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Crossbreeding strategy evaluation between Boer and local Indonesian goat based on pre-weaning traits

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Abstract The livestock industry in Indonesia is dominated by smallholder farmers. Crossbreeding between local and exotic breeds is a common practice by these farmers in order to improve productivity. This study is evaluated the crossbreeding strategy between Boer goat and Jawarandu goats by observing the pre-weaning traits. In total of 3,815 records were obtained from the kids born between 2012–2015. The recorded data of offspring from three mating scenarios: B×B (Boer and Boer), B×J (Boer and Jawarandu), and B×(B×J) (Boer bucks and B×J does) were investigated. The birth weight (BW), weaning weight (WW), and average daily gain (ADG) were analysed. For all traits, B×B kids were compared to the other sub-populations. Genetic parameters for each trait were estimated using univariate animal models and solved via average information restricted maximum likelihood (AI-REML) procedures. The heritability of BW were 0.38±0.12, 0.41±0.0 and 0.12±0.07, respectively, and weaning weights were 0.12±0.07, 0.24±0.07 and 0.08±0.06, respectively. The heritability for ADG were 0.13±0.07, 0.14±0.05, and 0.06±0.05 for B×B, B×J, and B×(B×J) sub-populations, respectively. Genetic correlations among pre-weaning traits were generally high (>70%), while the phenotypic correlations were low to moderate. A crossbreeding system in which the two parental breeds were maximally differed as the best scenario. It produced higher additive genetic variability, corresponding to the higher chance of improvement through between-breed selection on pre-weaning traits.

Keywords: Boer goat, Crossbreeding, Genetic parameters, Goat, Pre-weaning

Introduction

Goat is among the meat-producer species with good adaptability to tropical environments and limited quality feed resources. A type of local Indonesian goat with a high population is the Jawarandu, which is widespread in the archipelago but concentrated in the island of Java (Astuti *et al.,* 2007). Local goats are typically robust and highly resistant to tropical diseases, but their productivity is considerably low (Ørskov, 2011). Jawarandu goats result from uncontrolled mating between Etawah bucks and the indigenous Kacang

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does; however, information regarding their exact genetic background remains unknown. This breed is often subjected to crossbreeding to improve production performance (Elieser *et al.,* 2012). Crossbreeding of cattle has been vastly implemented in Indonesia since the 1980s and proved by Agus and Widi (2018) to successfully increase meat production. However, goat breeding practice, in general, is not under well-designed programs or any form of government initiatives; hence, less can be done to assess the achieved improvements.

Reports on the genetic parameters of local Indonesian goats, including Jawarandu, are minimal. This type of local goat is commonly reared by smallholder farmers in rural areas with very little awareness of the importance of livestock records (Elieser *et al.,* 2012; Ørskov, 2011). In local goat farming, pre-weaning traits are economically important (Barazandeh *et al.,* 2012) as they indicated the survival rate, growth potentials, and the profitability of meat farmers (Zhang *et al.,* 2009). Among the very few available information, a study on pre-weaning traits of Jawarandu reported that the mean birth weight and weaning weight (standardized for 120 days) were 2.36±0.98 kg, and 10.56±1.78 kg, respectively (Sulastri *et al.,* 2012). The same study employed a half-sib family design and obtained estimated heritability for birth and weaning weight of 0.14±0.07 and 0.22±0.08, respectively.

Boer goats are excellent in the meat production sense; they have high productivity, meat quality, and fertility (Schoeman *et al.,* 1997; Zhang *et al.,* 2008, 2009). Studies on the genetic parameters of Boer goat revealed that the direct heritability for birth weight was around 0.33–0.36 (Schoeman *et al.,* 1997) and 0.30±0.06 (Zhang *et al.,* 2009). For weaning weight at 90 days, the heritability values were 0.23±0.06 (Zhang *et al.,* 2009) and 0.27–0.60 (Schoeman *et al.,* 1997). These values suggested that genetic improvement of pre-weaning traits through the utilization of this breed's superiority is plausible.

The major benefit of crossbreeding is maximized the combination of the superior characteristics possessed by each parental breed (Falconer and Mackay, 1996). Breeders commonly practiced between-breed selection based on the desired traits to optimally utilize the breed differences and gained rapid genetic improvement (Bourdon, 2014). In order to conduct an efficient selection procedure, information about the genetic parameters of the traits of interest is needed to consider; thus, accurate estimation of genetic parameters will determine the effectivity of the breeding program (Falconer and Mackay, 1996; Lynch and Walsh, 1998; Zhang *et al.,* 2009). This study aimed to estimate the optimum strategy for crossbreeding by utilizing the benefit of between-breed selection properties. The genetic parameters of pre-weaning traits in three different sub-populations are purebred Boer goats, crossbred between Boer bucks and local Jawarandu. The crossbred between Boer bucks

and Boer × Jawarandu does were used as indicators. This information shall benefit the goat breeders and farmers in determining the most optimum selection and crossbreeding scenario.

Materials and methods

Data collection

Records were obtained from a private experimental farm of CV. Kambing Burja, Batu, Malang, East Java, Indonesia (7°50'00.9"S 112°33'52.3"E). The farm is located at 950 meters above sea level with precipitation of 139.17 mm/year and in averaged of 12 days of rain per month. The local weather station reported that the average temperature ranging from minimum of 24.16°C to a maximum of 26.60°C. The relative humidity was between 80-85%.

In total of 3,815 individual records were observed from the kids born between 2012 and 2015. The experimental population contained the offspring from three distinct mating scenarios, which were B×B (Boer bucks and Boer does; 463 records), B×J (Boer bucks and *Jawarandu* does; 2,169 records), and B×(B×J) (Boer bucks with B×J does; 1,183 records). Twenty-six Boer bucks and 107 Boer does which imported from Australia were used as the exotic breeding stock, whereas *Jawarandu* does were obtained from local breeding farms and livestock markets. The B×J does in this study were originated from the previous crossbreeding experiment on the same farm. The experiment started when the goats were roughly 8–10 months old, and the goats mated after they reached 12 months.

The mating system was designed to avoid inbreeding. Goats were kept under an intensive management system while the feed and water were given *ad libitum*. Does were housed in mix-breed colonies with 20–25 individuals per colony (pen). The mating period was planned to occur three times a year. Within each mating period, one male entered a female colony for 45 days. After the mating period, pregnant does were then shifted into separated pens, the does were allotted for the next mating period. Newborn kids were identified, and their pedigrees were recorded carefully. Birth weight prior to 24 hours (BW), weaning weight at 77 days (WW), and averaged daily gain (ADG) in kilogram were recorded as pre-weaning traits of interests.

Data analysis

Prior to analysis, the phenotype data were filtered to include individuals with complete information. Preliminary analysis was conducted by building a general linear model, including the effects of sex, birth year, dam age, and litter size. The model was fitted for all response variables with $\alpha = 0.05$. Factors were proven to significantly affect the response variables which used in the mixed model equation. The data were split into three sub-populations based on the following mating scenarios: B×B, B×J, and B×(B×J). The experimental population structure is presented in Table 1. Further data analyses were conducted separately for each sub-population.

Table 1. Number of records in different sub-populations (heads)

Observed Variables	Sub-populations		
	B×B	**B×J**	**B×(B×J)**
Bucks	12	22	24
Does	107	687	495
Offspring	461	2,169	1,183
Kids' sex			
Male	238	1,084	573
Female	225	1,085	610
Birth year			
2012	34	615	38
2013	123	750	218
2014	201	641	490
2015	105	163	437
Litter size (%)			
1	128 (27.65)	790 (36.42)	520 (43.96)
2	328 (70.84)	1328 (61.23)	653 (55.20)
3	7 (1.51)	51 (2.35)	10 (0.84)

Variance components were estimated according to the following basic univariate animal model and named as equation 1:

$$\mathbf{y = Xb + Za + e} \quad [1]$$

where **y** is a vector of phenotypic data, **b** is a vector of systematic effects that accounted for the effects of birth year, sex, and litter size. **X** is the incidence matrix corresponding to the fixed effects. **Z** is a matrix corresponding to the random additive genetic effect (**a**), with the (co)variance matrix being the additive genetic relationship matrix (**A**), where $\boldsymbol{a}|\boldsymbol{A}, \sigma_a^2 \sim MVN(0, \boldsymbol{A}\sigma_a^2)$. The random residual vector is **e**, with $\boldsymbol{e}|\boldsymbol{I}, \sigma_e^2 \sim MVN(0, \boldsymbol{I}\sigma_e^2)$.

The next model to estimate the genetic parameters was bivariate animal model (equation 2). We obtained both phenotypic and genotypic correlations using the bivariate approach, as we analyzed two traits at a time.

$$\begin{bmatrix} \boldsymbol{y_1} \\ \boldsymbol{y_2} \end{bmatrix} = \begin{bmatrix} \boldsymbol{X_1} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{X_2} \end{bmatrix} \begin{bmatrix} \boldsymbol{b_1} \\ \boldsymbol{b_2} \end{bmatrix} + \begin{bmatrix} \boldsymbol{Z_1} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{Z_2} \end{bmatrix} \begin{bmatrix} \boldsymbol{a_1} \\ \boldsymbol{a_2} \end{bmatrix} + \begin{bmatrix} \boldsymbol{I_1} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{I_2} \end{bmatrix} \begin{bmatrix} \boldsymbol{e_1} \\ \boldsymbol{e_2} \end{bmatrix} \quad [2]$$

where $\mathbf{y_1}$ and $\mathbf{y_2}$ are the vectors of trait 1 and trait 2, respectively. $\mathbf{X_1}$ and $\mathbf{X_2}$ are the incidence matrices related to the fixed effects of each trait, whereas $\mathbf{b_1}$ and $\mathbf{b_2}$ are the vectors of fixed effects (sex, birth year, and litter size). $\mathbf{Z_1}$ and $\mathbf{Z_2}$ are the incidence matrices corresponding to additive genetic effects $\mathbf{a_1}$ and $\mathbf{a_2}$ for

$$\begin{bmatrix} \boldsymbol{a_1} \\ \boldsymbol{a_2} \end{bmatrix} \sim \boldsymbol{N}\left(\begin{bmatrix} \boldsymbol{0} \\ \boldsymbol{0} \end{bmatrix}, \begin{bmatrix} \boldsymbol{\sigma^2_{a1}} & \boldsymbol{\sigma_{a12}} \\ \boldsymbol{\sigma_{a21}} & \boldsymbol{\sigma^2_{a2}} \end{bmatrix} \otimes \boldsymbol{A} \right)$$

where $\mathbf{A}$ is the additive genetic relationship matrix. Random residuals are represented as $\mathbf{e_1}$ and $\mathbf{e_2}$ for traits one and two, respectively, for

$$\begin{bmatrix} \boldsymbol{e_1} \\ \boldsymbol{e_2} \end{bmatrix} \sim \boldsymbol{N}\left(\begin{bmatrix} \boldsymbol{0} \\ \boldsymbol{0} \end{bmatrix}, \begin{bmatrix} \boldsymbol{\sigma^2_{e1}} & \boldsymbol{\sigma_{e12}} \\ \boldsymbol{\sigma_{e21}} & \boldsymbol{\sigma^2_{e2}} \end{bmatrix} \otimes \boldsymbol{I} \right)$$

where $\mathbf{I}$ is an identity matrix.

The univariate animal model in equation 1 and bivariate animal model in equation 2 were solved using the restricted maximum likelihood (REML) approach in the *breedR* package (Munoz and Sanchez, 2018) and custom script in R programming language (R Core Team, 2020). Direct additive heritability values were obtained as the proportion of additive genetic variance (σ_a^2) relative to the total variance ($\sigma_p^2 = \sigma_a^2 + \sigma_e^2$); hence, $h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_e^2)$. Genetic and phenotypic correlations were defined as $r_p = r_g\sqrt{h_1^2\, h_2^2} + r_e\sqrt{(1-h_1^2)(1-h_2^2)}$ (Roff, 1995).

Results

Preliminary analysis, a general linear model was constructed to discover the potential non-genetic factors. It resulted in three systematic, fixed effects that significantly affected these traits: sex, litter size, and birth year (results not shown). Hence, these factors were included in the mixed model equation for estimating the genetic parameters. The dam age factor was analyzed and found to be non-significantly affected on the pre-weaning traits in this study.

The another linear model with sub-population as the systematic fixed effect was built to obtain the least square means and standard deviations of BW, WW, and ADG, as summary statistics in Table 2. We observed that BW significantly differed ($P<0.05$) in all three sub-populations with B×B showing the highest, and followed by B×(B×J) then B×J. Whereas WW and ADG, the values in the B×B sub-population were significantly higher than both crossbred sub-populations.

Table 2. Summary statistics of the pre-weaning traits

Traits	Breed	N	Mean ± sd*	Median	Minimum	Maximum
Birth weight (kg)	B×B	461	3.197±0.605[a]	3.000	1.500	5.500
	B×J	2164	2.835±0.580[c]	3.000	1.500	5.500
	B×(B×J)	1179	3.003±0.618[b]	3.000	1.500	5.000
Weaning weight (kg)	B×B	461	15.069±3.652[a]	14.933	8.000	27.397
	B×J	2164	13.488±3.666[b]	13.151	5.490	26.111
	B×(B×J)	1179	13.518±3.942[b]	13.333	5.063	28.000
Average daily gain (kg)	B×B	463	0.154±0.046[a]	0.154	0.058	0.297
	B×J	2169	0.138±0.045[b]	0.135	0.032	0.287
	B×(B×J)	1183	0.137±0.049[b]	0.134	0.016	0.318

*sd = standard deviation; [a, b, c] values followed with different superscripts showed significant difference (α=0.05)

Genetic parameter estimated for BW, WW, and ADG for all three sub-populations are presented in Table 3. The results from both univariate and bivariate animal models showed similar estimates and trends for all parameters as well as the corresponding standard errors across the observed pre-weaning traits and sub-populations.

Table 3. Variance components of the pre-weaning traits

Traits	Breed	Variance ± se*			h^{2**}
		σ_a^2	σ_e^2	σ_p^2	
Univariate model					
Birth weight (kg)	B×B	0.111±0.046	0.214±0.035	0.325±0.081	0.337±0.127
	B×J	0.102±0.019	0.147±0.014	0.249±0.033	0.408±0.066
	B×(B×J)	0.034±0.020	0.241±0.019	0.275±0.039	0.121±0.072
Weaning weight (kg)	B×B	1.379±0.831	9.807±0.927	11.186±1.758	0.122±0.073
	B×J	2.754±0.788	8.536±0.692	11.290±1.480	0.242±0.065
	B×(B×J)	1.068±0.779	11.934±0.804	13.002±1.583	0.081±0.059
Average daily gain (kg)	B×B	$2.48e^{-4}$±$1.38e^{-4}$	$1.61e^{-3}$±$1.52e^{-4}$	$1.86e^{-3}$±$2.90e^{-4}$	0.132±0.072
	B×J	$2.61e^{-4}$±$1.08e^{-4}$	$1.55e^{-3}$±$9.44e^{-5}$	$1.81e^{-3}$±$2.02e^{-4}$	0.142±0.057
	B×(B×J)	$1.13e^{-4}$±$1.10e^{-4}$	$1.99e^{-3}$±$1.23e^{-4}$	$2.11e^{-3}$±$2.33e^{-4}$	0.061±0.051
Bivariate model					
Birth weight (kg)	B×B	0.111±0.045	0.214±0.035	0.325±0.080	0.338±0.125
	B×J	0.108±0.019	0.144±0.013	0.252±0.032	0.426±0.064
	B×(B×J)	0.041±0.020	0.235±0.019	0.276±0.039	0.149±0.072
Weaning weight (kg)	B×B	1.398±0.618	9.794±0.933	11.192±1.551	0.125±0.074
	B×J	2.768±0.690	8.530±1.129	11.298±1.819	0.244±0.057
	B×(B×J)	1.139±0.786	11.882±1.608	13.021±2.394	0.087±0.059
Average daily gain (kg)	B×B	$2.49e^{-4}$±$1.36e^{-4}$	$1.61e^{-3}$±$1.52e^{-4}$	$1.86e^{-3}$±$1.44e^{-4}$	0.134±0.072
	B×J	$3.5e^{-4}$±$9.80e^{-5}$	$1.47e^{-3}$±$8.48e^{-5}$	$1.82e^{-3}$±$1.83e^{-4}$	0.203±0.053
	B×(B×J)	$1.63e^{-4}$±$1.11e^{-5}$	$1.96e^{-3}$±$1.25e^{-4}$	$1.98e^{-3}$±$1.26e^{-4}$	0.076±0.054

*se = standard error; **h^2 = heritability; σ_a^2 = additive genetic variance; σ_e^2 = residual variance; σ_p^2 = phenotypic variance.

The pairwise phenotypic and genetic (±se) correlation among pre-weaning traits was also calculated and is presented in Table 4. The phenotypic correlations between BB and BW were moderate in all three sub-populations and ranged between 0.25 – 0.34. Phenotypic correlations between BW and ADG were considerably low.

Table 4. Phenotypic (above diagonal) and genetic (below diagonal) correlations and standard errors of the pre-weaning traits

Breed		BW	WW	ADG
B×B	BW	-	0.250±0.045	0.087±0.046
	WW	0.124±0.031	-	0.986±0.007
	ADG	-	0.964±0.036	-
B×J	BW	-	0.318±0.02	0.167±0.021
	WW	0.837±0.030	-	0.987±0.003
	ADG	0.763±0.001	0.698±0.010	-
B×(B×J)	BW	-	0.336±0.027	0.187±0.028
	WW	0.721±0.016	-	0.988±0.004
	ADG	0.617±0.005	0.980±0.005	-

BW = Birth weight; WW = weaning weight; ADG = Average Daily Gain

Discussion

In order to remove non-genetic factors that affected pre-weaning traits, the current study used does of approximately the same age at the beginning of the experiment, and they were used only for one to a maximum of three parities. As a result of the preliminary analysis, we were unable to conclude any significant effect of dam age on the pre-weaning traits. It supported the fact that the built linear model is corrected for the litter size effect, which to some extent, might be confounded by the effect of dam age. Other considered factors affecting pre-weaning traits were also analyzed for their effect on pre-weaning traits. A subset of the experimental data has been published in analyzing the environmental factor affecting BW and WW in the Boer goat crossbreeding population (Nugroho *et al.,* 2018).

Boer goats produced offspring with BWs of approximately 3.2±0.13 (Browning Jr. and Leite-Browning, 2011), 3.5±0.48 (Schoeman *et al.,* 1997), and 3.6±0.54 kg (Zhang *et al.,* 2008); these were comparable to the result of this study, which was 3.197±0.605 kg. Birth weight values of offspring from crossbreeding between Boer goat × Spanish goat were reported to be 2.79±0.05 (Rhone *et al.,* 2013), 3.38±0.13 kg, and 3.34±0.13 kg for crossbred kids between Boer and Kiko goat (Browning Jr. and Leite-Browning, 2011);

whereas the BW of our B×J kids was 2.835±0.580 kg (Table 2). Our study also included the B×(B×J) cross for which BW was 3.003±0.618 kg.

The weaning weight of B×B kids in this study was 15.069±3.652 kg, within the range of previous studies, which were 13.50±0.62 (Browning Jr. and Leite-Browning, 2011), and varied between 13.0±0.14 to 16.5±0.23 kg (Zhang *et al.,* 2009). The WW of B×J crossbred in our study was 13.488±3.666 kg while B×(B×J) crossbred was 13.518±3.942 kg. Reports from the preceding crossbreeding experiments showed that weaning weight for Boer × Spanish goat were 15.20±0.34 kg (Rhone *et al.,* 2013) and 14.19± 0.60 while for Boer × Kiko goat was 16.10±0.61 kg (Browning Jr. and Leite-Browning, 2011). Our crossbred goats had lower body weights at WW compared with the references since Jawarandu goats (the doe's breed) were considered a smaller goat breed with a WW of 10.56±1.78 kg at 120 days of age (Sulastri *et al.,* 2012).

Average daily gain until weaning in Boer goats was reported to be 0.16±0.004 kg (Schoeman *et al.,* 1997) and 0.17±0.006 kg (Browning Jr. and Leite-Browning, 2011). These values are similar to our B×B result of 0.154±0.046 kg. ADG of B×J and B×(B×J) were 0.138±0.045 and 0.137±0.049 kg respectively while the ADG until weaning of Boer × Spanish goat was 0.12±0.006 and Boer × Kiko goat was 0.14±0.006 kg (Browning Jr. and Leite-Browning, 2011).

Heritability values were highest in the B×J sub-population for BW, WW, and ADG, while the B×(B×J) sub-population had the lowest. These results were consistent in both univariate and bivariate models. The B×J sub-population was resulted to crossbreeding between Boer Bucks and Jawarandu does. Crossbreeding between two genetically distanced breeds lead to the emergence of the highest genetic variance (Bourdon, 2014; Nietlisbach and Hadfield, 2015). Contrastingly, the backcross offspring, with 75% of the sire's breed [as in B×(B×J)], are not genetically diversed as the half-breed (Bourdon, 2014). It is common knowledge that quantitative traits are under the influence of a large number of genes. Crossbreeding with more complex structures caused additional complexity to the genetic interactions system due to linkage and epistasis, thus reducing the genetic variance due to additive effects (Hospital, 2005), ultimately yield to be a lower heritability value.

The genetic correlation between BW and WW in the B×B sub-population was low. We were also unable to estimate the genetic correlation between BW and ADG in the B×B sub-population due to the nature of the dataset. There was a lack of information on covariance components between BW and ADG traits, as also seen in the very low phenotypic correlation value between these traits in the respective sub-populations. In B×J and B×(B×J), however, the genetic correlation for BW and WW were high (0.837 and 0.721, respectively),

whereas the genetic correlation for BW and ADG were 0.763 and 0.617, respectively. Both phenotypic and genetic correlations for WW and ADG were close to one. The results suggested that in B×J and B×(B×J), selection for BW might subsequently improve the offspring's WW and ADG, which are essential for growth and production traits in meat-type goats.

Reports on Boer goat birth weight heritability was estimated using the direct animal model were 0.327 – 0.357 (Schoeman *et al.,* 1997) and 0.30±0.05 (Zhang *et al.,* 2009). Heritability of birth weight was estimated to be 0.32±0.05 in Raini Cashmere goats (Barazandeh *et al.,* 2012), 0.39±0.06 in Draa goats (Boujenane and Hazzab, 2008), 0.30 in Emirati goats (Al-Shorepy *et al.,* 2002), 0.50±0.05 in African dwarf goats (Bosso *et al.,* 2007), and 0.39±0.06 in Djallonke goats (Bosso *et al.,* 2007). The results of BW heritability in our study were ranged the aforementioned references which they were 0.3378±0.127, 0.408±0.066, and 0.121±0.072 for B×B, B×J, and B×(B×J) sub-populations, respectively. The additive heritability of BW in B×B and B×J can be considered moderate. It suggested that 33–40% of the total variance in BW was due to additive genetic factors (σ_a^2) inherited directly from the parents. Breeders often practiced between-breed selection to optimally utilize breed differences and gained rapid genetic improvement in crossbreeding programs (Bourdon, 2014). Thus, selection for birth weight in Boer and Jawarandu goats as parental breeds has given the potential to improve their offspring, both in pure Boer goats and in B×J crossbred sub-populations. It would be given less efficient to conduct a selection program for BW of B×J does to obtain B×(B×J) sub-populations, as the heritability was low and less improvement can be expected.

Heritability estimates for WW in this study were 0.122±0.073, 0.242±0.073, and 0.081±0.059 for B×B, B×J, and B×(B×J) sub-populations, respectively (Table 3). These values were lower for the 90-day weaning weight heritability of Boer goats, which were 0.27 (Schoeman *et al.,* 1997) and 0.23±0.06 (Zhang *et al.,* 2009). Weaning weight (90 days) heritability was also reported in some other goat breeds: 0.15±0.06 in Raini Cashmere goats (Barazandeh *et al.,* 2012), 0.19±0.06 in Draa goats (Boujenane and Hazzab, 2008), 0.42 in Emirati goats (Al-Shorepy *et al.,* 2002), 0.43±0.07 in African dwarf goats, and 0.54±0.08 in Djallonke goats (Bosso *et al.,* 2007). The kids in our study were weaned early, at 77 days of age; thus, environmental factors may consider the larger effects on the change in management and feeding system. During this period, kids had shifted between having milk as the primary nutritional resource to fiber and starch-rich diet but poor in fat and simpler carbohydrates (Bas *et al.,* 1991; Nagpal *et al.,* 1995). Kids can be weaned at three to four weeks of age. However, it was compared to those weaned normally, abruptly early-weaned kids experienced severe weaning shock and

decreased body weight at a later age (Louca *et al.,* 1975; Lu and Potchoiba, 1988; Nagpal *et al.,* 1995; Palma and Galina, 1995).

Earlier studies on Boer goats showed that the heritability of ADG until weaned was 0.257 (Schoeman *et al.,* 1997) and 0.22±0.05 (Zhang *et al.,* 2009). In Raini Cashmere goats, ADG heritability was 0.17±0.05 (Barazandeh *et al.,* 2012), while in Emirati goats, the value varied between 0.18 and 0.42 (Al-Shorepy *et al.,* 2002). These heritability values were obtained when the kids were weaned at 90 days of age. Pre-weaning ADG is an important growth indicator in kids. The heritability values for ADG in this study were 0.132±0.072, 0.142±0.057, and 0.061±0.051 for B×B, B×J, and B×(B×J), respectively which lower than the previous studies. These values were closely followed the pattern for heritability of WW which ADG and WW were highly correlated both phenotypically and genetically. Early weaning practice in our study might be caused the low heritability in ADG traits, and explained as in the WW section. The weaning practice belongs to the farm management system, special considerations regarding cost and the kid's further growth need to be underlined. The best practice of weaning at 90 days could be applied.

According to the results, it is evident that Boer goats have the potential to be utilized as a male genetic resource for improving the performance of local goats as meat producers. The application of a crossbreeding system in which the two parental breeds came from distinct populations were proven to be the best scenario. However, the optimum balance of the obtained improvements among the traits of interests must be maintained, as too high a BW might cause reproductive problems for the does. Conducting a more comprehensive selection on multiple traits by considering both production and reproduction traits and farm management practice might be appropriated. These estimates serve as the starting point for further research to develop future selection and crossbreeding programs.

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