Iranian Society of Animal Science

Journal of Livestock Science and Technologies

Shahid Bahonar University of Kerman

ISSN: 2322-3553 (Print) ISSN: 2322-374X (Online)

**Paper type:** Original Research

# Sexual dimorphism in early body weight traits of Raeini Cashmere goat: sex-specific heritability and cross-sex correlations

*Morteza Mokhtari[1,*], Arsalan Barazandeh[1], Zahra Roudbari[1], Farhad Ghafouri-Kesbi [2] and Najmeh Kargar Borzi[3]*

[1]*Department of Animal Science, Faculty of Agriculture, University of Jiroft, P.O. Box 364, Jiroft, Iran*
[2]*Department of Animal Science, Faculty of Agriculture, Bu-Ali Sina University, Hamedan, Iran*
[3]*Animal Science Research Department, Kerman Agricultural and Natural Resources Research and Education Center, AREEO, Kerman, Iran*

*Corresponding author,
Tel: +983443347066
E-mail address:
msmokhtari@ujiroft.ac.ir

*Received:* 10 Apr 2022,
*Accepted:* 12 Jun 2022,
*Published online:* 15 Jun 2022,

**ORCID**
Morteza Mokhtari
0000-0002-3971-628X
Arsalan Barazandeh
0000-0001-7716-7624
Zahra Roudbari
0000-0002-3357-3126
Farhad Ghafouri-Kesbi
0000-0002-2219-055X
Najmeh Kargar Borzi
0000-0001-9907-1877

**Abstract** Pedigree and body weight records collected from 1979 to 2013 at the Breeding Station of Raeini Cashmere goat, south-east of Iran, were used for investigating genetic aspects of sexual dimorphism (SD) for birth weight (BW), weaning weight (WW) and six-month weight of the breed. The SD levels, calculated as male/female ratio at birth, weaning, and six months of age, were 1.08, 1.14, and 1.16, respectively. Genetic analyses for investigating the SD performed by applying six bivariate animal models included different combinations of direct additive genetic, maternal additive genetic, and maternal permanent environmental effects. Estimates of phenotypic variance ($\sigma_p^2$) were different between males and females and were more pronounced at weaning and six months of body weight. For all studied traits, direct additive genetic, residual, and phenotypic variances in male kids were higher than in female kids. Direct heritability estimates for BW, WW, and 6MW in male kids were 0.24, 0.17, and 0.10, respectively. The corresponding estimates in female kids were 0.21, 0.21, and 0.09, respectively. Cross-sex differences for direct heritability estimates for the studied traits were statistically non-significant, implying that body weight traits could be considered the same in male and female Raeini Cashmere kids. The estimates of between-sex correlations for each trait were positive and statistically significant. Direct genetic correlations between sexes were 0.90, 0.87, and 1.00 for BW, WW, and 6MW, respectively, indicating that selection for the investigated body weights in male kids would result in a correlated response in females and, consequently, would prevent phenotypic divergence. Furthermore, the high cross-sex genetic correlations for each trait implied a similar genetic structure in both sexes.

**Keywords:** genetic parameters, goat, growth, maternal effects, sexual dimorphism

## Introduction

The difference between the male and female of any species in phenotypic characteristics, such as the size and body weigth, is known as the sexual dimorphism (SD) (Andersson, 1994). In other words, SD is defined as the difference between phenotypic characteristics such as body weight and size of conspecific male and female animals (Badyaev, 2002). Several explanations have been presented for addressing SD (Darwin, 1871; Rensch, 1959; Badyaev, 2002). Darwin (1871) pointed out that due to different reproductive roles of the male and female, they are selected differentially to perform these roles, which bring about variations in the expression of phenotypic characteristics in different sexes. The empirical Rensch's rule, as a well-known established hypothesis explaining SD, notes that SD increases with body weight in species in which the males are the larger sex, and decreases with body size in those that females are larger (Rensch, 1959). Badyaev (2002) stated that SD is the outcome of the combined effects of sex-specific selection pressure, sex-biased arose phenotypic and genetic differences, and cross-sex genetic correlations.

Sexual dimorphism can be applied in breeding programs if supported by genetic differences between the sexes. Sex-related variance heterogeneity could be considered in the genetic evaluation programs by considering distinct traits in female and male individuals (Ghafouri-Kesbi et al., 2015). In small ruminant species such as sheep and goats, body weight is one of the most outstanding examples of sexual dimorphism (Ghafouri-Kesbi et al., 2015). Sexual dimorphism in body weight has been studied in several goat (Baneh et al., 2021; Mandal et al., 2022) and sheep (Ghafouri-Kesbi et al., 2015; Ghafouri-Kesbi and Notter, 2016; Ghafouri-Kesbi and Baneh, 2018; Noorian et al., 2021) breeds.

The Raeini Cashmere goat is a small-sized breed, with white light, grey and, dark brown cashmere colors. The breed, generally considered a dual-purpose, meat and Cashmere, is mainly kept by nomadic flock holders under traditional and low-input management systems. In this breed, large differences in growth were observed between males and females. Mokhtari et al. (2018) reported that males were significantly heavier than females at birth, weaning, and six months of age. If there are sizeable differences in inheritance patterns between the males and females, divergent selection could be achieved via sex-specific breeding programs. Due to the lack of information regarding the genetic and phenotypic aspects of SD in Raeini Cashmere goat, which are important for developing an efficient breeding program, the present study was carried out to study SD in early growth traits of the breed.

## Materials and methods

### *Data and flock management*

The pedigree and data used in the present investigation were collected from 1979 to 2013 at the Raeini Cashmere Goat Breeding Station in Baft, Kerman Province, south-east part of Iran. Mating occurred from August to October, and consequently kidding period lasted from January to March. The does were first exposed to bucks at about 18 months of age. Detailed information about flock management is reported by Mokhtari et al. (2018).

### *Evaluated traits*

The studied traits included birth weight (BW), weaning weight (WW), and six-month weight (6MW). Records with the unknown dam, sex, birth type and, birth year and those outside the range mean ±3×S.D. were removed from the data set. The cross-sex summary statistics of the data are shown in Table 1.

**Table 1.** Descriptive statistics for the studied body weight traits in Raeini Cashmere goat

| Item | Traits (kg) ¥ | | | | | |
|---|---|---|---|---|---|---|
| | BW | | WW | | 6MW | |
| | Male | Female | Male | Female | Male | Female |
| Numbers of records | 2313 | 2433 | 1602 | 1665 | 1374 | 1482 |
| Mean | 2.42 | 2.23 | 11.05 | 9.71 | 15.51 | 13.42 |
| Standard deviation | 0.41 | 0.39 | 3.17 | 2.64 | 3.93 | 3.17 |
| Minimum | 1.10 | 1.10 | 3.40 | 4.00 | 5.50 | 5.00 |
| Maximum | 5.00 | 4.30 | 27.50 | 22.00 | 32.00 | 31.20 |
| Coefficient of variation (%) | 16.94 | 17.49 | 28.69 | 27.19 | 25.34 | 23.62 |

¥ BW: birth weight; WW: weaning weight; 6MW: six-month weight.

### *Statistical analyses*

To identify significant fixed effects for inclusion in the models of genetic analysis, preliminary analyses were performed applying the general linear model (GLM) procedure (SAS, 2004). Fixed effects considered in the models were the age of dam at kidding, birth year, and birth type of kids. The ages of kids at weighing for weaning and six-month body weights (in days) were fitted as a linear covariate in the models for WW and 6MW, respectively. Sexual dimorphism in BW, WW and 6MW was evaluated by applying the Lovich and Gibbons ratio (Lovich and Gibbons, 1992). For species where males are larger than females, SD in body weight is calculated as M/F, and when females are larger, it is calculated as 2–F/M, where M and F are the mean body weights of males and females, respectively.

For genetic analysis of SD, the cross-sex phenotypic measurements of the trait of interest should be considered as a distinct trait (Maniatis et al., 2013). Genetic analyses for investigating the SD performed by applying six bivariate animal models included different combinations of direct additive genetic, maternal additive genetic, and maternal permanent environmental effects as follows:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix}\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \qquad \text{Model 1}$$

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix}\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Z_{pe1} & 0 \\ 0 & Z_{pe2} \end{bmatrix}\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \qquad \text{Model 2}$$

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix}\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Z_{m1} & 0 \\ 0 & Z_{m2} \end{bmatrix}\begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \qquad \text{Cov(a,m)=0} \qquad \text{Model 3}$$

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix}\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Z_{m1} & 0 \\ 0 & Z_{m2} \end{bmatrix}\begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \qquad \text{Cov(a,m)=}\mathbf{A}\sigma_{am} \qquad \text{Model 4}$$

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix}\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Z_{pe1} & 0 \\ 0 & Z_{pe2} \end{bmatrix}\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} Z_{m1} & 0 \\ 0 & Z_{m2} \end{bmatrix}\begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \qquad \text{Cov(a,m)=0} \qquad \text{Model 5}$$

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix}\begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Z_{pe1} & 0 \\ 0 & Z_{pe2} \end{bmatrix}\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} Z_{m1} & 0 \\ 0 & Z_{m2} \end{bmatrix}\begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \qquad \text{Cov(a,m)=}\mathbf{A}\sigma_{am} \qquad \text{Model 6}$$

where, indices 1 and 2 denote male and female kids, respectively; $\mathbf{y}_{1(2)}$, $\mathbf{b}_{1(2)}$, $\mathbf{a}_{1(2)}$, $\mathbf{pe}_{1(2)}$, $\mathbf{m}_{1(2)}$, and $\mathbf{e}_{1(2)}$ are vectors of records, fixed, direct additive genetic, maternal permanent environmental, maternal additive genetic, and residual effects, respectively. The matrices of $\mathbf{X}_{1(2)}$, $\mathbf{Z}_{a1(2)}$, $\mathbf{Z}_{pe1(2)}$, and $\mathbf{Z}_{m1(2)}$ are the corresponding design matrices associating the fixed, direct additive genetic, maternal permanent environmental, maternal additive genetic, and residual effects to the vector of records, respectively. It was assumed $\mathbf{a}$ ~ N(0, $\mathbf{A}\sigma_a^2$), $\mathbf{m}$ ~ N(0, $\mathbf{A}\sigma_m^2$), $\mathbf{pe}$ ~ N(0, $\boldsymbol{I_d}\sigma_{pe}^2$), and $\mathbf{e}$ ~ N(0, $\boldsymbol{I_n}\sigma_e^2$). **A** is the numerator relationship matrix and $\sigma_{am}$ presents covariance between direct additive and maternal additive effects. $\mathbf{I}_d$ and $\mathbf{I}_n$ are identity matrices of order equal to the number of dams and number of records, respectively; and $\sigma_a^2$, $\sigma_{pe}^2$, $\sigma_m^2$ and, $\sigma_e^2$ are additive genetic, maternal permanent environmental, maternal additive genetic, and residual variances, respectively.

The best bivariate animal model for each trait was selected applying the Bayesian Information Criterion (BIC; Schawarz, 1978). The model with the lowest BIC was considered the best model. Model fitting and genetic analysis were carried out using the WOMBAT program (Meyer, 2013).

Although heritability estimates are more easily understood, it has been argued that heritabilities do not provide a suitable means of comparing genetic variation between different traits, especially where the amount of environmental variations varies between traits (Houle, 1992). For such comparisons, coefficients of variation are more suitable than the non-standardized variance components (Houle, 1992). The additive coefficient of variation ($CV_a$) was calculated for each trait as:

$$CV_a = \frac{\sqrt{\sigma_a^2}}{\bar{x}} \times 100$$

where, $\sigma_a^2$ is the additive genetic variance and $\bar{x}$ is the arithmetic mean of the trait.

## Results and Discussion

In the present investigation, the mean body weight of male and female kids increased by, respectively, 6.41 and 6.02 times from birth to six months of age (Table 1). The male kids were 8.52%, 13.80%, and 15.57% heavier than female kids at birth, weaning and six months of age, respectively. The SD levels, calculated as M/F ratio (Lovich and Gibbons, 1992) at birth, weaning, and six months of age, were 1.08, 1.14, and 1.16, respectively, which indicated that from weaning to six months of age, males gained more weight than females compared to pre-weaning growth phase which resulted in a higher SD level at six months of age. The increasing trend for SD from birth to six months of age may be explained partly by differences in the endocrine system of males and females and the occurrence of sexual maturity (Noorian et al., 2021). Steroid hormones like testosterone and estrogen influence the growth of males and females in a different manner. In males, testosterone accelerates muscle growth by affecting the rate of protein synthesis. While, in females, estrogen modifies growth by limiting the length of long bones and leads to a smaller body size (Mateescu and Thonney, 2002). Snell and Turner (2018) pointed out SD may be the consequence of differences in circulating levels of gonadal sex hormones or, in mammals, activation of genes on the Y chromosome of males or inactivation of one of the two X chromosomes in females.

Baneh et al. (2021) reported the SD levels for the BW, WW and, 6MW of Markhoz goat as 1.09, 1.17 and 1.14, respectively. Mandal et al. (2022) studied sexual dimorphism in growth traits of Jamunapari goats of India and reported that male kids were 9.9, 6.8, and 9.3% heavier than female kids for BW, WW, and 6MW, respectively. They also noted the level of SD for BW, WW, and 6MW of Jamunapari kids as 1.10, 1.07, and 1.09, respectively. Polak and Frynta (2009) pointed out that during domestication, SD has decreased considerably in domestic animals, though it is still observed in livestock. The SD levels for adult body mass in wild and domestic goats were measured as 1.83 and 1.36, respectively (Polak and Frynta, 2009), higher than the values obtained in the present study. Sexual dimorphism could be significant in breeding so that where SD is present, it can easily be applied for developing efficient breeding programs for domestic animals.

### *Variance components and genetic parameters*

The BIC values for the studied traits under the investigated bivariate animal models are shown in Table 2. The most appropriate bivariate model for BW, WW, and 6MW contained the direct additive genetic and maternal permanent environmental effects (Model 2).

The estimated values of variance components and genetic parameters for the studied traits in male and female Raeini Cashmere kids under the best bivariate animal model are presented in Table 3. Heterogeneity of variance components was observed between male and female Raeini Cashmere kids for all the studied traits. Estimates of phenotypic variance ($\sigma_p^2$) were different between males and females and were more pronounced at weaning and six-month of body weight. For all studied traits, direct additive genetic, residual, and phenotypic variances in male kids were higher than in female kids. Similarly, Mandal et al. (2022) noted that male Jamunapari kids had greater $\sigma_p^2$ than female kids for all post-natal studied body weights. As shown in Table 3, for both sexes, the estimates of $\sigma_p^2$ for all the studied traits increased with increasing age. Similar increases in $\sigma_p^2$ of body weights with increasing age were reported in Markhoz (Baneh et al., 2021) and Jamunapari (Mandal et al., 2022) goat breeds.

The total resemblance among relatives can be quantified by $v^2 = 1 - e^2$, where $e^2$ is the ratio of residual variance to the phenotypic variance (Mandal et al., 2022). Values of $v^2$ were similar for BW of male and female kids. But $v^2$ estimates for WW and 6MW in female kids were greater than in male kids (Table 3). These differences would lead to a higher selection response in females for WW and 6MW. Contrary to us, Mandal et al. (2022) reported higher estimates of $v^2$ for BW, WW, and 6MW of male Jamunapari kids than female ones.

Direct heritability estimates for BW, WW, and 6MW in male kids were 0.24, 0.17, and 0.10, respectively. The corresponding estimates in female kids were 0.21, 0.21, and 0.09, respectively. Direct heritability estimates for BW and 6MW in male kids were 14.28 % and 11.11 % higher than those in female kids, respectively. On the other hand, direct heritability of WW in females was 23.53% higher than that in males. Similar trends were observed for $CV_a$ values. The estimated values for direct heritability of the studied traits in the present study were in the ranges reported in the literature. Mandal et al. (2022) reported heritability estimates of 0.06 and 0.09 for BW, 0.32 and 0.39 for WW, and 0.22 and 0.43 6MW in male and female Indian Jamunapari goats, respectively. Baneh et al. (2021) studied SD in body weight of the Markhoz goat breed and reported heritability estimates of 0.31 and 0.29 for BW, 0.13 and 0.15 for WW, and 0.13 and 0.20 for 6MW in male and female kids, respectively. Noorian et al. (2021) estimated direct heritabilities of 0.07, 0.10, and 0.08 for BW, WW, and 6MW of male Baluchi lambs, respectively. The corresponding estimates in female lambs were 0.07, 0.05, and 0.04, respectively.

Maternal permanent environmental variances and $pe^2$ estimates in female kids were higher than those of male kids. The $pe^2$ estimates for BW, WW and 6MW in male kids were 0.14, 0.12, and 0.13, respectively. The corresponding estimates in female kids were 0.17, 0.17, and 0.18, respectively. The $pe^2$ estimates for BW, WW, and 6MW of male Jamunapari kids were 0.12, 0.12, and 0.05, respectively. The corresponding estimates in female Jamunapari kids were 0.06, 0.09, and 0.12, respectively (Mandal et al., 2022). In a recently published paper, Baneh et al. (2021) reported $pe^2$ estimates of 0.12 and 0.10, 0.08 and 0.04, and 0.11 and 0.04 for BW, WW, and 6MW in male and female Markhoz goats, respectively. Ghafouri-Kesbi and Baneh (2018) studied SD in Iran-Black sheep and reported $pe^2$ estimates of 0.19 and 0.16 and 0.13 and 0.09 for WW and 6MW in male and female lambs, respectively. In another study, Ghafouri-Kesbi and Notter (2016) estimated 0.18 and 0.22 and 0.13 and 0.04 for $pe^2$ of BW and WW in male and female Afshari lambs, respectively.

**Table 2.** BIC values for the studied traits under investigated bivariate animal models

| Model | Traits ¥ | | |
|---|---|---|---|
| | BW | WW | 6MW |
| Model 1 | -4601.862 | 9399.252 | 9171.790 |
| Model 2 | **-4681.062** | **9387.562** | **9161.524** |
| Model 3 | -4673.392 | 9399.204 | 9175.228 |
| Model 4 | -4626.598 | 9423.464 | 9205.300 |
| Model 5 | -4661.066 | 9410.882 | 9184.956 |
| Model 6 | -4631.096 | 9436.840 | 9216.244 |

¥ BW: birth weight; WW: weaning weight; 6MW: six-month weight.

Although the estimates of $h^2$ and $pe^2$ varied between male and female kids (Table 3), the differences were not statistically significant. Noorian et al. (2021) also reported statistically non-significant between-sex differences in $h^2$ estimates for body weight traits in Baluchi sheep.

Between-sex estimates of correlations for the studied traits in Raeini Cashmere goat are shown in Table 4. All estimated correlations were positive and statistically significant. Direct genetic correlations between sexes were 0.90, 0.87, and 1.00 for BW, WW, and 6MW, respectively. Poissant et al. (2010) noted that cross-sex additive genetic correlation shows how similarities in phenotypes of males and females are co-inherited. The high estimated genetic correlations imply that the studied body weights in male and female Raeini Cashmere goats are controlled by many common genes, i.e., a similar genetic structure in both sexes. On the other hand, direct genetic correlation estimates between male and female Raeini Cashmere kids for BW and WW were lower than unity, implying some degree of dimorphism for these traits. Falconer and Mackay (1996) noted when the genetic correlation between two traits is less than unity, then these traits can be considered two distinct traits. Therefore, it is justified to analyze the traits by applying sex-specific models.

**Table 3.** Estimates of variance components and genetic parameters for the studied traits in male and female Raeini Cashmere kids

| Traits¥ | Sex | $\sigma_a^2$ | $\sigma_{pe}^2$ | $\sigma_e^2$ | $\sigma_p^2$ | $h^2$± S.E. | $pe^2$± S.E. | $v^2$ | CV$_a$ |
|---|---|---|---|---|---|---|---|---|---|
| BW | Male | 0.036 | 0.020 | 0.091 | 0.147 | 0.24±0.06 | 0.14±0.03 | 0.38 | 7.84 |
| | Female | 0.027 | 0.022 | 0.079 | 0.128 | 0.21±0.04 | 0.17±0.04 | 0.38 | 7.37 |
| WW | Male | 1.293 | 0.891 | 5.188 | 7.372 | 0.17±0.06 | 0.12±0.04 | 0.30 | 10.29 |
| | Female | 1.170 | 0.966 | 3.448 | 5.584 | 0.21±0.06 | 0.17±0.04 | 0.38 | 11.14 |
| 6MW | Male | 1.074 | 1.361 | 8.068 | 10.503 | 0.10±0.04 | 0.13±0.05 | 0.23 | 6.68 |
| | Female | 0.542 | 1.397 | 5.751 | 7.690 | 0.09±0.04 | 0.18±0.04 | 0.25 | 5.48 |

¥ BW: birth weight; WW: weaning weight; 6MW: six-month weight, $\sigma_a^2$: additive genetic variance, $\sigma_{pe}^2$: maternal permanent environmental variance, $\sigma_e^2$: residual variance, $\sigma_p^2$: phenotypic variance, $h^2$: direct heritability, $pe^2$: ratio of maternal permanent environmental variance to phenotypic variance, $v^2 = 1 - \frac{\sigma_e^2}{\sigma_p^2}$, CV$_a$: additive coefficient of variation, S.E.: standard error

Genetic correlations between male and female Markhoz kids for BW, WW, and 6MW were 0.95, 0.97, and 0.88, respectively (Baneh et al., 2021). In a recently published paper, Mandal et al. (2022) reported positive and high genetic correlation estimates of 1.00, 0.97 and 0.66 between male and female Jamunapari kids for BW, WW and 6MW, respectively. Ghafouri-Kesbi et al. (2015) reported cross-sex genetic correlation estimates between male and female Zandi lambs for BW, WW, and 6MW as 0.82, 0.92 and 0.92, respectively. Ghafouri-Kesbi and Notter (2016) estimated the genetic correlations as 0.98 and 0.99 for BW and WW in Afshari lambs, respectively.

Maternal permanent environmental correlation between sexes for BW (0.97) was lower than the corresponding direct genetic correlation (0.90). Maternal permanent environmental correlation estimates between sexes for WW and 6MW were 0.36 and 0.57, respectively, implying differential maternal permanent environmental effects of the doe on male and female kids. Mandal et al. (2022) reported cross-sex maternal permanent environmental correlation estimates of 0.77, 1.00 and, 1.00 for BW, WW, and 6MW of Jamunapari kids, respectively. Ghafouri-Kesbi and Baneh (2018) estimated a cross-sex maternal permanent environmental correlation of 1.00 and 0.66 for WW and 6MW of Iran-Black lambs, respectively. Phenotypic correlation estimates between sexes for the studied traits were lower than direct genetic and maternal permanent environmental estimates. Similarly, Noorian et al. (2021) estimated cross-sex phenotypic correlations of 0.26, 0.22, and 0.19 for BW, WW, and 6MW of Baluchi lambs, respectively.

## Conclusions

Male Raeini Cashmere kids were heavier at birth, weaning, and six months of age than their female counterparts, and had higher phenotypic, additive genetic, and residual variances for the studied body weight traits. The cross-sex differences for direct heritability estimates of the studied traits were non-significant, implying that body weight traits could be considered the same in male and female Raeini Cashmere kids. Sex-wise genetic correlations for body weight traits were positive and high, indicating that selection for body weights in male kids would result in a correlated response in females and, consequently, would prevent phenotypic divergence. Furthermore, the high cross-sex genetic correlations for each trait implied a similar genetic structure in both sexes.

**Table 4.** Cross-sex correlations for the studied body weight traits in Raeini Cashmere gost

| Traits ¥ | r$_a$ | r$_{pe}$ | r$_p$ |
|---|---|---|---|
| BW | 0.90±0.13 | 0.97±0.15 | 0.35±0.04 |
| WW | 0.87±0.07 | 0.36±0.10 | 0.13±0.05 |
| 6MW | 1.00±0.24 | 0.57±0.23 | 0.17±0.05 |

¥ BW: birth weight; WW: weaning weight; 6MW: six-month weight. r$_a$: direct genetic correlation, r$_{pe}$: maternal permanent environmental correlation, r$_p$: phenotypic correlation.

## Acknowledgments

The authors wish to thank the staff of Raeini Cashmere Breeding Station and Agriculture Jihad Organization of Kerman Province for helping in data collection and flock management.

## References

Andersson, M., 1994. Sexual Selection. Princeton, NJ, Princeton University Press.

Badyaev, A.V., 2002. Male and female growth in sexually dimorphic species: harmony, conflict, or both? *Comments on Theoretical Biology* 7, 11-33.

Baneh, H., Ghaderi-Zefrehei, M., Pouryaei, R., Mandal, A., 2021. Genetic analysis of sexual size dimorphism in Markhoz goat. *Tropical Animal Health and Production* 53, 67-78

Darwin, C., 1871. The Descent of Man, and Selection in Relation to Sex. Murray, London, UK.

Falconer, D.S., Mackay, T.F.C., 1996. Introduction to Quantitative Genetics. Harlow, Essex, UK.

Ghafouri-Kesbi, F., Baneh, H., 2018. Genetic aspects of sexual size dimorphism in a synthesized breed of sheep. *Meta Gene* 17, 177-183.

Ghafouri-Kesbi, F., Notter, D. R., 2016. Sex influence on genetic expressions of early growth in Afshari lambs. *Archives of Animal Breeding* 59, 9-17.

Ghafouri-Kesbi, F., Rahimi Mianji, G., Ansari Pirsaraei, Z., Hafezian, S. H., Baneh, H., Soleimani, B., 2015. A genetic study on sexual dimorphism of bodyweight in sheep*. Animal Production Science* 55, 101-106.

Houle, D., 1992. Comparing evolvability and variability of quantitative traits. *Genetics* 130, 195-204.

Lovich, J.E., Gibbons, J.W., 1992. A review of techniques for quantifying sexual size dimorphism. *Growth, Development and Aging* 56, 269-281.

Mandal, A., Baneh, H., Rout, P.K., Notter, D.R., 2022. Genetic analysis of sexual dimorphism in growth of Jamunapari goats of India. *Journal of Animal Breeding and Genetic*s 139, 1-14.

Maniatis, G., Demiris, N., Kranis, A., Banos, G., Kominakis, A., 2013. Genetic analysis of sexual dimorphism of body weight in broilers. *Journal of Applied Genetics* 54, 61-70.

Mateescu, R.G., Thonney, M.L., 2002. Gene expression in sexually dimorphic muscles in sheep. *Journal of Animal Science* 80, 1879-1887.

Meyer, K. 2013. WOMBAT- A Programme for Mixed Model Analyses by Restricted Maximum Likelihood. User Notes, Animal Genetics and Breeding Unit, Armidale, Australia.

Mokhtari, M.S., Moghbeli Damaneh, M. and Abdollahi Arpanahi, R., 2018. The application of recursive multivariate model for genetic evaluation of early growth traits in Raeini Cashmere goat: A comparison with standard multivariate model. *Small Ruminant Research* 165, 54-61.

Noorian, M., Joezy-Shekalgorabi, S., Emam Jomeh Kashan, N., 2021. Estimation of genetic parameters for sexual dimorphism in body weight of Baluchi sheep. *Journal of Livestock Science and Technologies* 9, 61-68.

Poissant, J., Wilson, A.J., Coltman, D.W., 2010. Sex-specific genetic variance and the evolution of sexual dimorphosm: A systematic review of cross-sex genetic correlation. *Evolution* 64, 97-107.

Polak, J., Frynta, D., 2009. Sexual size dimorphism in domestic goats, sheep, and their wild relatives. *Biological Journal of the Linnean Society* 98, 872-883.

Rensch, B., 1959. Evolution above the Species Level. London, Methuen and Co. Ltd.

SAS (Statistical Analysis System). 2004. SAS User's Guide, Version 9.1. SAS Institute Inc. Cary, North Carolina, USA.

Schawarz, G., 1978. Estimating the dimension of a model. *The Annals of Statistics* 6, 461-464.

Snell, D. M., Turner, J. M. A., 2018. Sex chromosome effects on male-female differences in mammals. *Current Biology* 28, R1313-R1324.