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GENETIC EVALUATION FOR FIBER LENGTH AND FIBER DIAMETER OF INNER MONGOLIA CASHMERE GOATS AT DIFFERENT STAPLE LENGTH

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Abstract

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The genetic parameters for fleece traits of Inner Mongolian Cashmere Goat at different staple length were investigated. Data was collected with 4178 repeat records from 2008 to 2011 in a breeding farm of Inner Mongolia White Cashmere Goats (IMCGs). IMCGs were divided into three types based on staple length which named short-staple length (SSL), intermediate-staple length (ISL) and long-staple length (LSL). The genetic parameters of fiber length (FL) and fiber diameter (FD) were estimated under the repeatability and multivariate animal model with the AIREML method using the WOMBAT software in the three types. The heritabilities were 0.21±0.04, 0.30±0.03 and 0.39±0.04 for FL of SSL, ISL and LSL, respectively, which belong to moderate heritability. Heritabilities for FD were moderate in SSL, ISL and LSL (0.23±0.03, 0.25±0.0.02 and 0.29±0.04). The genetic correlation between FL and FD were negative in the SSL, ISL and LSL (-0.23±0.01,-0.23±0.03 and -0.48±0.01). Phenotypic and genetic correlations of FL were higher than 0.48 and 0.93 in three types. And the phenotypic and genetic correlations for FD were higher than 0.60 and 0.95 in three types. The results show that the phenotypic selection for staple length are possible to increase the FL and decrease FD and genetic progress can be achieved quickly in IMCGs by selection the LSL as the breeding stock.

Key words: Cashmere goats; heritability; genetic correlation; phenotypic selection

Introduction

Cashmere is regarded as a specialty and luxury fiber owing to its scarcity and high economic value (Martin et al., 2015). For fiber quality assessment, it is technically very challenging to longer and thinner of cashmere fiber in cashmere breeding. Inner Mongolian Cashmere Goats (IMCGs) is an excellently breeding which kept for both cashmere and meat production by long-term natural selection and artificial selection (Xuewu et al., 2017). And IMCGs is famous for thin, soft, and white of cashmere in the world. The types of fleeces grown of IMCGs belong to double-coat. Staple is growth in the primary hair follicles and fiber is growth in secondary hair follicles of the IMCGs (Sumner et al., 1993). The estimation of genetic parameters and genetic progress for fleece traits of IMCGs have been studied by Xuewu et al. (2017), which illustrated that heritability of FL and FD is moderate. Therefore, genetic gain will be obtained by genetic evaluation (Zhang et al., 2014).

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Li et al (2001) had found that FL and staple length had high positive genetic correlation (0.69). And it has positive genetic correlation between staple length and FD (0.04) by (Xuewu et al., 2017). And other studies had shown different length effect on the staple strength (Greeff et al., 2013). So, it is possible for indirect selection fiber by selecting the staple length in breeding progress (NA Q, 2016).

Phenotypic selection refers to the development of a variety based on its physical appearance (Schlegel et al., 2003). The staple length was variety from 5cm to 30cm of IMCGs (Xuewu et al., 2017). Based on previous study, three types of SL in IMCGs were divided according to staple length, namely, short-staple length (SSL≤13cm), intermediate-staple length (13cm<ISL≤22cm) and long-staple length (LSL>22cm) (NA Q, 2016). And found every type was significant influence on the other fleece traits by significance test (NA Q, 2016). Fiber quality can be improved by phenotypic selection (Xuewu et al., 2016). And FL and FD can be early selected by genetic evaluation of fiber quality from IMCGs at different ages (Wang et al., 2015). But there are no studies about impacted on the fiber by staple length. The objective of this research is to realize the indirect selection of fiber across estimation genetic parameters (heritabilities and genetic correlations) for FL and FD in the IMCGs population at different staple length.

Materials and Methods

Data Sources

Data for this study was collected 4178 repeat records comes from 2008 to 2011 in breeding farm of Inner Mongolia White Cashmere Goats. This breeding farm located at the Ordos in southwestern Inner Mongolia in China (latitude 39°06' N and longitude 107°59'E). The cashmere goats, in the light of age and sex, were managed 12 different herds. In addition to the adult rams herd which had an average herd size of approximately 100, the other herds had an average herd size of about 200 goats, and the ratio of ewes to rams was about 1:200–300. The flock of goats mating occurred at the beginning of October in every year using artificial insemination. And record the breeding data that including ewe's identification number, mating times and the ram's identification number. Lambs were born from March to May in second year. All of lambs were clearly identified by identification number and recorded the lambing data (including lamb identification number, ewe's identification number, gender, weight of birth and date of birth). So, the genealogical record is detailed and accurate. Details on the feeding and management of this flock were described by Zhou H M et al. (2002), Bai J et al. (2006) and Dai S et al. (2015). Cashmere goats were weaned at the beginning of May. Patch samples of 10 cm^2 were collected from on the side of shoulder before combing. The fleece samples were taken and evaluated at Wool Analysis Laboratory of Inner Mongolia Agriculture University. Firstly, the samples were washed by petroleum ether to remove contaminants. Then, the hair were separated from the samples, the rest were cashmere. Staple length and FL were gauged with a standard ruler. The observations of staple length and FL were repeated 50 times, respectively. FD was measured with an OFDA2000BT fiber fineness tester. Overall, the performance and pedigree records were complete and explicit.

Statistical Analysis

Phenotypic and genetic parameters of FD and FL of IMCGs were different between yearling and other ages (Wang et al., 2015). So, FD and FL from individuals aged 2 to 7 years old were recorded and analyzed. The statistical results were described in Table 1. The significance of fixed effect was identified using a General Linear Model (GLM) procedure of the SAS program (SAS, 2004). Based on previous studies (Zhou et al., 2003; Wang et al., 2013; NA Q, 2016), the fixed effects tested in the model for traits of fiber quality were year of production (four levels), herd (twelve herds), individual age (2-7), sex (female and male) and staple types (SSL, ISL and LSL). And several reports had proved that fiber quality traits were not influenced by maternal effect (Wang et al., 2014; Xuewu et al., 2017).

Table 1

Detailed description of fiber length and fiber diameter at three types

Traits	Types	n	Mean	SD	CV (%)
FL (cm)	SSL	1034	9.91	1.47	14.83
	ISL	2258	10.47	1.66	15.85
	LSL	453	11.61	2.05	17.66
FD (um)	SSL	1034	14.77	0.98	6.64
	ISL	2258	14.74	0.96	6.51
	LSL	453	14.66	0.92	6.28

Therefore, the repeatability and multivariate animal model that include only direct additive genetic effects. Variance components and genetic parameters were estimated using the restricted maximum likelihood method (AIREML) method in the WOMBAT software (Meyer, 2007). The final model was as follows:

$$y = Xb + Za + e,$$

where y is a the vector of observed traits of animals; b is the vector of fixed effects of observed traits; a is the vector of direct additive genetic effects of animal for observed traits. X and Z are incidence design matrices respectively relating fixed effect and directs additive genetic effects; e is the vector of residuals.

Results

Basic statistical analysis

The analytic results of phenotypic for FL and FD at different staple types in IMCGs are shown in Table 1. The average values for FL of SSL, ISL and LSL were 9.91 cm, 10.47 cm and 11.61 cm, respectively. And the average FD values for the SSL, ISL and LSL types were 14.77 um, 14.74 um and 14.66 um for the bucks. The CV of FL for SSL, ISL and LSL were ranged from 14.83% to 17.66% showing more variation compared with FD ranged from 6.64% to 6.28%. The average value of FL was stretched with the staple length. But the average value of FD thinned down with the staple length. The standard deviation and coefficient of variation increased for FL and decreased for fiber diameter. It illustrated the phenotypic of FL and diameter was different in between SSL and LSL.

Estimates of genetic parameters

As showed in the Table 2, the variance components and heritabilities for FL and FD of IMCGs at different staple types. The estimated values vary from 0.21±0.04, 0.30±0.03 and 0.39±0.04 for FL at SSL to LSL. And heritabilities were 0.23±0.03, 0.25±0.02 and 0.29±0.04 for FD form SSL to LSL. The heritabilities of FL and FD belong to moderate heritability in three staple types.

The genetic and phenotypic correlations were summarized in Table 3. The genetic correlations between FL and FD at different staple length were negative and moderate, ranging from -0.23 to -0.48. For all traits, the genetic correlations were strong and positive at different staple types (0.93-0.98). Phenotypic correlations for each trait between any two types were high and positive (0.48-0.72) which less the genetic correlation.

Table 2
Variance component and heritability estimates for fiber quality traits at three types

Traits	Types	σ^2_a	σ^2_p	σ^2_e	h^2_T
FL	SSL	1.00	4.83	1.47	0.21±0.04
	ISL	1.01	3.32	1.41	0.30±0.03
	LSL	1.01	2.59	0.98	0.39±0.04
FD	SSL	0.21	0.91	0.61	0.23±0.03
	ISL	0.21	0.84	0.58	0.25±0.02
	LSL	0.20	0.67	0.50	0.29±0.04

Note: Direct additive genetic variance σ^2_a, residual variance σ^2_e, phenotypic variance σ^2_p, direct heritability h^2_T

Discussion

Basic statistical analysis

The average FL value for SSL, ISL and LSL cohorts ranged from 9.91 cm to 11.61 cm for the flock. The mean value for FL of LSL was maximum in three types. And the FL of LSL was 1.7cm longer than FL of SSL. The standard deviation and coefficient of variation increased was small for FL. It illustrated the FL was a few effected on environment. And coefficient of variation of SL was maximum at LSL, which explained the FL had high potential for improvement.

The average FD value for SSL, ISL and LSL cohorts ranged from 14.77 um to 14.66 um for the flock. The mean value of FD was thinnest at LSL, and it was 0.11 cm thinner than FD of SSL, but FD was not obvious changes. The standard deviation and coefficient of variation of FD was decreased with staple length which showed to decrease the FD more difficult. The result was consistent of study by NA Q (2016).

The basic statistical analysis result indicating the potential of the IMCGs was increased the FL and decrease the FD by selecting the cashmere goats of LSL as the breeding.

Estimates of genetic parameters

As showed in the Table 3, the heritabilities of FL were 0.21, 0.30 and 0.39 which belong to moderate heritability in SSL, ISL and LSL, respectively. In this study, the heritability estimate for fiber is similar to estimate of 0.32 and 0.21 reported by Zhang Y et al. (2014) and Bai J et al. (2005) on IMCGs.

In contrast, Younesi H N et al. (2008) showed that the heritability of FL in Cashmere Goats in Southern Khorasan

Table 3
Heritability (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for fiber the quality traits at three types

Traits	Types	1	2	3
FL	SSL	**0.21±0.04**	0.94±0.01	0.93±0.01
	ISL	0.51±0.17	**0.30±0.03**	0.95±0.04
	LSL	0.48±0.06	0.58±0.11	**0.39±0.04**
FL/FD		-0.23±0.01	-0.23±0.03	-0.48±0.01
FD	SSL	**0.23±0.03**	0.98±0.01	0.95±0.01
	ISL	0.61±0.06	**0.25±0.02**	0.98±0.01
	LSL	0.60±0.08	0.72±0.2	**0.29±0.04**

Note: FL/FD: genetic correlation between fiber length and fiber diameter

Province was 0.53, which was higher than that reported in this paper. This diversity result may be caused by different breed, genetic structure, and sample size. The heritabilities were moderate for FD with value of 0.23, 0.25 and 0.30 in SSL, ISL and LSL, respectively. And the moderate heritability for FD differs from those reported for Alashan Left Banner White Cashmere goats (Pallotti et al., 2017) and for South African Angora goats (Visser et al., 2009) where the heritability was found to be moderate with value of 0.41 and 0.45. For the FD, we found the heritability similar to those reported from previous studies on IMCGs (Xuewu et al., 2017) in which the heritability was moderate heritability (0.32).There have been no reported on the genetic variation of cashmere goats at different staple types. It may be due to micro multi-gene of FL and FL in LSL was more than SSL and ISL. And it explained the phenotype value of FL and FD was different in three types.

The FL showed positive genetic correlations with FD were variable among the three types, ranging from -0.48 to -0.23. And the direct additive genetic correlation between FL and FD increases with the increasing staple length. The genetic correlations between FL and FD was similar with the result by Bai.et al. (2006) and lower than the reported by Wang et al. (2015). It may be due to size of data, methods of research and genetic structure of breeding. The genetic correlations between FL and FD were low at SSL and ISL, but it was high at LSL. It also illustrated the genetic correlations between FL with FD will strength with increasing of staple length. The genetic correlations of FL among the three types were more and more strength. The FL of SSL showed positive genetic correlation with the FL of ISL and LSL (0.94 and 0.93). And FL of ISL showed positive genetic correlation with the FL of LSL (0.95). The genetic correlation between FD of SSL and FD of ISL and LSL were highly with value of 0.98 and 0.95. And the genetic correlation between FD of ISL and FD of LSL was highly with a value of 0.98. Phenotypic correlations were range from 0.48 (FL of SSL and LSL) to 0.72 (FD of ISL and LSL). It has been found that there were highly positive genetic and phenotypic correlation between the FL of ISL and LSL (0.95 and 0.58) and FD of ISL and LSL (0.98 and 0.72),so that the ISL and the LSL can be used as a type which named LSL. This study was the first to estimate genetic variation for FL and FD of Inner Mongolia Cashmere Goats at different staple length. So, there was no reported of estimating genetic parameters for FL and FD.

According to our study, the phenotypic selection for reducing FD and increasing FL were possible and the genetic progress can be achieved quickly in the IMCGs. And all traits have strong genetic and phenotypic correlation, which above the value of 0.60 and 0.48, respectively. Therefore, genetic gain for FL and FD of IMCGs can be obtained by phenotypic selection. So, it will increase FL and reduce FD by LLS as breeding stock.

Conclusion

The moderate heritabilities for FL and FD in three types demonstrated that genetic improvement can be achieved by phenotypic selection. And the moderate heritabilities for FL and FD of LSL were highest in three types. IMCGs are divided into two types of SSL and LSL base on genetic and phenotypic correlation. The positive genetic and phenotypic correlations between FL and FD were favorable for selection of length of fiber and fine cashmere while the selection for long staple length in IMCGs. And the genetic progress can be achieved quickly by selection LSL as breeding stock.

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