Short communication

Estimates of genetic parameters and genetic changes for fleece traits in Inner Mongolia cashmere goats

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ABSTRACT

Genetic parameters and genetic trends for staple length (SL), staple fineness (SF), fiber length (FL) and fiber diameter (FD) were estimated using 7798 repeat records of 4583 Inner Mongolia cashmere goats at different ages measured from 2008–2011. These goats were descendants of 110 sires and 2139 dams, born between 2003 and 2010 at the Inner Mongolia Arbas cashmere goat stock farm. Analyses were carried out by average information restricted maximum likelihood, fitting four single-trait repeatability animal models with various combinations of individual and maternal effects. The best model for each fleece trait was chosen after testing for improvement of the log-likelihood values. Genetic parameters were then estimated under the most appropriate model. Genetic trends were determined by regressing yearly estimated mean breeding values on year of birth. All the fleece traits were influenced by direct addictive genetic and individual permanent environment effects. Estimates of direct heritability for SL, SF, FL and FD were 0.30, 0.27, 0.18 and 0.32, respectively. Genetic correlations among the fleece traits (SL–SF and FL–SF) were negative and high (−0.50 and −0.48). For the other fleece traits (SL–FL and SF–FD), the genetic correlation was moderate and positive (0.26 and 0.31). The phenotypic correlation among all fleece traits was low, ranging from −0.22 to 0.23. Compared with other traits, fleece traits were not objective traits in previous breeding programs; they presented irregular changes across year of birth. Estimates of genetic parameters and analyses of genetic trends would be helpful for designing a breeding program for the genetic improvement of fleece traits in Inner Mongolia cashmere goats.

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1. Introduction

Compared with milk goats and meat goats, superior dedicated cashmere goat breeds around the world are rare. Goats make vital contributions to the development of rural zones. Developing countries own approximately 98% of the goat population and a 76% share of the breeds. There are over 30 indigenous "improved breeds" that are under-used and potentially important. The largest populations are in Asia (480 million) and Africa (169 million). This includes 77% of the world population and 42% of the breeds (Devendra, 2010). Cashmere goats are being raised by an increasing number of countries because of the important economic values of cashmere and the variety of uses of cashmere goats. The total worldwide goat population

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Table 1
Description of the dataset for fleece traits.

Traits	No. of records with progeny	No. of lambs	No. of sires	No. of dams	Mean	SD	C.V
Staple length (cm)	7747	4562	109	2139	14.89	4.93	0.3311
Staple fineness (um)	7798	4585	107	2136	59.43	10.58	0.1780
Fiber length (cm)	7775	4582	110	2134	10.51	1.78	0.1694
Fiber diameter (μm)	7784	4583	110	2138	14.42	1.06	0.0735

in 2007 was about 851 million and includes 1156 breeds. China contributes 23% or 197 million animals (FAOSTAT, 2007). Cashmere yield was the highest in China and its production accounts for two-thirds of the total global cashmere.

In China, Inner Mongolia, as a unique natural prairie, has become a very important livestock production base. Inner Mongolia Arbas cashmere goats (IMACGs) are a dual-purpose breed used to produce meat and cashmere. The cashmere produced by Arbas cashmere goats is characterized by its brightness, color, elasticity, thin diameter and softness (Bai et al., 2006). It represents the finest cashmere produced by China. However, declining market demand and undesirable sale prices for cashmere over recent years has resulted in more attention being paid to meat production and fleece yield, as in other cashmere goat breeds (Rashidi et al., 2008; Maghsoudi et al., 2009; Barazandeh et al., 2012). Olivier et al. (2005) stated that goat production in developing counties is mostly aimed at meat production, probably caused by lower fiber product prices in recent years. The quality of the cashmere from Arbas cashmere goats is declining.

Fleece traits determine the quality of mohair product, which is the trait that most affects profits. Many researchers (Visser et al., 2009; McGregor and Butler, 2009a,b; Olayemi et al., 2011) have studied fleece traits. There are few reports concerning fleece traits of IMACGs, probably because of limited conditions and the low price of the fiber product. Zhou et al. (2002, 2003) and Bai et al. (2006) performed studies regarding fleece traits of IMACGs. In China, cashmere is sold according to its grades and since 2008 more precise measurements of fleece traits have been possible using improved measurement methods. Selective breeding has been the major tool for genetic improvement. The purpose of this study was to estimate the genetic parameters for fleece traits of IMACGs using repeat records, and to compare the results with those of yearling IMACGs studied by Wang et al. (2012). If the results were similar, we could design a breeding plan based on early records of fleece traits. Meanwhile, the genetic trends of fleece traits obtained by estimated breeding values between 2003 and 2010 were discussed, including the indirect determination of a genetic relationship between fiber diameter and cashmere yield weight. Our results lay the foundation for an optimal breeding program in IMACG.

2. Material and methods

2.1. Traits and data

Data were collected from 7798 repeat records on progeny from eight birth years (2003–2010) in the IMACG

flock. Zhou et al. (2002, 2003) and Wang et al. (2012) described the details of management and production for this flock. Four fleece traits were considered in this study: staple length (SL), staple fineness (FD), fiber length (FL) and fiber diameter (FD). The method of measurement and specific definition of each fleece trait were provided by Wang et al. (2012). The description of the data is shown in Table 1.

2.2. Statistical analysis

The models were fitted to account for known environmental effects, including year of production (4 years from 2008–2011), herd (12 herds), birth status (simple or twin), ages of kids (1–7 years) and ages of the dams at kidding (2–7 years). (Co) variance components and genetic parameters were estimated by average information restriction maximum likelihood (AIREML) (Gilmour et al., 1995; Mohammadi et al., 2012a,b) using WOMBAT software. By ignoring or including maternal direct additive genetic effects or maternal permanent environmental effects, four univariate linear animal models were fitted for all traits to obtain heritability estimates. The likelihood ratio test ($-2 \log L$) was performed to obtain the appropriate model (Maghsoudi et al., 2009; Di et al., 2011). When the variances of function values in Simplex were less than 10^{-8}, convergence of AIREML solutions was considered to be reached. These models were:

Model 1: $y_i = X_i b_i + Z_i a_i + E_i c_i + e_i$
Model 2: $y_i = X_i b_i + Z_i a_i + E_i c_i + W_i m_i + e_i$
Model 3: $y_i = X_i b_i + Z_i a_i + E_i c_i + Q_i q_i + e_i$
Model 4: $y_i = X_i b_i + Z_i a_i + E_i c_i + W_i m_i + Q_i q_i + e_i$

The key parameters involved in all the models are shown in Table 2. X_i, Z_i, E_i, W_i and Q_i are design matrices relating observations to the corresponding effects. It is assumed that direct addictive genetic effects, maternal addictive genetic effects, individual permanent

Table 2
Definition of parameters in all models.

parameters	Definition
y_i	The vector of observations for the ith trait
b_i	The vector of fixed effects for the ith trait
a_i	The vector of direct additive genetic effects for the ith trait
c_i	The vector of individual environment effects for the ith trait
m_i	The vector of maternal additive genetic effects for the ith trait
q_i	The vector of maternal permanent environmental effects for the ith trait
e_i	The vector of maternal permanent environmental effects for the ith trait