

Estimation of genetic parameters for horn traits and essential economic traits in Inner Mongolia Cashmere goats

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Abstract: Horns are unique cranial appendages in ruminants, and horn traits are useful in indirect selection of growth traits in goat. However, genetic parameters for horns have not been estimated in Inner Mongolia Cashmere goats. In this study, we collected pedigree information with 7 632 records from 2 049 Inner Mongolia Cashmere goats during 2017 to 2019 to study horn base interval (HBI), horn length (HL) and horn base circumference (HBC), as well as four essential economic traits including cashmere length (CL), staple length (SL), cashmere weight (CW) and live body weight (LBW). Genetic parameters and (co)variances were estimated by a multivariate animal model, average information restriction maximum likelihood method in WOMBAT software. The estimates of heritability for HBI, HL, HBC, CL, SL, CW and LBW were 0.31, 0.25, 0.30, 0.10, 0.34, 0.21 and 0.12, respectively, indicating moderate heritability of horn traits in Cashmere goats. We found out that coefficients of genetic correlations between three horn traits were –0.31 to 0.78, while those between three horn traits and four economic traits ranged from –0.05 to 0.52. Strong genetic correlations were observed between horn traits (HBC-HL, HBC-HBI). In addition, a strong phenotypic correlation was revealed for horn and economic traits (HL-LBW). In summary, this study uncovered genetic characteristics and relationships for horn traits in Cashmere goats, which will facilitate the breeding practices of Cashmere goats by providing easier measurement than common economic traits.

Keywords: genetic parameter; Inner Mongolia Cashmere goat; horn and economic traits

Similarly like in other ruminants, horns are typical features of goats. Horn shapes are different in various goat breeds. In actual production processes, horn

traits among individuals in the same population are also different, indicating the complex genetic basis of horns affected by modified genes and hormones.

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Johnston et al. (2010) developed microsatellite markers in a targeted region of the Soay sheep genome and refined the location of the Horns locus (Ho) to a ~7.4 cM interval on chromosome 10 (level of development = 8.78). The genetic variation in both horn type and horn length is attributable to the same chromosomal region. Wang et al. (2014) reported that the horn in Laoshan dairy goat has a significant effect on milk production. However, only a few studies on horn traits in Cashmere goats have been reported so far, especially their genetic evaluation. For example Han (2000) demonstrated that the high and positive phenotype correlation was obtained between the horn base interval and cashmere production in the offspring of Liaoning Cashmere goats and Ningxia local Cashmere goats. The Inner Mongolia Cashmere goats (IMCGs) are a famous local breed in China with dual-purpose long-term natural selection and artificial selection, producing both pleasant meats known as ginseng in meat and excellent cashmere known as soft gold. IMCGs cashmere is special for its brightness, elasticity, thin diameter, and softness (Wang et al. 2019). Previous studies focused on growth, reproductive and fleece traits in IMCGs (Biggam et al. 1993; Zhou et al. 2002; McGregor and Butler 2009; Visser et al. 2009; Wang et al. 2013), but not on genetic parameters of horn traits. Therefore, in this study, we analysed three horn traits (horn base interval, HBI; horn length, HL; horn base circumference, HBC) and four essential economic traits (cashmere length, CL; staple length, SL; cashmere weight, CW; live body weight, LBW) to estimate their genetic parameters and detect indirect selection among traits in IMCGs. The results will be helpful to make a reasonable breeding plan and speed up genetic progress of generations in IMCGs.

MATERIAL AND METHODS

Animals and phenotype

Pedigree information with 7 632 records was collected from 2 049 adult goats (two years old) of IMCGs Arbas Stock (latitude 39°06'N and longitude 107°59'E) in the southwest of Inner Mongolia in China during three years (2017 to 2019). The feeding mode of the 2 049 animals was half grazing (during the day) and half house feeding (at night) for supplementary feeding.

The 2 049 goats included 117 sires reared in one herd and 1 932 dams reared in six herds with an average herd size of about 240 goats. The seven herds were reared by different herdsmen with half grazing and half house feeding. All the goats were subjected to artificial insemination. The ratio of sires to dams was about 1 : 200 to 300. Kids were born between March and May. Each animal was assigned a unique number. And the information about mother, birth weight, gender and other information were recorded. Combined with mating information records, pedigree data was obtained, including individual, sire and dam. Three horn traits were analysed in this study. The length between the base of the horn and the other horn on the skull was measured as HBI (cm). The length from the base to the tip of the horn along the outer curvature of the spiral was measured as HL (cm). The circumference around the base of the horn at the closest point to the skull was measured as HBC (cm). Four goat economic traits (CL, SL, CW, LBW) were also analysed. Moulded cashmere was harvested once a year by combing in May and weighed using an electronic scale, and CW (g) was recorded. After combing, LBW (kg) was measured by an electronic scale. Fibre samples were taken back to the laboratory. Cashmere and guard hair were then separated. Cashmere was then washed with petroleum ether to get cleaned samples. SL and CL were gauged with a standard ruler. The observations of SL and CL were repeated 50 times, respectively. Both traits were measured to the nearest 1 mm, respectively.

Statistical analysis

Phenotypic data within mean \pm 3 times of standard deviation were maintained for subsequent analysis. Generally, fixed effect of each trait in the model was identified by General Linear Model (GLM) procedure using SAS program as follows:

$$y_{ijklmn} = \mu + Y_i + H_j + A_k + D_l + T_m + e_{ijklmn} \quad (1)$$

where:

- y_{ijklmn} – the n^{th} observation of the m^{th} animal;
- μ – the mean;
- Y_i – the year effect (three levels, 2017–2019);
- H_j – the herd effect (seven herds, 1–7);
- A_k – the individual age effect (2–7);
- D_l – the dam age effect (4–10);

T_m – the birth-type effect (single or twin);
 e_{ijklmn} – the residuals effects.

a_i – the vector of direct additive genetic effects of animal for trait i ;
 p_i – the vector of individual permanent environmental effects for trait i ;
 e_i – the vector of random residuals effects for trait i .

There are seven herds in this flock, including six adult dam herds and one adult sire herd. Wang et al. (2013) reported that neither maternal environment nor maternal genetic effects were significant in adult animals. Therefore, we applied the restricted maximum likelihood method (AIREML) to estimate the variance components of each trait. AIREML was an animal model with random animal genetic and permanent effects.

Then heritability for each trait was computed by AIREML in WOMBAT software. The default convergence criterion was 10^{-8} . The formula for this model was:

$$y_i = X_i b_i + Z_i a_i + W_i p_i + e_i \quad (2)$$

where:

y_i – the vector of observation of animals for trait i ;
 X_i , Z_i and W_i – design matrices of the corresponding effects, respectively;
 b_i – the vector of fixed effects for trait i ;

RESULTS AND DISCUSSION

Basic statistical analysis

Descriptive statistics of phenotypic data in IMCGs are shown in Table 1. The average values of HBI, HL, HBC, CL, SL, CW and LBW were 2.49 cm, 31.11 cm, 12.09 cm, 6.50 cm, 19.94 cm, 749.76 g and 38.16 kg, respectively. The CV of HBI and HL were 20.30% and 28.75%, respectively, showing more variation compared with HBC.

Determination of fixed effects

The GLM was used to determine the non-genetic factors of each trait (Table 2). Year, herd and in-

Table 1. Descriptive statistics of trait data

Traits	No. of records	Mean	SD	CV (%)	Minimum	Maximum
HBI (cm)	3 438	2.49	0.51	20.30	0.70	5.30
HL (cm)	3 438	31.11	8.94	28.75	7.00	90.00
HBC (cm)	3 438	12.09	2.66	9.97	5.00	22.00
CL (cm)	3 438	6.50	1.22	18.78	2.00	12.00
SL (cm)	3 438	19.94	5.10	25.56	5.00	30.00
CW (g)	3 438	749.76	181.99	24.28	290.00	1 580.00
LBW (kg)	3 438	38.16	9.28	24.32	15.00	99.50

CL = cashmere length; CW = cashmere weight; HBC = horn base circumference; HBI = horn base interval; HL = horn length; LBW = live body weight; SL = staple length

Table 2. Fixed effects that had a significant influence on each trait

Factors	Year	Herd	Individual age	Dam age	Birth type
HBI	$P < 0.01$	$P < 0.01$	$P < 0.05$	ns	ns
HL	$P < 0.05$	$P < 0.01$	$P < 0.01$	ns	ns
HBC	$P < 0.01$	$P < 0.05$	$P < 0.01$	ns	ns
CL	$P < 0.01$	$P < 0.01$	$P < 0.05$	$P < 0.01$	ns
SL	$P < 0.05$	$P < 0.01$	$P < 0.01$	ns	ns
CW	$P < 0.01$	$P < 0.01$	$P < 0.05$	$P < 0.01$	$P < 0.01$
LBW	$P < 0.01$	$P < 0.01$	$P < 0.01$	ns	$P < 0.01$

CL = cashmere length; CW = cashmere weight; HBC = horn base circumference; HBI = horn base interval; HL = horn length; LBW = live body weight; ns = not significant; SL = staple length;

dividual age had significant effects on all studied traits ($P < 0.01$). Dam age had a significant influence on CW and CL ($P < 0.01$), but other traits in this study were not affected by dam age ($P > 0.05$). Birth type had a significant influence on LBW and CP ($P < 0.01$), but other traits in this study were not affected by birth type ($P > 0.05$). The results were in agreement with the previous study of economic traits in goat (Bai et al. 2006).

Heritability estimates

As shown in Table 3, direct heritability was moderate to high for HBI (0.31), HBC (0.30) and lower for HL (0.25). To investigate the genetic correlation with economic phenotypic observations, CL, SL, CW and LBW were also considered in our study. The heritability of SL and CW was 0.34 and 0.21, respectively, when it was moderate heritability of both traits. And the heritability of CL and LBW was 0.10 and 0.12, respectively, indicating lower heritability of the two traits. The results of economic traits were in accordance with previous studies. For example, the heritability for CL was 0.10. The heritability of CL in IMCGs estimated by Dai et al. (2012), Zhang et al. (2014), Bai et al. (2006) and Zhou et al. (2002) was 0.11, 0.17, 0.21 and 0.23, respectively; the differences in estimates might be reasoned by different breeding program designs. For SL, heritability estimates in Newland cashmere goats (Biggam et al. 1993) and Australian goats (Pattie and Resatll 1989) were 0.57 and 0.70, respectively, which were higher than our results. This might reflect the different data and the breeds.

Direct heritability of SL was 0.34, which was higher than the values estimated by Pattie and Resatll (1989), Wang et al. (2013) and Li et al. (2001) (0.27, 0.29 and 0.29, respectively). Heritability estimates for SL in yearling Merino sheep (Swan et al. 2008), Ultrafine Merino sheep (Wuliji et al. 2001) and Targhee sheep (Notter et al. 2007) were 0.34, 0.59 and 0.64, respectively, which were higher than our results. The differences between studies are probably caused by the source of breeds, the design of models and the data structure.

Direct heritability of CW was 0.21 in this study, which was similar to IMCGs intermediate-staple length values (0.22), but lower than long-staple length (0.33), and higher than short-staple length (0.14) estimated by Li et al. (2018). In other goat breeds, the heritability of CW was higher than that of our study. For instance, heritability of CW in Liaoning Cashmere goats was 0.34 (Ma et al. 2008), and heritability of FL in Nanjiang Cashmere Goats in Xinjiang was 0.70 (Tao 2012).

Direct heritability of LBW was 0.12 in IMCGs, which was similar to the value (0.10) estimated by Bangar et al. (2020) and lower than the value (0.21) estimated by Bai et al. (2006). The differences between studies are probably caused by the design of the models.

Genetic and phenotype correlations

The genetic correlation of HBI-HL was -0.31 , and that of HBI-HBC was -0.50 (Table 4). The phenotype correlation between HBI and HL was -0.12 , between HBI and HBC -0.23 (Table 3). A positive and high genetic correlation was observed between

Table 3. Estimates of variance components and heritability

Traits	σ_{σ}^2	σ_c^2	σ_e^2	σ_p^2	h_T^2	SE of h_T^2
HBI	0.08	0.07	0.11	0.26	0.31	0.04
HL	6.34	5.80	13.52	25.66	0.25	0.04
HBC	0.70	0.56	1.10	2.36	0.30	0.04
CL	0.15	0.10	1.20	1.45	0.10	0.02
SL	8.23	6.34	9.31	23.88	0.34	0.05
CW	5 856.90	4 328.70	17 962.40	28 148.00	0.21	0.04
LBW	3.00	2.12	20.77	25.89	0.12	0.03

σ_{σ}^2 = direct additive genetic variance; σ_c^2 = individual permanent environmental variance; σ_e^2 = residual variance; σ_p^2 = phenotypic variance; CL = cashmere length; CW = cashmere weight; h_T^2 = direct heritability; HBC = horn base circumference; HBI = horn base interval; HL = horn length; LBW = live body weight; SL = staple length

Table 4. Genetic (\pm SE; below the diagonal) and phenotypic (\pm SE; above the diagonal) correlations between horn traits and economic traits, the diagonal is heritability (\pm SE) of each trait

Traits	HBI	HL	HBC	CL	SL	CW	LBW
HBI	0.31 \pm 0.04	-0.12 \pm 0.02	-0.23 \pm 0.02	-0.04 \pm 0.01	-0.03 \pm 0.02	-0.03 \pm 0.04	-0.07 \pm 0.04
HL	-0.31 \pm 0.02	0.25 \pm 0.04	0.68 \pm 0.02	0.02 \pm 0.01	0.21 \pm 0.02	0.16 \pm 0.03	0.51 \pm 0.04
HBC	-0.50 \pm 0.04	0.78 \pm 0.01	0.30 \pm 0.04	0.05 \pm 0.02	0.17 \pm 0.02	0.29 \pm 0.04	0.44 \pm 0.04
CL	-0.30 \pm 0.03	0.52 \pm 0.02	0.37 \pm 0.03	0.10 \pm 0.02	0.23 \pm 0.04	0.29 \pm 0.03	0.05 \pm 0.04
SL	-0.44 \pm 0.05	0.38 \pm 0.03	0.36 \pm 0.04	0.43 \pm 0.03	0.34 \pm 0.05	-0.05 \pm 0.04	-0.02 \pm 0.03
CW	-0.10 \pm 0.01	0.19 \pm 0.04	0.16 \pm 0.05	0.36 \pm 0.04	-0.10 \pm 0.04	0.21 \pm 0.04	0.09 \pm 0.02
LBW	-0.26 \pm 0.02	0.28 \pm 0.05	0.37 \pm 0.04	-0.05 \pm 0.05	-0.19 \pm 0.02	-0.06 \pm 0.01	0.12 \pm 0.03

CL = cashmere length; CW = cashmere weight; HBC = horn base circumference; HBI = horn base interval; HL = horn length; LBW = live body weight; SL = staple length

HL and HBC (0.78). This positive genetic correlation indicates that an improvement of one trait would have positive impacts on the other trait. For HBI, its genetic correlations with CL, SL, CW and LBW were -0.30, -0.44, -0.10 and -0.26, respectively. Regarding the phenotype correlation between HBI and essential economic traits, it was close to zero (from -0.03 to -0.07). For another horn trait, HL, its genetic correlations with CL, SL, CW and LBW were 0.52, 0.38, 0.19 and 0.28, respectively. Its phenotype correlations with CL, SL, CW and BW were 0.02, 0.21, 0.16 and 0.51, respectively. These positive and strong genetic correlations indicate the evidence of common genetic and physiological mechanisms controlling those traits. In other words, the longer the HL, the longer the CL and SL, and the heavier the CW and LBW are. HBC trait is closely correlated with HL trait (Table 4).

In addition, we also analysed the relationships for four economic traits. The genetic correlations of CL with SL, CW and LBW were 0.43, 0.36 and -0.05, respectively, while the phenotype correlations were 0.23, 0.29, and 0.05, respectively. A positive and high genetic correlation was observed between CL, SL and CW, indicating that the genetic improvement of CL could increase SL and CW traits. The genetic correlations of SL-CW and SL-LBW were -0.15 and -0.19, while their phenotype correlations were -0.05 and -0.02, suggesting that it was difficult to improve SL, CW and LBW simultaneously. The genetic correlation between CW and LBW was -0.06, and the phenotype correlation between CW and LBW was 0.09. These results show that these traits might be influenced by the same genetic and environmental factors.

CONCLUSION

In this study, we estimated the genetic parameters of three horn traits and four economic traits and detected indirect selection among traits in 2 049 IMCGs. The results indicated that the heritability of horn traits was moderate. Also, moderate genetic correlations between the important economic traits were observed. As the horn traits are easier to measure than other economic traits, we also expect that these results will facilitate future studies to elucidate the relationship between horn traits and economic traits in IMCG breeds by reducing labour and material expenses.

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Conflict of interest

The authors declare no conflict of interest.

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