6]. In beef cattle, selection based on yearling weight would not affect birth weight which lead to the difficulty in giving birth. Other trait, such as yearling weight, shows negative selection for optimal birth weight.

As reported in our previous study [2], Bali cattle still has large variation in the phenotype which need to be improved. In the aim to improve Bali cattle performance via selection, therefore this study aimed to know the phenotypic and genetic correlation among growth traits. Thus, the information can be useful as effective strategy in breeding process.

2. Methodology

Study location and Bali cattle rearing

The current study was performed in Pulukan Breeding Center, Denpasar, Bali, Indonesia (8°25'35.6"S 114°51'49.9"E). In total 20 males, 132 females and 160 calves which born from 2013 until 2016 were used in this study. During the study, cattle were reared in extensive management, one one-hectare paddock consist of 25-30 head. Cattles were freely graze, but concentrate was given limited once a day and water was freely access.

Growth traits data

The data collected were sex, year of birth, birth season, male and growth traits (phenotype) namely birth weight (BW), weaning weight (WW), yearling weight (YW) and mature weight (MW). All the weight data are in kilogram basis. The WW, YW, MW were standardized using the following formula according to Hardjosubroto (1994) [7]:

1. Weaning Weight at 205 days (WW\textsubscript{205})
   \[ WW_{205} = \left( \frac{\text{actual weight} - BW}{\text{interval}} \times 205 \right) + BW \]

2. Yearling Weight at 365 days (YW\textsubscript{365})
   \[ YW_{365} = \left( \frac{\text{actual weight} - WW}{\text{interval}} \times 160 \right) + WW_{205} \]

3. Mature Weight at 730 days (MW\textsubscript{730})
   \[ MW_{730} = \left( \frac{\text{actual weight} - YW}{\text{interval}} \times 365 \right) + YW_{365} \]

Data analysis

First, incomplete cattle data were omitted from further analysis in this study. The estimation of variance component was done by using bivariate animal model and genetic parameter estimates. Later, a phenotypic and genetic correlation was analyzed using bivariate by analyzing two traits at once. The following equation was used to analyse the data.

\[
\begin{pmatrix}
Y_1 \\
Y_2
\end{pmatrix} = \begin{pmatrix}
X_2 \\
Z_2
\end{pmatrix} \begin{bmatrix}
\beta_2 \\
\alpha_2
\end{bmatrix} + \begin{pmatrix}
Z_2 \\
Z_2
\end{pmatrix} \begin{bmatrix}
\alpha_2 \\
\varepsilon_2
\end{bmatrix} + \begin{pmatrix}
U \\
X_2
\end{pmatrix} \begin{bmatrix}
\gamma_1 \\
\sigma_2
\end{bmatrix} + \begin{pmatrix}
U \\
X_2
\end{pmatrix} \begin{bmatrix}
\gamma_2 \\
\sigma_2
\end{bmatrix} + \begin{pmatrix}
\varepsilon_1 \\
\varepsilon_2
\end{pmatrix}
\]
where:
- \( y_1 \) and \( y_2 \) = vectors of traits 1 and trait 2
- \( X_1 \) and \( X_2 \) = incidence matrix related to the fixed effects of trait 1 and trait 2
- \( b_1 \) and \( b_2 \) = vectors of fixed effect (birth year)
- \( Z_1 \) and \( Z_2 \) = incidence matrix corresponding to additive genetic
- \( a_1 \) and \( a_2 \) = additive genetic effect, where:

\[
\begin{bmatrix}
\sigma^2_e \\
\sigma^2_a
\end{bmatrix} \sim N \left( \begin{bmatrix}
0 \\
0
\end{bmatrix}, \begin{bmatrix}
\sigma^2_e & \sigma^2_{ea} \\
\sigma^2_{ae} & \sigma^2_a
\end{bmatrix} \right) \], A is the additive genetic relationship matrix.

\( e_1 \) and \( e_2 \) = random residual, where:

\[
\begin{bmatrix}
e_1 \\
e_2
\end{bmatrix} \sim N \left( \begin{bmatrix}
0 \\
0
\end{bmatrix}, \begin{bmatrix}
\sigma^2_e & \sigma^2_{ea} \\
\sigma^2_{ae} & \sigma^2_a
\end{bmatrix} \right) \], I is identity matrix.

Bivariate animal models were analyzed with Restricted Maximum Likelihood (REML) using a `breedR` package and custom script using the R programming language [8]. The heritability value \( h^2 \) is obtained as a proportion of additive genetic variance \( \sigma^2_a \) which is related to total variance \( \sigma^2 = \sigma^2_e + \sigma^2_a \). The phenotypic and genetic correlation is:

\[
r_y = r_g \sqrt{h^2} = \frac{r_g \sqrt{h^2}}{1 - h^2},
\]

3. Result and discussion

Bali cattle growth traits

According to the record during observation, we found the mean of Bali cattle growth traits as tabulated in Table 1. This result was in accordance with the previous study which found BW, WW, YW and MW Bali cattles were 16.8, 82.9 ± 8.2, 127.5 ± 5.7 and 170.4 ± 17.4 kg respectively [9].

| Growth traits (kg) | Mean±sd       | Min | Max |
|--------------------|---------------|-----|-----|
| BW                 | 17.94 ± 1.95  | 15  | 25  |
| WW205              | 82.52 ± 15.24 | 61  | 124 |
| YW365              | 122.46 ± 18.29| 89  | 168 |
| MW730              | 192.43 ± 39.83| 128 | 300 |

Heritability

The calculation of \( h^2 \) growth traits is shown in Table 2. According to that value, we can see \( h^2 \) is categorized as low to moderate. The highest \( h^2 \) was found in MW (0.63±0.18), while the lowest was in WW (0.22±0.12). Heritability is a reflection of genetic factor inherited from its parent to the offspring for specific trait. Different genetic, breed, and environment will give difference value of \( h^2 \) as listed in Table 3.

For example, \( h^2 \) of WW in this study is 0.22±0.12, when compared to \( h^2 \) which listed in Table 3 in the same breed, its show lower. This indicates that WW is strongly influenced by environmental factors. This was in accordance with the previous report [13], which states that WW is heavily influenced by environmental factors rather that parent genetic. Low WW heritability is because the changes of environment during the cattle growth [14]. Before weaning, calf depend on milk produced by its mother, later after nearly weaning calf will start to be independent by consuming the feed which is available such grass.

Differences in the heritability values of the growth characteristics of Bali cattle are thought to be caused by differences in genetic diversity, environment, amount of data and analytical methods used. In cattle the same genetic diversity occurs due to the system of mating and selection carried out in livestock populations, while the diversity of the environment will be experienced by livestock during their lifetime which will lead to differences in diversity. Differences in cattle and locations with
different natural conditions will be related to genetic diversity and the influence of uncontrolled factors will also affect the value of heritability. Differences results of $h^2$ estimation occur due to differences in breed, genetic variation in populations, environmental conditions and statistical analysis used [15].

Table 2. Heritability of Bali cattle growth trait

| Growth traits (kg) | $\sigma^2_{sd}$ | $\sigma^2_{sd}$ | $\sigma^2_{sd}$ | $h^2_{sd}$ |
|--------------------|-----------------|-----------------|-----------------|-----------|
| BW                 | 1.77 ± 0.57     | 2.31 ± 0.47     | 4.08 ± 1.04     | 0.43 ± 0.12 |
| WW$_{205}$         | 62.67 ± 35.36   | 220.66 ± 34.87  | 283.33 ± 70.23  | 0.22 ± 0.12 |
| YW$_{365}$         | 222.70 ± 93.59  | 349.50 ± 78.82  | 572.20 ± 172.41 | 0.39 ± 0.15 |
| MW$_{730}$         | 1,823.50 ± 589.01 | 1,052.50 ± 456.95 | 2,876 ± 1045.96 | 0.63 ± 0.18 |

$\sigma^2$ = genetic variance; $\sigma^2$ = error variance; $\sigma^2$ = phenotype variance; $h^2$ = heritability

Table 3. Heritability of beef cattle growth trait in Indonesia

| Beef Cattle | Growth trait kg | References |
|-------------|-----------------|------------|
| Bali        | BW              | WW$_{205}$ | YW$_{365}$ | MW$_{730}$ |
| Brahman CROSS | 0.09±0.07      | 0.33±0.09  | 0.43±0.10  | -          | [3]        |
| Madura      | 0.33±0.24       | 0.87±0.45  | 0.27±0.29  | -          | [11]       |
| Aceh        | 0.15±0.13       | 0.48±0.58  | 0.49±0.58  | 0.56±0.69  | [12]       |

Phenotypic and genetic correlation

The value of phenotype and genetic correlation of Bali cattle growth traits in this study, were shown in Table 4.

Table 4. Phenotypic correlation (above diagonal) and genetic correlation (below diagonal)

| Traits       | BW    | WW$_{205}$ | YW$_{365}$ | MW$_{730}$ |
|--------------|-------|------------|------------|------------|
| BW           | -     | 0.16       | 0.11       | 0.34       |
| WW$_{205}$   | 0.53  | -          | 0.61       | 0.25       |
| YW$_{365}$   | 0.76  | 0.70       | -          | 0.31       |
| MW$_{730}$   | 0.47  | 0.48       | 0.64       | -          |

The phenotypic correlation value of the study results is between 0.11-0.61, categorized as low to moderate. The phenotypic correlation was found low in BW x WW$_{205}$, BW x YW$_{365}$, WW$_{205}$ x MW$_{730}$, while BW x MW$_{730}$, WW$_{205}$ x YW$_{365}$ and YW$_{365}$ x MW$_{730}$ was medium. The phenotypic correlation value of BW was higher than BW x WW$_{205}$ and BW x YW$_{365}$ (0.07 and 0.14) in Bali cattle, but BW x WW$_{205}$ was lower than Madura (0.40), the phenotypic correlation of WW$_{205}$ x YW$_{365}$ was higher than Madura and Aceh Cattles (0.21 and 0.48) [11,16,17]. The results of this study indicate that selection of BW, WW and YW will increase the selection response to MW$_{730}$ weight.

The genetic correlation of the results of the study 0.47-0.76 is positive with a moderate to high category. The genetic correlation was found low in BW x WW$_{205}$, BW x YW$_{365}$, WW$_{205}$ x MW$_{730}$, while BW x MW$_{730}$, WW$_{205}$ x YW$_{365}$ and YW$_{365}$ x MW$_{730}$ was medium. The genetic correlation value of BW was higher than BW x WW$_{205}$ and BW x YW$_{365}$ (0.07 and 0.14) in Bali cattle, but BW x WW$_{205}$ was lower than Madura (0.40), the phenotypic correlation of WW$_{205}$ x YW$_{365}$ was higher than Madura and Aceh Cattles (0.21 and 0.48) [11,16,17]. This result is lower than the genetic correlation of BW with WW$_{205}$ and YW$_{365}$ in Bali cattle, respectively 0.03 and 0.09 [16]. This result is lower than the genetic correlation of BW with WW$_{205}$ in Aceh cattle which has a genetic correlation value of 0.56 [12]. Genetic correlation between WW$_{205}$ and YW$_{365}$ and MW$_{730}$ respectively 0.70 and 0.48. Genetic correlation between YW$_{365}$ and MW$_{730}$ (0.64), including the medium category. This correlation is the same as the literature on research in the Zebu cattle, ranging from 0.54-0.63 (WW$_{205}$ x YW$_{365}$ and MW$_{730}$) and 0.62-0.80 (YW$_{365}$ x MW$_{730}$) [18].

The phenotypic and genetic correlation values of Bali cattle growth trait are positive from low to high criteria. The low correlation is likely due to environmental variations and post-recovery compensatory growth causing a bias in the phenotypic covariance between WW$_{205}$ and YW$_{365}$ [14]. Low phenotypic correlation of BW x WW$_{205}$ and BW x YW$_{365}$ was due to environmental stress.
Moderate to high phenotypic and genetic correlations indicate selection in one trait will improve the other trait. The highest phenotypic correlation is between WW\textsubscript{205} x YW\textsubscript{365}, while genetic correlation was high in BW x YW\textsubscript{365} and WW\textsubscript{205} x YW\textsubscript{365}. This shows that the selection in BW and WW\textsubscript{205} will increase YW\textsubscript{365}. However, it is better to make a selection on BW, because BW has a higher phenotypic and genetic correlation with MW\textsubscript{730} compared to WW\textsubscript{205}.

4. Conclusion

According to the result, it can be concluded that heritability of growth trait Bali cattle was categorized as moderate to high. Selection of these traits has potential to improve the genetic quality in the population. Phenotypic correlations of growth characteristics in the low to moderate categories, while genetic correlations of growth characteristics are medium to high. This shows the influence of environment and management to the growth of Bali cattle. Due to its correlation, selection at BW would be beneficial for further growth.

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