Heritability of Test Day Somatic Cell Counts and Its Relationship with Milk Yield and Protein Percentage in Dairy Ewes

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ABSTRACT

A total of 6620 monthly test day records of SCC, milk yield, and protein percentage from single lactations of 2374 Spanish Churra ewes from 10 flocks was used to estimate genetic and environmental parameters. A subset of 4278 records containing data from healthy udders (SCC ≤250,000 cells/ml) was also analyzed. Genetic parameters were estimated by REML using an animal model.

Herd test date, parity, and lactation stage contributed significantly to variation of most variables, and birth type significantly affected milk yield only. The SCC increased markedly as parity number and stage of lactation increased.

Heritabilities (±SE) for test day milk yield, log SCC, protein percentage, and log SCC (≤250,000 cells/ml) were 0.18 (0.03), 0.09 (0.02), 0.16 (0.03), and 0.03 (0.02), respectively. The corresponding repeatabilities were 0.54, 0.38, 0.38, and 0.10. Genetic correlations of log SCC with milk yield and protein percentage were −0.23 and 0.18, respectively. Phenotypic correlations were −0.15 and 0.16.

Genetic and environmental reduction of SCC for dairy ewes could be achieved using practices similar to those for dairy cows. The negative genetic correlation between milk yield and SCC suggested that selection for increased milk yield alone is expected to result in a decrease in SCC.

(Key words: heritability, test day, somatic cell counts, dairy ewes)

Abbreviation key: HTD = herd test date, P% = protein percentage.

INTRODUCTION

The dairy industry has regarded milk of dairy ewes as a raw material necessary for producing the cheeses typically consumed in Mediterranean countries and highly valued in other markets. Therefore, milk yield presents the principal criterion for ewe culling and ram selection in the Mediterranean region (12).

Mastitis is one of the most expensive health problems of dairy cows and ewes because it results in a marked reduction in milk yield and changes in levels of specific milk components (16, 19). This problem has motivated extensive research toward improved udder sanitation and mastitis control with the final aim of increasing milk yield and quality. Test day SCC has been introduced in many milk recording schemes for both dairy ewes and cows as an indicator of mastitis and milk quality and as a possible selection criterion for resistance to mastitis (7, 16).

Studies on dairy cattle have indicated that heritability of log₂ SCC is around 10 to 12% (2, 5). For dairy ewes, there is a lack of information on the inheritance of SCC and its genetic relationships with milk yield and composition. The only available genetic study indicates that heritability of test day ln(SCC) was 4% (4).

Gonzalo et al. (17) mentioned that, in order to prove the validity of test day SCC as a diagnostic method of subclinical mammary infection, it is necessary to be able to estimate the cell threshold between infected and uninfected udders. Such threshold values may be used to provide valid criteria for interpretation of SCC inheritance and may offer farmers accurate information on the udder status of ewes, thereby helping them to make management and selection decisions. Working with test day records of dairy sheep, some studies (8, 14) recommended values between 250 and 300 × 10³ cells/ml as most satisfactory discrimination thresholds between healthy and infected udders. These thresholds correctly identified the great majority of ewes with intermammary infections.
Within a population of dairy ewes, SCC presents an acceptable indicator of mastitis. However, in a sample including SCC data that were lower than a certain discrimination threshold between healthy and infected udders, SCC may be expected to be no more than a composition character of milk. Therefore, SCC in these two cases may have different degrees of importance to genetic selection.

The aim of this study was to investigate the inheritance of test day SCC, on the one hand, using all data considering SCC as an indicator of mastitis and, on the other, using a data subset of records for healthy udders of ewes using a threshold value of $250 \times 10^3$ cells/ml. In both cases, environmental factors, heritabilities, repeatabilities, and genetic and phenotypic correlations among log SCC, milk yield, and protein percentage ($P\%$) were estimated.

**MATERIALS AND METHODS**

**Data**

Data were supplied by the National Association of Spanish Churra Breeders (ANCHE, Palencia, Spain). Test day records of milk yield, milk composition, and SCC were taken at monthly intervals following an alternative a.m.-p.m. recording scheme. Although milking intervals for the commercial flocks used in this study were almost 12 h, adjustment factors for milking intervals were used by ANCHE to estimate the daily milk yield. Protein percentage was measured by the automated method of infrared absorption spectrophotometry (Milk-o-Scan; Foss Electric, Hillerød, Denmark), and SCC were determined using the Fossomatic method as described by Gonzalo et al. (15); both were conducted at the analysis service of the milk testing program for the local government. Data were collected between June 1994 and December 1996, and only one lactation per ewe was considered. The first test day record was obtained at least 3 d following weaning, between the 31st and 75th day postpartum, and at approximately monthly intervals thereafter. Lactations were normally 120 d. Therefore, the maximum number of test day records per lactation ranged between three and four records.

Two data sets were considered. The first was the total data for which SCC were considered as an indicator of mastitis. For the second, a data subset was considered that included independently from the ewe only test day records for those SCC $\leq 250 \times 10^3$ cells/ml. This discrimination threshold between healthy and infected sheep udders is within the most satisfactory range according to results from analyses of intermammary infection (8, 14).

The first data set corresponds to 6620 test day records for 2374 ewes belonging to 10 flocks that were integrated in the nucleus scheme of the breed. The total number of sheep in pedigree were 3747, of which 3523 were ewes and 224 were rams. Of the total rams, 105 were used for natural service under good pedigree control and 119 were used for AI, of which 56 had offspring in different flocks. Therefore, many genetic links existed among flocks because of the wide use of rams through AI. The second data set corresponds to 4278 test day records with SCC $\leq 250 \times 10^3$ cells/ml for 1992 ewes, and the total number of animals in the pedigree file was 3293.

**Statistical Analysis**

Records of SCC were transformed to their logarithmic form (1) to meet the characteristics of hypothesis testing. In order to account for the circumstances of the day of test within herd, contemporary groups were formed on the basis of herd test date (HTD) (3, 28). Only one lactation per ewe was considered.

The data were analyzed with the following multivariate repeatability animal model:

$$ Y_{ijklmn} = A_i + PE_i + HTD_j + P_k + S_l + B_m + e_{ijklmn} $$

where

$$ Y_{ijklmn} = \text{test day records of milk yield, P\%, log SCC or log SCC (} \leq 250,000 \text{ cells/ml);} $$

$$ A_i = \text{additive genetic random effect of the individual i;} $$

$$ PE_i = \text{permanent environmental random effect on the individual i;} $$

$$ HTD_j = \text{fixed effect of HTD j;} $$

$$ P_k = \text{fixed effect of parity k;} $$

$$ S_l = \text{fixed effect of stage of lactation l;} $$

$$ B_m = \text{fixed effect of the type of birth m; and} $$

$$ e_{ijklmn} = \text{random residual effect.} $$

All known relationships among individuals were considered in the animal model. There were 7 categories for parity (parities 1 through 6 and 7 or later), 4 for month of lactation (mo 1 to 4), 2 for birth type (single or multiple), and 205 for HTD levels.

Genetic parameters were estimated employing a multitrait repeatability animal model by the derivative-free REML procedure of Thompson and Hill (31). Initially, estimates for heritability and the proportion of permanent environmental variance and
TABLE 1. Descriptive statistics of test day traits.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean (X)</th>
<th>Standard Deviation (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield, ml</td>
<td>948</td>
<td>482</td>
</tr>
<tr>
<td>SCC, × 10⁻³ cells/ml</td>
<td>734</td>
<td>1716</td>
</tr>
<tr>
<td>Log SCC</td>
<td>5.26</td>
<td>0.67</td>
</tr>
<tr>
<td>SCC (≤250,000), × 10⁻³ cells/ml</td>
<td>87</td>
<td>57</td>
</tr>
<tr>
<td>Log SCC (≤250,000)</td>
<td>4.84</td>
<td>0.31</td>
</tr>
<tr>
<td>Protein, %</td>
<td>5.62</td>
<td>0.86</td>
</tr>
</tbody>
</table>

their standard errors were made through a single-trait analysis for each of the variables studied following the average information REML method given by Gilmour et al. (13). These single-trait estimates were used as starting values for derivative-free REML to facilitate convergence of the multitrait analysis. The average information REML presents an improved derivative-based procedure for the estimation of variance and covariance parameters by REML. It has convergence properties that are similar to the Fisher scoring algorithm and yet avoids the computing burdens of that approach (13). Environmental effects were estimated using a fixed model, including the same environmental fixed effects appearing in the mixed model used for estimating the genetic parameters.

RESULTS AND DISCUSSION

Means and standard deviations of the test day traits are in Table 1. Reported results (4, 11, 16) for test day milk yield and P% were similar to those for Churra ewes. Mean SCC obtained from the current study was lower than other values reported for Churra ewes (4, 16) and higher than means recorded for the French Lacaune breed (22, 23). Birth type was highly significant (P < 0.001) for milk yield only and had no significant effect on the rest of variables. Similar results were reported for the same breed (4).

The ANOVA results for milk yield, log SCC, P%, SCC (≤250,000) cells/ml, and log SCC (≤250,000) are given in Table 2. Flock test date, parity, and stage of lactation contributed significantly to variation of all variables, except for log SCC (≤250,000), which was not affected by stage of lactation. Similar results for HTD (4) and for parity and stage of lactation (11, 16, 22, 23) were reported for Churra and Lacaune breeds.

The proportion of variance explained by the HTD factor was calculated by dividing the variance component of the HTD factor by the sum of both the residual and the HTD variances. This HTD variance proportion was 0.23 for test day milk yield, 0.19 for log SCC, and 0.24 for P%. These results demonstrate the importance of HTD as it is associated with the actual circumstances of the herd on the day of testing. Similar results for test day milk yield and SCC were reported for the same breed (4, 9). For dairy cows, Ptak and Schaeffer (28) noted that adjustment for HTD reduced the residual variance considerably, indicating the importance of taking into account effects specific to the day of test within each herd.

Table 3 shows the effect of the stage of lactation on the variables studied. A contrast test was not carried out for the absolute values of both SCC and SCC (≤250,000) cells/ml because of their biased distributions. The lactation curve of milk yield was related inversely to the lactation curves of log SCC and P%. The decrease of milk yield as lactation progressed was accompanied by a significant increase in both log SCC and P%; log SCC (≤250,000) were not affected by the stage of lactation. The dilution effect of milk volume may also explain some of the differences in curves for SCC and P%. The increase in SCC as lactation continued could also depend on the worsening of subclinical mastitis. These results are in agreement with those of Gonzalo et al. (16) and Lagriffoul et al. (22)

TABLE 2. Analysis of variance results for test day variables.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Milk yield</th>
<th>Log SCC</th>
<th>Protein percentage</th>
<th>df</th>
<th>SCC (≤250,000)</th>
<th>Log SCC (≤250,000)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Flock test date</td>
<td>204</td>
<td>10.47***</td>
<td>8.27***</td>
<td>11.11***</td>
<td>200</td>
<td>5.65***</td>
<td>6.79***</td>
</tr>
<tr>
<td>Parity, no.</td>
<td>6</td>
<td>13.54***</td>
<td>29.62***</td>
<td>12.18***</td>
<td>6</td>
<td>3.34**</td>
<td>3.06**</td>
</tr>
<tr>
<td>Type of birth</td>
<td>1</td>
<td>69.31***</td>
<td>0.48NS</td>
<td>0.74NS</td>
<td>1</td>
<td>0.30NS</td>
<td>0.21NS</td>
</tr>
<tr>
<td>Stage of lactation</td>
<td>3</td>
<td>404.73***</td>
<td>8.70***</td>
<td>652.81***</td>
<td>3</td>
<td>2.78*</td>
<td>1.95NS</td>
</tr>
<tr>
<td>Remainder</td>
<td>6405</td>
<td></td>
<td></td>
<td></td>
<td>4067</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*P < 0.05.
**P < 0.01.
***P < 0.001.
1P > 0.05.
for Churra and Lacaune ewes and are supported in this study by the nonsignificant effect of stage of lactation on log SCC from healthy udders.

The results presented in Table 4 show the influence of parity. All variables were affected significantly by parity except for log SCC (≤ 250,000). Values for log SCC increased greatly as parity number increased, which was in agreement with other results for dairy ewes (15, 18, 23) and cows (2, 5, 20, 24, 25, 30).

Cell counts increased incrementally to almost 100% between the first and the fourth lactations (Table 4). The increase in SCC with advancing age is attributable to the increase in prevalence of infection in older udders. In this sense, parity effect had no significant effect on healthy udders (SCC ≤ 250,000 cells/ml).

Type of birth had a highly significant effect (P < 0.001) on test day milk yield but no significant effect on the rest of the variables. Ewes giving birth to multiple lambs had higher milk yield (958 ml) than did dams of single lambs (880 ml). This result agrees with the findings of others (4, 11, 16) for the same breed.

Univariate REML estimates of heritability (± SE) for test day records of milk yield, log SCC, log SCC (≤ 250,000), and P% were 0.18 (0.04), 0.08 (0.02), 0.03 (0.02), and 0.17 (0.03), respectively. The corresponding univariate REML estimates of the permanent environmental variances (± SE) for the same variables were 0.36 (0.04), 0.26 (0.03), 0.07 (0.03), and 0.22 (0.03), respectively. Table 5 presents values for heritabilities, the proportion of permanent environmental variance, and repeatabilities for test day milk yield, log SCC, log SCC (≤ 250,000), and P% that were obtained from multivariate analysis. All of the univariate estimates were similar to those from the multivariate analysis (Table 5).

The heritability of log SCC was three times as high as the heritability of log SCC (≤ 250,000). This result indicates clearly different behavior on the part of the inheritance of SCC under the two cases carried out in this study. As an indicator of mastitis, SCC presented moderately low heritability, and heritability of SCC from healthy udders was almost nil (0.03 ± 0.02).

The heritability of log SCC from this study (0.09) was much higher than that (0.04) recorded by Baro et al. (4) for ln(SCC) of the same breed and is within the range (0.08 to 0.16) reported for dairy cows (2, 5, 24, 26). These results suggest that genetic and environmental strategies that were similar to those currently used for dairy cattle such as removal of sires when their daughters are predisposed to high SCC

### TABLE 3. Least squares means of test day variables by stage of lactation.

<table>
<thead>
<tr>
<th>Variable</th>
<th>45 d</th>
<th>75 d</th>
<th>105 d</th>
<th>135 d</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield, ml</td>
<td>1258&lt;sup&gt;a&lt;/sup&gt;</td>
<td>1000&lt;sup&gt;b&lt;/sup&gt;</td>
<td>766&lt;sup&gt;c&lt;/sup&gt;</td>
<td>650&lt;sup&gt;d&lt;/sup&gt;</td>
</tr>
<tr>
<td>SCC, × 10&lt;sup&gt;3&lt;/sup&gt; cells/ml</td>
<td>746</td>
<td>843</td>
<td>889</td>
<td>970</td>
</tr>
<tr>
<td>Log SCC</td>
<td>5.25&lt;sup&gt;c&lt;/sup&gt;</td>
<td>5.33&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.37&lt;sup&gt;a&lt;/sup&gt;</td>
<td>5.41&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>SCC (≤ 250,000), × 10&lt;sup&gt;3&lt;/sup&gt; cells/ml</td>
<td>86</td>
<td>89</td>
<td>92</td>
<td>96</td>
</tr>
<tr>
<td>Log SCC (≤ 250,000)</td>
<td>4.89&lt;sup&gt;a&lt;/sup&gt;</td>
<td>4.85&lt;sup&gt;a&lt;/sup&gt;</td>
<td>4.86&lt;sup&gt;a&lt;/sup&gt;</td>
<td>4.89&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>Protein, %</td>
<td>5.03&lt;sup&gt;d&lt;/sup&gt;</td>
<td>5.54&lt;sup&gt;c&lt;/sup&gt;</td>
<td>6.04&lt;sup&gt;b&lt;/sup&gt;</td>
<td>6.37&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>Test days, no.</td>
<td>1877</td>
<td>1896</td>
<td>1674</td>
<td>1173</td>
</tr>
</tbody>
</table>

<sup>a,b,c,d</sup>Means in a row with different superscripts differ (P < 0.05).

### TABLE 4. Least squares means of test day variables by parity.

<table>
<thead>
<tr>
<th>Variable</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>≥7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield, ml</td>
<td>888&lt;sup&gt;d&lt;/sup&gt;</td>
<td>928&lt;sup&gt;c&lt;/sup&gt;</td>
<td>978&lt;sup&gt;a&lt;/sup&gt;</td>
<td>942&lt;sup&gt;b&lt;/sup&gt;</td>
<td>972&lt;sup&gt;a&lt;/sup&gt;</td>
<td>916&lt;sup&gt;e&lt;/sup&gt;</td>
<td>812&lt;sup&gt;c&lt;/sup&gt;</td>
</tr>
<tr>
<td>SCC, × 10&lt;sup&gt;3&lt;/sup&gt; cells/ml</td>
<td>491</td>
<td>655</td>
<td>834</td>
<td>967</td>
<td>950</td>
<td>1154</td>
<td>979</td>
</tr>
<tr>
<td>Log SCC</td>
<td>5.13&lt;sup&gt;e&lt;/sup&gt;</td>
<td>5.24&lt;sup&gt;d&lt;/sup&gt;</td>
<td>5.30&lt;sup&gt;c&lt;/sup&gt;</td>
<td>5.38&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.40&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.44&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.47&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>SCC (≤ 250,000), × 10&lt;sup&gt;3&lt;/sup&gt; cells/ml</td>
<td>85</td>
<td>86</td>
<td>87</td>
<td>92</td>
<td>92</td>
<td>96</td>
<td>99</td>
</tr>
<tr>
<td>Log SCC (≤ 250,000)</td>
<td>4.83&lt;sup&gt;b&lt;/sup&gt;</td>
<td>4.83&lt;sup&gt;b&lt;/sup&gt;</td>
<td>4.84&lt;sup&gt;b&lt;/sup&gt;</td>
<td>4.87&lt;sup&gt;b&lt;/sup&gt;</td>
<td>4.86&lt;sup&gt;b&lt;/sup&gt;</td>
<td>4.87&lt;sup&gt;b&lt;/sup&gt;</td>
<td>4.91&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>Protein, %</td>
<td>5.63&lt;sup&gt;c&lt;/sup&gt;</td>
<td>5.67&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.69&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.70&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.76&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.91&lt;sup&gt;b&lt;/sup&gt;</td>
<td>5.84&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>Test days, no.</td>
<td>1858</td>
<td>1520</td>
<td>1188</td>
<td>912</td>
<td>542</td>
<td>292</td>
<td>308</td>
</tr>
</tbody>
</table>

<sup>a,b,c,d</sup>Means in a row with different superscripts differ (P < 0.05).
TABLE 5. Heritabilities, proportions of permanent environmental variance (c²), and repeatabilities (r) and their approximate standard errors for test day variables.

<table>
<thead>
<tr>
<th>Variable</th>
<th>h²</th>
<th>SE</th>
<th>c²</th>
<th>SE</th>
<th>r</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield</td>
<td>0.18</td>
<td>0.04</td>
<td>0.36</td>
<td>0.04</td>
<td>0.54</td>
<td>0.01</td>
</tr>
<tr>
<td>Log SCC</td>
<td>0.09</td>
<td>0.02</td>
<td>0.29</td>
<td>0.03</td>
<td>0.38</td>
<td>0.01</td>
</tr>
<tr>
<td>Log SCC (≤250,000)</td>
<td>0.03</td>
<td>0.02</td>
<td>0.07</td>
<td>0.03</td>
<td>0.10</td>
<td>0.02</td>
</tr>
<tr>
<td>Protein, %</td>
<td>0.16</td>
<td>0.03</td>
<td>0.22</td>
<td>0.03</td>
<td>0.38</td>
<td>0.01</td>
</tr>
</tbody>
</table>

TABLE 6. Genetic correlations (below diagonal) and phenotypic correlations (above diagonal) among test day variables studied.

<table>
<thead>
<tr>
<th></th>
<th>Milk yield</th>
<th>Log SCC</th>
<th>Protein percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield</td>
<td>–0.15</td>
<td>–0.28</td>
<td></td>
</tr>
<tr>
<td>Log SCC</td>
<td>–0.23</td>
<td></td>
<td>0.16</td>
</tr>
<tr>
<td>Protein, %</td>
<td>–0.38</td>
<td>0.18</td>
<td></td>
</tr>
</tbody>
</table>

and adoption of good management practices (6, 21) could be applied to dairy ewes, too, in order to reduce high SCC. Heritabilities for both milk yield and P% fell within the range found for Churra and Lacaune ewes (3, 4, 9).

Table 5 shows repeatabilities for milk yield, log SCC, and P% of 0.54, 0.38, and 0.38, respectively, and proportions of permanent environmental variance of 0.36, 0.29, and 0.22, respectively. The repeatability estimates obtained from this study were moderate and comparable with estimates for the same breed in a study (11) carried out under experimental conditions. Moreover, the repeatability for log SCC obtained from this study was in the range found for Lacaune ewes (23). These results suggested that the recording scheme carried out for Churra ewes has acceptable validity under field conditions for test day milk yield, SCC, and P% of dairy ewes. Results in Table 5 show that repeatability for log SCC (≤250,000) was clearly lower than that for log SCC (0.10 vs. 0.38). These results coincide with those for heritabilities obtained for both cases in this study.

Genetic and phenotypic correlations among milk yield, log SCC, and P% are shown in Table 6. Genetic correlations of milk yield with log SCC (–0.23) and P% (–0.38) were negative, and the genetic correlation between log SCC and P% was positive (0.18). These results were generally in agreement with those of Baro et al. (4) who found a negative genetic correlation (–0.37) between milk yield and ln(SCC), positive and lower correlation (0.08) between milk yield and P%, and positive and higher correlation (0.37) between ln(SCC) and P%. For dairy cows, many studies have reported genetic correlations of the logarithmic form of SCC and yield traits (2, 5, 6, 20, 24, 25, 30). Estimates from these studies were contradictory, and some estimates were positive for the first lactation and negative for the subsequent ones. Table 6 shows that the genetic correlation between SCC and milk yield was weak to moderate and negative. Therefore, correlated response in SCC with selection for increased milk yield would be favorable, or at least not antagonistic.

Genetic correlations of log SCC (≤250,000 cells/ml) with milk yield and P% were –0.66 and 0.07, respectively. The lower heritability (0.03) obtained for log SCC (≤250,000) and the relatively lower number of records used in this data set, both inversely related to the accuracy, may suggest that future verifications using larger data sets are needed. The corresponding phenotypic correlations of log SCC (≤250,000 cells/ml) with milk yield and P% were –0.08 and 0.08, respectively.

Phenotypic correlations between log SCC and yield traits are given in Table 6. Correlations were positive between log SCC and P% (0.16) and negative between milk yield and both log SCC (–0.15) and P% (–0.28). The results concur with other results for dairy ewes (4, 11, 16, 17, 23). The negative phenotypic correlation between milk yield and SCC suggested that high SCC in milk, as a possible result of subclinical mastitis, are associated with low milk yield. This result has been found before for both dairy ewes (11) and cows (10, 27, 29). The positive phenotypic correlation between log SCC and SCC suggested that an increase in protein percentage occurred with higher SCC in milk samples. As in dairy cows, this increase could be due to the accompanying increase in blood proteins (Ig and BSA) during infection (27, 29).

CONCLUSIONS

The heritability of SCC found in this study (9%) falls within the range reported for dairy cows. Therefore, genetic and environmental methods that are similar to those practiced for dairy cattle, such as the
culling of sires when their daughters are predisposed to high SCC and maintenance of good management practices, are also recommended for dairy sheep. However, the negative genetic correlation between log SCC and milk yield suggests that genetic selection for milk yield only is expected to result in a genetic decrease in SCC in Churra ewes. More research is needed to investigate the heritability of SCC and its genetic relationship with yield traits in other breeds of milking ewes.

Differences in heritability and repeatability between SCC as a mastitis indicator and SCC from healthy udders suggested that these two traits could be different biologically and have different implications for genetic selection.

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REFERENCES
