



## Genetic and non-genetic parameter estimates for growth traits and Kleiber ratios in Dorper × indigenous sheep



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### ABSTRACT

Genetic improvement programme will only be successful when accompanied by a good understanding of the influence of different environmental factors, knowledge of the genetic parameters and the genetic relationships between the traits of interest. This study aimed to evaluate the influence of non-genetic factors on growth traits and Kleiber ratios and to estimate genetic parameters for early growth traits in Dorper × indigenous crossbred sheep. The effects of fixed factors were analysed by the general linear model procedure of statistical analysis system, while the genetic parameters were estimated using a WOMBAT computer program fitted animal model. The overall least-square mean for birth weight (**BRW**), weaning weight (**3MW**), six-month weight, nine-month weight, and yearling weight were  $3.03 \pm 0.02$ ,  $14.5 \pm 0.18$ ,  $20.4 \pm 0.26$ ,  $24.8 \pm 0.31$ , and  $28.3 \pm 0.40$  kg, respectively. The overall least-square mean for Kleiber ratio from birth to weaning (**KR1**), weaning to six months, six to nine months and nine months to yearling age were  $16.8 \pm 0.10$ ,  $6.41 \pm 0.17$ ,  $4.55 \pm 0.21$  and  $3.38 \pm 0.20$  g/kg of metabolic weight, respectively. The inclusion of maternal genetic effect had a significant influence on BRW, and it explains 20% of the phenotypic variation. The total heritability estimates for BRW, 3MW, birth to weaning average daily weight gain and KR1 were 0.10, 0.14, 0.16 and 0.12, respectively. The phenotypic correlation varied from  $-0.11 \pm 0.05$  to  $0.98 \pm 0.02$ , whereas the direct genetic correlation ranged from  $-0.32 \pm 0.40$  to  $0.98 \pm 0.17$ . The mean inbreeding coefficient was 0.105% with an annual rate of 0.02%. The heritability estimates for growth traits and Kleiber ratio suggest that slow genetic progress would be expected from the selection. However, the integration of selection with crossbreeding programme can enhance genetic gain. Therefore, selection should be conducted based on breeding values estimated from multiple information sources to increase the selection response.

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### Implications

Integration of crossbreeding with selection is vital to increase the rate of genetic progress through efficient use of both the additive and non-additive genetic effects. To do so, estimation of genetic parameters and identification of systematic factors for trait of interest are essential. In this study, the genetic progress was evaluated; the heritability, inbreeding level and genetic correlation among early growth traits were estimated. These results may assist the genetic improvement programme through selection. Besides, knowledge of the genetic trend and inbreeding level in the flock

enable the breeders to make the right intervention and to improve the genetic progress.

### Introduction

Sheep farming is a major part of Ethiopia's livestock sector and plays a significant role in ensuring food security due to its higher reproductive rate and low initial capital requirements (Tibbo, 2006). There are around nine sheep breeds (Gizaw et al., 2008) and 31.30 million heads of sheep (CSA, 2018). However, the productivity of indigenous sheep breeds in Ethiopia is not adequate to meet the rapidly growing population's red-meat demand (Getachew et al., 2016). Thus, it has been suggested that sheep productivity be increased by crossing indigenous sheep with more

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productive genotypes. Accordingly, the Romney, Corriedale, Hampshire, Rambouillet, and Awassi sheep breeds have been imported to Ethiopia in various years since 1944 (Getachew et al., 2016). However, the contribution of these breeds except Awassi sheep was negligible (Tesema and Shenkute, 2019).

The Ethiopian Sheep and Goat Productivity Improvement Program (ESGPIP) was launched in 2007 to improve meat production by crossbreeding indigenous ewes with Dorper sire. The ESGPIP has followed two breeding strategies: nucleus breeding and crossbreeding. The nucleus breeding programme focuses on multiplying imported Dorper sheep, and the crossbreeding programme focuses on producing crossbreds by crossing imported Dorper sheep with indigenous sheep breeds (Menz, Tumele, Afar, Black head Ogaden, and Doyogena sheep). To realise this breeding programme, two nucleus farms and ten breeding, evaluation, and distribution (BED) sites have been established. One of the BED sites has been established as Sirinka Agricultural Research Center to cross the indigenous Tumele sheep ewes with Dorper sires. Since 2012, Sirinka Agricultural Research Center has been disseminating Dorper × Tumele (50% Dorper level) crossbred rams to sheep producers of the area to improve meat production through crossbreeding.

Live weight and growth rate are economically important traits, requiring particular attention in any breeding programme intended to improve meat production. Besides growth, the selection of sheep for feed utilisation is a better strategy to increase the efficiency of meat production (Faid-Allah et al., 2016). Direct selection for this trait is difficult, particularly in the tropics, due to the absence of feed intake data for individual animals. However, the use of Kleiber ratio as an indicator of feed efficiency has been reported in literature (Arthur et al., 2001; Faid-Allah et al., 2016; Ghafouri-Kesbi and Gholizadeh, 2017; Mokhtari et al., 2019).

Integration of crossbreeding programme with selective breeding is imperative to enhance genetic gain and reduce the declining performance of crossbreds in subsequent generations (Gizaw et al., 2012). Growth traits and Kleiber ratio are under the influence of genetic and non-genetic factors (Farokhad et al., 2010). The phenotypic expression of these traits in the progeny is affected by direct additive genetic effect and maternal genetic effect or the ability of the dam to provide optimum nurturing conditions (Tesema et al., 2020a; Behrem, 2021). Thus, considering both direct and maternal effects in selection programme could maximise the genetic gain particularly when the direct-maternal genetic correlation is negative (Meyer, 1997). The design of such type of combined genetic improvement programme will only be successful when accompanied by a good understanding of the influence of different environmental factors, knowledge of the genetic parameters, and the genetic relationships between the traits of interest. Genetic parameters for various sheep breeds including Dorper and their crosses were estimated by several scholars (Inyangala et al., 1992; Kiriro, 1994; Farokhad et al., 2010; Kariuki et al., 2010; Mohammadi et al., 2010; Ghafouri-Kesbi et al., 2011; Prakash et al., 2012; Khorsand et al., 2014; Mandal et al., 2015; Faid-Allah et al., 2016; Areb et al., 2021). However, the genetic parameter estimates of a trait are under the influence of population, time, and environment. Therefore, the objectives of this study were to evaluate the influence of non-genetic factors on growth traits and Kleiber ratios and to estimate genetic parameters for early growth traits and Kleiber ratio in Dorper × indigenous crossbred sheep.

## Material and methods

### Location

The study was conducted at the sheep and goat farm of Sirinka Agricultural Research Center which is located 508 km northeastern

of Addis Ababa (11°45'00"N latitude and 39°36'36"E longitude) at an altitude of 1850 m.a.s.l. The mean annual rainfall amount of the area is on average about 950 mm. The area is a moderately warm temperature zone with a mean daily temperature ranges from 13.7 to 26.4 °C.

### Flock management

Flocks were reared under semi-intensive management, i.e. graze from 0900 to 1100 hrs in the morning and 1400 to 1600 hrs in the afternoon and supplemented with 0.1 to 0.4 kg of commercial concentrate composed of *Noug* cake, wheat bran and salt based on their age and physiology when returned from grazing. Besides suckling, lambs were supplemented with 0.10 kg concentrate feed per day until weaning (90 days). Both weaned male and female lambs were supplemented with 0.20 kg day<sup>-1</sup> animal<sup>-1</sup> concentrate mix once in the afternoon. During the late gestation and early lactation period, 0.40 kg of concentrate mixture was provided per day per animal in the evening after grazing/browsing. All animals had access to water three times a day. Sheep greater than six months of age were vaccinated against Anthrax, Sheep and Goat pox, and Pestis Des Petites Ruminants diseases. In addition, animals were treated regularly for internal and external parasites at the beginning and end of the rainy season (Tesema et al., 2020b).

Tumele sheep are indigenous to the study area, and ewes required to form the foundation flock at the Sirinka Agricultural Research Center's BED site were purchased from nearby local markets at the start of the study. The pure Dorper sires needed to begin the crossbreeding programme were acquired from the nucleus farms (Fafen, Worer, and Debre Birhan). A natural controlled mating method was used, and one ram was assigned to 20–30 ewes. The assigned rams were kept with ewes for 45 days during the daytime. During mating, herdsman were assigned to each mating group to collect the mating data and pedigree information. The pure indigenous (Tumele) ewes were crossed with pure Dorper rams to produce the F1 crossbreds with a 50% Dorper level. To evaluate the performance of crossbreds with different Dorper levels, female crossbreds with 50% Dorper level were crossed with pure Dorper rams to produce crossbreds with 75% Dorper level. Age, physical defect, and poor reproductive performance were the major criteria for culling animals. Ewes that were old and infertile have been culled. Additional indigenous ewes were purchased as and when required over the study period. Sires have been replaced by new sires from the nucleus farm when they have completed their mating services and are culled.

### Data collection and studied traits

Data were collected for Dorper × indigenous crossbred sheep born from 2009 to 2018. A growth trait includes birth weight (BRW), weaning (3MW), six-month weight (6MW), nine-month weight (9MW), and yearling weight (12MW). Birth weight was taken within 24 hours of the birth of a lamb, and 3-, 6-, 9-, and 12-month weights were taken on exact dates. In addition, average daily gain (g day<sup>-1</sup>) from birth to weaning (ADG1), from weaning to 6 months (ADG2), from 6 months to 9 months (ADG3), and from 9 months to yearling age (ADG4) were computed and considered in this study. Kleiber ratios in different growth phases were computed as follows: KR1 = ADG1/3MW<sup>0.75</sup>, KR2 = ADG2/6MW<sup>0.75</sup>, KR3 = ADG3/9MW<sup>0.75</sup> and KR4 = ADG4/12 MW<sup>0.75</sup>.

### Data analysis

Data on growth performance and Kleiber ratio were analysed using the general linear model procedure of statistical analysis system (SAS, 2002) for determining the fixed effects that have a signif-

ificant influence on the traits investigated. The model considered fixed effects of type of birth in two classes (single and twin), sex of lamb in two classes (male and female), the Dorper blood level of lambs in two classes (50 and 75%), year of lambing in ten classes (2009–2018) and season of birth in three classes (dry, short rain, and main rain). The mean temperature for dry, short rain and main rain season were 17.9, 21.5, and 21.4 °C, respectively. The average rainfall for dry, short rain and main rain season were 335, 772, and 2076 mm, respectively. Tukey-Kramer test was employed for making all possible comparisons of means. Only significant effects ( $P < 0.05$ ) were included in the models, which were subsequently used for the genetic analysis. Genetic parameters for BRW, 3MW, ADG1, and KR1 were estimated by the Average Information Restricted Maximum Likelihood (AI-REML) method fitting an animal model using a WOMBAT computer program (Meyer, 2007). The genetic parameters for postweaning growth traits were not estimated due to a lack of enough sample size. A detailed description of the data structure and pedigree is presented in Table 1.

When there were missing records for one of the two traits, multivariate analysis performed much better than single trait, however, when there were no missing records, both techniques gave similar reliability (Guo et al., 2014). In addition, the power of various tests of significance in multivariate technique could be affected due to the high correlation between the traits (Foster et al., 2006). Moreover, multivariate techniques need a large sample of data to give meaningful; otherwise, the results are meaningless due to high standard errors. Thus, in this study, a univariate animal model was fitted due to data structure. Direct additive genetic effect, maternal genetic effect and maternal permanent environmental effect had a considerable effect on the phenotypic expression of traits (Tesema et al., 2020a; Behrem, 2021). Therefore, four models (including these random effects) were fitted and evaluated for each trait.

The number of progeny per dam is small in this study. According to Meyer (1997) and Heydarpour et al. (2008), including direct-maternal covariance with this data structure may result in negative and higher direct-maternal genetic correlation estimates. Besides, David et al. (2015) reported that the influence of the direct-maternal genetic correlation on the total estimated breeding value is minimal and suggested setting the direct-maternal genetic correlation to 0 for genetic evaluation purposes. Therefore, the direct-maternal genetic covariance was not included in this study. The four single-trait animal models were shown below:

$$y = X\beta + Z_1a + \varepsilon \tag{1}$$

$$y = X\beta + Z_1a + Z_2m + \varepsilon \text{ with } \text{Cov}(a, m) = 0 \tag{2}$$

$$y = X\beta + Z_1a + Z_2c + \varepsilon \tag{3}$$

$$y = X\beta + Z_1a + Z_2m + Z_3c + \varepsilon \text{ with } \text{Cov}(a, m) = 0 \tag{4}$$

where  $y$  is the vector of records;  $\beta$ ,  $a$ ,  $m$ ,  $c$  and  $\varepsilon$  are vectors of fixed (fixed effects which had a significant effect), additive direct genetic, maternal additive genetic, permanent environmental effects of the dam and residual effects, respectively;  $X$ ,  $Z_1$ ,  $Z_2$  and  $Z_3$  are incidence matrices that relate these effects to the records. The (co)variance structure for the model was as follows:

$$\begin{aligned} \text{Var}(a) &= A\sigma_a^2, \quad \text{Var}(m) = A\sigma_m^2, \quad \text{Var}(c) = I_Dc^2, \quad \text{Var}(\varepsilon) \\ &= I_K\varepsilon^2 \quad \text{and} \quad \text{Cov}(a, m) = A\sigma_{am}, \end{aligned}$$

where  $A$  is the numerator relationship matrix between animals;  $I_D$  and  $I_K$  are identity matrices with orders equal to the number of dams and the number of kids, respectively.

Likelihood ratio test (LRT) was used to determine the most appropriate model for each trait. The significance of model comparison was done from univariate analysis of animal models with and without including the effects as a random effect and compared log-likelihoods (Maximum log L) by chi-square ( $\chi^2$ ) distribution (Chen et al., 2006; Wilson et al., 2010).

$$\chi^2_{1df} = 2[\text{ML}(x)_f - \text{ML}(x)_r]$$

where  $\text{ML}(x)_f$  = maximum likelihood for full model,  $\text{ML}(x)_r$  = maximum likelihood for reduced model. A random effect was considered significant when its inclusion in the model caused a significant ( $P < 0.05$ ) increase in the log-likelihood value, i.e. when  $\chi^2_{1df}$  is greater than the critical value. However, when the difference between the values of log-likelihood is not greater than a critical value of chi-square ( $\chi^2$ ), the simplest model was considered to be the best model. A chi-square distribution for  $\alpha = 0.05$  and one degree of freedom (3.841) was used as the critical test statistic to compare the model which includes one random effect with two random effects.

Genetic and phenotypic correlations were estimated using bivariate analysis. The genetic trend was obtained by regression of the average breeding value on lamb birth year (Tesema et al., 2020a). The inbreeding coefficient for individual animals was estimated and extracted from the additive relationship matrix. The total heritability ( $h_t^2$ ) was estimated according to Willham (1972):

$$h_t^2 = (\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am}) / \sigma_p^2$$

where  $\sigma_a^2$  is the additive genetic variance,  $\sigma_m^2$  is the maternal genetic variance,  $\sigma_p^2$  is the phenotypic variance, and  $\sigma_{am}$  is the covariance between additive direct and maternal genetic effects.

**Table 1**  
Description of data structure for early growth traits in Dorper × indigenous sheep.

Items	Traits			
	BRW	3MW	ADG1	KR1
Number of records	537	453	449	449
Number of sire	21	20	20	20
Number of dam	260	229	229	229
Number of progeny per sire	25.6	22.6	22.4	22.4
Number of progeny per dam	2.06	1.97	1.96	1.96
Number of animals with paternal grandsire	50	36	36	36
Number of animals with paternal granddam	50	36	36	36
Number of animals with maternal grandsire	146	109	109	109
Number of animals with maternal granddam	138	99	97	97
Mean (kg)	3.03	14.5	127.2	16.8
SD	0.68	3.87	41.2	2.30
Minimum	1.20	8.60	40.0	9.97
Maximum	5.00	27.5	260.8	23.2
CV (%)	19.3	22.9	28.1	12.2

BRW = birth weight; 3MW = weaning weight; ADG1 = birth to weaning average daily weight gain; KR1 = birth to weaning Kleiber ratio.

## Results

### Live weight and the effect of non-genetic factors

The least-square mean live weights at various ages of Dorper crossbred lambs and factors affecting live weight are presented in Table 2. Birth type had a significant ( $P < 0.01$ ) influence on the live weight of crossbred lambs at various ages. Single-born lambs had a higher live weight in all growth phases than twin-born lambs. The sex of lambs is the other important ( $P < 0.01$ ) source of variation, and males appear to grow faster than respective female lambs. The growth performance of crossbreds was not increased with Dorper blood level, i.e. crossbred lambs with 50% and 75% Dorper blood level had similar ( $P > 0.05$ ) live weight in all growth phases.

Lambs born during the short rainy season had higher ( $P < 0.0001$ ) BRW than lambs born during the dry and main rainy seasons. However, the 6MW of lambs born during the dry season was greater ( $P = 0.0059$ ) than lambs born in the other seasons. Although the trend was not consistent, the year of lambing had a significant influence ( $P < 0.0001$ ) on the live weight of crossbred lambs. The lowest 3MW and 6MW were observed for lambs born during 2011, 2014, and 2017 compared to lambs born in the other years.

### Weight gain and the influence of environmental factors

The least-square mean and standard errors for the weight gain of lambs at different growth phases and the influence of non-genetic factors are presented in Table 3. Generally, the growth rate showed a decreasing trend when the age of lambs increases. In particular, higher weight gain of crossbred lambs was observed during the preweaning period. Single-born lambs had a higher ( $P < 0.0001$ ) preweaning growth rate than twin-born lambs. However, the postweaning growth rate of twins and single-born lambs was found to be similar ( $P > 0.05$ ). Except for ADG2, the weight gain of male lambs was superior to female lambs. Lambs with a 50%

Dorper blood level had lower ( $P < 0.05$ ) preweaning weight gain than lambs with a 75% Dorper blood level. Nevertheless, the weight gain of both genotypes was found to be similar ( $P > 0.05$ ) during the postweaning growth phases. Season of birth had a considerable influence on the ADG2 and ADG3 of crossbred lambs. However, the effect of season on ADG1 and ADG4 was found to be non-significant ( $P > 0.05$ ). The weight gain of crossbred lambs was significantly ( $P < 0.01$ ) different across years.

### Kleiber ratio and the effect of non-genetic factors

The least-square mean and standard errors for Kleiber ratio (KR) of lambs are presented in Table 4. The highest KR was observed from birth to weaning growth phase, and the lowest KR was observed between nine months and yearling age. Single-born crossbred lambs had a higher ( $P < 0.0001$ ) Kleiber ratio during the preweaning growth phase and that higher performance was not continued thereafter, i.e. twin-born lambs had a higher Kleiber ratio during the postweaning age. Sex of lambs had not a significant ( $P > 0.05$ ) influence on Kleiber ratio in different growth phases. Season of lambing affects ( $P < 0.001$ ) the KR2 and KR3. Lambs born during dry and short rain seasons had lower KR3 and KR2, respectively, than lambs born in the other seasons. Year of lambing also had a significant ( $P < 0.0001$ ) influence on Kleiber ratios of crossbred sheep except for KR2.

### Variance components and heritability estimate for early growth traits

Estimates of genetic parameters for BRW, 3MW, ADG1, and KR1 along with their likelihood values for each analysis under the four different models are summarised in Table 5. As per the log-likelihood test, the model, which includes direct additive and maternal genetic effects (model 2), was sufficient to explain the variation in the BRW. Likewise, a combination of direct additive and maternal permanent environmental effect (model 3) was the optimal model for 3MW and ADG1. However, the model, which includes only the direct additive genetic effect

**Table 2**  
Live weight (kg) of Dorper × indigenous sheep at a specific age (LSM ± SE).

Source of variation	BRW		3MW		6MW		9MW		12MW	
	N	LSM ± SE	N	LSM ± SE	N	LSM ± SE	N	LSM ± SE	N	LSM ± SE
Overall	531	3.03 ± 0.02	450	14.5 ± 0.18	349	20.4 ± 0.26	284	24.8 ± 0.31	210	28.3 ± 0.40
CV		19.3		22.9		21.2		17.5		15.5
Birth type		$P < 0.0001$		$P < 0.0001$		$P = 0.0030$		$P = 0.0014$		$P = 0.0094$
Single	440	3.13 ± 0.03	377	14.9 ± 0.14	290	20.6 ± 0.28	232	25.2 ± 0.33	173	28.7 ± 0.45
Twin	91	2.55 ± 0.07	73	12.2 ± 0.43	59	19.5 ± 0.68	52	23.1 ± 0.79	37	26.3 ± 0.79
Dorper level		$P = 0.6575$		$P = 0.0030$		$P = 0.1566$		$P = 0.3297$		$P = 0.2794$
50%	450	3.03 ± 0.03	388	14.4 ± 0.18	308	20.3 ± 0.28	258	24.6 ± 0.32	196	28.1 ± 0.14
75%	81	3.00 ± 0.07	62	15.2 ± 0.59	41	21.4 ± 0.66	26	26.3 ± 1.28	14	29.6 ± 1.94
Sex		$P = 0.0060$		$P = 0.0050$		$P = 0.0017$		$P < 0.0001$		$P = 0.0008$
Female	270	2.93 ± 0.04	233	13.9 ± 0.21	186	19.6 ± 0.32	165	23.6 ± 0.34	138	27.3 ± 0.45
Male	261	3.13 ± 0.04	217	15.1 ± 0.29	163	24.1 ± 0.42	119	26.5 ± 0.53	72	30.0 ± 0.75
Season		$P < 0.0001$		$P = 0.4333$		$P = 0.0059$		$P = 0.0643$		$P = 0.1222$
Dry	171	2.97 ± 0.05 <sup>b</sup>	151	14.9 ± 0.36	121	21.5 ± 0.53 <sup>a</sup>	77	25.5 ± 0.59	56	28.6 ± 0.66
Main rain	114	2.65 ± 0.05 <sup>c</sup>	91	13.4 ± 0.41	59	20.0 ± 0.66 <sup>b</sup>	51	25.4 ± 0.86	37	28.9 ± 0.95
Short rain	246	3.25 ± 0.04 <sup>a</sup>	208	14.7 ± 0.22	169	19.8 ± 0.31 <sup>b</sup>	156	24.2 ± 0.39	117	27.8 ± 0.57
Year		$P < 0.0001$		$P < 0.0001$		$P < 0.0001$		$P < 0.0001$		$P < 0.0001$
2009	72	3.10 ± 0.06 <sup>abc</sup>	68	15.3 ± 0.44 <sup>bcd</sup>	55	19.6 ± 0.62 <sup>cde</sup>	52	26.6 ± 0.66 <sup>abc</sup>	38	31.2 ± 0.77 <sup>ab</sup>
2010	66	3.39 ± 0.07 <sup>a</sup>	64	14.8 ± 0.31 <sup>cd</sup>	58	20.3 ± 0.42 <sup>cd</sup>	54	22.1 ± 0.45 <sup>de</sup>	42	22.3 ± 0.44 <sup>e</sup>
2011	59	3.26 ± 0.06 <sup>ab</sup>	57	12.8 ± 0.31 <sup>ef</sup>	45	17.8 ± 0.47 <sup>de</sup>	30	23.0 ± 0.58 <sup>de</sup>	28	28.5 ± 0.70 <sup>bc</sup>
2012	66	3.16 ± 0.07 <sup>ab</sup>	52	14.1 ± 0.50 <sup>de</sup>	29	20.2 ± 0.71 <sup>cd</sup>	25	23.5 ± 1.08 <sup>cde</sup>	15	27.4 ± 1.67 <sup>cd</sup>
2013	24	3.18 ± 0.11 <sup>ab</sup>	14	16.6 ± 0.99 <sup>ab</sup>	10	23.1 ± 1.66 <sup>ab</sup>	5	28.5 ± 2.51 <sup>a</sup>	–	–
2014	32	2.45 ± 0.11 <sup>f</sup>	24	12.2 ± 0.82 <sup>f</sup>	13	18.4 ± 1.21 <sup>de</sup>	11	24.6 ± 0.77 <sup>bcd</sup>	8	30.5 ± 1.12 <sup>ab</sup>
2015	55	2.62 ± 0.09 <sup>ef</sup>	44	16.0 ± 0.66 <sup>abc</sup>	37	22.8 ± 0.90 <sup>ab</sup>	36	27.9 ± 0.92 <sup>ab</sup>	31	31.9 ± 0.97 <sup>a</sup>
2016	67	3.01 ± 0.10 <sup>bcd</sup>	56	15.2 ± 0.57 <sup>bcd</sup>	49	21.8 ± 0.67 <sup>bc</sup>	40	26.7 ± 0.90 <sup>abc</sup>	29	30.8 ± 1.09 <sup>ab</sup>
2017	52	2.74 ± 0.08 <sup>def</sup>	44	12.4 ± 0.39 <sup>f</sup>	29	17.5 ± 0.88 <sup>e</sup>	26	20.8 ± 0.87 <sup>e</sup>	19	25.4 ± 0.99 <sup>d</sup>
2018	30	3.13 ± 0.11 <sup>ab</sup>	27	17.2 ± 0.93 <sup>a</sup>	24	24.8 ± 1.40 <sup>a</sup>	5	29.3 ± 4.01 <sup>a</sup>	–	–

LSM = least square mean; BRW = birth weight; 3MW = weaning weight; 6MW = six-month weight; 9MW = nine-month weight; 12MW = yearling weight. Least square mean with different superscripts within the same column and class are statistically different.

**Table 3**  
Weight gain (g day<sup>-1</sup>) of Dorper × indigenous sheep at different growth phases.

Source of variation	ADG1		ADG2		ADG3		ADG4	
	N	LSM ± SE	N	LSM ± SE	N	LSM ± SE	N	LSM ± SE
Overall	446	127.3 ± 1.95	345	64.1 ± 1.99	274	51.9 ± 2.26	208	44.4 ± 2.58
CV		28.1		54.5		60.1		64.0
Birth type		<i>P</i> < 0.0001		<i>P</i> = 0.1232		<i>P</i> = 0.5352		<i>P</i> = 0.0735
Single	373	131.3 ± 2.09	286	61.7 ± 2.13	223	52.6 ± 2.53	177	43.8 ± 2.90
Twin	73	106.7 ± 4.59	59	75.9 ± 5.19	51	49.3 ± 5.00	31	47.1 ± 5.64
Dorper level		<i>P</i> = 0.0003		<i>P</i> = 0.3802		<i>P</i> = 0.1978		<i>P</i> = 0.5134
50%	384	125.9 ± 2.00	305	64.8 ± 2.01	248	52.1 ± 2.33	194	44.8 ± 2.64
75%	62	135.7 ± 6.40	40	58.9 ± 6.28	26	50.1 ± 8.54	14	38.5 ± 8.80
Sex		<i>P</i> = 0.0019		<i>P</i> = 0.2082		<i>P</i> = 0.0019		<i>P</i> = 0.0354
Female	231	121.9 ± 2.23	184	62.1 ± 2.60	159	46.7 ± 2.75	137	40.9 ± 2.92
Male	215	133.0 ± 3.22	161	66.5 ± 3.08	115	59.3 ± 3.72	71	51.2 ± 4.99
Season		<i>P</i> = 0.1707		<i>P</i> = 0.0001		<i>P</i> < 0.0001		<i>P</i> = 0.0641
Dry	149	132.6 ± 3.91	121	75.5 ± 3.31 <sup>a</sup>	75	43.8 ± 3.49 <sup>b</sup>	56	43.9 ± 4.74
Main rain	91	119.3 ± 4.46	57	65.9 ± 5.25 <sup>a</sup>	51	59.2 ± 5.45 <sup>a</sup>	37	46.2 ± 5.72
Short rain	206	126.9 ± 2.41	167	55.3 ± 2.66 <sup>b</sup>	148	53.6 ± 3.26 <sup>ab</sup>	115	44.1 ± 3.65
Year		<i>P</i> < 0.0001		<i>P</i> = 0.0076		<i>P</i> < 0.0001		<i>P</i> < 0.0001
2009	68	136.2 ± 4.60 <sup>bc</sup>	55	53.0 ± 4.31 <sup>c</sup>	49	81.7 ± 4.55 <sup>a</sup>	38	59.4 ± 6.09 <sup>a</sup>
2010	64	127.0 ± 3.19 <sup>c</sup>	58	61.4 ± 3.16 <sup>abc</sup>	52	23.9 ± 1.86 <sup>d</sup>	40	2.88 ± 3.48 <sup>b</sup>
2011	57	106.2 ± 3.28 <sup>d</sup>	45	55.9 ± 3.04 <sup>c</sup>	30	52.9 ± 5.17 <sup>bc</sup>	28	59.8 ± 6.02 <sup>a</sup>
2012	52	121.2 ± 5.48 <sup>cd</sup>	29	52.5 ± 5.76 <sup>abc</sup>	22	58.4 ± 8.25 <sup>abc</sup>	15	44.0 ± 4.99 <sup>a</sup>
2013	14	147.4 ± 10.9 <sup>ab</sup>	10	62.1 ± 10.6 <sup>abc</sup>	5	49.7 ± 11.1 <sup>bc</sup>	–	–
2014	24	106.9 ± 8.63 <sup>d</sup>	11	61.6 ± 8.98 <sup>abc</sup>	11	60.4 ± 12.3 <sup>abc</sup>	8	55.3 ± 10.7 <sup>a</sup>
2015	44	148.0 ± 7.24 <sup>ab</sup>	36	76.8 ± 7.29 <sup>ab</sup>	35	52.8 ± 6.23 <sup>bc</sup>	31	52.9 ± 6.08 <sup>a</sup>
2016	56	133.9 ± 5.96 <sup>bc</sup>	49	78.3 ± 6.06 <sup>ab</sup>	40	51.8 ± 6.92 <sup>bc</sup>	29	48.8 ± 7.30 <sup>a</sup>
2017	40	103.8 ± 5.49 <sup>d</sup>	28	60.9 ± 9.11 <sup>abc</sup>	26	37.9 ± 7.42 <sup>cd</sup>	19	54.6 ± 5.53 <sup>a</sup>
2018	27	156.7 ± 10.2 <sup>a</sup>	24	83.3 ± 10.9 <sup>a</sup>	4	74.4 ± 7.43 <sup>ab</sup>	–	–

LSM = least square mean; ADG1 = weight gain from birth to weaning; ADG2 = weight gain from weaning to six months; ADG3 = six months to nine months; ADG4 = weight gain from nine months to yearling age.

Least square mean with different superscripts within the same column and class are statistically different.

**Table 4**  
Kleiber ratio (g/ kg of metabolic weight) for Dorper × indigenous sheep (LSM ± SE).

Source of variation	KR1		KR2		KR3		KR4	
	N	LSM ± SE	N	LSM ± SE	N	LSM ± SE	N	LSM ± SE
Overall	446	16.8 ± 0.10	345	6.41 ± 0.17	274	4.55 ± 0.21	208	3.38 ± 0.20
CV		12.2		48.3		66.9		67.3
Birth type		<i>P</i> < 0.0001		<i>P</i> = 0.0011		<i>P</i> = 0.2834		<i>P</i> = 0.0098
Single	373	16.9 ± 0.11	286	6.09 ± 0.18	223	4.58 ± 0.22	177	3.27 ± 0.22
Twin	73	15.9 ± 0.29	59	7.94 ± 0.48	51	4.45 ± 0.55	31	3.88 ± 0.52
Dorper level		<i>P</i> = 0.0017		<i>P</i> = 0.1063		<i>P</i> = 0.6526		<i>P</i> = 0.4327
50%	384	16.7 ± 0.11	305	6.49 ± 0.18	248	4.66 ± 0.22	194	3.44 ± 0.21
75%	62	17.2 ± 0.35	40	5.76 ± 0.56	26	3.54 ± 0.77	14	2.57 ± 1.00
Sex		<i>P</i> = 0.2079		<i>P</i> = 0.5643		<i>P</i> = 0.1661		<i>P</i> = 0.2576
Female	231	16.7 ± 0.13	184	6.37 ± 0.24	159	4.31 ± 0.29	137	3.24 ± 0.22
Male	215	16.9 ± 0.17	161	6.45 ± 0.26	115	4.89 ± 0.28	71	3.65 ± 0.41
Season		<i>P</i> = 0.0568		<i>P</i> < 0.0001		<i>P</i> = 0.0001		<i>P</i> = 0.0525
Dry	149	17.0 ± 0.21	121	7.42 ± 0.25 <sup>a</sup>	75	3.69 ± 0.33 <sup>b</sup>	56	3.24 ± 0.41
Main rain	91	16.6 ± 0.26	57	6.54 ± 0.48 <sup>a</sup>	51	5.20 ± 0.50 <sup>a</sup>	37	3.71 ± 0.45
Short rain	206	16.7 ± 0.13	167	5.63 ± 0.25 <sup>b</sup>	148	4.77 ± 0.30 <sup>a</sup>	115	3.34 ± 0.28
Year		<i>P</i> < 0.0001		<i>P</i> = 0.1341		<i>P</i> < 0.0001		<i>P</i> < 0.0001
2009	68	17.3 ± 0.22 <sup>abc</sup>	55	5.46 ± 0.38	49	6.86 ± 0.34 <sup>a</sup>	38	4.38 ± 0.42 <sup>ab</sup>
2010	64	16.7 ± 0.17 <sup>bcd</sup>	58	6.33 ± 0.29	52	2.31 ± 0.19 <sup>c</sup>	40	0.25 ± 0.34 <sup>c</sup>
2011	57	15.5 ± 0.22 <sup>e</sup>	45	6.38 ± 0.28	30	4.99 ± 0.48	28	4.76 ± 0.55 <sup>ab</sup>
2012	52	16.4 ± 0.33 <sup>cde</sup>	29	5.29 ± 0.56	22	5.88 ± 1.13 <sup>ab</sup>	15	3.64 ± 0.37 <sup>ab</sup>
2013	14	17.7 ± 0.51 <sup>ab</sup>	10	5.74 ± 0.77	5	4.24 ± 1.10 <sup>ab</sup>	–	–
2014	24	15.9 ± 0.50 <sup>de</sup>	11	6.65 ± 0.91	11	5.38 ± 1.08 <sup>abc</sup>	8	4.16 ± 0.73 <sup>ab</sup>
2015	44	18.1 ± 0.39 <sup>a</sup>	36	6.94 ± 0.64	35	4.25 ± 0.50 <sup>abc</sup>	31	3.89 ± 0.45 <sup>ab</sup>
2016	56	17.1 ± 0.31 <sup>abc</sup>	49	7.62 ± 0.58	40	3.84 ± 0.60 <sup>bc</sup>	29	3.20 ± 0.68 <sup>b</sup>
2017	40	15.7 ± 0.37 <sup>de</sup>	28	6.31 ± 0.85	26	4.00 ± 0.86 <sup>bc</sup>	19	–
2018	27	18.1 ± 0.52 <sup>a</sup>	24	7.12 ± 0.79	4	6.52 ± 1.18 <sup>ab</sup>	–	–

LSM = least square mean; KR1 = Kleiber ratio from birth to weaning; KR2 = Kleiber ratio from weaning to six months; KR3 = Kleiber ratio from six to nine months; KR4 = nine months to yearling age.

Least square means with different superscripts within the same column and class are statistically different.

(model 1), was appropriate in estimating heritability for KR1. Based on optimal models, the direct heritability ( $h_a^2$ ) was varied from 0.003 for BRW to 0.16 for ADG1. The inclusion of maternal genetic effect in the model had a significant influence on BRW,

reduces the  $h_a^2$  estimate, and it explains 20% of the phenotypic variation. However, 21% of the phenotypic variation in 3MW and 19% in ADG1 were explained by a maternal permanent environmental effect ( $c^2$ ).

**Table 5**  
Genetic parameter estimates for early growth traits of Dorper × indigenous sheep.

Trait	M	$\sigma_a^2$	$\sigma_m^2$	$\sigma_c^2$	$\sigma_e^2$	$\sigma_p^2$	$h_d^2 \pm SE$	$h_m^2 \pm SE$	$c^2 \pm SE$	$e^2$	$h_t^2$	Log (L)
BRW	1	0.14			0.23	0.37	0.37 ± 0.12			0.63	0.38	-6.026
	2	0.001	0.07		0.28	0.35	0.003 ± 0.08	0.20 ± 0.06		0.79	0.10	-1.646
	3	0.001		0.08	0.26	0.34	0.003 ± 0.07		0.23 ± 0.06	0.77	0.00	-0.548
	4	0.001	0.02	0.06	0.27	0.35	0.003 ± 0.08	0.06 ± 0.11	0.17 ± 0.11	0.76	0.03	-0.395
3MW	1	2.51			9.28	11.8	0.21 ± 0.12			0.78	0.21	-777.41
	2	1.59	1.59		8.64	11.8	0.13 ± 0.13	0.13 ± 0.07		0.73	0.20	-775.65
	3	1.67		2.47	7.75	11.9	0.14 ± 0.13		0.21 ± 0.07	0.65	0.14	-773.37
	4	1.67	0.001	2.47	7.75	11.9	0.14 ± 0.13	0.00 ± 0.13	0.21 ± 0.13	0.65	0.14	-773.37
ADG1	1	255.7			1 091	1 346	0.19 ± 0.12			0.81	0.19	-1797.4
	2	200.9	172.8		987.2	1 360	0.15 ± 0.13	0.13 ± 0.07		0.72	0.21	-1795.9
	3	221.7		265.7	886.3	1 374	0.16 ± 0.13		0.19 ± 0.07	0.64	0.16	-1794.3
	4	221.4	0.009	265.4	886.8	1 373	0.16 ± 0.14	0.00 ± 0.12	0.19 ± 0.13	0.65	0.16	-1794.3
KR1	1	0.54			3.87	4.41	0.12 ± 0.10			0.87	0.12	-562.43
	2	0.49	0.33		3.61	4.44	0.11 ± 0.13	0.07 ± 0.06		0.81	0.15	-561.85
	3	0.55		0.59	3.33	4.48	0.12 ± 0.13		0.13 ± 0.07	0.74	0.12	-561.12
	4	0.56	0.001	0.59	3.32	4.48	0.12 ± 0.13	0.00 ± 0.11	0.13 ± 0.12	0.74	0.13	-561.12

M = model; Log (L) = Maximum log-likelihood value.

$\sigma_a^2$  = direct genetic variance;  $\sigma_m^2$  = maternal genetic variance;  $\sigma_c^2$  = maternal permanent environmental variance;  $\sigma_e^2$  = residual variance;  $\sigma_p^2$  = phenotypic variance;  $h_d^2$  = heritability of direct genetic effects;  $h_m^2$  = heritability of maternal genetic effects;  $c^2$  = maternal permanent environmental variance as a proportion of phenotypic variance;  $e^2$  = residual variance as a proportion of phenotypic variance;  $h_t^2$  = total heritability.

BRW = birth weight; 3MW = weaning weight; ADG1 = weight gain from birth to weaning and KR1 = Kleiber ratio from birth to weaning age.

### Genetic and phenotypic correlation

The phenotypic and genetic correlation estimates among early growth traits are presented in Table 6. The phenotypic correlation varied from -0.11 to 0.98, whereas the direct genetic correlation ranges between -0.32 and 0.98. The antagonistic phenotypic and genetic relationship was observed between BRW and KR1. On the other hand, high and positive genetic correlations were observed among 3MW and other preweaning growth traits (ADG1 and KR1).

### Genetic trend and inbreeding coefficient (F)

The genetic trend for preweaning growth traits of Dorper crossbred sheep is presented in Fig. 1. Except for BRW, all traits showed an undulating genetic trend. The coefficient for genetic trend for BRW, 3MW, ADG, and KR1 was 0.001 kg year<sup>-1</sup>, -0.105 kg year<sup>-1</sup>, -1.103 g year<sup>-1</sup>, and -0.044 g/metabolic weight/year, respectively. The overall mean probability of the two alleles at a randomly chosen locus being identical by descent (inbreeding coefficient) was 0.105% with an annual rate of 0.021%. The average inbreeding level for inbred sheep was found to be 14.1%.

## Discussion

### Non-genetic factors

The BRW, 3MW, 6MW of crossbred lambs in this study are higher than the report of Abebe et al. (2016) for Dorper × Afar crossbred sheep (2.57 kg BRW, 9.45 kg 3MW and 13.2 kg 6MW) and Dorper × Menz crossbred sheep (2.77 kg BRW, 12.3 kg 3MW and 17.2 kg 6MW). Likewise, a relatively lowest yearling weight (22.5 kg) than the current result was reported for Washera × Farta crossbred sheep (Mekuriaw et al., 2013). However, the yearling weight of crossbred lambs in this study is lower than the result (31.3 kg for Dorper × Menz sheep) reported by Abebe et al. (2014). Generally, the live weight of Dorper crossbred sheep observed in the present study is superior to most of the non-improved indigenous breeds (Washera, Farta, Horo, Adilo, Menz, Wollo sheep) reported by several scholars (Tibbo, 2006; Gizaw and Getachew, 2009; Mekuriaw et al., 2013; Gemiyo et al., 2014). The export market (Middle East countries) needs lambs weighing 25–30 kg at yearling age. In this study, the crossbred lambs could

attain the minimum requirement of the export market standard starting from nine months of age.

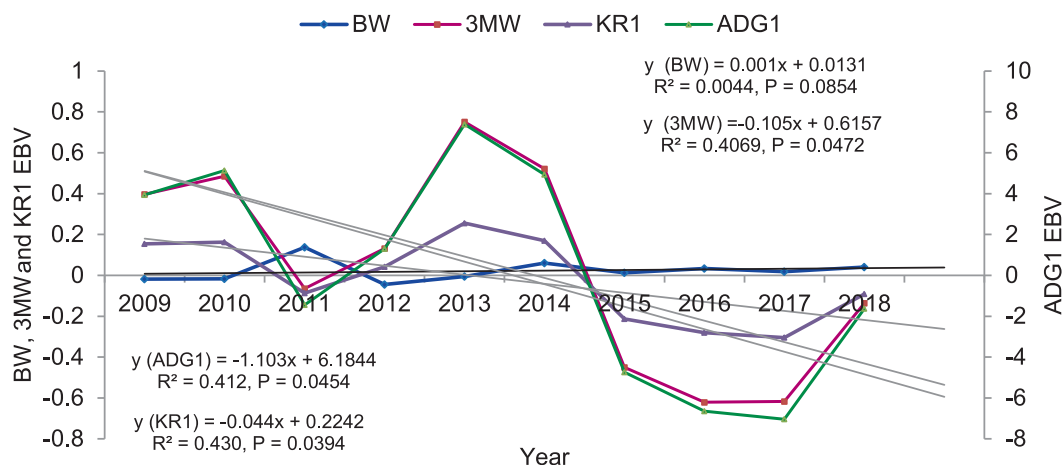
The higher live weight of single-born lambs than twins in this study is in agreement with several studies (Mohammadi et al., 2010; Mekuriaw et al., 2013; Lakew et al., 2014; Mandal et al., 2015). The heavier weight of single-born lambs could be attributed to the pre- and postnatal availability of nutrients, i.e. enough capacity of the maternal uterus space to gestate offspring and less competition for milk among the single than twin-born lambs. This carry-over effect is there up to yearling age (Abegaz et al., 2002). The higher live weight of males than females has been reported by several authors (Tibbo, 2006; Lakew et al., 2014; Teklebrhan et al., 2014; Mandal et al., 2015). This difference could be due to more influence of sex hormones (androgen) on muscle development of males than females. However, oestrogen limits skeleton growth in females (Ghafouri-Kesbi and Gholizadeh, 2017). Besides, ewes that carry male lambs had higher cotyledon numbers and heavier placental weight than ewes that carry females (Jawasreh et al., 2009), this may be the other possible reason for the higher performance of male lambs. The higher exotic inheritance must be accompanied by improved management to enable them to express their full genetic potential. Otherwise, using 50% crossbreds would be compatible with the existing management level. Moderate level of drought in 2011 and 2014 and also high disease prevalence during 2017 were the possible reasons for the observed lowest performance of lambs. According to Tesema et al. (2020b), Gastrointestinal parasites, Pneumonia and Septicemia were the major diseases in the station where sheep were raised. Besides, the variability of rainfall across the years may also be the other factor for observed variation as it is associated with the quality and quantity of forage.

The reduction of weight gain when the age of lamb increases is consistent with several studies (Ghafouri-Kesbi et al., 2011; Jalil-Sarghale et al., 2014; Ghafouri-Kesbi and Gholizadeh, 2017). This lower weight gain could be explained by the reduction of maternal effect as lambs grew old. The fastest growth rate of single-born lambs during preweaning age in this study is in line with Teklebrhan et al. (2014) and Abebe et al. (2014). Single and twin-born lambs had a similar growth trend after weaning, and a similar observation has been made by several authors (Taye et al., 2009; Mohammadi et al., 2010; Mekuriaw et al., 2013; Lakew et al., 2014). This is not surprising, because the maternal effect during the preweaning period is higher than the effect during the post-

**Table 6**  
Direct genetic (above the diagonal) and phenotypic (below the diagonal) correlation estimates for early growth traits of Dorper × indigenous sheep.

	BRW	3MW	ADG1	KR1
BRW		0.43 ± 0.32	0.10 ± 0.32	-0.32 ± 0.40
3MW	0.30 ± 0.05		0.98 ± 0.17	0.70 ± 0.25
ADG1	0.13 ± 0.05	0.98 ± 0.02		0.87 ± 0.11
KR1	-0.11 ± 0.05	0.89 ± 0.01	0.94 ± 0.01	

BRW = birth weight; 3MW = weaning weight; ADG1 = weight gain from birth to weaning and KR1 = Kleiber ratio from birth to weaning age.



**Fig. 1.** Genetic trend for preweaning growth traits of Dorper crossbred sheep. BRW, birth weight; 3MW, weaning weight; ADG1, weight gain from birth to weaning and KR1, Kleiber ratio from birth to weaning age; EBV, estimated breeding value.

weaning period, i.e. single-born lambs are favoured during preweaning periods than twin lambs in terms of nutrients.

Consistent with the current result, the higher weight gain of male lambs was noted in previous studies (Mohammadi et al., 2010; Ghafouri-Kesbi and Gholizadeh, 2017). This could be ascribed to the secretion and function of hormones. According to Ghafouri-Kesbi and Gholizadeh (2017), oestrogen limits the growth of the long bones in females whereas testosterone has a positive effect on growth in males. The lower preweaning weight gain of lambs with 50% Dorper level is in line with the report of Teklebrhan et al. (2014) for Dorper × Hararghe Highland and Doper × Black Head Ogaden lambs. The influence of season and year of kidding on weight gain is in agreement with those reported in the literature (Mekuriaw et al., 2013; Lakew et al., 2014; Teklebrhan et al., 2014). The difference in weight gain across year and season of lambing could be attributed to the variability of feed availability, climatic condition, and disease distribution.

Kleiber ratio could be used as a useful indicator of feed conversion and an important selection criterion for the efficiency of growth as suggested by several scholars (Kleiber, 1947; Köster et al., 1994; Ghafouri-Kesbi et al., 2011). The lower postweaning Kleiber ratio in this study is in agreement with Ghafouri-Kesbi and Gholizadeh (2017) who noted a higher growth rate and Kleiber ratio in the preweaning growth phase than postweaning. The KR1 observed in this study is comparable with the value (16.8) reported by Mandal et al. (2015), higher than the value (15.6) reported by Mohammadi et al. (2010), and Abegaz et al. (2005) for Horo sheep (15.3), but lower than the report (18.2) of Ghafouri-Kesbi et al. (2011). The observed variation among breeds could be due to the variability of the genetic potential of breeds, the weaning age of lambs, forage abundance, and other husbandry practices.

The higher postweaning Kleiber ratio of multiple-born lambs than single-born could be due to compensatory growth of lambs, i.e. the period of amplified growth after a spell of limited development and growth. Animals that have a high Kleiber ratio are con-

sidered efficient users of feed (Ghafouri-Kesbi et al., 2011), i.e. single-born lambs were more efficient in feed utilisation than twin contemporaries during the preweaning period and the reverse is true during postweaning. The sizable influence of year and season on Kleiber ratios was documented in previous studies (Mohammadi et al., 2010; Mandal et al., 2015; Faid-Allah et al., 2016). The variation across year and season could be due to the variability of climatic conditions that are directly or indirectly associated with feed availability, quality of forage, and disease prevalence.

#### Genetic parameter estimates

As per the log-likelihood ratio test, the model including direct additive and maternal genetic effects was sufficient to explain the variation in the birth weight of crossbred lambs. This result is in line with the report of Eskandarinasab et al. (2010) and Mohammadi et al. (2010). The model included both direct additive genetic effect and maternal permanent environment effect to be the most appropriate model for evaluating 3MW and ADG1. This result is consistent with the report of Rashidi et al. (2008) for Kermani lambs, Prakash et al. (2012) for Mapura lambs and Mandal et al. (2015) for Muzaffarnagari sheep. Thus, the exclusion of maternal effect from the model could overestimate the direct heritability of these traits. However, for KR1, the inclusion of maternal effect did not improve log-likelihood significantly ( $P > 0.05$ ) and thus, model 1 was sufficient to explain the variation for KR1. This result is in line with the report of Eskandarinasab et al. (2010) and Prakash et al. (2012).

The direct heritability ( $h_a^2$ ) for ADG1 and KR1 in the present study is higher than the value (0.11 for ADG, and 0.10 for KR1) reported by Ghafouri-Kesbi et al. (2011). However, higher estimates (0.16 for BRW, 0.27 for 3MW, 0.26 for ADG and 0.15 for KR) than the present results were noted by Mohammadi et al. (2010). Likewise, higher  $h_a^2$  (0.164) and lower  $c^2$  (0.078) than the current result were

reported by Khorsand et al. (2014) for Afshari sheep. The variability of estimates among studies could be ascribed to the type of breeding programme (crossbreeding or selection), selection intensity, data structure, the model used for estimation, and overall management of the flock.

The higher maternal heritability ( $h_{m}^2$ ) estimates ranging from 0.18 to 0.24 for BRW were documented in several studies (Roshanfekar et al., 2011; Rashidi, 2012; Shokrollahi and Zandieh, 2012; Khorsand et al., 2014; Faid-Allah et al., 2016). This depicts that birth weight is strongly influenced by the maternal gene than by the lambs' own gene and this suggests that maternal genetic effects need to be considered in selecting early growth traits. The  $c^2$  of 3MW in this study was higher than those reported for dual purpose (0.09), meat (0.19), and wool (0.10) sheep (Safari et al., 2005). These results indicate that maternal genetic effect is more important in birth weight than other traits. This result is in line with Prakash et al. (2012) who noted that the maternal genetic effects directly affect the lamb's birth weight and its effect usually diminishes slowly as the age of lamb increases. The variability of milking ability and nursing behaviour of dams, which result in variable maternal care for lambs, could be the reason for high  $c^2$ . The influence of genetic and non-genetic maternal effect on early growth traits suggests that intervention in ewes (improving dam nutrition at the last stage of gestation, selection based on maternal behaviour and milking ability) may have a considerable influence on the preweaning growth performance of lambs.

When the maternal genetic effect is considered in the model, the total heritability estimate is ideal for the estimation of selection response based on phenotypic values. Higher total heritability estimates for BRW than the current study were reported by Abegaz et al. (2005) for Horo sheep and Mandal et al. (2015) for Muzaffarnagari sheep. However, the estimates for 3MW (0.12) and ADG1 (0.13) of Horo sheep were lower than the present estimates. In general, the heritability estimates in this study were found within a lower range and this could be explained by the inconsistency of management, fodder quality, and malnourishment of flock, as these factors increase the proportion of phenotypic variance due to environmental variance (Mandal et al., 2015; Ghafouri-Kesbi and Gholizadeh, 2017). The heritability estimates for preweaning growth traits and Kleiber ratio suggest slow genetic progress would be expected through selection. According to Cassel (2009) and Faid-Allah et al. (2016), when the heritability is below 0.15, the selection of animals based on their performance is less effective. Therefore, selection for both early growth traits and Kleiber ratio should be according to the breeding values estimated from multiple information sources such as progeny, pedigree, sibs, and other relative information besides to own performance record.

Higher direct genetic correlations for BRW-3MW (0.72) and BRW-ADG1 (0.52) than the current finding were noted by Jalil-Sarghale et al. (2014). The direct genetic correlation estimate for BRW-3MW, BRW-ADG1, 3MW-KR1, and 3MW-ADG1 was reported to be 0.29, 0.04, 0.74, and 0.96, respectively, according to Abegaz et al. (2005), and these values were lower than the current estimates. The variation of correlation estimate among breeds or studies is likely due to the variation of sample size, data structure, management, number of random and fixed factors considered. A lower genetic correlation among BRW and KR1 than the current estimate was reported by Mohammadi et al. (2010), Mandal et al. (2015), and Faid-Allah et al. (2016). This suggests that these two traits cannot be improved simultaneously through selection, and thus, selection should focus on the trait of the highest importance. The higher genetic correlation of 3MW with ADG1 and KR1 is in line with previous studies (Prakash et al., 2012; Mandal et al., 2015). This suggests that genes that influence these traits were in a similar direction or the presence of linkage between these genes,

and thus, selection could be carried out based on either one of them.

#### Genetic trend and inbreeding level

Evaluation of the genetic trend and inbreeding level is important to indicate the way forward. Except for BRW, all investigated traits were decreased genetically by a determined coefficient per year. On the contrary, a positive genetic trend (0.028 kg year<sup>-1</sup>) was noted by Areb et al. (2021) for the weaning weight of Bonga sheep under selection. Differences in trends among breeds can be explained by selection criteria and selection intensity, which varied among breeds. The observed fluctuation of a genetic trend over years and negative genetic trend for 3MW, KR1 and ADG1 from 2013 to 2017 could be due to the absence of selection for rams and ewes based on their estimated breeding value, variation of nutritional level and pasture quality. Hence, the selection of rams and ewes based on their estimated breeding value and reducing environmental variation/ improving the animal management could enhance the genetic progress.

A relatively higher inbreeding level than this result was reported by Patiabadi et al. (2016) for Iranian Shal sheep (F = 6.28%), Tesema et al. (2021) for Boer crossbred goats (F = 0.58%), and Areb et al. (2021) for Bonga sheep (F = 0.36%). The observed inbreeding level could be ascribed to excessive use of very few rams (a high number of progenies per ram) and the absence of a periodic evaluation of the flock. According to Ryan (2018), the inbreeding coefficient of up to 6.25% is acceptable. Thus, inbreeding depression is unlikely to occur in the flock as the inbreeding level is below the maximum threshold level, as expected for crossbred sheep.

#### Conclusion

The result of this study indicates that birth type, sex, season, and year of lambing are the main determinants of growth traits and Kleiber ratios and should be taken into account in genetic evaluations. Besides to direct genetic effect of animal, maternal genetic effect and maternal permanent environmental effects also need to be considered for genetic evaluation of early growth traits. The observed low heritability estimates for growth traits and Kleiber ratio suggest that slow genetic progress would be expected from the selection. However, the integration of selection with crossbreeding programmes and improving the flock management could further enhance the genetic gain. Therefore, selection should be conducted based on breeding values estimated from multiple information sources to improve its efficiency.

#### Ethics approval

Not applicable.

#### Data and model availability

None of the data were deposited in an official repository. However, the data that support the study findings are available to reviewers, available from authors upon request.

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## Author contributions

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**Negus Belayneh, Alemu Kefale, Mekonnen Shibesh, Asres Zegeye, Liuel Yizengaw and Getachew Worku Alebachew:** Conceptualisation, data curation, methodology and writing.

**Solomon Tiruneh, Shanbel Kiros, Mengesha Asfaw and Molla Bishaw:** Data curation, resources and revision of manuscript.

## Declaration of interest

None.

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