Genetic Parameters for Milk Somatic Cell Scores and Relationships with Production Traits in French Lacaune Dairy Sheep

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ABSTRACT

Records from 94,445 and 45,499 French Lacaune dairy ewes in first and second lactations, respectively, were used to estimate genetic parameters for somatic cell scores. Somatic cell count data came from an extensive recording scheme and sample testing that began in 1999 using the flocks enrolled in the official milk recording system. Somatic cell count data were from 2 to 4 test days per lactation. Lactation average and single test-day somatic cell scores were considered in multitrait sire models.

The heritability estimate of lactation somatic cell score was close to 0.13 and similar for first and second parity. Heritabilities of somatic cell scores increased from first to fourth test day (from 0.07 to 0.11 in first lactation and from 0.05 to 0.13 in second lactation). Genetic correlations between somatic cell scores were high, usually more than 0.91, but lower between first test day and later test days in first lactation (0.64 to 0.88). The genetic correlations between lactation somatic cell score and milk yield, between lactation somatic cell score and fat content, and between lactation somatic cell score and protein content were 0.18, 0.04, and 0.03 in first lactation, respectively. The genetic antagonism between test day somatic cell score and milk yield measured in first lactation increased from beginning to the end of the lactation (0.05 to 0.23). This antagonism was slightly lower for somatic cell score in second lactation (from 0.09 to 0.14, and 0.08 for lactation mean). Environmental correlations in first lactation between lactation somatic cell score and milk yield, between lactation somatic cell score and fat content, and between lactation somatic cell score and protein content were -0.18, 0.13, and 0.30, respectively.

(Key words: dairy sheep, somatic cell count, production traits, genetic parameters)

Abbreviation key: LSCS = lactation mean SCC.

INTRODUCTION

In dairy sheep, mastitis mainly consists of subclinical infections caused by coagulase-negative staphylococci. Under these conditions, SCC is an accurate, indirect measure to predict mammary gland infection. Indeed, specific IMI diagnosis rules based on SCC have been developed for different sheep breeds and countries (Bergonier et al., 1994; Green, 1984; Gonzalez-Rodriguez et al., 1995; Mavrogenis et al., 1995). Therefore, SCC could be used as an indirect selection criterion for mastitis resistance, as is widely done in dairy cattle (Mrode and Swanson, 1996; Boichard and Rupp, 1997; Boettcher et al., 1998). Moreover, selection for mastitis resistance in dairy sheep could mainly focus on selection against subclinical mastitis using SCC, considering the low incidence of clinical cases in this species (~5%), compared with dairy cattle for which clinical cases occur frequently (20 to 40% affected lactations; Heringstad et al., 2000). Further genetic research on clinical mastitis is needed to make assumptions on indirect response in clinical cases in dairy sheep.

Genetic studies of SCC in dairy sheep are more recent and are scarcer than in dairy cattle. Reported results, however, are consistent and show that the trait exhibits genetic variation in this species. Initial results based on repeatability test day models for SCS, i.e., log transformed SCC to achieve normality of distribution, indicated low heritability estimates, ranging from 0.04 (Baro et al., 1994) to 0.09 (El Saied et al., 1998). But more recent studies reported higher heritability estimates for the lactation mean SCS, from 0.11 to 0.18 (El Saied et al., 1999; Mavrogenis et al., 1999; Barillet et al., 2001; Rupp et al., 2001). These results were very similar to values from the dairy cattle literature (Mrode and Swanson, 1996; Heringstad et al., 2000). Thus, the level of genetic variability of SCC in dairy sheep appears sufficient to implement selection. Genetic correlation estimates with milk yield, however, are quite inconsistent across dairy sheep studies, ranging from antagonistic, i.e., from 0.09 to 0.20 (Mavrogenis et al., 1999; Barillet et al., 2001; Rupp et al., 2001), to favorable, i.e., from

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–0.15 to –0.37 (Baro et al., 1994; El Saied et al., 1998 and 1999).

Following the first genetic analyses on experimental data (Barillet et al., 1999, 2001), an extensive recording procedure for SCC has been implemented for French dairy sheep breeds as part of the milk recording system. The consistent database should allow further research and genetic evaluation of SCS.

The objective of this study was to estimate genetic parameters for SCS in first and second lactations using records from the national database. Models based on lactation means and multitrait within-lactation approaches were used. Relationships with dairy production traits were also investigated. Results should allow us to define a model to be used for genetic evaluation for SCS.

MATERIALS AND METHODS

Data

Data originated from Lacaune flocks of the French nucleus breeding scheme. Out of 1,300,000 dairy ewes milked in France, 60% are of the Lacaune breed, and 20% in each breed are involved in the nucleus scheme. Exhaustive monthly recording of SCC, usually available in dairy cattle, is prohibitive in sheep. Therefore, in order to record a large number of animals at a reduced cost, a simplified method of sampling for SCC was implemented. This method, similar to the sampling scheme for fat and protein content (Barillet, 1985), is as follows: For first and second lactations, information includes two to four individual SCC per lactation. Test-day SCC are collected after a 25-d suckling period among the first four monthly records for milk yield. SCC are measured by a Fossomatic cell counter from a sample of the milk collected during the morning milking. Individual daily milk yield is estimated from individual morning recording adjusted with the bulk tank milk of the second daily milking (ICAR, 1992).

From 1999 to 2001, the Lacaune database includes SCC records for 204,256 first and second lactations of ewes in 384 flocks, in addition to production trait information (fat and protein content, milk yield, pedigrees, etc.). To avoid bias due to selection, information gathered during parity 2 was considered only if information for parity 1 was available. Moreover, ewes had to be sired by either proven sires born after 1992 who have at least 100 daughters, or sampling sires, born from 1996 to 1999 who have at least 20 daughters. After edits, the dataset included 94,474 first lactations and 45,499 second lactations of Lacaune ewes. Selected ewes originated from 1221 and 171 sampling and proven sires, respectively. The average number of SCC records per lactation was 2.9, and most ewes (87%) had three records per lactation. For milk yield, an average of 5.1 test day records per

lactation were available. Characteristics of the data set are summarized in Table 1.

Variables

Test-day SCC were transformed to SCS by the logarithmic transformation of Ali and Shook (1980). SCS were then adjusted for DIM. The adjustment procedure has been defined from a previous study based on healthy ewes with four to seven SCC records per lactation and is described in Barillet et al. (2001). Lactation mean SCS (**LSCS**) were computed as the weighted arithmetic mean of test-day SCS adjusted for DIM. Weights were r^2 , where r is the correlation between one measure and the mean of all other records.

Monthly SCS were also considered as independent, single traits according to DIM at test-day: 25–55 (SCS1), 56–85 (SCS2), 86–115 (SCS3), and 116–145 (SCS4).

Milk yield per lactation was estimated using the Fleischmann method and was adjusted for milking length on a reference period of 160 d (Barillet, 1985). Lactation traits for fat and protein content were defined as the arithmetic mean of test-days' record adjusted for DIM, following the same procedure as for LSCS.

Methods

Variance components were estimated by REML applied to multitrait sire models, using the VCE package (Neumaier and Groeneveld, 1998), which is based on a derivative-free iterative algorithm (Quasi Newton) for parameter estimation. As only 3 yr of data were available, with few dam-daughter pairs with performance records, the sire model will imply a limited loss of information compared to an animal model. A sire group effect was fitted with one level for each proven sire and one level by year of birth for sampling sires. Therefore, proven sires were treated as fixed, and only sampling sires contributed to the estimation of variance components. Underestimation of genetic variance due to highly selected rams was avoided.

Because of computation limitations, a maximum of four traits were analyzed simultaneously. To take into account the selection process from first to second lactation, which is based on milk production and somatic cell counts, all analyses including traits in second lactation also included average milk yield and LSCS in first lactation. The model for lactation measures in first or second parity was:

$$y_{ijklmn} = FY_i + M_j + A_k + L_l + G_m + S_n + e_{ijklmn} \quad (1)$$

where:

y_{ijklmn} = LSCS, average milk yield, fat content, or protein content in first or second lactation;

Table 1. Structure of the dataset.

Breed	Lacaune
Study period	1999–2001
Number of flocks	384
Number of flock*year combination	1143
Number of first lactations ¹	94,474
Number of second lactations ^{1,2}	45,499
Number of test-day SCC in first lactation	273,975
Number of test-day SCC in second lactation	131,947
Average milk yield in first lactation, liters	230
Milking length, days	145
Number of sampling sires (>20 daughters, born after 1995)	1221
Average number of daughters per sampling sire	42
Number of proven sires (>100 daughters, born after 1992)	171
Average number of daughters per proven sire	386

¹Lactations with information for milk yield.

²Second lactations considered only if information for parity one was available.

FY_i = fixed effect of flock × year combination *i* (1143 and 680 levels for first and second lactations, respectively);

M_j = fixed effect of month at lambing *j* within parity (5 levels);

A_k = fixed effect of age at lambing *k* within parity (5 and 3 levels for first and second lactation, respectively);

L_l = fixed effect of the number of lambs born (2 levels: 1 vs. 2 or more);

G_m = fixed sire group effect (one level per sire for proven rams and one level per birth year for sampling rams);

S_n = random genetic effect of sire (within sire group);

e_{ijklmn} = random residual effect.

The four single test-day SCS traits (SCS1 to SCS4) defined according to DIM were considered as different traits in a multiple-trait test-day model approach. The model used was similar to (1) and also included the fixed effect of days in milk at sampling (15 levels with 2-day steps). Three generations of ancestors were considered to compute the pedigree file, which included 4390 individuals.

RESULTS AND DISCUSSION

Basic Statistics

Basic statistics for SCS are presented in Table 2. Mean LSCS and increase of SCS from beginning to the end of the lactation were in agreement with previous French reports (Barillet et al., 2001). However, no increase in LSCS with parity was observed, contrary to trends usually reported (Gonzalo et al., 1994; Fuertes et al., 1998). Further investigation showed that ewes culled at the end of first lactation, completed in 1999 or 2000, had much higher somatic cell counts (3.60 and 690,000 cells/ml, for LSCS and average SCC, respectively) than ewes that were allowed to start a second lactation (3.00 or 330,000 cells/ml, for LSCS and average SCC, respectively). This showed that breeders started to use SCC in culling strategies as soon as this information had been made available to them. It may explain the absence of an increase in SCC from first to second lactation, and makes it necessary to perform multitrait analyses that include milk and somatic cell count in first lactation when REML is applied to second lactation SCS data.

Genetic Parameters for Somatic Cell Scores

Heritabilities. The heritability of LSCS was moderate (0.13) and similar in first and second lactation (Table

Table 2. Number of records and mean for somatic cell score traits.

Trait ¹	First lactation		Second lactation	
	N	Mean (SD)	N	Mean (SD)
LSCS	94,445	3.13 (1.53)	45,499	3.15 (1.46)
SCS1	62,454	2.92 (1.81)	8849	2.83 (1.72)
SCS2	88,761	3.03 (1.77)	35,930	2.89 (1.64)
SCS3	82,018	3.25 (1.79)	38,755	3.13 (1.68)
SCS4	25,527	3.36 (1.80)	30,148	3.41 (1.76)

¹LSCS = lactation mean SCS, and single test days according to DIM: SCS1 = 25 to 55; SCS2 = 56 to 85; SCS3 = 86 to 115; SCS4 = 116 to 145.

Table 3. Genetic parameters for lactation mean SCS (LSCS) in first and second lactation and correlations with production traits in first lactation (heritabilities on the diagonal, genetic correlations above the diagonal, and environmental correlation under the diagonal).¹

	LSCS		Production traits in first lactation		
	1st Lactation	2nd Lactation	Milk yield	Fat content	Protein content
LSCS					
1st Lactation	0.13	0.93	0.18	0.04	0.03
2nd Lactation	0.31	0.12	0.08		
Milk yield	-0.18	-0.02	0.28	-0.48	-0.53
Fat content	0.13		-0.22	0.41	0.60
Protein content	0.30		-0.37	0.39	0.51

¹Standards errors between 0.004 and 0.008 for heritabilities. Standard errors between 0.002 and 0.008 for environmental correlations. Standards errors between 0.013 and 0.040 for genetic correlations.

3). Results were in agreement with previous French studies (Barillet et al., 2001; Rupp et al., 2001). These studies were based on data from ewes of 38 Lacaune flocks between 1993 and 1999 with 5 to 6 test-day SCC per lactation. Heritabilities of LSCS, estimated with an animal model, ranged from 0.14 to 0.15 in these studies. The value estimated presently would have been a little higher if an animal model instead of a sire model could have been used. Comparable heritabilities for LSCS (0.12) were also reported from Spanish Churra flocks (El Saied et al., 1999) and in recent dairy cattle studies (Mrode and Swanson, 1996; Boettcher et al., 1998; Rupp and Boichard, 1999).

Heritability estimates for SCS1 to SCS4 (Tables 4 and 5) were lower than the estimate for LSCS. Heritabilities of SCS increased from 0.07 for SCS1 to 0.11 for SCS4 in first lactation, and from 0.05 for SCS1 to 0.13 for SCS4 in second lactation. This increase of heritability with DIM reflected an increase of the genetic variance (Table 6). Conversely, the environmental variance was quite stable, although slightly higher at the beginning of the lactation. This result confirms similar trends observed in previous Spanish (Baro et al., 1994) and French (Barillet et al., 2001) studies. In the latter studies, heritabilities in the first 2 mo of lactation were lower (0.01 to 0.05) than the present study.

Genetic and environmental correlations. The genetic correlation between LSCS in first and second lactation (Table 3) was high (0.93), as observed previously (Rupp et al., 2001), and in agreement with dairy cattle data (Mrode and Swanson, 1996; Boettcher et al., 1998). This finding suggested that LSCS in first and second lactation were essentially the same trait genetically. Similarly, genetic correlations between single traits SCS1 to SCS4 and LSCS (Tables 4 and 5) and among single traits were high (0.64 to 0.99), especially for SCS2 to SCS4. However, SCS1 exhibited a lower correlation with SCS2 to SCS4, which could be due to the influence of both the suckling period (for 1 mo following lambing) and a biological effect of starting lactation for the first time in primiparous ewes. Environmental correlations (Tables 4 and 5) were highest between successive test day SCS and decreased with increasing interval between measures, i.e., from 0.55 to 0.36, reflecting a repeatability of monthly SCS of approximately 0.4 (Barillet et al., 2001).

Relationships between SCS and Milk Production Traits

Genetic parameters for production traits (Table 3) were in accordance with the ovine literature. Heritabilities for milk yield were about 0.30, and heritabilities for fat and

Table 4. Heritability (on the diagonal), genetic (above the diagonal), and environmental (below the diagonal) correlations between single test-day¹ SCS traits (SCS1 to SCS4) and genetic correlations with lactation mean SCS (LSCS) in first lactation.²

Trait ¹	SCS1	SCS2	SCS3	SCS4	LSCS
SCS1	0.07	0.87	0.64	0.88	0.88
SCS2	0.51	0.09	0.93	0.94	0.99
SCS3	0.41	0.55	0.10	0.98	0.97
SCS4	0.36	0.54	0.54	0.11	0.99

¹LSCS = lactation mean SCS, and single test days according to DIM: SCS1 = 25 to 55; SCS2 = 56 to 85; SCS3 = 86 to 115; SCS4 = 116 to 145.

²Standards errors between 0.002 and 0.004 for heritabilities. Standard errors between 0.002 and 0.004 for environmental correlations. Standards errors between 0.01 and 0.07 for genetic correlations.

Table 5. Heritability (on the diagonal), genetic (above the diagonal), and environmental (below the diagonal) correlations between single test-day SCS traits (SCS1 to SCS4) in second lactation and genetic correlation with lactation mean SCS (LSCS) in first lactation.^{1,2}

Trait	SCS1	SCS2	SCS3	SCS4	LSCS
SCS1	0.05	0.99	0.98	0.82	0.97
SCS2	0.55	0.07	0.94	0.91	0.87
SCS3	0.42	0.57	0.09	0.96	0.92
SCS4	0.38	0.47	0.56	0.13	0.89

¹LSCS = lactation mean SCS, and single test days according to DIM: SCS1 = 25 to 55; SCS2 = 56 to 85; SCS3 = 86 to 115; SCS4 = 116 to 145.

²Standards errors between 0.002 and 0.004 for heritabilities. Standard errors between 0.002 and 0.007 for environmental correlations. Standards errors between 0.002 and 0.16 for genetic correlations.

protein content were between 0.40 and 0.60 (Barillet and Boichard, 1987; Barillet and Boichard, 1994; Sanna et al., 1997; Barillet et al., 2001).

Genetic correlations between LSCS and fat and protein content were close to zero (Table 3). As expected, the genetic correlation (Table 3) between milk yield in first lactation and LSCS in second lactation (0.08) was slightly lower than the genetic correlation between milk yield in first lactation and LSCS in first lactation (0.18). These values reflected a moderate genetic antagonism between the two traits and were in the range of values previously reported on a smaller French dataset (Rupp et al., 2001). Indeed, Rupp et al. (2001) found genetic correlations between LSCS and milk yield ranging from 0.09 to 0.19. Such a genetic antagonism is also reported from dairy cattle data (Mrode and Swanson, 1996; Boichard and Rupp, 1997; Rupp and Boichard, 1999). El Saied et al. (1998 and 1999), however, found negative and favorable genetic correlations (−0.15 to −0.23) between SCC and milk yield in the ovine Churra breed. This discrepancy could be due to both the structure of data and the model used (Barillet et al., 2001).

The unfavorable genetic relationship between SCS and milk yield increased during first lactation, from 0.05 at first test day to 0.23 at fourth test day (Table 7). The

very low correlation between SCS at first test day and milk yield may be related to the low heritability of SCS1. Nevertheless, results did not confirm the favorable correlation at first test day (−0.48) observed previously (Barillet et al., 2001), but standard errors were substantial in some cases. In the present study, all first and second lactation results showed genetic antagonism between milk yield and SCS, indicating that the udder health may be deteriorating under selection for production traits. As reported by others (Mrode and Swanson, 1996; Barillet et al., 2001), environmental correlation between milk yield and SCS are of opposite sign (e.g., negative), reflecting the reduction in the production ability of the mammary gland when an infection occurs.

CONCLUSIONS

Genetic parameters for SCS were estimated using a large dataset from the newly implemented recording procedure for SCC in the French Lacaune breed. Heritability of LSCS was approximately 0.13 and was comparable in

Table 6. Genetic and environmental variance for lactation mean SCS (LSCS) and for single test-day SCS1 to SCS4 according to parity.

	Genetic variance	Environmental variance
Trait in first lactation ¹		
LSCS	0.066	2.08
SCS1	0.051	2.99
SCS2	0.065	2.87
SCS3	0.075	2.91
SCS4	0.085	2.86
Trait in second lactation ¹		
LSCS	0.062	1.99
SCS1	0.032	2.69
SCS2	0.045	2.51
SCS3	0.060	2.62
SCS4	0.092	2.77

¹Single test days according to DIM: SCS1 = 25 to 55; SCS2 = 56 to 85; SCS3 = 86 to 115; SCS4 = 116 to 145.

Table 7. Genetic and environmental correlations between milk yield in first lactation and single test day somatic cell score traits (SCS1 to SCS4) in first or second lactation. Reported values are means of three to four multitrait analyses.

	Correlation with milk yield in first lactation	
	Genetic ²	Environmental ³
Trait in first lactation ¹		
SCS1	0.05	−0.21
SCS2	0.18	−0.16
SCS3	0.17	−0.10
SCS4	0.23	−0.06
Trait in second lactation ¹		
SCS1	0.14	−0.03
SCS2	0.07	−0.04
SCS3	0.09	−0.02
SCS4	0.09	−0.01

¹Single test days according to DIM: SCS1 = 25 to 55; SCS2 = 56 to 85; SCS3 = 86 to 115; SCS4 = 116 to 145.

²Standards errors between 0.036 and 0.130 for genetic correlations.

³Standard errors between 0.002 and 0.007 for environmental correlations.

first and second lactation, with high genetic correlation between parities (>0.90). Antagonism between SCS and milk production was confirmed (genetic correlation 0.05 to 0.23), suggesting that including SCS in the breeding goal may be useful. Depending on the emphasis placed on SCS, we expect to, at least, stop the deterioration in SCS that is a consequence of selection for production traits. Genetic evaluation using lactation average SCS in first and second lactation is justified and could be easily implemented. However, the increasing heritability and increasing genetic antagonism with milk yield as days in the lactation increase suggests that models for test day records, accounting for complex (co)variance structure within and across lactation, may increase accuracy of genetic evaluation for SCS when compared to lactation models.

REFERENCES

- Ali, A. K. A., and G. E. Shook. 1980. An optimum transformation for somatic cell concentration in milk. *J. Dairy Sci.* 63:487–490.
- Barillet, F. 1985. Amélioration génétique de la composition du lait des brebis: l'exemple de la race Lacaune. Ph.D. Thesis, Institut National Paris-Grignon, Paris, France.
- Barillet, F., and D. Boichard. 1987. Studies on dairy production of milking ewes. I. Estimates of genetic parameters for total milk composition and yield. *Génét. Sélect. Evol.* 19:459–474.
- Barillet, F., and D. Boichard. 1994. Use of first-lactation test-day data for genetic evaluation of the Lacaune dairy sheep. Pages 111–114 in *Proc. 5th World Congr. Genet. Appl. Livest. Prod., Guelph, Canada. XIX*.
- Barillet, F., R. Rupp, S. Mignon, J. M. Astruc, M. Jacquin, and G. Lagriffoul. 1999. Genetic analysis for mastitis resistance and somatic cell score in French Lacaune dairy sheep. Pages 393–399 in *Proc. 6th Int. Symp. of the Milking of Small Ruminants, Athens, Greece. Wageningen Pers, Wageningen, The Netherlands*.
- Barillet, F., R. Rupp, S. Mignon-Grasteau, J. M. Astruc, and M. Jacquin. 2001. Genetic analysis of mastitis resistance and somatic cell score in French Lacaune dairy sheep. *Genet. Sel. Evol.* 33:397–415.
- Baro, J. A., J. A. Carriedo, and F. San Primitivo. 1994. Genetic parameters of test-day measures for somatic cell count, milk yield, and protein percentage of milking ewes. *J. Dairy Sci.* 77:2658–2662.
- Bergonier, D., A. Van De Wiele, J. M. Arranz, F. Barillet, G. Lagriffoul, D. Condorcet, and X. Berthelot. 1994. Detection of subclinical mammary infections in the ewe by mean of somatic cell counts: proposal of physiological thresholds. Pages 41–47 in *Proc. Int. Symp. on Somatic Cells and Milk of Small Ruminants, Bella, Italy. Wageningen Pers, Wageningen, The Netherlands*.
- Boettcher, P. J., J. C. M. Dekkers, and B. W. Kolstad. 1998. Development of an udder health index for sire selection based on somatic cell score, udder conformation, and milking speed. *J. Dairy Sci.* 81:1157–1168.
- Boichard, D., and R. Rupp. 1997. Genetic analysis and genetic evaluation for somatic cell score in French dairy cattle. Pages 54–60 in *INTERBULL Bull. No. 15. Int. Bull Eval. Serv., Uppsala, Sweden*.
- El Saied, U. M., J. A. Carriero, and F. San Primitivo. 1998. Heritability of test day somatic cell counts and its relationship with milk yield and protein percentage in dairy ewes. *J. Dairy Sci.* 81:2956–2961.
- El Saied, U. M., J. A. Carriero, and L. F. De La Fuente. 1999. Genetic parameters of lactation cell counts and milk and protein yield in dairy ewes. *J. Dairy Sci.* 81:2956–2961.
- Fuertes, J. A., C. Gonzalo, J. A. Carriedo, and F. San Primitivo. 1998. Parameters of test-day milk yield and milk components for dairy ewes. *J. Dairy Sci.* 81:1300–1307.
- Gonzalez-Rodriguez, M. C., C. Gonzalo, F. San Primitivo, and P. Carmenes. 1995. Relationship between somatic cell count and intramammary infection of the half udder in dairy ewes. *J. Dairy Sci.* 78:2753–2759.
- Gonzalo, C., J. A. Carriedo, J. A. Baro, and F. San Primitivo. 1994. Factors influencing variation of test-day milk yield, somatic cell count, fat, and protein in dairy sheep. *J. Dairy Sci.* 77:1537–1542.
- Green, T. J. 1984. Use of somatic cell counts for detection of subclinical mastitis in ewes. *Vet. Rec.* 114:43.
- Heringstad, B., G. Klemetsdal, and J. Ruane. 2000. Selection for mastitis in dairy cattle: a review with focus on the situation of the Nordic countries. *Livest. Prod. Sci.* 64:95–106.
- ICAR. 1992. International regulations for milk recording in sheep. Institut de l'Élevage, Paris, France.
- Mavrogenis, A. P., A. Koumas, C. K. Kakoyiannis, and C. K. Taliotis. 1995. Use of somatic cell counts for the detection of subclinical mastitis in sheep. *Small Rum. Res.* 17:79–94.
- Mavrogenis, A. P., A. Koumas, and G. Gavrielidis. 1999. The inheritance of somatic cell counts (index of mastitis) in Chios sheep. Pages 389–392 in *Proc. 6th Int. Symp. of the Milking of Small Ruminants, Athens, Greece. Wageningen Pers, Wageningen, The Netherlands*.
- Mrode, R. A., and G. J. T. Swanson. 1996. Genetic and statistical properties of somatic cell count and its suitability as an indirect means of reducing the incidence of mastitis in dairy cattle. *Anim. Breed. Abstr.* 64:847–857.
- Neumaier, A., and E. Groeneveld. 1998. Restricted maximum likelihood estimation of covariances in sparse linear models. *Genet. Sel. Evol.* 30:3–26.
- Rupp, R., and D. Boichard. 1999. Genetic parameters for clinical mastitis, somatic cell score, production, udder type traits, and milking ease in first lactation Holsteins. *J. Dairy Sci.* 82:2198–2204.
- Rupp, R., G. Lagriffoul, J. M. Astruc, and F. Barillet. 2001. Genetic parameters for milk somatic cell count across first three parities and relationships with production traits in French Lacaune dairy sheep. Page 280 in *Proc. 52nd Annu. Mtg. Eur. Assoc. Anim. Prod., Budapest, Hungary. Wageningen Pers, Wageningen, The Netherlands*.
- Sanna, S. R., A. Carta, and S. Casu. 1997. (Co)variance component estimates for milk composition traits in Sarda dairy sheep using bivariate animal model. *Small Rum. Res.* 25:77–82.
- Wiggans, G. R., and G. E. Shook. 1987. A lactation measure of somatic cell count. *J. Dairy Sci.* 77:2666–2672.