Genetic parameters for somatic cell score in dairy goats estimated by random regression

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ABSTRACT

The objective of the study was to estimate genetic parameters of somatic cell score (SCS = $\log_2$ of somatic cell count / 1000) in New Zealand mixed-breed dairy goats using a random regression model. The dataset comprised 37,051 herd-test records of somatic cell counts (SCC) from 3,688 does kidding between 2000 and 2007 distributed in 47 herds. The mixed model included the fixed effects of contemporary group (herd-year-month of kidding), lactation number (1st, 2nd and 3rd), and the covariables day-of-month, proportion of Saanen, Nubian, Alpine and Toggenburg breeds, heterosis, and a second-order orthogonal polynomial of days in milk across all data and for each lactation number. The random effects included a second order random regression polynomial for the additive animal effect and the doe permanent environmental effect within parity and doe permanent environmental effect across parities. The residual variance was assumed heterogeneous, with different residual variances for each of the nine months of lactation. Estimates of heritability increased from 0.12 to 0.25 from the beginning to the end of the lactation and estimates of repeatability ranged from 0.46 to 0.59, also increasing from the beginning to the end of lactation. These results show that genetic improvement can be achieved in SCC by including SCS in selection index.

Keywords: somatic cell score; dairy goats; genetic parameters; test-day model.

INTRODUCTION

Somatic cells in dairy goats comprise the white blood cells in milk and a relatively small number of epithelial cells from milk-secreting tissues. These cells are an important component of part of the natural defence of the animal against udder diseases. When udder tissue is injured or becomes infected, the number of somatic cells in milk is significantly increased.

Somatic cell score (SCS = $\log_2$ of somatic cell count / 1000) has been the preferred trait to select for mastitis resistance in New Zealand dairy cattle (Harris *et al*., 2005) because measurement of SCS is less expensive and more consistent than an assessment of clinical mastitis. Also, SCS has a high correlation with bacteriological status of milk and hence subclinical mastitis, which in turn causes an economic loss for dairy goat farmers. There are few studies linking these parameters in dairy goats.

Normal goat milk has a higher somatic cell count (SCC) than normal milk from cows. This has been a concern of the goat industry because there is limited information on the relationship between SCC and milk quality in goats. Despite this, in New Zealand, a seasonally adjusted monthly average SCC is used as an industry standard as a threshold in the milk payout.

Genetic improvement for SCS involves the processing and use of information for timely identification of animals of high genetic and phenotypic merit to improve the net financial return to the farm business (Singireddy *et al.,* 1997). One important advantage of the test-day model for genetic evaluation is the most efficient use of serial observations, making better estimates of genetic values, and the possibility of using incomplete lactation records (Freeman, 1998).

In dairy sheep, SCS is moderately heritable and therefore suitable for a genetic improvement programme (De la Fuente *et al.,* 1997; Bergonier *et al.,* 2003). However, SCS is not included in the breeding objective of the United States (Wiggans, 2001), France (Boyazoglu & Morand-Fehr, 2001) and New Zealand dairy goats. The objective of this study was to estimate genetic parameters for SCS in New Zealand dairy goat using a random regression model allowing consideration of whether udder health could be included in the breeding objective.

MATERIALS AND METHODS

Pedigree information and herd-test records of SCC dairy goats kidding between 2000 and 2007 were obtained from the Livestock Improvement Corporation database. After editing for incomplete information, there were 37,051 test-day records of SCC from 3,688 does distributed in 47 herds across the North Island of New Zealand. Only lactation records from first to third parity does were considered. Contemporary group was defined as does kidding in the same herd, year and month,

resulting in 215 contemporary groups. Breed composition of each doe was described in terms of the proportion of Saanen, Nubian, British, Toggenburg and "unknown" breeds. Instead of specific heterosis, only total heterosis was considered because there were insufficient numbers of crossbred animals in all possible specific breed combinations.

Variance components for SCS for each day of the lactation were obtained using the software package ASREML (Gilmour *et al*., 2002) with the following test-day random regression model:

$$y_{jklt} = c_j + p_k + \beta_1 dm + \beta_2 h + \sum_{q=1}^{4} \beta_q r_q + \sum_{m=0}^{2} \theta_m p_m + \sum_{m=0}^{2} \theta_{mk} p_{mk} + \sum_{m=0}^{2} \alpha_{ml} p_{ml} + \sum_{m=0}^{2} \alpha_{mkl} p_{mkl} + d_l + e_{jklt}$$

where

- y_{jklt} is the SCS record measured on doe l, at the t^{th} day in milk of parity k and contemporary group j;
- c_j is the fixed effect of contemporary group j;
- p_k is the fixed effect of parity number k;
- β_1 is the regression coefficient of the linear fixed effect of the day of month (dm) on SCS;
- β_2 is the linear regression coefficient of the fixed effect of total heterosis (h) on SCS;
- β_q is the q^{th} regression coefficient of the fixed linear effect of proportion of breed r on SCS (the Saanen breed was set to zero for comparison);
- θ_m is the m^{th} fixed regression coefficient of the Legendre polynomial of order 2 modelling all records of SCS throughout the lactation;
- θ_{mk} is the m^{th} fixed regression coefficient of the Legendre polynomial of order 2 modelling records of SCS throughout the lactation for parity k;
- α_{ml} is the m^{th} random regression coefficient of the Legendre polynomial of order 2 modelling records of SCS throughout all lactations of doe l;
- α_{mkl} is the m^{th} random regression coefficient of the Legendre polynomial of order 2 modelling records of SCS throughout the lactation of doe l and parity k;
- d_l is the random permanent environmental effect of the doe l across all parities;
- e_{jklt} is the random residual effect unique to observation y_{jklt}

Coefficients of the Legendre polynomial at day t were calculated as follows:

$p_0 = \sqrt{1/2}$, $p_1 = z \times \sqrt{3/2}$ and

$p_2 = [(3/2) \times z^2 - (1/2)] \times \sqrt{5/2}$ where

$z = -1 + 2[(t - 270)/(1 - 270)]$.

It was assumed that the random effects (α_{ml}, α_{mlk}, d_l, and e_{ijklm}) had means of zero and were uncorrelated. The variances of α_{ml}, α_{mlk}, and d_l, were modeled as $\mathbf{K_A} \otimes \mathbf{A}$, $\mathbf{K_P} \otimes \mathbf{I_N}$ and $\mathbf{I}\sigma^2_{Pe}$, where $\mathbf{K_A}$ and $\mathbf{K_P}$ are the covariance matrix for the coefficients of the Legendre polynomial of the animal additive genetic and permanent environmental effects, respectively. The residual variance was assumed to be heterogeneous, with different residual variances for each of the nine months of lactation.

RESULTS AND DISCUSSION

The average and standard deviation of daily SCS were 9.35 and 1.69, respectively, while the corresponding average of SCC was 653 x 10^3 cells/mL of milk. This was higher than the average reported in the United States for the year 2004 (570 x 10^3 cells/mL; Paape *et al.,* 2007) and Chile (450 x 10^3 cells/mL; Marín *et al.,* 2007). Somatic cell score increased from parity one to three (Table 1) as observed in other studies with goats (Paape *et al.,* 2007), sheep (Serrano *et al.,* 2003) and cows (Harris *et al.,* 2005).

Breed and heterosis effects are shown in Table 2. Saanen does had a lower SCS than Nubian, Alpine and Toggenburg does, however breed differences were not significant. Total heterosis for SCS represented 0.8% of the mean and was not significantly different from zero. In United States, Paape *et al.* (2007) reported that Saanen does had significantly lower average SCS than Alpine and Toggenburg does but similar average SCS to Nubian does.

The trends of additive genetic, permanent environmental and residual variances of SCS through the lactation are shown in Figure 1. Permanent environmental variance was higher at the beginning and at the end than in the middle of lactation and was higher than the additive genetic and residual variances during all days of the lactation. The additive genetic variance tended to increase at the end of the lactation.

Heritability for SCS during the first month of the lactation was 0.12 and increased to 0.25 at the end of the lactation (Figure 2). Similarly repeatability increased from 0.46 for the first month to 0.59 at the ninth month of the lactation.

TABLE 1: Effect of parity on somatic cell count (SCC) and somatic cell score (SCS = $\log_2$ of SCC / 1000) in dairy goats. SE = Standard error.

Parity number	SCS (± SE)	SCC[2] ($\times 10^3$/mL milk)
First[1]	0.0	0.0
Second	0.141 ± 0.038	67
Third	0.728 ± 0.047	428

[1] First parity effect was set to zero for comparison.
[2] Back-transformed somatic cell count.

TABLE 2: Breed and heterosis effects for somatic cell count (SCC) and somatic cell score (SCS = $\log_2$ of SCC / 1000) in dairy goats. SE = Standard error.

Breed effect	SCS (± SE)	SCC[2] ($\times 10^3$/mL milk)
Saanen[1]	0	0
Nubian	0.220 ± 0.273	107
Alpine	0.031 ± 0.272	14
Toggenburg	0.079 ± 0.107	37
Unknown	-0.100 ± 0.101	-44
Heterosis	0.072 ± 0.063	33

[1] Breed effect of Saanen was set to zero for comparison.
[2] Back-transformed somatic cell count.

There is a dearth of genetic parameters estimates for SCS in dairy goats, the authors were not aware of any heritability estimates. Boettcher *et al*. (2005) estimated the repeatability of SCS at 0.34 using a finite mixture model and 0.31 using a linear mixed model. Estimates of heritability for SCS in dairy sheep based on repeatability test day range from 0.04 to 0.17 (Bergonier *et al*., 2003). The estimates of heritability from this study are in close agreement with estimates in dairy cattle (Rupp & Boichard, 2003).

The estimates of additive genetic variability of SCS from this study appear sufficient to implement SCS into a breeding programme aimed at reducing SCC as implemented in dairy cattle (Harris *et al.,* 2005). However, there are important differences between SCC in cows and goats with regard to the significance and interpretation of SCC levels. Some studies indicate that SCS can lead to errors in the diagnosis of subclinical intramammary infections and in the application of discriminatory standards for sheep and goat milk quality (Bergonier *et al.,* 2003; Droke *et al.,* 1993). Even between these two species of small ruminants there are important differences with regards to the significance and interpretation of SCC levels (Bergonier *et al.,* 2003). To avoid these problems more studies on SCC in dairy goats are required, especially aspects related to infection status and production and technological aspects of milk that could justify the inclusion of SCS into the breeding programme.

FIGURE 1: Additive genetic (■), permanent environmental (▲) and residual (○) variances of somatic cell score (SCS = $\log_2$ of somatic cell count / 1000) in dairy goats.

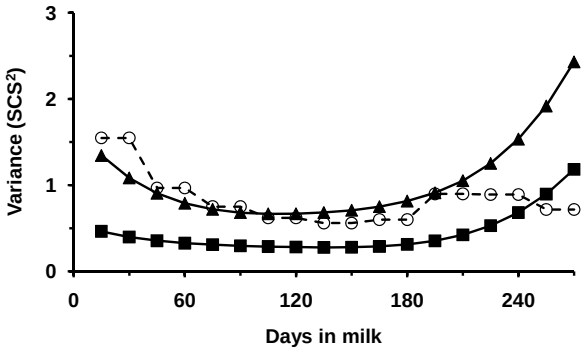
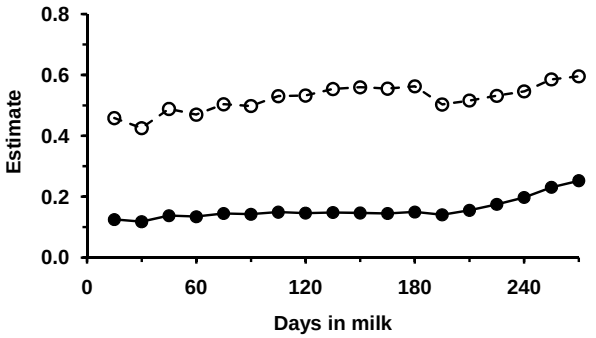


FIGURE 2: Repeatability (○) and heritability (●) of somatic cell score (SCS = $\log_2$ of somatic cell count / 1000) in dairy goats.



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