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Short communication

Genetic trends for growth and wool traits of Chinese superfine Merino sheep using a multi-trait animal model

Jiang Di[a,*], Lazate Ainiwaer[a], Xin-Ming Xu[a], Yan-Hua Zhang[a], Li-Juan Yu[a],
Wu-Chen Li[b]

[a] *Animal Science Institute, Animal Science Academy of Xinjiang Uygur Atonomous Region, Urumqi 830000, China*
[b] *Xinjiang Gonaisi Fine Wool Sheep Breeding Farm, Xinyuan 835808, China*

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ABSTRACT

The objective of the present study was to estimate genetic trends for birth weight (BW), weaning weight (WW), weaning staple length (WSL), yearling liveweight (YLW), and greasy fleece weight (YGFW), staple length (YSL), mean fibre diameter (YFD), fibre diameter standard deviation (YFDSD) and fibre diameter variation (YFDCV) at first shearing, which are essential to design a more efficient selection breeding programme for Chinese superfine Merino sheep. Data was collected on progeny from eight birth years (2001–2008) in the Chinese superfine Merino breeding flock maintained at Xinjiang Gongnaisi Fine Wool Sheep Breeding Farm. Different appropriate models for investigation of each trait using multivariate analysis were applied. (Co)variance components were estimated by average information restricted maximum likelihood (AIREML) and breeding values of individuals were predicted with Best Linear Unbiased Prediction (BLUP) methodology under multi-trait animal models. Genetic trends of studied traits were estimated by regressing mean of breeding values on birth year. Genetic trends were negative and significant for YFD and YFDSD ($p < 0.01$) being 0.059 and 0.005 μm/year respectively. The genetic changes for other traits were insignificant and maintained at the level of base year. Our results herein form a practical basis for designing optimal breeding schemes in Chinese superfine Merino.

1. Introduction

The international wool market tendencies have shown the economic advantages of producing fine and superfine wool during the last few decades, and selection on fibre diameter of wool in Merino has been a focus point in many countries. In 2000, a breeding programme was started with the aim to breed superfine bloodline in Chinese Merino and subsequently a breeding flock was constructed in Xinjiang Gonaisi Fine Wool Sheep Breeding Farm. Since the genetic parameters of economic traits were lacking for the flock at the early stage, and literature estimates of genetic parameters for FD was high from 0.59 to 0.62 in other Merino strains (Coelli et al., 1998; Safari et al., 2005), the stud were selected based on individual fibre diameter in the flock. Recently, several breeding plans of state are implemented sequentially in the flock to further decrease fibre diameter, and simultaneously to improve genetic gain of other growth and fleece traits. For achieving these targets, genetic parameters of the economically important traits have been estimated in the flock by Jiang Di et al. (2011), and accordingly, a more efficient selection programme needs to be devised.

Genetic correlations between traits may impact estimates of breeding values depending on their strength and direction. Multiple-trait analyses should be used rather than single-trait analyses when estimating genetic changes because of the impact including correlated traits have estimates of breeding values of other traits (Hanford et al., 2006).

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* Corresponding author. Tel.: +86 0991 4835207;
fax: +86 0991 4835207.
E-mail address: dijiang1@hotmail.com (J. Di).

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Many studies have estimated genetic trend of growth and fleece traits for different sheep breeds. However, few studies have been conducted on it in Chinese Merino sheep. The major objectives of this study were to estimate the genetic trend with estimated breeding values for live weight traits at different ages and fleece traits at weaning and first shearing in Chinese superfine Merino sheep, with Best Linear Unbiased Prediction (BLUP) methodology using a multi-traits animal model, in order to evaluate the current breeding programme and develop strategies for a future programme in Chinese superfine Merino sheep.

2. Materials and methods

2.1. Data

The foundation flock of approximately 1000 ewes was established in 2000 according to fibre diameter from 12,000 Chinese Merino sheep raised in Xinjiang Gongnaisi Fine Wool Sheep Breeding Farm, located in Xinyuan County, Xinjiang Province of China. Details of the management and production of the flock have been described in our previous study (Jiang Di et al., 2011). The data used in the present study covered eight birth years from 2001 to 2008, and comprised 37 sire groups. All pedigree was recorded and the age of dams was also recorded for comparison of these maternal effects. The traits investigated were birth weight (BW), weaning staple length (WSL), live weight (WW), yearling greasy fleece weight (YGFW), live weight (YLW), staple length (YSL), mean fibre diameter (YFD), fibre diameter standard deviation (YFDSD) and fibre diameter variation (YFDCV) across the staple. The number of available records, mean, standard deviation, coefficient of variation, number of sires and dams of the traits studied are presented in Table 1.

2.2. Statistical and genetic analysis

The multi-trait animal model was fit to estimate (Co)variance components for investigated traits by average information restricted maximum likelihood (AIREML) with using DMUv6-R4.7 software. Statistical and genetic analysis of investigated traits in our previous study revealed the important fixed and random effects for analyzing each trait (Jiang Di et al., 2011), which are presented in Table 2. Therefore, the most appropriate models that our previous studies indicated were used in the present multivariate analysis. In matrix notation, the general model for multi-trait animal model can be written as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Z}_3\mathbf{c} + \mathbf{e},$$

with

$$var\begin{pmatrix} a \\ m \\ c \\ e \end{pmatrix} = \begin{pmatrix} A\otimes G & 0 & 0 & 0 \\ 0 & I\otimes M & 0 & 0 \\ 0 & 0 & I\otimes C & 0 \\ 0 & 0 & 0 & I\otimes R \end{pmatrix},$$

where y is a vector of all observations of nine traits; b, a, m and c are vectors and $\mathbf{X}$, $\mathbf{Z}_1$, $\mathbf{Z}_2$ and $\mathbf{Z}_3$ are corresponding design matrices related to fixed effects: direct additive genetic effects, maternal additive genetic effects, maternal common environmental effects respectively, and e is the vector of the residual effects. $\boldsymbol{A}$ is the numerator relationship matrix; $\boldsymbol{I}$ is an identity matrix; and $\otimes$ is the direct product operator. $\boldsymbol{G}$ and $\boldsymbol{R}$ are the animal direct additive genetic and the error variance–covariance 9×9 matrix among nine traits respectively. $\boldsymbol{M}$ is the maternal additive genetic variance–covariance 2×2 matrix among BW and YGFW. $\boldsymbol{C}$ is the maternal common environmental genetic variance–covariance 4×4 matrix among WW, YLW, YFDSD and YFDCV. We assume, as usual, that the random effects $\boldsymbol{c}$ and $\boldsymbol{e}$ are independently distributed among animals and the relationship matrix accounts for correlations of the additive genetic effects among animals.

Breeding values of individual animals were predicted with Best Linear Unbiased Prediction (BLUP) methodology using the trait Co(variances) from the multi-trait analyses. Genetic trends were estimated by regressing means of estimated breeding values on year of birth using procedure of SAS9.1.

3. Results and discussion

3.1. Fibre diameter traits

Means of estimates of breeding value by year of birth showed the oppositely fluctuant changes for YFD and YFDCV after base year (Fig. 1A), with a consistent decrease for YFD and a consistent increase for YFDCV over time except the year of 2002 and 2006, and which could be attributed to the high and negative genetic correlation (−0.84) between them. The abrupt changes in yearly mean predicted values of YFD and YFDCV in 2002 were evidently owing to the unexpected death of several outstanding rams and the poor replacers having been used, and the slightly abrupt changes in 2006 may be due to selection of inferior rams. Means of estimates of breeding value on year of birth showed a consistent decrease with few fluctuations for YFDSD (Fig. 1A). The estimates of genetic changes were significant ($p < 0.01$) for YFD and YFDSD and insignificant for YFDCV (Table 3).

Direct genetic trends for fibre diameter were estimated in several fine wool sheep breeds. Selection based on breeding values resulted in a higher reduction of 0.157 μm/year for fibre diameter in the Grootfontein Merino (Olivier et al., 1995). The selection of emphasizing fleece weight and maintaining fibre diameter acceptably led to a lower genetic change of −0.011 μm/year for fibre diameter in Dohne Merino (Cloete and Scholtz, 1998). Application or no. of selection pressure to reduce FD resulted in a significantly high genetic change of −0.129 μm/year and insignificantly lower genetic trend (−0.015 μm/year) for FD in Cradock fine wool sheep respectively (Cloete et al., 2007). The low genetic trends of −0.005 μm/year and −0.004 μm/year for FD were also reported in Merino population divergently selected for maternal multiple rearing ability by Cloete et al. (2005). Estimate of significantly direct genetic trend −0.059 μm/year for FD in current study was lower than the results reported by Olivier et al. (1995) and Cloete et al. (2007), and higher than that reported by