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Non-genetic factor and genetic parameter analysis for growth traits in Sumba Ongole (SO) cattle

W.P.B. Putra*, P.P. Agung and S. Said
Laboratory of Animal Reproduction, Breeding and Cell Culture,
Research Center for Biotechnology, Indonesian Institute of Science,
Jl. Raya Bogor-Jakarta Km. 46 Cibinong, Bogor 16911 - Indonesia
**Corresponding E-mail: widya.putra.lipi@gmail.com*

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ABSTRAK

Penelitian ini bertujuan untuk mengevaluasi pengaruh non-genetik dan parameter genetik pada sifat pertumbuhan sapi Sumba Ongole (SO). Sifat pertumbuhan yang diamati meliputi bobot lahir (BL), bobot sapih (BS), bobot setahunan (BY), pertambahan bobot badan harian prasapih ($PBBH_1$) dan pascasapih ($PBBH_2$). Data catatan produktivitas ternak tahun 2011 - 2016 dari 143 ekor sapi SO yang dipelihara di PT. KAR digunakan dalam penelitian ini untuk dianalisis. Analisis *General Linear Model* (*GLM*) digunakan untuk mengkaji pengaruh non-genetik yang meliputi jenis kelamin, tahun kelahiran, generasi dan musim. Selanjutnya, untuk mengevaluasi perameter genetik maka dilakukan perhitungan heritabilitas (h^2) dan korelasi genetik (r_g) menggunakan metode korelasi saudara tiri sebapak (*Paternal Halfsib Correlation*). Hasil penelitian menunjukkan bahwa jenis kelamin tidak berpengaruh nyata (P>0,05) terhadap BL, BS dan BY sedangkan tahun kelahiran berpengaruh nyata terhadap ketiga sifat tersebut. Faktor musim hanya berpengaruh nyata terhadap BS. Estimasi nilai h^2 yang diperoleh termasuk kategori tinggi (h^2 >0,30) dan handal (h^2 >SE) pada BL (0,66±0,42), BS (0,65±0,44), BY (0,67±0,42), $PBBH_1$ (0,68±0,45) dan $PBBH_2$ (0,70±0,43). Estimasi nilai r_g termasuk kategori tinggi (r_g>0,50) dan handal (r_g>SE) diperoleh pada BL-BS (0,87±0,63); BL-BY (0,95±0,87); $PBBH_1$-BS (0,99±0,34); BS-BY (0,98±0,48) dan $PBBH_1$-BY (0,95±0,51). Disimpulkan bahwa sifat BS dapat digunakan sebagai kriteria seleksi ternak untuk meningkatkan BY pada sapi SO karena memiliki nilai r_g yang tinggi.

Kata kunci: genetik, heritabilitas, korelasi genetik, faktor non-genetik, sifat pertumbuhan

ABSTRACT

The aim of this study was to evaluate non-genetic factors and genetic parameters of the growth traits in Sumba Ongole (SO) cattle. The growth traits were consisted of birth weight (BW), weaning weight (WW), yearling weight (YW), average daily gain of pre-weaning (ADG_1) and post-weaning (ADG_2). Data from 143 heads of SO cattle (year 2011 to 2016) which raised at PT KAR were used in this study. Generalized Linear Model (GLM) analysis was performed to evaluate non-genetic effect including sex, year of birth, generation and season. Therefore, to evaluate genetic parameters, the heritability (h^2) and genetic correlation (r_g) were performed using Paternal Halfshib Correlation method. The results showed that sex of calf had no significant effect (P>0.05) on BW, WW and YW, but year of birth had significant effect on those traits. The factor of season had significant effect on WW. The estimation of h^2 values of growth traits were included high category (h^2>0.30) and accurate (h^2>SE) on BW (0.66±0.42), WW (0.65±0.44), YW (0.67±0.42), ADG_1 (0.68±0.45) and ADG_2 (0.70±0.43). The estimation of r_g values were included high category (r_g>0.50) and accurate (r_g>SE) on BW-WW (0.87±0.63); BW-YW (0.95±0.87); ADG_1-WW (0.99±0.34); WW-YW (0.98±0.48) and ADG_1-YW

(0.95±0.51). It was concluded that trait of WW could be used as selection criteria to increase YW trait in SO cattle.

Keywords: genetic, heritability, genetic correlation, non-genetic factors, growth traits

INTRODUCTION

Sumba Ongole (SO) cattle is one of Indonesian local cattle that adapted well in Sumba Island, East Nusa Tenggara Province. This cattle was declared to be Indonesian native cattle through decision of Indonesian Ministry of Agriculture No: 427/Kpts/SR.120/3/2014. The SO cattle was included *Bos indicus* breeds and was kept as beef cattle in Indonesia. There are a few information about SO cattle productivity in Indonesia. Previous studies reported that the average of dressing percentage in SO bull was 51.73 - 52.40 kg (Paskah *et al.,* 2016) and the average of body weight in SO bull at ± 2.5 years age was 353.86 - 474.08 kg (Said *et al.,* 2016a). Moreover, the birth weight of SO cattle reached of 23.86±5.68 kg (male) and 19.77±3.19 kg (female) as reported by Said *et al.* (2016b). Selection and breeding program for SO cattle in Indonesia is very important to increase meat production in Indonesia. Total estimation of meat (beef) production in Indonesia in 2016 was 524.110 ton, lower than total consumption in the same year (623.480 ton). Therefore, amount of 99.370 ton (16%) must be supplied from import (Kementan RI, 2016).

Selection of SO cattle may be initiated with evaluation of the genetic parameters and non-genetic effect to the growth traits. In beef cattle, body weight is an important trait for selection criteria, especially weaning and yearling weights (Supriyantono *et al.,* 2011). Evaluation of genetic parameters for growth traits in cattle could be measured through estimation of heritability (h^2), genetic correlation (r_g) and repeatability (r) values. Estimation of h^2, r_g and r values can be evaluated if the records data of livestock productivity were available. Unfortunately, the data records for repeatability estimation in this study was not available. Estimation of r value was needed to estimate most probable producing ability (MPPA) and commonly used for cow's selection (Said *et al*., 2016b). Heritability value could be used to identify the proportion of genetic variance to phenotypic variance in the population (Warwick *et al*., 1990). The h^2 values consisted of three category which were low ($h^2<0.10$), moderate ($0.11< h^2 < 0.30$) and high ($h^2 >0.30$). A traits with high of h^2 value indicated that this trait can be used for selection criteria to increase selected trait in the next generation (Falconer and Mackay, 1996). Moreover, the h^2 value was used to estimate breeding value and response selection. Besides, the r_g value was used to measure the correlation between two selected traits. The r_g values were consisted of three category of low ($r_g <0.30$), moderate ($0.31<r_g< 0.50$) and high ($r_g >0.50$). Two traits with high of r_g value indicated that selection on one trait can be affected by other traits. The r_g value between growth traits in beef cattle according to Warwick *et al.* (1990) were ranged from 0.25 to 0.50.

Several studies showed that weaning and yearling weight had high value of h^2 in Indonesian beef cattle such as Bali (Kaswati *et al.,* 2013; Gunawan and Jakaria, 2011), Ongole grade (Hartati e*t al.,* 2015), Simmental (Putra *et al.,* 2017), Aceh (Sari *et al.,* 2016) and Brahman cross (Duma and Tanari, 2008). In addition, weaning and yearling show high category of r_g in Indonesian beef cattle such as Bali (Prajoga and Talib, 2008), Madura (Karnaen, 2008) and Simmental (Suhada *et al.,* 2009). The non-genetic effect of sex, generation, year and season were important to evaluate as basic information for breeding strategy. Several studies reported that non genetic effect of year and season were significantly affecting birth weight and reproductive performance of cattle (Bayou *et al.,* 2015). This study was carried out to evaluate genetic factor (h^2 and r_g) and non-genetic factor (sex, generation, year and season) of growth traits for the genetic improvement in SO cattle.

MATERIALS AND METHODS

Research Site and Animals

The research was conducted at the breeding station of PT. Karya Anugerah Rumpin (KAR) at Rumpin District, Bogor Regency, West Java Province, Indonesia. This area is located at along latitude 06°26'30" S to 06°26'50" S and longitude 106°38'50" E to 106°39'15" E about 3500 to 4000 m above the sea level. The humidity 70% to 80% with temperature 28°C to 30°C and rainfall average occuring ±2500 mm/year. Amount of 143 progeny records data were used in this study. Body condition score (BCS) of cows in the present study was 3.0 (scale: 1 to 5). All of cows were about 3 years old and in the first calving status. Data records of progeny consisted of birth weight (BW), weaning weight (WW), yearling weight (YW) and average daily gain of pre-weaning (ADG_1) and average daily gain of post-weaning (ADG_2). Weight measurements were taken from each animal using a digital weighing scale. Data of calves were collected from herd book during 2011 to 2015.

Management of Animals

Calves were kept with their dam (cow) until ± 5 months in the colony stall. Therefore, the weaning calves (5-7 months of age) were kept in individual stall. The weaning calves were grouped based on sex into colony stall until yearling age (±12 months of age). The breeding bulls were kept in the individual stall. An artificial insemination (AI) and natural mating methods were managed at the breeding station. The BW was measured at 1 hours after birth and continued every 3 months. Colostrum milk was given to weekly calves (1-7 days of age) with portion of 4 L/head/day. Whereas, fresh milk was given to the monthly calves (7-30 days of age) with portion of 6 L/head/day. Calves with 2-3 months of age were given fresh milk and milk replacer (3 L/head/day) and concentrate (1 kg/head/day). Calves with 3-6 months of age were given fresh milk and milk replacer (4 L/head/day), concentrate (3-4 kg/head/day) and forages (7 kg/head/day). The yearling cattle were given concentrate (20 kg/head/day) and forages (10 kg/head/day). Forages used in this breeding station were Napier grass (*Pennisetum purpureum*) and corn leaf. The forages was chopped using chopper machine before given to cattle. The nutritional content of concentrate feed is presented inTable 1.

Data Correction

The data used in this study were collected from the breeding station during the period from year 2013 to 2016. Data of birth weight in female calf were corrected to male calf based on Hardjosubroto (1994) as follows:

$$CF_{sex} = \frac{\text{The average BW of male calf}}{\text{The average BW of female calf}}$$

$$BW_C = BW \times CF_{sex}$$

Where:

CF_{sex} = correction factor for sex

BW_C = corrected birth weight

BW = actual birth weight for female calf

Data of weaning and yearling weights were corrected to 205 days of age using the formula from Hardjosubroto (1994) as follows:

$$WW_{205} = \left(\frac{W - BW}{T} \times 205 \right) + BW_C$$

Where:

YW_{365} = corrected weaning weight at 365 days of age

WW_{205} = corrected weaning weight at 205 days of age

WW = actual weaning weight

W = actual weight at measured

BW = actual birth weight

BW_C = corrected birth weight

T = actual age at measured (days)

The average daily gain (ADG) was estimated using formula as follows:

$$ADG_1 = \frac{WW_{205} - BW_C}{T_1}$$

$$ADG_2 = \frac{YW_{365} - WW_{205}}{T_2}$$

Where:

ADG_1 = average daily gain of pre-weaning weight (kg/days)

ADG_2 = average daily gain of post-weaning weight (kg/days)

BW_C = corrected birth weight (kg)

WW_{205} = weaning weight at205 days of age (kg)

YW_{365} = yearling weight at 365 days of age (kg)

T_1 = actual age at measured or weaning age (days)

T_2 = period between weaning and yearling (days)

Data Analysis

Non-genetic factor. Data of BW, WW, YW and ADG were analyzed to determine the effect of

Table 1. The Nutritional Content of Feed for SO Cattle at the Breeding Station

Nutrient	Starter	Grower	Finisher
Dry matter (%)	89.10	89.26	88.65
Crude protein (%)	14.36	14.15	13.66
Crude fat (%)	4.80	4.79	4.56
Crude fiber (%)	12.08	12.50	12.83
Total digestible nutrient (%)	68.41	68.96	69.27
Metabolizable energy Mcal (%)	2.11	2.07	2.33
Starch (%)	32.09	36.55	40.31
Lignin (%)	3.31	3.39	4.02
Calcium (%)	1.66	1.63	1.52
Phospor (%)	0.56	0.58	0.40

sex, year, generation and season. Season of birth in the year were consisted of dry (April - September) and rainy (Oktober - March). The data were analyzed using General Linear Model (GLM) with formula according to Becker (1992) as follow:

$$Y_{ijkl} = \mu + s_i + t_j + g_k + m_l + e_{ijkl}$$

Where:

Y_{ijk} = observation of the BW, WW, YW and ADG

μ = common mean

s_i = effect of the i^{th} sex of calves (male and female

t_j = effect of the j^{th} years at birth (year 2011 to 2016)

g_k = effect of the k^{th} generations

m_l = effect of the l^{th} seasons (dry and rainy)

e_{ik} = experimental error

Genetic parameters. Genetic parameters of h^2 and r_g values were analyzed with a paternal hafshib correlation model. In the heritability model, sire was included as a random effect in the model which account for the genetic effect. The total variance and covariance components were sorted into additive and non-additive (environmental and residual genetic) with a mathematical model according to Becker (1992) as follows:

$$Y_{ik} = \mu + \alpha_i + e_{ik}$$

Where:

Y_{ik} = observation of the BW, WW, YW and ADG

μ = common mean

α_i = effect of the i^{th} sire

e_{ik} = experimental error

Heritability and genetic correlation were estimated based on Becker (1992) as follow:

$$h^2 = 4t$$

$$t = \frac{Var_s}{Var_s + Var_w}$$

$$SE\left(h^2\right) = 4\sqrt{\frac{2(1 - t)^2[1 + (k - 1)(t)]^2}{k(k - 1)(S - 1)}}$$

and

$$k = \frac{1}{S - 1}\left(N - \frac{\sum n_i^2}{N}\right)$$

Where:

h^2 = heritability

r_g = genetic correlation

Var_{rg} = variance of genetic correlation

Var_s = variance component of sire

Var_w = variance component of individu

h^2 = heritability

r_g = genetic correlation

Var_{rg} = variance of genetic correlation

Var_s = variance component of sire

Var_w = variance component of individu

Cov_s = covariance component of sire

SE (h^2) = standard error of heritability

SE (r_g) = standard error of genetic correlation

k = constanta

S = the number of sire

N = the number of progeny

n_i = the number of progeny per sire

RESULTS AND DISCUSSION

Effect of Sex

The average values of growth traits in male animals were higher than those in female animals, but it was not significantly different between the treatments (Table 2). Similar study reported that sex had no significant effect on BW and WW in several breeds cattle such as Friesian Holstein (Bakir e*t al.,* 2004), Fogera cross (Addisu *et al.,* 2010), Bali (Gunawan and Jakaria, 2011), Horro (Abera *et al.,* 2013), Baggara cross (Ibrahim *et al.,* 2015) and Friesian cross (Rahman *et al.,* 2015). In addition, sex had significant effect to BW, WW and YW in several breeds cattle such as Friesian Holstein (Aksakal and Bayram, 2009); Asturiana de los Valles (Goyache *et al.,* 2003), Ogaden (Getinet *et al.,* 2009), Simbra (Smith, 2010), Swedish Red and White (Aksakal *et al.,* 2012), Ongole grade (Hartati *et al.,* 2015), Sheko (Bayou *et al.,* 2015), Sistani (Bazzi, 2011), Brown Swiss (Tilki *et al.,* 2008), Brahman (Hemandez *et al.,* 2015) , Vrindavani (Sagar *et al.,* 2017), Gudali, Wakwa (Ndofor-Foleng *et al.,* 2011), Nellore (Lopes *et al.,* 2013), Mashona (Mangwiro *et al.,* 2013), Brahman (Hemandez *et al.,* 2015), Charolais and Horro (Abera *et al.,* 2013). Moreover, sex had significant effect to ADG in several breeds cattle such as Friesian Holstein (Abera *et al.,* 2013), Sheko (Bayou *et al.,* 2015), Charolais (El-Saied *et al.,* 2006) and Ogaden (Getinet *et al.,* 2009), but it was not significant in Red Chittagong (Tapasy *et al.,* 2009), Fogera (Addisu *et al.,* 2010) and Friesian cross (Rahman *et al.,* 2015). The mechanism of sex hormonal (androgen) can cause the growth rate in male animal that was faster and heavier than those in female animal (Soeparno, 2005).

Effect of Year

Year had significant effect on BW, WW_{205} and YW_{365} (Table 2). The average of WW_{205} value was increasing since year 2012 to 2016 and YW_{365} was increasing since 2013 to 2016. The average of WW at year 2016 was significantly higher than other years ($P<0.05$). Differences observed in the growth traits between years can be caused by the difference of feed availability between years due to variation in total precipitation and the distribution of rainfall in the breeding station. The significant effect of year could be attributed to variability in management and climate. The growth traits of cattle can be increased per year through selection program in several breeds cattle such as Brahman cross (Duma and Tanari, 2008), Northeastern Thai (Intaratham *et al.,* 2008), Bali (Supriyantono *et al.,* 2011) and Aceh cattle (Putra *et al.,* 2014).

Effect of Generation

The generation did not have significant effect on BW, WW and YW but had significant effect on pre-weaning daily gain (ADG_1) and post-weaning daily gain (ADG_2) as presented in Table 2. The average value of YW in the second generation was higher than first generation. Similar finding was reported by Hartati *et al.* (2015) that generation did not have significant effect on BW, WW and YW. The ADG_1 of second generation was higher than those of first generation ($P<0.05$) and it described that selection in the SO cattle in this study increased the ADG_1 of the second generation.

Effect of Season

The season did not have significant effect on BW and YW but had significant effect to WW (Table 2). Significant effect of season to WW were reported in several breeds cattle such as Bali (Gunawan and Jakaria, 2011), Sheko (Bayou *et al.,* 2015), Gudali and Wakwa (Ndofor-Foleng *et al.,* 2011). Despite, several study were reported that season did not have significant effect to WW in *Bos indicus* breeds cattle such as Fogera (Addisu *et al.,* 2010), Ongole grade (Hartati *et al.,* 2015), Brahman (Hernandez *et al.,* 2015) and

Table 2. Means and Standard Deviation for Growth traits in SO Cattle

Variable	BW$_C$ (n)	WW$_{205}$ (n)	YW$_{365}$ (n)	ADG$_1$ (n)	ADG$_2$ (n)
Sex					
Male	24.29±5.30 (50)	121.53±38.57 (50)	181.34±44.69 (43)	1.13±0.83^{a} (50)	0.78±0.71^{a} (43)
Female	21.89±5.18 (93)	105.25±29.61 (84)	157.92±34.93 (62)	0.73±0.38^{b} (84)	0.57±0.48^{b} (62)
Year					
2011	26.33±0.89^{ac} (12)	116.66±32.04^{acd} (8)	-	1.10±0.45 (16)	-
2012	29.64±4.29^{c} (14)	84.01±28.13^{ab} (6)	178.90±33.73^{a} (9)	1.54±1.46 (11)	-
2013	24.83±5.93^{a} (52)	98.86±15.83^{a} (27)	85.00±7.43^{b} (2)	0.85±0.28 (21)	-
2014	22.31±4.30^{ab} (45)	103.78±28.53^{a} (21)	136.20±22.92^{a} (3)	1.14±0.14 (2)	-
2015	24.57±4.65^{a} (14)	106.86±25.06^{ac} (36)	157.74±29.71^{a} (59)	0.90±0.43 (10)	-
2016	27.60±8.79^{ac} (6)	136.09±28.87^{d} (10)	157.46±36.45^{a} (5)	1.04±0.32 (6)	-
Generation					
1	24.75±5.40 (115)	107.69±33.57 (106)	165.05±40.82 (94)	0.78±0.41^{a} (94)	0.56±0.52^{a} (80)
2	23.31±4.89 (35)	97.30±29.54 (35)	188.70±36.25 (10)	0.99±1.30^{b} (30)	0.98±0.77^{b} (19)
Season					
Dry	26.51±5.36 (53)	110.32±26.19^{a} (58)	173.18±41.62 (82)	-	-
Rainy	23.38±4.93 (70)	107.19±40.47^{b} (59)	147.29±30.11 (23)	-	-
Total	22.73±5.33 (143)	111.33±34.02 (134)	167.51±40.70(105)	0.88±0.62 (134)	0.66±0.59 (105)

$^{a,b,c,d)}$different of letters in the same section within column shows significantly different ($P<0.05$); n = number of observation; BW$_C$ = corrected birth weight; WW$_{205}$ = weaning weight at 205 days of age; YW$_{365}$ = yearling weight at 365 days of age.

Table 3. The Variance Component for Heritablity Estimation of Growth Traits in SO Cattle

Growth Traits	NS	N$_{prog}$	k	Var$_S$	Var$_W$	h^2	SE
BW$_C$	7	127	17	8.55	43.59	0.66	0.42
WW$_{205}$	7	106	15	196.44	1009.77	0.65	0.44
YW$_{365}$	7	100	20	255.76	1263.78	0.67	0.42
ADG$_1$		113	15	0.11	0.57	0.68	0.45
ADG$_2$	7	101	20	0.18	0.85	0.70	0.43

N$_S$ = number of sire; N$_{prog}$ = number of progeny; k = constanta; Var$_S$ = variance component of sire; Var$_W$ = variance component of individu; h^2 = heritability; SE = standard error for heritability; BW$_C$ = corrected birt weight; WW$_{205}$ = weaning weight at 205 days of age; YW$_{365}$ = yearling weight at 365 days of age; ADG$_1$ = average daily gain of pre-weaning; ADG$_2$ = average daily gain of post-weaning.

Table 4. The Heritability (h^2) Values of Growth Traits in Several Breeds of Cattle

Breeds	*Group*	Research Area	Growth Traits				
			BW	WW	YW	ADG$_1$	ADG$_2$
Gudali[1]	*Bos indicus*	Cameroon	0.33	0.29	0.39	0.23	-
Wakwa[1]	*Bos indicus*	Cameroon	0.21	0.32	0.50	0.03	-
Nguni[2]	*Bos indicus*	South Africa	0.36	0.29	0.25	-	-
Madura[3]	*Bos indicus*	Indonesia	0.33±0.24	0.87±0.45	0.27±0.29	0.55±0.41	0.23±0.28
Ongole grade[4]	*Bos indicus*	Indonesia	0.28±0.12	0.47±0.15	0.63±0.17	-	-
Aceh[5]	*Bos indicus*	Indonesia	0.15±0.13	0.48±0.58	0.49±0.58	0.53±0.58	0.64±0.64
Bhagnari[6]	*Bos indicus*	Pakistan	0.09±0.02	0.09±0.01	-	0.01±0.01	-
Red Chittagong[7]	*Bos indicus*	Bangladesh	0.50±0.01	0.50±0.10	0.50±0.10	0.48±0.10	0.49±0.17
Brahman[8]	*Bos indicus*	Botswana	0.57±0.11	0.53±0.10	-	-	-
Horro[9]	*Bos indicus*	Ethiopia	0.62±0.04	0.40±0.05	-	0.20±0.05	-
Fogera[10]	*Bos indicus*	Ethiopia	0.06±0.02	0.08±0.03	-	0.06±0.03	-
Nellore[11]	*Bos indicus*	Brazil	0.37±0.02	0.33±0.01	0.36±0.01	0.28±0.02	0.31±0.01
Romosinuano[12]	*Bos indicus*	Colombia	0.25±0.00	0.34±0.06	-	0.32±0.06	0.17±0.05
Tswana[13]	*Bos taurus*	South Africa	0.45	0.37	0.39	0.34	0.31
Bonsmara[8]	*Bos taurus*	Botswana	0.36±0.08	0.69±0.08	-	-	-
Tuli[8]	*Bos taurus*	Botswana	0.21±0.11	0.36±0.12	-	-	-
Charolais[14]	*Bos taurus*	Spain	0.36±0.04	0.36±0.01	-	0.22±0.01	-
Brown Swiss[15]	*Bos taurus*	Mexico	0.19	0.27	0.34	-	-
Gelbvieh cross[16]	*Bos taurus*	Mexico	0.30±0.03	0.20±0.04	-	-	-
Fr. Holstein[17]	*Bos taurus*	Egypt	0.28±0.10	0.13±0.09	-	-	-
Limousin[18]	*Bos taurus*	South Africa	0.09±0.02	0.19±0.04	0.16±0.03	-	-
Hereford[19]	*Bos taurus*	South Africa	0.30	0.10	0.11	-	-
Simmental[20]	*Bos taurus*	Indonesia	0.11±0.09	0.39±0.16	0.43±0.19	-	0.46±0.20
Native Thai[21]	-	Thailand	0.40±0.08	0.27±0.06	-	-	-
Vrinda vani[22]	*B.tau x B. ind*	India	0.29	0.03	0.40	-	-
Bali[23]	*B. javanicus*	Indonesia	0.85±0.44	0.51±0.32	0.54±0.32	-	-

[1]Ebangi *et al.* (2002); [2]Norris *et al.* (2004); [3]Karnaen (2008); [4]Hartati *et al.* (2015); [5]Sari *et al.* (2016); [6]Waheed *et al.* (2003); [7]Afroz *et al.* (2011); [8]Rakwadi *et al.* (2014); [9]Abera *et al.*(2013); [10]Bekele *et al.* (2016); [11]Regatieri *et al.* (2012) and Araujo *et al.* (2014); [12]Sarmiento and Garcia (2007); [13]Raphaka (2008); [14]El-Saied *et al.* (2006); [15]Chin-Colli *et al.* (2016); [16]Marquez *et al.* (2004); [17]Atil *et al.* (2005); [18]Niekerk and Neser (2006); [19]Marle-Koste *et al.* (2000); [20]Suhada *et al.* (2009); [21]Intaratham *et al.* (2008); [22]Singh *et al.* (2010); [23]Kaswati *et al.* (2013). BW= birth weight; WW = weaning weight; YW= yearling weight; ADG$_1$= average daily gain of pre-weaning; ADG$_2$= average daily gain of post-weaning

crossbred cattle between *Bos indicus* and *Bos taurus* (Mostari *et al.,* 2017). In addition, Wijono *et al.* (2006) reported that season had significant effect to YW but did not have significant effect to WW in Ongole grade cattle. The average WW and YW of SO cattle in the dry season were higher than those in the rainy season and similar to Fogera (Addisu *et al.,* 2010), Bali (Gunawan and Jakaria, 2011) and Ongole grade (Hartati e*t al.,* 2015). Rainy season can increase the desease risk, especially diarrhea, bovine ephemeral fever (BEF), Helminthiasis and Myasis (Subronto, 2008).

Heritability

The estimation of heritability (h^2) values of growth traits in SO cattle were presented in Table 3. The h^2 value of BW in this study was in the high category. The h^2 value of BW, WW and YW in this study were more than 0.60 and it was similar to Horro, Bonsmara and Ongole grade (Table 4). The h^2 value of YW in SO cattle was 0.77±0.68 (Said *et al.,* 2016a) that was and higher than those in this study. Heritability value of 0.60 can be explained that more than 60% of variation in the growth traits of SO cattle in this study were affected by genetic. Differences results in this study compared to previous study was caused by differences of breeds, statistical analysis, selection pressure in the population, sample size (number of sire, dam and progeny) and environmental effect (Rabeya *et al.,* 2009). Low of h^2 value of growth traits in Fogera cattle (Table 4) could be explained that most of the variation in the population was affected by environmental factors. Goyache and Gutierrez (2001) reported that low h^2 value could be explained by 1) less number of animal for estimation, 2) the environmental factor is dominant to influence some traits, 3) the decrease of genetic variability coming from the culling policy, 5) failure to consider the influence of some other traits, 6) the use of fitted models that can not explain sufficiently the population structure. Moreover, low of h^2 value could be either due to deterioration in management resulting to poor nutritional status of the animals, or due to the use of the same sire for a number of years, which could decrease genetic variation (Ndofor-Foleng e*t al.,* 2012).

Low of h^2 value in the population was indicated that selection based on individual performance was not effective to increase gain of growth traits (Bekele e*t al., 2*016). The standrad error (SE) of h^2 was explained the accuracy of the estimation regarding to explain the additive genetic variation. The SE of h^2 values in this

Table 5. The covariance component for genetic correlations estimation among growth traits in SO cattle

Correlation Traits	N_S	$N_{prog.}$	N_i	Cov_S	Cov_W	r_g	SE
BW_C - WW_{205}	6	60	10	35.80	2.23	0.87	0.63
BW_C - YW_{365}	6	54	9	44.65	5.75	0.95	0.87
BW_C - ADG_1	6	60	10	1.03	-0.13	0.02	0.01
BW_C - ADG_2	6	54	9	0.45	-0.56	0.01	0.03
WW_{205} - YW_{365}	6	60	10	219.19	829.46	0.98	0.48
WW_{205} - ADG_2	6	54	9	8.36	1.53	0.18	0.10
ADG_1 - WW_{205}	6	60	10	4.81	16.40	0.99	0.34
ADG_1 - YW_{365}	6	60	10	5.29	16.24	0.95	0.51
ADG_2 - YW_{365}	6	60	10	5.41	1.94	0.98	1.02
ADG_1 - ADG_2	6	60	10	0.13	-0.07	0.02	0.01

N_S = number of sire; $N_{prog.}$ = number of progeny; N_i = number of progeny per sire; Cov_S = covariance component of sire; Cov_W = covariance component of individu; r_g = genetic correlation; SE = standard error for genetic correlation; BW_C = corrected birth weight; WW_{205} = weaning weight at 205 days of age; YW_{365} = yearling weight at 365 days of age; ADG_1 = average daily gain of pre-weaning weight; ADG_2 = average daily gain of post-weaning weight.

Table 6. The Genetic Correlations (r_g) among Growth Traits in Several Breeds Cattle

Breeds	Research Area	Genetic Correlations								
		BW - WW	BW - YW	BW - ADG_1	BW - ADG_2	WW - YW	WW - ADG_2	ADG_1 - WW	ADG_1 - YW	ADG_2 - YW
Bali[1]	Indonesia	-	0.72±0.03	-	-	-	-	0.27±0.06	0.86±0.02	-
Madura[2]	Indonesia	0.43±0.31	-	0.38±0.28	-	0.59±0.11	0.47±0.24	-	-	-
Simmental[3]	Indonesia	0.29±0.27	0.46±0.33	-	0.27±0.39	0.68±0.16	0.01±0.30	-	-	0.57±0.21
Aceh[4]	Indonesia	0.56±0.60	0.52±0.62	0.55±0.54	0.63±0.62	0.46±1.00	0.50±0.96	0.34±0.81	0.39±0.91	0.51±0.95
Limousin[5]	South Africa	0.41±0.15	0.37±0.10	-	-	0.99±0.03	-	-	-	-
Brangus[6]	South Africa	0.78±0.06	0.57±0.08	-	-	0.86±0.05	-	-	-	-
Nguni[7]	South Africa	0.53±0.04	0.51±0.05	-	-	0.95±0.03	-	-	-	-
Hereford[8]	South Africa	0.33	0.50	-	-	0.93	-	-	-	-
Tswana[9]	Botswana	0.44	-	0.29	0.16	-	0.28	0.97	-	-
Gudali[10]	Cameroon	0.53	0.39	-	-	0.88	-	-	-	-
Fogera[11]	Ethiopia	0.60±0.23	-	0.50±0.27	-	-	-	0.99±0.00	-	-
Canchim[12]	Brazil	0.42±0.07	0.41±0.07	-	-	-	-	-	-	-
Nellore[13]	Brazil	0.79	-	-	-	-	-	-	-	-
Red Chittagong[14]	Bangladesh	0.53	-	-	-	-	-	-	-	-
Hereford[15]	USA	-	-	-	-	0.47±0.05	-	-	-	-
Brown Swiss[16]	Mexico	0.51	0.44	-	-	0.84	-	-	-	-
Charolais[17]	Spain	-0.11	-	-0.16	-	-	-	-	-	-
Friesian Holstein[18]	Egypt	0.80±0.07	-	-	-	-	-	-	-	-
Vrindavani[19]	India	-0.06	-0.11	-	-	-	-	-	-	-

[1]Sukmasari *et al.* (2002); [2]Karnaen (2008); [3]Suhada *et al.* (2009); [4]Putra *et al.* (2014); [5]Niekerk and Neser (2006); [6]Neser *et al.* (2012); [7]Niekerk *et al.* (2004); [8]Marle-Koster *et al.* (2000); [9]Raphaka (2008); [10]Ndofor-Foleng *et al.* (2012); [11]Bekele *et al.* (2016); [12]Pires *et al.* (2016); [13]Kamei *et al.* (2017); [14]Rabeya *et al.* (2009); [15]Vazquez (2016); [16]Chin-Colli *et al.* (2016); [17]El-Saied (2006); [18]Atil *et al.* (2005); [19]Singh *et al.* (2010)

study were lower than h^2 values and indicating that the estimation was usable to measure the additive genetic contain in population (Putra *et al.,* 2014). In Addition, low SE value could be conducted to little number of animal available in estimation (Warwick *et al.,* 1990) included of sire, dam and progeny. High of h^2 values of growth traits in this study were indicated that selection of

Genetic Correlation

The estimation of genetic correlation (r_g) values among growth traits in SO cattle are presented in Table 5. Based on the Table 5, four r_g values of BW-ADG$_1$, BW-ADG$_2$, WW-ADG$_2$ and ADG$_1$-ADG$_2$ were included of low category. Previous study reported that low of r_g value were observed in correlation between BW-WW in Simmental, Charolais and Vrindavani as presented in Table 6. Therefore, the r_g value of BW-ADG$_2$ and WW-ADG$_2$ in Tswana and Simmental cattle were included of low category and similar to this study. Differences results in this study among previous study was conducted by differences of breeds, statistical analysis and number of animal for analysis. Low of r_g value between two different traits suggested that no linear association and if selection were carried out, there would be minor changes expected among them (Pires *et al.,* 2016). Positive and negative correlation in the Table 6 suggested that two different traits had positive or negative impact to another trait. The SE values in correlation of BW-ADG$_2$ and ADG$_2$-YW were higher than r_g values and indicated that the estimation was not accurate. The r_g value of WW-YW in this study was more than 0.90 and similar to Limousin and Nguni cattle (Table 6). Traits of WW and YW in this study had high positive correlation and suggested that WW could be used as selection criteria to increase YW gain of SO cattle. The WW trait could be used for individual selection and cow selection (Hardjosubroto, 1994). A calves with higher WW than average herd was described that their cow had good mathering ability.

CONCLUSION

The heritability estimation of growth traits in SO cattle were included of high category with low of standard error. The genetic correlation value between weaning and yearling weights showed high category with low of standard error. Practically, selection to increase yearling weight gain could be carried out through weaning weight selection.

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