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Estimation of breeding values and genetic trend of some growth traits in Merino sheep

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ABSTRACT

The aim of this study was to estimate the genetic trends for growth traits of Merino sheep managed under the National Sheep and Goat Improvement Project's breeding program. the analysis included data belonging to 3116 lambs born to 83 rams and 1129 ewes. The data [birth weight (BW), live weight at 45th day (LW45), weaning weight (WW-90th day) and average daily gain from birth to weaning (ADG)] were collected over a period of 6 years. BW demonstrated a positive and significant genetic correlation with all growth traits, but had a low direct heritability (0.02 ± 0.02). Birth weight had high genetic correlation with all growth traits. Except for the high correlation between LW45 and WW (0.51), the remaining traits had medium or low phenotypic correlations. While the genetic trend values for LW45 in lambs, ADG, WW and growth index (GI) in rams and ADG, LW45 and GI in ewes were all positive, they were not statistically significant. However, the genetic progression for GI, WW and ADG in lambs were found to be negative and significant ($p < 0.05$). Genetic trend estimates indicated that there wasn't a positive genetic improvement in the growth traits studied in Merino sheep. Thus, it is proposed to improve genetic trends by the implementation of selection as based on BLUP.

1. Introduction

The evaluation of genetic trends for economic traits in animal breeding plays the most critical role in successfully planning future breeding programs. Moreover, it allows for the documentation of any improvements resulting from previous selection implementations (Eteqadi et al., 2016). Reliable estimates of genetic trends, i.e. the annual rate of genetic change, enable comparisons of expected and realized genetic change in experimental situations and assessment of progress in a given trait (Mallick et al., 2016). Hence, it allows for the evaluation of a designed genetic improvement program. If an applied program advances toward determined targets, optimization becomes possible, but if the program fails or deviates from predetermined targets, redesign becomes viable (Bekana, 2019).

Apart from this, accurate estimation of breeding values of candidate animals is one of the most useful tools for maximizing the responses to be obtained from selection programs. The estimated breeding value (EBV) is a measure of an animal's genetic potential expressed relative to the population average. Therefore, the most critical decision that breeders and experts are required to make in sheep breeding is determining which animals will be kept as parents for future generations. Rapid genetic improvement is achievable only through designating the best rams as reserve rams. These are the animals that will uncover their superior genetic potential when provided with a suitable environment. The only method of selecting genetically-superior animals is to focus on the top highest quality 5 %−10 % of the animals. For this reason, in order for sheep breeders to select rams that are likely to produce superior lambs, they must consider not only their appearances, but also their genetic merit or breeding value. The genetic trend, expressed as a ratio of the theoretical change expected in the average breeding value calculated for the trait under selection, has been used to evaluate a breeding program's performance (Jurado et al., 1994; Rajkumar et al., 2021).

Early growth traits of lambs are of particular interest for the profitability of any sheep production enterprise. Establishing the effect share of each trait in variance by examining the genotype and environmental factors affecting growth rate in lambs is very important for guiding future research. Knowledge on genetic variation and correlations among traits is required for both designing effective sheep breeding programs and accurately predicting genetic progress (Supakorn et al., 2013).

The selection index is a method for estimating the breeding value of an animal by combining all available relevant data on the animal and its

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relatives. Breeding goals involving multiple traits can be achieved most efficiently with the use of a selection index. Sorting rams is simple when performance information associated with a trait is used. The number of breeding goals or selection programs focused on a single trait, however, is quite low. Most of the targets of Türkiye's Merino Sheep Breeding Program include fleece yield and quality and growth traits. Selection indices are generally one of the most useful genetic tools for describing the animals that are most likely to achieve the population's breeding goal. In this way, in order to assign an index value to each animal, the sets of information from all the traits are combined (Paswan et al., 2016).

The most primary element of the National Sheep and Goat Improvement Project is to maintain records and estimate genetic parameters and EBV. Moreover, estimating genetic trend is critical for testing the effectiveness of a breeding scheme and providing information for the development of future selection programs. For this reason, the aim of the present study is to estimate breeding values for growth traits in animals included in the National Sheep and Goat Improvement Project and to determine the genetic trend.

2. Materials and methods

2.1. Data

In this study, the pedigree and data file obtained between 2011 and 2016 from a flock within Türkiye's National Sheep and Goat Improvement Project (TAGEM/41KBM2011-01) was evaluated. The pedigree file includes 117 sires, 1129 dams, and a total of 4216 animals. The data of sires with one and two progeny were omitted and only data of 3116 animals with progeny from 83 sires were used. The birth weight (BW), live weight of the 45th day (LW45), average daily gain from birth to weaning (ADG) and weaning weight (WW-90th day) of these lambs were determined.

2.2. Statistical analysis

The (co)variance components and the breeding values were estimated by MTDFREML in the BLUP univariate animal model (Boldman et al., 1995). The fixed effects included the model are the birth year, birth season, birth type and sex. Moreover, for the LW45 the BW and for WW, the suckling period the BW and the LW45 were considered as covariates. In order to determine the correlations between the traits, the bivariate analysis was performed. To determine the most suitable model for each growth trait in the investigation, six distinct models were fitted, ignoring or including maternal additive genetic effects, maternal permanent environmental (common) effects, as well as the additive genetic relationship between direct and maternal effects. The model with the lowest Bayesian Information Criterion (BIC) was selected as the optimal model for the estimation of genetic parameters. The model with direct additive and common environmental influence is the most suitable for BW, LR45, and ADG. However, it was determined that the most appropriate model for WW included maternal genetic effects in addition to the previous ones.

These model can be written as follows:

$$y = Xb + Za + Sc + e$$

$$y = Xb + Za + Wm + Sc + e \qquad Cov(a, m) = A\sigma_{am}$$

in which **y** denotes the observation vector for each trait, **b** indicates the fixed effects (birth year, birth season, birth type and sex) vector, **a, m, c** and **e** refer to direct additive genetic effects (animal), maternal additive genetic effects, common environment effect for litters and random residual effect, respectively. **X, Z, W** and **S** are the design matrices belonging to these effects. **A** is the numerator relationship matrix. The assumptions implemented in the analysis are as follows:

$$V(a) = \boldsymbol{A}\sigma_a^2, V(m) = \boldsymbol{A}\sigma_m^2, Vc(c) = \boldsymbol{I_c}\sigma_c^2, Cov(a, m) = \boldsymbol{A}\sigma_{am}, V(e) = \boldsymbol{I_n}\sigma_e^2$$

where; $\boldsymbol{I_c}$ ve $\boldsymbol{I_n}$ are identity matrices with orders equal to number of litter groups and animals, σ_a^2, σ_m^2, σ_c^2, σ_{am} ve σ_e^2 direct additive genetic variance, maternal additive genetic variance, common environmental variance, covariance between additive direct and maternal effects and environmental variance, respectively. By dividing these variance components by phenotypic variance, the direct heritability (h_d^2), maternal heritability (m^2) and common environmental effects (c_m^2) were calculated. In flocks where multiple births are common, it is useful to categorize the maternal permanent environmental effects over the years into maternal effects and litter effects. As the source of the maternal common environment, the litter effect was taken into consideration in this study. Moreover, the total heritability was calculated via $h_T^2 = (\sigma_a^2 + 0.5\sigma_m^2 + 1.5\sigma_{am})/\sigma_P^2$ (Willham, 1972).

The genetic trend was calculated in this study by determining the change in the means of the breeding values according to the birth years of the animals. Annual genetic improvement was determined via the regression of the predicted breeding values for each trait on the birth years. Since the minimum and the maximum values of breeding values and phenotypic values for all traits are distinct, it is difficult to depict them on the same scale in the same figure. To achieve this, the breeding values and the phenotypic values were transformed into the standard normal distribution. This was accomplished by extracting a value from the mean of the trait and dividing it by its standard deviation. Additionally, an index called the Growth Index (GI), which is constructed by combining the breeding values for each trait to reflect the growth traits' general trend. ADG was expressed in kg. The GI of an animal was calculated by multiplying the four standard breeding values by 0.25 and taking their sum.

3. Results

Direct heritability was determined to be 0.01–0.05 for growth traits and 0.02 for WW in the study. The share of common environmental variance resulting from litters was found to be higher than the direct and maternal heritability, ranging between 0.24 and 0.54 (Table 1). Therefore, to obtain an accurate and unbiased estimation of genetic parameters and breeding values, common environmental effects should be accounted for in breeding programs. The genetic correlations between direct and maternal effects were found to be positive and close to the biological reach for WW. Heritabilities for growth traits, both direct and maternal, were low in the flock (Table 1). Low heritability implies a low possibility of achieving rapid genetic progress through phenotypic selection.

In the study, the genetic and the phenotypic trends for growth traits in all lambs were shown in Fig. 1. Here, the means of the standardized breeding values and phenotypic values of the animals were used for each trait. As presented in Fig. 1, the genetic trend for ADG decreased from

Table 1
Estimates of genetic parameters for growth traits in Merino sheep.

Traits	$h_d^2 \pm SE$	$m^2 \pm SE$	c_m^2	$r_{am} \pm SE$	h_t^2
BW	0.02 ± 0.02		0.27 ± 0.03		
LW45	0.01 ± 0.02		0.53 ± 0.03		
ADG	0.05 ± 0.02		0.54 ± 0.03		
WW	0.05 ± 0.03	0.02 ± 0.03	0.24 ± 0.04	1.00 ± 1.06	0.09

[a] Direct heritabilities (h_d^2), standard error (SE), maternal heritabilities (m^2), the ratio of maternal permanent environmental variance to phenotypic variance (c_m^2), genetic correlation between direct and maternal additive genetic effects (r_{am}), total heritabilities (h_t^2).

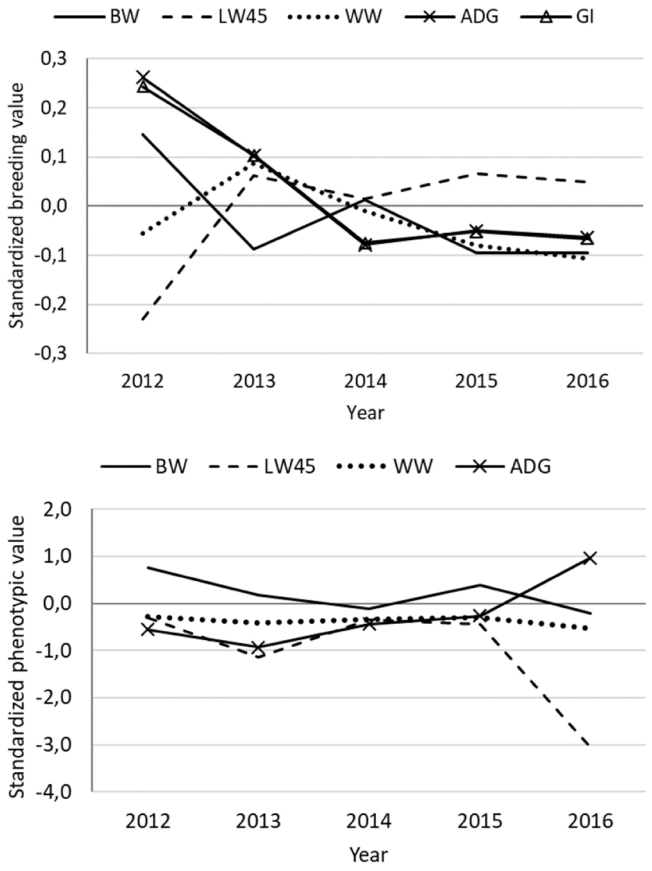


Fig. 1. Genetic (upper) and phenotypic (lower) trends for some growth traits in Merino lambs.

2012 to 2014 and subsequently stabilized. The genetic trend for BW was comparable to that of ADG and GI, indicating a downward trend following 2012. Among all qualities, the genetic trend for LW45 began increasing in 2012 and continued to be positive in 2016. On the other hand, WW and GI were steady until 2013, when they began to decline. From 2012–2015, the phenotypic trend for all traits remained steady. While ADG increased in 2015, LW45 declined significantly. What is ideal and expected is a genetic trend that continues to increase, even by a small margin. Although the genetic trend did not increase at a fixed rate, that it decreased in some years can be considered an indication that a genetic selection is either not occurring or is ineffective for the listed traits. It is intriguing that the trend for GI, which was initially slightly positive, shifted to the negative in the three years since the research was conducted.

Birth weight had high genetic correlation with LW45, WW and ADG (Table 2). The genetic correlation between LW45 and WW was high (1.00). In the present study, except for the negative and low phenotypic correlations between BW and WW (−0.08), all other phenotypic correlations were positive or medium-low. The high and positive genetic correlations between the growth traits of Merino lambs showed that improving one trait through selection will result in positive progress in the others. In other words, it indicates that indirect selection can be employed effectively.

Table 2
Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations among growth traits in Merino sheep.

Traits	BW	LW45	ADG	WW
BW		0.35	0.01	-0.08
LW45	0.94		0.35	0.51
ADG	0.99	0.62		0.29
WW	0.79	1.00	1.00	

The estimated genetic gain for growth traits is presented in Table 3. When analyzed in terms of rams, a positive but statistically insignificant genetic gain for ADG, WW, and GI can be observed (Table 3). Negative genetic gain, on the other hand, was found to be minor (−0.256) for LW45 but significant (−0.256) for BW ($p < 0.01$). Except for BW and WW, genetic gain for growth traits in sheep was positive, although none was significant. In lambs, all traits except LW45 demonstrated a negative trend. However, the values for ADG, WW, and GI are statistically significant ($p < 0.01$). Additionally, genetic gain was negative for lambs, although it was positive for ram and ewes.

Between 2010 and 2013, the genetic trend for BW in rams decreased steadily, while it increased for WW (Fig. 2). The genetic trend for LW45, on the other hand, climbed until 2012 and then decreased. ADG and GI had a genetic trend of −0.840 kg, but increased by 1.488 and 1.428 kg, respectively, in 2013. This fluctuation in some traits may imply that these traits are overlooked during selection or that rams are not effectively selected. The presence of sudden declines and increases, in particular, leads us to believe that any selection or increase made in earlier years might not have been purposeful.

When the genetic trend is analyzed in terms of ewes, BW and WW have remained consistent over time, LW45 demonstrated a significant upward trend in 2013, and ADG and GI have shown a strong upward trend since 2012. (Fig. 3). Therefore, it can be concluded that there has been a significant improvement in the growth traits of ewes since 2012.

4. Discussion

Numerous studies have identified genetic trends for early growth traits in lambs of various breeds (Hossein-Zadeh, 2012; Javed et al., 2013; Mallick et al., 2016; Yadav et al., 2018). Genetic parameters should be recognized for accurate genetic evaluations and effective selection for economically important traits. There is a need for a comprehensive evaluation of implementations to ensure that breeding programs obtain the maximum possible gain (Lamuno et al., 2018). The maternal effect is defined as a situation in which the phenotype of the offspring is determined not only by its own environment and genotype, but also by that of their dams. For this reason, due to genetic or environmental differences between ewes, maternal effects are important in the development and expression of economic traits. The inclusion of maternal effects in the model reduces bias and increases the precision of genetic parameters (Rajkumar et al., 2021). Estimates of correlations between direct and maternal genetic effects (r_{am}) cover a wide range of values in the literature. For example, Kariuki et al. (2010) reported $r_{am} = -0.94$ for WW in the Dorper breed, whereas in the present study, we found $r_{am} = 1.00$ for WW in Merino. The biological interpretation of extreme values is perplexing and has generated considerable discussion. Often, inconsistencies among published results are due to differences in the structure of the data and pedigree information employed. We can conclude that there is no conflict between direct and maternal genetic effects on weaning weight in this Merino sheep population.

Genetic correlation plays an important role in the success of a breeding program. For instance, while selection for a trait increases the performance in another positively-related trait, it reduces the

Table 3
Annually genetic improvement (regression coefficients of estimated breeding values of ram on birth year).

Trait	Ram	Ewe	Lamb
BW, kg	-0.0021 ± 0.002^{ns}	-0.0001 ± 0.0002^{ns}	-0.0010 ± 0.0005^{ns}
LW45, kg	-0.0024 ± 0.008^{ns}	0.0006 ± 0.0017^{ns}	0.0035 ± 0.0020^{ns}
ADG, g	-0.3010 ± 0.652^{ns}	0.3580 ± 0.2060^{ns}	0.0200 ± 0.1310^{ns}
WW, kg	-0.0005 ± 0.013^{ns}	-0.0021 ± 0.0013^{ns}	-0.3130 ± 0.0104^{ns}
GI	-0.0770 ± 0.162^{ns}	0.0891 ± 0.0510^{ns}	-0.0792 ± 0.0245*

ns: Not significant ($p > 0.05$).
* ($p < 0.05$).

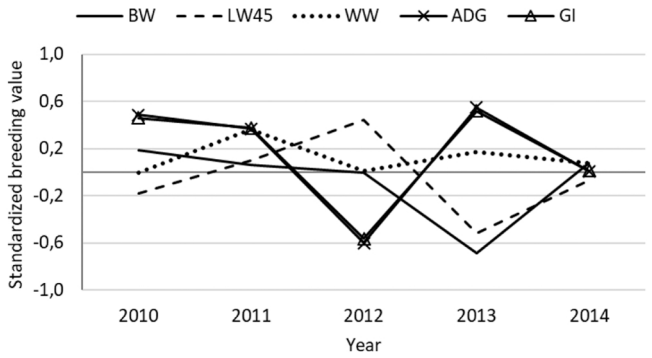


Fig. 2. Genetic trend for some growth traits in Merino rams.

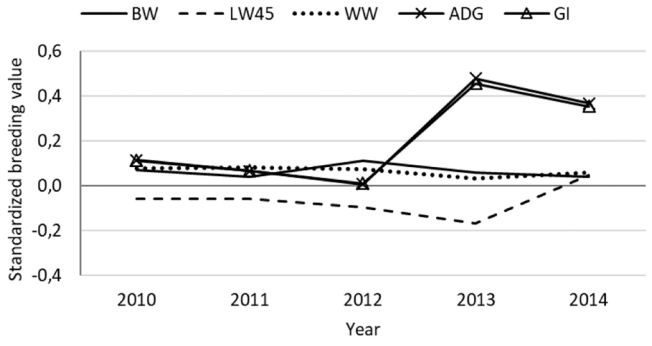


Fig. 3. Genetic trend for some growth traits in Merino ewes.

performance of a negatively-related trait (Rajkumar et al., 2021). Genetic correlation between two traits occurs naturally due to the pleiotropic effects of genes on both traits. Therefore, genetic correlations are essential for the determination of the optimal breeding strategies required for genetic progress of the lambs' growth traits. This study indicates a high and positive genetic correlation between BW, and that the other growth traits and genes, which are responsible for increasing BW, increase the other traits as well. In other words, the high relationship of BW with the other traits indicates that selection for BW will result in a positive response in the other traits. For example, the high, positive correlation between LW45 and WW (1.00) showed that the lambs growing more rapidly in the pre-weaning period would grow more rapidly throughout the weaning period, too.

The high genetic correlation found in this study between all growth traits indicates that a GI encompassing all of them can be used for selection. The genetic gain for GI was estimated to be 0.118 and 0.087 kg/year in rams and ewes, respectively (Table 3). A response obtained through the application of a multitrait selection index will be smaller than a response realized individually for each trait. Hence, making a selection for any of these traits might result in a positive expectation for another growth trait. However, upon examination of the Figures, it is observed that the results did not hold true in this manner and there were fluctuations over the years in all the traits. Hence, based on the growth traits of this flock, it can be concluded that no genetic selection was made or that the selection that was made was ineffective. Several previous studies (Mohammadi et al., 2015; Haile et al., 2018; Habtegiorgis et al., 2020) have also reached similar findings. On the contrary, there are also studies indicating that there is a weak relationship between BW and the subsequent live weights (Duguma et al., 2002; Gizaw and Joshi, 2004). These researchers reported that the absence of a strong correlation between BW and live weights in the subsequent period favored selection for each trait independently of the others.

Accurate prediction of the breeding value of growth traits of lambs is an integral component of the majority of genetic improvement breeding programmes (Eteqadi et al., 2016; Baneh and Ahmadpanah, 2018, Yadav et al., 2018). As seen in Table 3, the genetic trend had irregular fluctuations and resulted in genetic gain for ADG (−0.132 kg/year) ($p < 0.05$) and WW (−0.047 kg/year) ($p < 0.05$) in lambs over a 5-year period. Except for LW45, the growth traits of lambs did not improve over the years in Merino lambs (Fig. 1). Similarly, Aguirre et al. (2016) reported margianlly negative genetic trend of −0.001 kg/year for BW and positive genetic trend of 0.04 kg/year for WW in Santa Ines sheep. Jawasreh et al. (2018) reported significant ($p < 0.01$) negative genetic trends of −0.0005 and −0.006 kg/year for BW and WW in Awassi sheep, respectively. Yadav et al. (2018) obtained negative genetic trends of −0.09 and −0.25 kg/year for BW and WW in Munjal sheep, respectively. Habtegiorgis et al. (2020) reported negative genetic trends of −0.0026 kg/year for BW, and positive genetic trends 0.048 kg/year for WW in Doyogena sheep ($p > 0.05$). Farokhad et al. (2011), on the other hand, reported significant ($p < 0.01$) and positive genetic trends of 2 and 7 g/year for BW and WW in Arman sheep, respectively. Eteqadi et al. (2016) reported significant positive direct genetic trends of 0.51 and 5.56 g/year for BW and WW in Iran sheep, respectively ($p < 0.001$). Mallick et al. (2016) discovered significant positive genetic trends of 0.005 kg/year for BW and non-significant positive genetic trends of 0.0008 kg/year for WW in Bharat Merino sheep ($p < 0.01$). Ahmadpanah et al. (2016) reported significant and positive direct genetic trends of 0.93 and 43.74 g/year for BW and WW in Iranian-Black sheep, respectively ($p < 0.01$). Baneh and Ahmadpanah (2018) observed significant positive direct genetic trends of 2.34 and 46.20 g/year for BW and WW in Ghezel sheep, respectively. In the present study, the trend fluctuation observed in the lambs might be due to insufficient or ineffective ram selection or changes in feeding regimes and management practices over time. Optimal environmental conditions should be provided in order to align phenotypic and genetic trends and achieve a greater genetic improvement. However, annual genetic improvement was observed in all other traits except for WW, ADG and GI in rams, but it was statistically insignificant.

5. Conclusions

A factor contributing to insufficient genetic improvement in the flock where the study was conducted was the low direct heritability. Genetic changes within a flock over the years are smaller than the effects of environmental changes. A significant effect can be realized only after the implementation of the same breeding goal for several years. It is an intriguing finding that despite two generations of selection, the desired response could not be obtained, particularly for the rams. As demonstrated in this study, the implemented breeding program prevented a possible genetic gain in growth traits, particularly for rams. A considerable rate of genetic improvement in growth traits could be obtained by selecting rams based on their breeding values. The results generally indicated the importance of developing an effective selection program to improve the growth traits of Merino lambs. As a result, increasing additive genetic variance for these traits and basing selection on BLUP will almost certainly improve the response.

Declaration of Competing Interest

None of the authors have any conflict of interest to declare.

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