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Genetic analysis of somatic cell score and other milk traits in several lactations of Manchega ewes. Mean lactation approach

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SUMMARY – Somatic Cell Score (SCS) as indicator of udder health was analysed using 36,873 data of this trait in Manchega ewes. Firstly genetic parameter estimation was carried out using multivariate animal models including Somatic Cell Score Lactation mean (SCSL) and other milk traits (milk yield and protein and dry matter contents). Analysis were made within 1st, 2nd and 3rd lactations separately and also with multiple lactations under repeatability and multivariate approaches considering SCSL as the same or different trait throughout lactations. Heritability estimates of SCSL under models without repeatability were higher, 0.12-0.24, than estimates obtained when the permanent environmental effect was fitted, 0.04. Also this fact occurred for the other milk traits. Genetic correlations among SCSL in different lactations were moderate to high, 0.54-0.98. Genetic correlation between SCSL and milk yield was low and negative, –0.12 to –0.16, indicating a slightly favourable genetic relationship between these traits, however was positive between SCSL and protein content, 0.22. Pearson and Spearman correlation coefficients of estimated breeding of animals showed modest favourable correlations between the Estimated Breeding Value (EBV) for SCSL and milk yield (–0.15 to –0.28) and positive between SCSL and protein content (0.13-0.33).

Key words: Somatic cell score, models, multiple lactations, genetic parameters, sheep.

RESUME – *"Analyse génétique du comptage de cellules somatiques et autres caractères laitiers sur plusieurs lactations chez les brebis de race Manchega. Approche d'une lactation moyenne". Le nombre de cellules somatiques (SCS) comme indicateur de la santé de la mamelle est analysé en utilisant 36 873 données de ce caractère chez la brebis Manchega. L'estimation des paramètres génétiques est réalisée sous des modèles animaux multivariés, qui comprennent le nombre cellulaire moyen par lactation (SCSL) et d'autres caractères laitiers (production de lait et de protéine, contenu de matière sèche). Les analyses comprennent les 1ère, 2ème et 3ème lactations séparément et aussi toutes les lactations sous un modèle avec répétabilité et des approximations multivariées en considérant le SCSL comme un seul ou plusieurs caractères au long des lactations. Les estimations de l'héritabilité de SCSL sous des modèles sans répétabilité sont plus hautes, 0,12-0,24, que les estimations obtenues quand l'effet d'environnement permanent est considéré, 0,04. La même tendance est observée chez les autres caractères laitiers. La corrélation génétique estimée entre SCSL dans les différentes lactations est modérée-haute, 0,54-0,98. La corrélation génétique entre SCSL et la production laitière est basse et négative, –0,12 à –0,16, indiquant une faible relation génétique favorable entre ces caractères, mais qui est positive entre SCSL et le taux protéique, 0,22. Les coefficients de corrélation de Pearson et de Spearman des valeurs génétiques estimées (EBV) des animaux montrent des corrélations légèrement favorables entre celles de SCSL et celles de production laitière (–0,15 to –0,28) et positives entre SCSL et taux protéique (0,13-0,33).*

Mots-clés : *Nombre de cellules somatiques, modèles, multiples lactations, paramètres génétiques, brebis.*

Introduction

Mastitis is recognized as one of the most costly diseases of the dairy industry and one of the main causes of culling dairy ewes. Clinical (CM) and Sub Clinical Mastitis (SCM) produce economic losses by a decrease of milk yield, changes in milk and cheese quality (Pellegrini *et al.*, 1994; Dekkers, 1995) and the increase of culling rate and cost of veterinary treatments. Data of CM and SCM are scarcely available in most breeding programs. However development of Somatic Cell Count (SCC) testing in milk recording as indicator of udder health, has opened opportunities for the indirect measurement of mastitis incidence and the practical genetic improvement of mastitis resistance.

Results from dairy cattle literature (Banos and Shook, 1990; Da *et al.*, 1992; Mrode and Swanson, 1996; Rupp and Boichard, 1999) indicate that SCC and CM do not seem to be the expression of the same trait, since genetic correlation between these traits is 0.7. However Somatic Cell Score (SCS) has higher heritability (0.10 to 0.15) than CM (0.02) and therefore it could be used as a tool to improve milk quality through selection programs in this specie.

In sheep there are scarce literature about SCC (Baro *et al.*, 1994; El Saied *et al.*, 1998, 1999; Barillet *et al.*, 2001) and less about CM and SCM traits (Mavrogenis *et al.*, 1998; Barillet *et al.*, 2001) because only in experimental herds there are collection of mastitis data and only few breeds have systematic recording of SCC. In this specie intramammary infections are characterized by a lower incidence of clinical mastitis, 5%, (Barillet *et al.*, 2001) than in dairy cattle, reported to be between 20% and 40% (Mrode and Swanson, 1996; Rupp and Boichard, 1999). By the other hand studies of SCC in sheep show great variability in their results.

Many papers had been focused in statistical treatment of SCC under a mean lactation approach and test-day models in cattle (Schutz *et al.*, 1990; Da *et al.*, 1992; Reents *et al.*, 1994, 1995) and ewes (Baro *et al.*, 1994; El Saied *et al.*, 1998, 1999; Barillet *et al.*, 2001). The best genetic treatment of SCC by adjustment of test-day data in a single lactational measure or by a test-day approach, with repeatability or multivariate animal models along lactations, still remains an open question.

In this work, a study SCS along lactations under a mean lactation approach is presented. Variance component estimation within and among lactation were developed. Finally, genetic animal evaluation under some of previous models and genetic parameters was made.

Material and methods

Data

Data from Manchega Spanish breed were available. These animals are raised in a semiarid region of Central Spain, the Autonomous Community of Castilla-La Mancha. Since 1998 data of individual SCC are collected in this breed. Data consisted of 71,710 lactation records of ewes belonging to 118 herds, in which data of SCC were available for one, two, three or four test-day. Only lactations with at least two SCC test-day ranging between 50,000-7,000,000 cell/ml and pertaining to the first three lactations were considered in analyses (36,873 lactations, 103,792 test-day records). Also, most of these lactations (32,844) had records of standardised to 120 days milk yield in kg (120dMY) and protein (120d%P) and dry matter (120d%DM) contents. Because SCC have a highly skewed distribution, SCS are defined by a logarithmic transformation [$SCS = \log_2(SCC/100000)+3$] of individual SCC test-day values (Ali and Shook, 1980). Classical models to analyse SCS in cattle and ewes involves calculation of a measure of the cell count lactation mean computed as the arithmetic mean of test-day SCS preadjusted for some environmental factors and days in milk. In this case test-day SCS data were preadjusted (ASCS) by lactation stage as proposed by Wiggans and Shook (1987) and by month of test-day. After preadjustment, a Somatic Cell Score Lactation mean (SCSL) was computed as the arithmetic mean of ASCS. In pedigree only artificial insemination sires were considered. This males allow connection among flocks. Table 1 shows data and pedigree characteristics. Table 2 shows basic statistics of SCC and SCS test-day records in each lactation. Table 3 shows statistics of lactation mean SCS (SCSL) and standardized to 120 days milk yield, protein content and dry matter content for first, second and third lactations.

Statistical analysis

Variance component estimation was made with REML methodology using VCE 4.2.5 software (Groeneveld and García-Cortés, 1998) in all cases. Variance component estimation with multivariate animal models were carried out including SCSL and standardised to 120 days milk yield (120dMY), protein content (120d%P) and dry matter content (120d%DM). Analyses were carried out with first lactation records, second lactation records and third lactation records separately. Also analysis with multiple lactation under a repeatability animal model and with a multivariate approach (only for SCSL) considering SCSL along lactations as different traits were made.

Different models were applied for SCSL and the other milk traits. Models included herd-year-season of lambing (season in four periods: 1 = December-February; 2 = March-May; 3 = June-August; 4 = September-November), age at lambing (in months), number of lambs born (one, two and three or more), lambing-first test-day period only in the case of milk traits (1 = <45 days; 2 = 45 to 52 days; 3 = >52 days) and lactation number (only in the case of multiple lactations) as fixed effects. Additive genetic and permanent environmental (in the case of multiple lactations) were the random effects included in the models.

Table 1. Data and pedigree characteristics[†]

Pedigree (animals)	47,808
Sires	526
Average number of daughters per sire	13
Dams	16,562
Animals with known sire and dam	6,640
Animals with known dam	17,238
Animals with unknown sire and dam	23,930
SCSL records	36,873
1st SCSL lactation records	13,448
2nd SCSL lactation records	12,938
3rd SCSL lactation records	10,487
Animals with data	28,694
Dams with data	1,744
Dams number of data	2,314
Milk traits records	32,844
1st 120dMY, 120d%P and 120d%DM lactation records	12,025
2nd 120dMY, 120d%P and 120d%DM lactation records	11,568
3rd 120dMY, 120d%P and 120d%DM lactation records	9,251

[†] SCSL = mean lactation somatic cell score; 120dMY = standardised to 120 days milk yield in kg; 120d%P = standardised to 120 days protein content; 120d%DM = standardised to 120 days dry matter content.

The equations of the multivariate animal models applied for SCSL and milk traits data of single lactations and multiple lactations were the following:

Single lactations: model (1)

SCSL: $y_{ijkom} = \mu + hys_i + age_j + nlb_k + g_m + \varepsilon_{ijklom}$

Milk traits: $y_{ijklomn} = \mu + hys_i + age_j + nlb_k + ipc_l + g_{mn} + \varepsilon_{ijklomn}$

Multiple lactations: model (2)

SCSL: $y_{ijkom} = \mu + hys_i + age_j + nlb_k + pnu_o + g_m + p_m + \varepsilon_{ijklom}$

Milk traits: $y_{ijklomn} = \mu + hys_i + age_j + nlb_k + ipc_l + pnu_o + g_{mn} + p_{mn} + \varepsilon_{ijklomn}$

In the case of multiple lactations of SCSL treated as different traits, the equation of the multivariate animal model used was the following:

SCSL along lactations as different traits: model (3)

$$y_{ijkmn} = \mu + hys_{in} + age_{jn} + nlb_{kn} + g_{mn} + \varepsilon_{ijklmn}$$

where:

y_{ijkom} = SCSL records in each single lactation (model 1) or in multiple lactations under a repeatability animal model (model 2).

$y_{ijklomn}$ = 120dMY, 120d%P or 120d%DM records in each lactation (model 1) or in multiple lactations under a repeatability animal model (model 2).

y_{ijkmn} = SCSL in each lactation, 1st, 2nd and 3rd treated as different traits (model 3).

μ = Population mean.

hys = Fixed effect of herd-year-season of lambing (651 levels for first lactation, 640 for second lactation, 619 for third lactation and 737 for multiple lactations).

age = Fixed effect age at lambing (19 levels for first lactation, 19 levels for second lactation, 16 levels for third lactation and 40 levels for multiple lactations).

nlb = Fixed effect number of lambs born (3 levels).

ipc = Fixed effect lambing-first test-day period, only for milk traits (3 levels).

pnu = Fixed effect parity number, in the case of multiple lactations (3 levels).

g = Additive genetic effect (47,808 levels).

p = Permanent environmental effect, only in the case of multiple lactations (28,694 levels).

ε = Residual.

Finally a genetic evaluation of animals with PEST (Groeneveld and Kovac, 1990) was made using the multivariate repeatability animal model described above and the genetic parameters previously estimated. Pearson and Spearman correlation coefficients were calculated by SAS statistical package (SAS, 1990) for ewes and sires rankings of all traits considered.

Results and discussion

Table 2 shows basic statistics of test-day SCC and SCS of 1st, 2nd and 3rd lactations. Mean SCC was higher than the value found in Lacaune breed (Barillet *et al.*, 2001) and lower than that of Churra (El Saied *et al.*, 1998). SCC values show an increase from first to fourth test-day in all lactations. Also an increase in SCC values was observed from 1st to 3rd lactation. SCC values of 3rd lactation were higher than the legal limit established for sheep milk in the United States, 0.75×10^6 cell/ml (Paape *et al.*, 2001). Official rules for establishing a legal SCC limit have not yet been imposed in EU for small ruminants. Mean of SCS data ranged from 3.76 to 4.01 in first lactation, from 4.06 to 4.28 in second lactation and from 4.21 to 4.44 in third lactation. SCS values in first lactation were higher than those found in Lacaune breed, 3.08 to 3.43, (Barillet *et al.*, 2001) and lower than that found in Churra ewes, 4.95, mean of test-day of several lactations (Fuertes *et al.*, 1998). Skewness and kurtosis of SCS were near to normal values.

Table 3 shows mean, standard deviations and coefficient of variation of lactation mean SCS (SCSL) and standardised to 120 days milk yield (120dMY), protein content (120d%P) and dry matter content (120d%DM) for first, second and third lactation data. A 12% increase in SCSL occurs between the first and third lactation. Similar results are pointed out by Paape *et al.* (2001) for the first fourth lactations in ewes. Also 120dMY, 120d%P and 120d%DM showed the same trend, with increases of 10%, 3% and 2% from first to third lactation, respectively. SCSL mean of first lactation data, 3.80, was slightly higher than value found in Lacaune breed, 3.29 (Barillet *et al.*, 2001). For the whole data, mean of SCSL was 4.08 which was smaller than those of Churra ewes, 5.27 (El Saied *et al.*, 1999).

Table 4 shows genetic parameters (heritability, genetic and phenotypic correlations) estimated for first, second, third lactations (model 1) and multiple lactations (model 2). Under model (1) SCSL heritability increased from 1st to 3rd lactation, 0.12 to 0.24. Similar heritability values were found in Lacaune (Barillet *et al.*, 2001) with first lactation data, in Churra ewes (El Saied *et al.*, 1999) with multiple lactations and also in recent studies in cattle (Mrode and Swanson, 1996; Rupp and Boichard, 1999). 120dMY and 120d%DM heritability estimates were very similar in 1st, 2nd and 3rd lactation, 0.26-

0.27 and 0.23-0.26, respectively. However heritability of protein content decrease along lactations from 0.44 to 0.27.

Table 2. Mean, standard deviation (SD), coefficient of variation (%CV), skewness (SKE) and kurtosis (KUR) of test day data in 1st, 2nd and 3rd lactation

	Test-day	N[†]	Mean	SD	%CV	SKE	KUR
SCC (x10^3)[††]							
1st lactation							
	1st	10,962	512.0	1,240	242.4	4.12	17.20
	2nd	10,362	547.5	1,326	242.3	3.85	14.62
	3rd	8,995	601.5	1,381	229.5	3.62	12.84
	4th	7,322	683.2	1,460	213.6	3.28	10.39
2nd lactation							
	1st	10,560	676.7	1,466	216.7	3.31	10.46
	2nd	10,327	720.2	1,530	212.4	3.20	9.57
	3rd	8,957	718.8	1,500	208.6	3.22	9.81
	4th	6,949	797.8	1,585	198.6	2.93	7.90
3rd lactation							
	1st	8,379	761.3	1,566	205.8	3.03	8.45
	2nd	8,202	799.3	1,585	198.2	2.94	7.91
	3rd	7,137	817.3	1,600	195.0	2.90	7.70
	4th	5,640	854.5	1,603	187.6	2.78	7.08
SCS[†††]							
1st lactation							
	1st	10,962	3.76	1.76	46.80	1.31	1.21
	2nd	10,362	3.75	1.81	48.34	1.35	1.20
	3rd	8,995	3.86	1.90	49.38	1.16	0.55
	4th	7,322	4.01	2.00	49.92	0.98	0.03
2nd lactation							
	1st	10,560	4.06	1.91	47.22	1.08	0.36
	2nd	10,327	4.15	1.94	46.74	1.01	0.20
	3rd	8,957	4.16	1.96	47.09	0.93	0.02
	4th	6,949	4.28	2.03	47.45	0.83	−0.24
3rd lactation							
	1st	8,379	4.21	1.99	47.24	0.95	0.02
	2nd	8,202	4.32	2.00	46.39	0.84	−0.18
	3rd	7,137	4.37	2.01	46.15	0.78	−0.27
	4th	5,640	4.44	2.05	46.25	0.70	−0.46

[†] N = number of observations.
[††] SCC = test day somatic cell count.
[†††] SCS = test day somatic cell score.

In the analysis with separate lactations model (1) genetic correlations between SCSL and 120dMY were low and negative in all cases, −0.12 to −0.15. Also a favourable relation between these traits had been observed in Churra ewes under classical, −0.15, (El Saied *et al.*, 1999), and test-day, −0.37, (Baro *et al.*, 1994) approaches. However in Lacaune (Barillet *et al.*, 2001) and in cattle (Reents *et al.*, 1994) unfavourable genetic relationship between SCC and milk yield were found (0.11-0.14). Genetic correlation between SCSL and 120d%P in first lactation (0.23) was higher than those found in 2nd and 3rd lactations, which were near to zero. In Churra ewes (El Saied *et al.*, 1999) this genetic correlation was almost nill (−0.03). However in cattle Rupp and Boichard (1999) found a genetic correlation between SCSL and protein content near our estimates (0.20). Genetic correlation between SCSL and 120d%DM were almost nill in all cases. As were expected, genetic correlations between 120dMY and contents were moderated and negatives and between contents high and positives. Phenotypic correlations were lower and with the same sign than the genetic ones in all cases. Same values were found by El Saied *et al.* (1999) in Churra ewes.

Table 3. Mean, standard deviation (SD) and coefficient of variation (%CV) of lactation traits for first, second and third lactations

Lactation	Trait[†]	N	Mean	SD	%CV
1st lactation	SCSL	13,448	3.80	1.41	37.20
	120dMY	12,025	137.84	55.91	40.56
	120d%P	12,025	5.71	0.51	8.98
	120d%DM	12,025	18.74	1.85	9.90
2nd lactation	SCSL	12,938	4.17	1.51	36.31
	120dMY	11,568	146.08	60.43	41.37
	120d%P	11,568	5.88	0.54	9.22
	120d%DM	11,568	18.95	1.87	9.86
3rd lactation	SCSL	10,487	4.34	1.58	36.54
	120dMY	9251	153.00	62.94	41.14
	120d%P	9251	5.90	0.57	9.71
	120d%DM	9251	19.05	1.91	10.03

[†] SCSL = mean lactation somatic cell score; 120dMY = standardised to 120 days milk yield in kg; 120d%P = standardized to 120 days protein content; 120d%DM = standardised to 120 days dry matter content.

Table 4. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) estimated by REML with first, second and third lactation records separately (model 1) and multiple lactation records (model 2)[†]

	Trait[††]	SCSL	120dMY	120d%P	120d%DM
1st lactation	SCSL	*0.12*	–0.12	0.23	–0.04
	120dMY	–0.08	*0.27*	–0.37	–0.37
	120d%P	0.16	–0.27	*0.44*	0.76
	120d%DM	0.10	–0.24	0.53	*0.25*
2nd lactation	SCSL	*0.19*	–0.14	0.09	0.02
	120dMY	–0.14	*0.26*	–0.37	–0.20
	120d%P	0.14	–0.26	*0.30*	0.78
	120d%DM	0.09	–0.21	0.55	*0.23*
3rd lactation	SCSL	*0.24*	–0.15	0.08	–0.00
	120dMY	–0.15	*0.26*	–0.38	–0.35
	120d%P	0.13	–0.29	*0.27*	0.88
	120d%DM	0.04	–0.22	0.55	*0.26*
1st, 2nd and 3rd lactations	SCSL	*0.04*	–0.16	0.22	0.04
	120dMY	–0.13	*0.18*	–0.32	–0.25
	120d%P	0.17	–0.24	*0.26*	0.80
	120d%DM	0.09	–0.23	0.50	*0.17*

[†] Standard errors of ratios ranged from 0.01 to 0.09.

[††] SCSL= mean lactation somatic cell score; 120dMY = 120 days standardised milk yield kg; 120d%P = 120 days standardised protein content; 120d%DM = 120 days standardised dry matter content.

In the multiple lactation model (2) SCSL heritability were 0.04. In this case genetic variance estimate was lower, 0.083, than those found in analysis with separate lactations and permanent environmental variance was four times higher than the genetic one, 0.373 (data not shown). Da *et al.* (1992) in analysis with three SCSL lactation measures in cattle, found permanent environmental variance two times higher than the genetic, 0.27 and 0.14 respectively, which show similar trend than results here observed. This heritability value is smaller than those found in Lacaune (Barillet *et al.*, 2001), 0.15, in Churra ewes (El Saied *et al.*, 1999), 0.12, and in cattle studies (Da *et al.*, 1992; Zhang *et al.*, 1994), 0.10 to 0.14. However, is near to that estimate in Lacaune (Barillet *et al.*, 2001) under a repeatability test-day model with first lactation data, 0.08. This results suggest that scarce repeated measures per animal and pedigree relationships did not allow separate permanent environmental effect from the genetic one. For the other milk traits, genetic and permanent environmental variances had more similar values. In general genetic correlations among traits had similar magnitudes than previous estimates in within lactation analyses. However genetic correlation between SCSL and 120d%P, 0.22, was similar to 1st lactation estimate and higher than values found in 2nd and 3rd lactations. Repeatabilities (not shown in table) were 0.24, 0.35, 0.42 and 0.29 for SCSL, 120dMY, 120d%P and 120d%DM, respectively. In Churra ewes (El Saied *et al.*, 1999) higher repeatability was estimated for SCSL (0.35) and smaller for 120d%P (0.38). In cattle Da *et al.* (1992) found similar heritability-repeatability relation for SCSL (0.14 and 0.35 respectively) to our estimates. In our case, repeatability was about five times as high as heritability. Phenotypic correlations showed the same trend of previous analyses.

Table 5 shows genetic parameters from multivariate analysis considering SCSL in 1st, 2nd and 3rd lactations as different traits (model 3). Heritability estimates for the three lactations were slightly higher than the value found for the repeatability model, 0.04-0.10. Similar estimates for the first three lactations were found in cattle (Da *et al.*, 1992) with a multivariate model considering first three lactations as different traits.

Table 5. Genetic parameters: heritability (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) estimated under a multivariate animal model considering lactation mean SCS of first, second and third lactations as different traits (model 3)[†]

Trait[††]	SCSL1	SCSL2	SCSL3
SCSL1	*0.04*	0.70*	0.98
SCSL2	0.20	*0.10*	0.54*
SCSL3	0.20	0.30	*0.06*

[†] Standard errors of ratios ranged from 0.01 to 0.03.
[††] SCSL1 = mean lactation of SCS in first lactation; SCSL2 = mean lactation of SCS in second lactation; SCSL3 = mean lactation of SCS in third lactation.
*Standard errors of these ratios were 0.1.

Genetic correlations among SCSL of all lactations were moderate to high and positive. Lower genetic correlations were found in cattle (Da *et al.*, 1992), 0.54-0.55, in similar analysis. Phenotypic correlations were lower than the genetic, ranging from 0.20 to 0.30. However these results need to be interpreted with caution, because the high standard errors estimated for genetic correlations.

Finally Table 6 shows Pearson and Spearman correlation coefficients for Estimated Breeding Values (EBV) rankings of ewes and sires, predicted under a multivariate repeatability animal model (2) using all lactations data.

A slightly antagonism between sire (−0.15 and −0.16) and ewes (−0.27 and −0.28) EBV for SCSL and 120dMY was observed, indicating a favourable relation between these traits. For SCSL and 120d%P EBVs small and positive correlations were found. As expected, moderate negative correlations of EBV for 120dMY and contents were found indicating the antagonism between milk yield and milk quality. High and positive correlations showed EBVs of contents.

Opposite results were found by Zhang *et al.* (1994) in cattle. In this case Pearson correlation coefficients between SCSL and milk yield of sires for several lactations were positives (0.05 to 0.12) and nearly null for SCSL and protein content (0.00 to −0.02).

Table 6. Pearson and Spearman correlation coefficients among ranking of breeding values predicted for lactation traits for ewes and sires under model 2[†]

	Trait[††]	SCSL	120dMY	120d%P	120d%DM
Ewes					
Pearson					
	SCSL	1.00	−0.28	0.33	0.12
	120dMY		1.00	−0.36	−0.26
	120d%P			1.00	0.90
	120d%DM				1.00
Spearman					
	SCSL	1.00	−0.27	0.33	0.14
	120dMY		1.00	−0.33	−0.25
	120d%P			1.00	0.88
	120d%DM				1.00
Sires					
Pearson					
	SCSL	1.00	−0.16	0.21	0.00
	120dMY		1.00	−0.40	−0.27
	120d%P			1.00	0.87
	120d%DM				1.00
Spearman					
	SCSL	1.00	−0.15	0.13	−0.03
	120dMY		1.00	−0.31	−0.23
	120d%P			1.00	0.84
	120d%DM				1.00

[†] $P < 0.0001$ in all cases.

[††] SCSL = mean lactation somatic cell score; 120dMY = standardised to 120 days milk yield; 120d%P = standardised to 120 days protein content; 120d%DM = standardised to 120 days dry matter content.

Conclusions

In the basis of some studies of SCC in cattle and sheep, it seems that this trait has different behaviour and maybe different genetic basis in these species, since in cattle SCC is a moderate good indicator of clinical mastitis but only of subclinical infection in ewes. Since moderate to high genetic correlations were found among SCSL in different lactations, repeatability models considering a mean lactation measure of preadjusted SCS records (SCSL) could be a good approach to evaluate this trait along lactations in dairy ewes. The smaller heritability found for SCS under a repeatability animal model, 0.04, than with models without repeated measures suggest that more repeated measures per animal and complete pedigrees are needed to separate the permanent environmental effect from the genetic one. Low favourable genetic correlation found between SCSL and 120dMY revealed that selection in this breed to improve milk yield might not affect mastitis resistance. Differences and agreements with results found in other sheep breeds and in cattle could be due to selection process of animals. Thus, in species or breeds with a large selection history, 30 years in Lacaune and more than 50 years in dairy cattle, to improve milk yield, a decrease of mastitis resistance due to a linkage disequilibrium or a pleiotropy effect could be occurred. However scarce pedigree relationships and repeated measures per animal present in our data, indicates that more studies are needed.

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