Relationships between somatic cell count and milk yield in the Sarda dairy sheep breed.

S. Salaris, S. Sechi, S. Casu and A. Carta

Research Unit: Genetics and Biotechnology, DIRPA-AGRIS Sardegna, S.S. 291 Sassari-Fertilia, Km. 18.6, 07100 - Sassari, Italy

Abstract

In dairy sheep, Somatic Cell Count (SCC) in bull milk has been used as an indicator of hygiene, animal welfare and prevalence of sub-clinical mastitis. SCC is also included in the parameters considered for the determination of the milk price. SCC individual recording has been implemented in several European sheep to detect sub-clinical mastitis and for selection purposes. In Sardinia a Regional Plan aimed at improving animal welfare and using as target the reduction of bulk milk SCC was launched. Simultaneously, a simplified recording system of individual value of SCC was applied in the selected population to evaluate the potential introduction as selection criterion. In this situation, it is crucial to assess the relationships between SCC and production traits. This work showed that raw relationships between somatic cell count and milk yield, even if negligible, are negative only in animals with high probability to have an infected udder.

Keywords: genetic parameters, test-day recording, mastitis

Introduction

In recent years there has been increasing emphasis on reducing milk somatic cell count (SCC) to improve milk quality in ruminants. In dairy sheep, SCC in bulk milk has been used as an indicator of hygiene (Gonzalo et al., 2005), animal welfare (Foddis et al., 2006) and prevalence of subclinical mastitis (Bergonier et al., 2003). SCC is also included in the parameters considered for the determination of milk price in several European countries (Pirisi et al., 2007).

In Europe, SCC individual recording has been implemented for several breeds (Carta et al., 2009): Lacaune and Pyrenean breeds in France, Sarda in Italy and Manchega, Churra, and Latxa in Spain. However, SCC has been included as selection criterion only in the Lacaune breed's selection scheme (Barillet et al., 2007).

In Sardinia, a specific part of the Rural Development Plans is aimed at improving animal welfare (RAS, 2007). The bulk milk SCC is the main indicator for evaluating if the farmer may access to the economic subsidies. In particular, farmers who adhere to the plan must have an annual geometric mean of bulk SCC lower than 1,500,000 cells/ml (RAS, 2011).

Moreover, SCC is considered an indirect measure of subclinical mastitis in dairy sheep (Berthelot et al., 2006). Although relationships between subclinical mastitis and milk yield are well known, relationships between SCC and production traits are controversial. In this situation, it is crucial to assess the relationships between SCC and the production traits both to show to the farmers the potential effects on production traits and to assess the profitable economic weights of SCC in milk pricing. The raw relationship between SCC and milk yield and contents has been evaluated in few researches in cattle (Durr et al., 2008; Hand et al.,

2008). A recent study on this relationship were carried out in sheep (Arias et al., 2012). In this species relationship is often deduced indirectly from the fact that infected ewes show a higher SCC and contemporarily a lower milk yield (Cuccuru et al., 2011; Leitner et al., 2008; Rupp et al., 2003). Some authors (Green et al., 2006; de los Campos et al., 2009; Koop et al., 2010) studied the effect of dilution effect, e.g. low milk yield correspond to higher percentages either for fat and protein or somatic cells, in cattle and goat milk. This is a crucial point for the farmer which may be induced to incorrectly conclude that there is a negative effect of SCC on milk yield and vice versa a positive one on contents. Moreover, farmers involved in selection schemes are debating the inclusion of SCC as selection criterion. The genetic relationship between SCC and milk yield antagonistic in dairy cattle, are quite inconsistent across dairy sheep studies. Genetic correlation estimates with milk yield ranged from antagonistic (0.08 to 0.23) to favourable (-0.15 to -0.30) (Rupp et al., 2010 for a review).

The aim of this study was either to evaluate the raw relationship between SCC and milk yield and to estimate the genetic correlation between them in view of including SCC as selection criterion against subclinical mastitis.

Material and methods

From 2000 to 2011, 123,006 test day (TD) records of 14,977 lactations of 6,043 ewes were collected from two flocks of AGRIS. In the first flock (FL1), TD records were monthly recorded. In this flock voluntary culling based on milk yield and udder morphology was performed. The second flock (F2), was composed by a Sarda×Lacaune backcross population from 2000 to 2004. In the following years ewes were mated with Sarda rams so that offspring showed an increasing proportion of Sarda blood. TD records were fortnightly recorded and each cohort was simultaneously slaughtered at the end of 4th lactation without voluntary culling.

After editing, only TD recorded between 30 to 240 days from lambing and lactations above 100 days in milking with the first TD within 82 days from lambing were considered. A description of data from the two flocks is shown in Table 1.

Table 1 – Description of data from two experimental flocks (FL1 and FL2) recorded between 2000 and 2011.

	FL1	FL2	Total
Years	12	12	12
Test Day records	24,187	92,590	116,777
Lactations	4,646	9,352	13,998
Ewes	2,742	3,046	5,788
Test Day records/Year	2,016	7,716	9,732
Lactations/Year	387	779	1,166
Test Day records/Lactation	5.21	9.90	8.34
Lactations/Ewe	1.69	3.07	2.42

Individual daily milk (MYd), fat (FYd) and protein (PYd) yields were computed with A4 method. Daily fat (FCd) and protein (PCd) contents and SCC (SCCd) were calculated weighting for corresponding milk yields of the morning and afternoon milkings. In addition SCCd scores (SCSd) were calculated according to Ali and Shook (1980).

Lactation yields of milk (MY), fat (FY), protein (PY) and somatic cells (SCT) were calculated with Fleishmann method. Missing data of milk composition (10% of the total values for SCCd) were estimated interpolating the closest TD records. Lactation contents of fat (FC), protein (PC) and SCC were computed as ratio of respective quantities with MY. SCC was then log transformed as before (SCS).

Empirically, lactations were considered performed by animals with high probability to be "infected" when at least 2 SCCd were above 600 K (K= x 10^3 cells/ml) or one SCCd was above 1,500 K. Therefore TD data were split into two classes of health status: 0 if referred to lactations performed by ewes with "health" udder and 1 if referred to lactations performed by ewes with "infected" udder (as described above). Descriptive statistics and correlations of somatic cells with production traits were calculated by flock and HSC.

To investigate the effect of decreasing (increasing) trend of milk yield with lactation stage on the relationship between somatic cells and milk yield, the expected SCCd (SCCf) was calculated on the basis of the amount of somatic cells at the first TD as:

$SCCf = (MYd_1 \times SCCd_1)/MYd_n$ where subscripts indicate TD order and the related score
$SCSf = \log_2 (SCCf/100) + 3$

The product $MYd_1 \times SCCd_1$ was assumed to be the individual base level of somatic cells. Thus, SCSf trend with lactation stage is only affected by milk yield and measures the dilution effect. Correlation of SCSf with milk yield is expected to measure the relationships caused by the decreasing of milk yield. Analogously, the difference between SCSd and SCSf (DSC) is expected to measure the deviation of SCSd from that due to the dilution effect on the SCSd base level. In order to estimate the relationship between deviations from the base levels of SCSd and MYd, the single TD milk yield deviation (DMY) from the first TD milk yield was calculated. The correlation between DSC and DMY was calculated by flock and HSC excluding TD of lactations with a first SCCd greater than 600 x K to increase the probability of not including animals with an infected udder at the beginning of the lactations which can bias the calculations.

Genetic parameters and correlations between lactation milk yield and somatic cell score were calculated by flock with the following bi-trait repeatability animal model:

$$y = YALS + APM + ML + A + PE + e$$

where *y* is MY and SCS, *YALS* is the fixed effect of Year x Age x Lambing Season combination (7 levels), *APM* is the fixed effect of Age x Parity x Lambing month combination (5 levels), *ML* the fixed effect of Milking Length class (14 levels), *A* is the random genetic effect, *PE* is random permanent environmental effect, *e* is the random residual effect. Known relationships until to grand-grandparents were considered in the pedigree file (4835 and 4739 individuals for FL1 and FL2).

Results and discussion

Descriptive statistics of TD and lactation yields according to flock and HSC were showed in Table 2 and Table 3 respectively. Production traits were similar but slightly higher in FL2 than in FL1. SCCd and SCC in FL1 were approximately twice than in FL2. The percentage of lactations included in HSC 0 were 47.4% in FL1 (11,277 TD) and 59.3% in FL2 (53,532 TD). The different percentage of infected animals does not seem sufficient to explain the difference in SCC suggesting that other management factors are involved (Arias et al., 2012).

Table 2 - Number of records (N) and mean ± standard deviation for TD milk (MYd), fat (FCd) and protein (PCd) content, fat (FYd) and protein (PYd) yield, somatic cell content (SCCd), somatic cell score (SCSd), expected somatic cell score (SCSf) according to flock (FL1 and FL2) and health status class (HSC=0 health; HSC=1 infected).

Flock	FL1			FL2		
HSC	0	1	0+1	0	1	0+1
N	11,277	12,910	24,187	53,532	39,058	92,590
MYd (L/d)	1.45 ± 0.46	1.37 ± 0.48	1.41 ± 0.47	1.51 ± 0.54	1.45 ± 0.56	1.48 ± 0.55
FCd (%)	6.17 ± 1.06	6.19 ± 1.09	6.18 ± 1.08	6.44 ± 1.15	6.48 ± 1.06	6.46 ± 1.11
PCd (%)	4.93 ± 0.55	5.19 ± 0.63	5.06 ± 0.61	5.20 ± 0.57	5.39 ± 0.58	5.28 ± 0.58
FYd (g/d)	88 ± 26	84 ± 27	86 ± 26	94 ± 30	91 ± 33	93 ± 31
PYd (g/d)	71 ± 21	71 ± 22	71 ± 22	77 ± 25	76 ± 27	77 ± 26
SCCd (K[1])	206 ± 209	2023 ± 3524	1164 ± 2720	171 ± 163	1227 ± 2472	616 ± 1693
SCSd	3.5 ± 1.1	5.8 ± 2.2	4.7 ± 2.1	3.4 ± 1.0	5.2 ± 1.9	4.2 ± 1.7
SCSf	3.4 ± 1.2	5.3 ± 2.3	4.5 ± 2.1	3.4 ± 1.1	5.1 ± 2.0	4.1 ± 1.8

[1]K = 10^3 cells x ml^{-1}

Table 3 - Number of records (N) and mean ± standard deviation for lactation milk (MY), fat (FY) and protein (PY) yield, fat (FC) and protein (PC) content, somatic cell count (SCC), score of SCC (SCS), milking period length (ML) according to flock (FL1 and FL2) and health status class (HSC=0 health; HSC=1 infected).

	FL1			FL2		
Variable/HSC	0	1	Total	0	1	Total
N	2203	2443	4646	5545	3807	9352
MY (L)	221 ± 56	220 ± 60	221 ± 58	255 ± 70	259 ± 69	257 ± 69
FC (%)	6.04 ± 0.62	6.09 ± 0.68	6.07 ± 0.65	6.25 ± 0.73	6.32 ± 0.71	6.27 ± 0.72
PC (%)	4.9 ± 0.41	5.16 ± 0.48	5.04 ± 0.47	5.09 ± 0.36	5.28 ± 0.36	5.16 ± 0.37
FY (Kg)	13.4 ± 3.8	13.4 ± 3.9	13.4 ± 3.8	16.0 ± 4.8	16.3 ± 4.7	16.1 ± 4.7
PY (Kg)	10.8 ± 3.0	11.3 ± 3.2	11.1 ± 3.1	13.0 ± 3.8	13.7 ± 3.7	13.3 ± 3.8
SCC (K)	206 ± 117	2096 ± 2295	1200 ± 1915	165 ± 83	1177 ± 1308	577 ± 974
SCS	3.8 ± 0.8	6.8 ± 1.3	5.4 ± 1.8	3.6 ± 0.7	6.0 ± 1.2	4.6 ± 1.5
ML (day)	153 ± 30	160 ± 32	157 ± 31	173 ± 31	183 ± 30	177 ± 31

[1]K = 10^3 cells x ml^{-1}

The overall correlation between SCS and MY were close to zero (-0.06 in FL1 and -0.02 in FL2). However, it showed an opposite sign in HSC 0 and 1: 0.08 and -0.18 in FL1 and 0.10 and -0.20 in FL2 for class 0 and 1 respectively. These results indicate that a moderate negative relationship between lactation milk yield and SCS is detected only in ewes with a higher probability to have an infected udder.

At TD level, the overall correlation between SCSd and MYd was moderately negative in both flocks (-0.20 in FL1 and -0.19 in FL2). Similarly to lactation level analysis, the correlation was higher in HSC 1 (-0.23 in FL1 and -0.24 in FL2) than in HSC 0 (-0.15 in FL1

and -0.15 in FL2). Finally, the relationships are generally higher in the TD analysis than lactation one, suggesting a potential impact of the dilution effect.

The average SCSd of HSC 1 ewes in FL1 was significantly higher than SCSf (Table 2). This result is determined by the higher level of SCSd along with lactation than SCSd of the first TD in infected ewes. The overall correlation between MYd and SCSf was -0.25 in FL1 and -0.33 in FL2. This result shows that the actual relationship between milk yield and somatic cells is lower than that due to mere effect of dilution. The explanation is that at the end of lactation the amount of somatic cells is lower than the initial one. This difference is more evident in "health" ewes as showed by the higher correlation values in HSC 0: -0.29 FL1 and -0.38 in FL2.

The percentage of first TDs with SCCd below 600 K was 75% in FL1 and 87% in FL2. The average amount of somatic cells in the first TD ($SCCd_1$*MYd_1) was 270 x 10^6 cells in FL1 and 280 x 10^6 cells in FL2 whereas the average MYd of the first TDs was 1.65 L/d in FL1 and 1.94 L/d in FL2.

DSC was on average 0.79 in FL1 and 0.27 in FL2 whereas DMY was -0.22 L in FL1 and -0.45 L in FL2. The overall correlation between DSC and DMY was close to zero (-0.04 in FL1 and 0.11 in FL2). This result demonstrates that the negative correlation found between SCSd and MYd is likely to be affected by dilution effect.

The correlation between DSC and DMY was positive in HSC 0 (0.13 FL1 and 0.26 in FL2) and negative or close to zero in HSC 1 (-0.09 in FL1 and 0.03 in FL2). These results indicate that the detrimental effect of SCSd on milk yield is negligible and it exists only in ewes with a high probability to be "infected". Moreover this result is not repeatable between flocks. On the contrary in "health" animals the relationships is moderately positive.

The genetic parameters and correlations between lactation SCS and MY were showed by flock in table 5. Repeatability of MY was 0.50±0.02 in FL1 and 0.61±0.01 in FL2. Repeatability of SCS was 0.33±0.02 in FL1 and 0.38±0.01 in FL2.

Table 4 – Hereditability (diagonal), genetic (above diagonal) and phenotypic correlation (below diagonal) of milk yield (MY) and somatic cell score (SCS) by flock (FL1 and FL2). The parameter estimates are followed by their approximate standard errors.

Flock	FL1		FL2	
	MY	SCS	MY	SCS
MY	0.37±0.04	0.18±0.14	0.47±0.03	-0.06±0.08
SCS	-0.15±0.02	0.12±0.03	-0.18±0.02	0.22±0.03

Higher heritabilities estimated in FL2 are probably due to the better accuracy of measures and consistency of data (Table 1). Both MY and SCS hereditabilities are in agreement with estimates in other breeds including Spanish Churra, Manchega and Latxa (El-Saied et al., 1999; Othmane et al., 2002; Legarra and Ugarte, 2005), French Lacaune (Barillet et al., 2001; Rupp et al., 2003) and Italian Valle del Belice (Riggio et al., 2007). The genetic correlations were low, discordant between two flocks and with high standard errors. These findings support the hypothesis that the true genetic correlations between SCS and MY are around zero. In particular, the different sign in the two flocks may be interpreted in the same way of differences found in literature between breeds. Indeed, in FL1 where a higher level of SCC was observed, the genetic correlation was unfavorable and in agreement with the values founded in dairy cow (Rupp and Boichard, 2003) and in Lacaune breed (Barillet et al., 2001; Rupp et al., 2003). On the contrary in FL2 the genetic correlation was favorable and in agreement with the values founded in Spanish breed (El-Saied et al., 1998 and 1999; Othmane

et al., 2002). Moreover, the different behavior of the two flocks suggests that genetic parameters estimate for SCS at population level should be checked by flock or at least flock class.

Conclusion

This work showed that raw relationships between somatic cell count and milk yield, even if negligible, are negative only in animals with high probability to have an infected udder. In any case the dilution effect should be considered when TD yields are analyzed. As far as the genetic parameter estimates is concerned, the level of heritabilities for SCS found in this study are in the range of literature. On the other hand, genetic correlations with milk yield are low and different in sign in the two analyzed flocks. The overall results coupled with the asymptomatic nature of subclinical mastitis makes particularly difficult to convince farmers to select against SCC mainly in the absence of an adequate payment system. In this situation the implementation of selection for udder morphology, that was shown to be favorable related to machine milkability and udder health (Casu et al., 2010), may be an efficient and already available way for genetically improving udder health.

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