Genetic parameters of different measures of somatic cell counts in the Rendena breed

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ABSTRACT

The objective of this study was to consider different and alternative methods of using somatic cell count (SCC) data recorded according to the Italian official milk recording system, estimating its genetic parameters and the correlations with the yield traits (milk, fat, and protein) in the Rendena breed. The SCC traits defined for genetic evaluation were somatic cell score, log of the total daily SCC (LTSCC, i.e., SCC multiplied by daily milk yield) individually recorded in a day of official control, and 3 different thresholds ($\geq 80,000$, $\geq 150,000$, and $\geq 400,000$ cells/mL) for somatic cells. A total of 187,052 test-day monthly records of milk, fat, and protein yields and SCC belonging to 11,718 cows were used to estimate heritability and genetic correlations between SCC and yield traits via a bi-trait repeatability test-day model using a Bayesian approach. The heritability values estimated for the threshold traits ranged from 0.036 to 0.065, less than those observed for monthly somatic cell score and LTSCC traits that were equivalent to 0.088 and 0.103, respectively. Higher genetic correlations were estimated between LTSCC trait and all productive traits (0.379 for milk, 0.240 for fat, and 0.370 for protein). The other SCC traits considered have shown low or almost null genetic correlations with the productive traits (from 0.008 between fat yield and SCC $\geq 150,000$ cells/mL to 0.234 between protein yield and SCC $\geq 400,000$ cells/mL) and almost all estimates included zero in the 95% highest posterior density region interval. These results indicated that genetic selection for milk, fat, and protein production negatively affects the LTSCC content and SCC $\geq 400,000$ cells/mL but does not negatively influence the other somatic cell and threshold SCC traits in the Rendena breed. However, the complete framework of genetic relationships of SCC with all traits under selection should be considered

when deciding on the possible inclusion of SCC in the breeding program of this small cattle population.

Key words: dual-purpose breed, genetic parameters, somatic cell count, threshold somatic cell count

INTRODUCTION

In many countries, including Italy, the SCC, regularly recorded according to the Italian official milk recording system, provides some information about milk quality and is considered to be the most common and suitable indicator of mastitis, in light of its high positive genetic correlation with mastitis and a greater heritability (Carlén et al., 2004; Koivula et al., 2005; Vallimont et al., 2009). Mastitis is an inflammation of the mammary gland, and it is a frequent and costly disease in dairy cattle (Nielsen, 2009). Considering the economic consequence of mastitis, selection for mastitis resistance should not be neglected in a dairy breeding program, but the genetic evaluation of mastitis is difficult because of its low heritability (Urioste et al., 2010; Koeck et al., 2012). Recent studies (Macciotta et al., 2012; Bobbo et al., 2014) reported that other traits than somatic cells, such as lactose, pH, lactoferrin, and minerals, could also be used as udder health indicators. However, at present SCC remains the most widespread method for controlling udder health. In most countries (Miglior et al., 2005), the genetic evaluation of udder health is based on the logarithmic transformation of SCC into SCS to achieve a normality of distribution (Ali and Shook, 1980). During the years, alternative SCC traits have been proposed as a new method of highlighting mastitis, suggesting a possible improvement in methods of genetic evaluation for mastitis resistance. The new traits studied should clarify the dynamic nature of mastitis and be flexible enough to accommodate sudden changes in SCC, especially when resulting from cases of clinical mastitis. For example, Urioste et al. (2010) used the measures of days sick during lactation as a trait for controlling mastitis resistance in dairy cattle. On the other hand, peak patterns have been suggested by de Haas et al. (2008) to better

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describe the dynamic nature of mastitis cases. Other traits have been derived directly from SCC by defining a test-day (TD) SCC threshold to distinguish between healthy or unhealthy cows, or to suggest the occurrence of subclinical or clinical mastitis (de Haas et al., 2008; Urioste et al., 2010). Current selection indices in specialized dairy cattle breeds typically include udder health indicators such as SCS to counteract the negative effects of selection for yield on health, longevity, and reproduction (e.g., Miglior et al., 2005; Oltenacu and Broom, 2010). Recently, udder health indicators have also been introduced in the selection indices of some dual-purpose breeds such as Austrian Simmental (Fuerst-Waltl et al., 2016), for which the udder health index includes both mastitis (70%) and SCS (30%). However, health indicators in genetic improvement have not yet been considered in many dual-purpose populations. This is the case in small autochthonous local breeds spread across Italy such as the Rendena, an Italian dual-purpose breed native to Trento province in the eastern Italian Alps (Mazza et al., 2014). In this breed, the current selection program does not include SCC and only TD SCC information has been routinely recorded and stored since 1996 (ANARE, 2016). In addition, milk production in the breed is increasing, and considering the positive correlation with the incidence of mastitis, interest in mastitis control is increasing. Milk yield is the most important trait under selection in the dual-purpose breeding scheme of the Rendena (65% of incidence in the global selection index), and possible new selection strategies regarding udder health indicators are currently under consideration by the National Association of Breeders of Rendena cattle. In light of this new possible breeding goal for this particular breed, the present study investigated genetic parameters for different SCC traits for feasible inclusion in the Rendena breeding program. It considered different and alternative methods of using SCC data routinely recorded under the national official milk recording system, as well as investigated the genetic parameters of SCC and correlations with other milk

production traits currently under selection. The study could also provide an example of investigation on the possible introduction of somatic cells as breeding goal in local dual-purpose breeds.

MATERIALS AND METHODS

Data and Editing

Production, quality traits (fat and protein content), SCC, and population genealogic data were provided by the National Association of Breeders of Rendena cattle. The SCC has been routinely collected by official milk recording systems in Rendena cattle since 1996. The initial data set used in the present study consisted of 437,616 monthly TD records for milk, fat, and protein yields and SCC recorded between 1999 and 2014. For this study, only complete TD records for milk, fat, and protein yields and SCC were retained considering that milk recording in not carried out on unhealthy cows. Only TD in the first 3 lactations with the first TD record obtained within 45 DIM were allowed to enter the data set. Furthermore, only TD collected between 5 and 305 DIM were retained. Considering the extremely low lethality rate for clinical mastitis (Seegers et al., 2003), and knowing that the optimal decision policy often deals with the treatment of mastitic cows rather than with their culling (Houben et al., 1994), we hypothesized that the probability of a cow being culled because of 2 or 3 consecutive peaks of SCC within the same lactation was low. Only lactations with at least 4 TD records and the herd TD within a lactation with at least 2 TD records were retained for analysis. The final edited data set included 187,052 TD records for milk, fat, and protein yields and SCC of 23,858 lactations, belonging to 11,718 cows in 211 herds. Simple descriptive statistics of the data set used are reported in Table 1. The pedigree file obtained for genetic analysis was generated by tracing back the pedigrees up to the last known generation. The resulting pedigree file included 18,503 animals up to the eleventh generation.

Table 1. Descriptive statistics for productive traits, SCC, SCS, and log of total SCC in daily milk production (LTSCC) in the data sets used for the study

Item	Mean	SD	Minimum	Maximum
Milk, kg/d	17.04	5.70	0.60	47.10
Fat, kg/d	0.60	0.21	0.02	2.13
Protein, kg/d	0.56	0.19	0.02	1.55
SCC, $\times 1,000$ cells/mL	188	312	1	22,007
SCS ¹	2.83	1.90	-3.64	10.78
LTSCC	4.96	1.27	-0.51	10.54

¹SCS = $3 + \log_2(\text{SCC}/100,000)$.

Definition of SCC Traits

Five alternative SCC traits were defined as udder health indicators for further genetic evaluation. The TD SCC converted by logarithm transformation to SCS [$SCS = 3 + \log_2(SCC/100,000)$] was the first trait considered. In line with Urioste et al. (2010), and to avoid the possible effects of milk dilution, a second trait considering the total amount of SCC was considered: the TD SCC was multiplied by TD milk yield to obtain the total number of cells and then log transformed (**LTSCC**). Finally, knowing that the TD SCC has been reported in other studies as an indication of mammary gland health (de Haas et al., 2008; Urioste et al., 2010), the 3 different thresholds traits [80,000 (**SCC80**), 150,000 (**SCC150**), and 400,000 (**SCC400**) cells/mL] of somatic cells were defined as possible different levels of mammary infection or inflammation, assuming for the Rendena breed a similar relationship with udder health as reported in literature when mastitis diagnosis was available (Urioste et al., 2010). The thresholds used in this study were then chosen on the basis of information available in the literature and taken from current European regulation. Specifically, the threshold of SCC400 is reported in Regulation (EC) No 853/2004 of the European Parliament and of the Council of 29 April 2004 in which specific hygiene rules for food of animal origin (European Community, 2004; Jayarao et al., 2004) have been laid down. This threshold was chosen as a legal limit for the purchase of milk, as is the case in many countries including Italy (Jayarao et al., 2004). Concerning the other 2 thresholds, these have been chosen to separate a record occurring in a possible case of subclinical mastitis or not (SCC80) and a record occurring during a possible case of clinical mastitis or not (SCC150). Thresholds derived from literature on other breeds have assumed for Rendena the same udder behavior with respect to the relationship with SCC. However, the sensitivity and specificity of SCC80 and SCC 150 thresholds remain unknown considering they have been recruited from literature and particularly from studies that correlated them with the events of clinical and subclinical mastitis registered at the same individual TD recording. de Haas et al. (2008) chose a threshold of SCC150 because it represents the lowest threshold used by the Dutch national recording system. The same threshold was used by Windig et al. (2010) to predict mastitis. Therefore, this threshold seems to be a reliable indicator for the occurrence of a clinical mastitis event. Concerning the SCC80 threshold, Urioste et al. (2010, 2012) used a threshold of SCC between 41,000 and 80,000 cells/mL to identify healthy cows on the basis of a clustering method (Urioste et al., 2010). In all threshold traits, each TD SCC was individually

classified as a binary trait depending on the threshold considered. For SCC80, a TD SCC $\geq 80,000$ cells/mL was registered as 1; otherwise, it was registered as 0. A TD SCC $\geq 150,000$ cells/mL (SCC150) was registered as 1; otherwise, it was registered as 0. Finally, the presence or absence of a TD record with $\geq 400,000$ cells/mL (SCC400) was scored as 1 or 0.

Statistical Analysis

Bi-trait repeatability TD animal model analyses were run for the 3 productivity traits (milk, fat, and protein) with each of the alternative SCC traits to estimate the genetic parameters and genetic correlations between traits. The linear model applied, following the official method adopted by the national breeders association for animal genetic evaluation (Guzzo et al., 2009; Sartori et al., 2018), was as follows:

$$y_{ijklmn} = \mu + \text{HTD-LN}_i + \text{GEST}_j + \sum_{r=0}^3 \varphi_r \text{AP-LN}_k + \sum_{r=0}^3 \psi_r \text{MP-LN}_l + \text{Pe}_m + a_m + e_{ijklmn},$$

where y_{ijklmn} is the TD record n of milk, fat, and protein yield and alternative SCC traits of the cow m ; μ is the overall mean; HTD-LN $_i$ is the fixed effect of herd TD within lactation number i (12,520 levels); GEST $_j$ is the fixed effect of the days of gestation class j (18 classes: the first class means no gestation, the further classes account for 15-d intervals from 1 to 240 d of gestation, and the last class considers ≥ 241 d of gestation); AP-LN $_k$ is the fixed effect of age at parity within lactation k (42 classes in total); MP-LN $_l$ is the fixed effect of the month of parity l (36 classes corresponding to single months of a year within lactation n); Pe $_m$ is the random permanent environmental component, $N(0, \sigma_{pe}^2)$; a_m is the additive genetic component, $N(0, \sigma_a^2)$; and e_{ijklmn} is the random residual term, $N(0, \sigma_e^2)$. The shape of the lactation curve was described by fourth order Legendre polynomials for the fixed effects of AP-LN and MP-LN with φ and ψ as random regression coefficients for the Legendre polynomial of order r varying between 0 and 3.

The assumptions on estimated (co)variances for the bi-trait analyses were obtained as $\mathbf{G} \otimes \mathbf{A}$, $\mathbf{P} \otimes \mathbf{I}$, and $\mathbf{R} \otimes \mathbf{I}$, with $\mathbf{G}$, $\mathbf{P}$, and $\mathbf{R}$ corresponding to the following 2×2 matrices:

$$\mathbf{G} = \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a1a2} \\ \sigma_{a1a2} & \sigma_{a2}^2 \end{bmatrix},$$

$$\mathbf{P} = \begin{bmatrix} \sigma_{pe1}^2 & \sigma_{pe1pe2} \\ \sigma_{pe1pe2} & \sigma_{pe2}^2 \end{bmatrix},$$

$$\mathbf{R} = \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e1e2} \\ \sigma_{e1e2} & \sigma_{e2}^2 \end{bmatrix},$$

where $\mathbf{G}$ is the matrix of additive genetic (co)variances σ_{a1}^2 , σ_{a2}^2 , and σ_{a1a2} for traits 1 and 2; $\mathbf{P}$ is the matrix of permanent environmental (co)variances σ_{pe1}^2 , σ_{pe2}^2 , and σ_{pe1pe2} ; and $\mathbf{R}$ is the matrix of residual (co)variances σ_{e1}^2 , σ_{e2}^2 , and σ_{e1e2} ; $\mathbf{A}$ and $\mathbf{I}$ are the additive relationships matrix and an identity matrix; and $\otimes$ is the Kronecker product.

Data were analyzed using a Bayesian approach and running a Gibbs sampling algorithm that considered flat priors for systematic effects. Variance components and genetic parameter estimates for SCS and LTSCC were obtained using the “gibbs3f90” program, and the “thrgibbs1f90” was used for traits expressed as a binary (Misztal, 2008). A single Gibbs chain of 480,000 iterations was run for each bivariate analysis. In all cases, the first 30,000 samples were discarded as burn-in. Samples were stored every 150 iterations to leave 3,000 samples for inferences. The posterior mean of the samples (i.e., common output of the post-Bayesian analysis produced by the “postgibbsf90” program; Misztal, 2008) was used as a point estimate of the (co)variance component and the related parameters. The lower and upper bounds of the 95% highest posterior density (HPD) interval were obtained from the estimated marginal densities of (co) variance components and from the derived marginal densities obtained for heritability and genetic correlations. The values of variance components, heritability, and genetic correlations obtained for the threshold traits were reported in a liability scale.

RESULTS

The basic statistics for yield traits, SCC, SCS, and LTSCC are presented in Table 1. The means of milk, fat, and protein yields were 17.04, 0.60, and 0.56 kg/d, and the traits showed similar coefficients of variation (0.33, 0.35, and 0.34, respectively). The mean values for SCC, SCS, and LTSCC were 188,000 cells/mL, 2.83, and 4.96, respectively. A very large standard deviation was observed, particularly for SCC. Compared with milk, fat, and protein production, the SCC and SCS traits showed greater variability, with coefficients of variation of 1.66 and 0.67, respectively. Conversely, the LTSCC trait exhibited a lower coefficient of variation than values obtained for SCC and SCS (0.25). The TD records in threshold SCC80 were equally distributed below (0.50) and above (0.50) the threshold of 80,000 cells/mL. For SCC150 and SCC400 traits the percentage of TD records below the thresholds was greater (0.68 and 0.89, respectively) than the percentage of records above the thresholds of 150,000 and 400,000 cells/mL. Table 2 presented the mean point estimates of marginal posterior densities for additive genetic, permanent environment, and residual variances obtained from bivariate analyses for the studied traits. The additive genetic variances estimated for the SCS and LTSCC were greater than those for the threshold traits (SCC80, SCC150, SCC400), which showed additive genetic variability comparable with or greater than those of fat and protein yield.

Posterior heritability values expressed on the liability scale ranged from 0.036 to 0.065, and heritability values on a normal scale were set at 0.088 and 0.103 for SCS and LTSCC traits, respectively. As expected, productive traits showed higher heritability estimates, i.e., 0.199 for milk yield, 0.162 for fat yield, and 0.167 for protein yield. The HPD 95% for heritability of all analyzed traits indicated asymmetry in the marginal

Table 2. Estimates¹ of genetic variance (σ_a^2), permanent environmental variance (σ_{pe}^2), residual variance (σ_e^2), and heritability (h^2) of productive traits and threshold SCC traits

Trait ²	σ_a^2	σ_{pe}^2	σ_e^2	h^2
Milk	2.510 (2.177; 2.874)	3.919 (3.651; 4.184)	6.216 (6.172; 6.261)	0.199 (0.174; 0.225)
Fat	0.003 (0.003; 0.004)	0.005 (0.004; 0.005)	0.013 (0.013; 0.013)	0.162 (0.142; 0.185)
Protein	0.002 (0.002; 0.003)	0.004 (0.004; 0.004)	0.007 (0.007; 0.007)	0.167 (0.144; 0.192)
SCS	0.247 (0.198; 0.301)	0.655 (0.613; 0.700)	1.900 (1.886; 1.914)	0.088 (0.070; 0.106)
LTSCC	0.134 (0.109; 0.161)	0.285 (0.265; 0.306)	0.881 (0.875; 0.887)	0.103 (0.084; 0.123)
SCC80	0.014 (0.011; 0.017)	0.040 (0.032; 0.036)	0.154 (0.153; 0.155)	0.065 (0.051; 0.080)
SCC150	0.012 (0.009; 0.015)	0.034 (0.032; 0.036)	0.142 (0.141; 0.143)	0.063 (0.049; 0.077)
SCC400	0.004 (0.003; 0.005)	0.014 (0.013; 0.015)	0.084 (0.083; 0.085)	0.036 (0.025; 0.047)

¹Mean of marginal posterior densities of the parameters. Bounds of the 95% high posterior density interval are within parentheses.

²SCS = $3 + \log_2(\text{SCC}/100,000)$; LTSCC = log daily total SCC; SCC80 = test-day (TD) record of SCC $\geq 80,000$ cells/mL; SCC150 = TD record of SCC $\geq 150,000$ cells/mL; SCC400 = TD record of SCC $\geq 400,000$ cells/mL. For SCC80, SCC150, and SCC400 values, 0 was assigned for TD below the threshold and 1 for TD above the threshold; values are expressed on a liability scale.

posterior distribution with a greater dispersion in heritability for productive traits, SCS, and LTSCC. The standard deviation for all the analyzed traits was on average very low.

The point estimate of the genetic correlations between productive traits and all SCC traits were almost null except for LTSCC. The point estimate (mean of the posterior distribution) of genetic correlations between milk yield and SCS, LTSCC, SCC80, SCC150, and SCC400 were 0.122, 0.379, 0.068, 0.082, and 0.205, respectively (Table 3). The posterior density obtained for the genetic correlations (Figure 1) between milk yield and SCS (HPD 95% 0.006; 0.244), SCC80 (HPD 95% -0.055; 0.193), SCC150 (HPD 95% -0.041; 0.207), and SCC400 (HPD 95% 0.057; 0.362) traits were overlapped, and estimates for SCC80 and SCC150 included zero. Conversely, the posterior density for the genetic correlations between milk yield and LTSCC was positive and ranged from 0.271 to 0.484. The point estimates (mean of the posterior distribution) for genetic correlations of fat yield were 0.028, 0.240, 0.008, 0.005, and 0.081 with SCS, LTSCC, SCC80, SCC150, and SCC400, respectively. Almost all estimates included zero in the 95% HPD region interval. Finally, protein yield showed values of the point estimates (mean of the posterior distributions) for genetic correlations of 0.139, 0.370, 0.088, 0.096, and 0.234 with SCS, LTSCC, SCC80, SCC150, and SCC400, respectively. Only estimates for SCC80 and SCC150 included zero in the 95% HPD region interval.

DISCUSSION

Local breeds, such as most of the dual-purpose cattle, have been receiving recent interest due to their connections with landscape conservation and the maintenance of local economies, thanks to typical products such as protected designation of origin cheeses (Gandini and Villa, 2003). These breeds are usually known to

be more robust and adaptable than specialized dairy or beef breeds (Medugorac et al., 2009), and breeding programs, when present, generally involve just the improvement of the productive traits of interest (Krupová et al., 2016). The importance of including functional characteristics (health, survival, reproduction) in addition to productive traits in nonspecialized breeds such as dual-purpose cattle and single- or multiaptitude local breeds has already been highlighted (Sölkner et al., 2000). Also in these breeds, functional traits generally have substantial effect on profitability due to the lower costs involved (e.g., for health issues) and the greater milk quality obtained (Krupová et al., 2016). Furthermore, consumer interest in animal welfare is increasing (Hietala et al., 2014). Among functional characteristics, the extra-economic benefit of accounting for traits related to somatic cells has also been reported (Oltenu and Broom, 2010; Sadeghi-Sefidmazgi et al., 2011). Nonetheless, functional traits such as mammary gland health indicators have only been included in the total merit indexes of wide-spread dual-purpose cattle such as Italian and Austrian Simmental (Sandri et al., 2015; Fuerst-Waltl et al., 2016) and Nordic breeds such as Finnish Ayrshire (Negussie et al., 2008). These traits have not yet been considered within the breeding objectives of most local dual-purpose cattle. Inclusion has been recently studied in only a few breeds, such as Slovak Pinzgau cattle (Krupová et al., 2016) and Rendena (Sartori et al., 2018).

Rendena is a local breed traditionally selected for dual-purpose production (milk and meat) that presents daily production levels that are on average much less than those reported by the Italian Breeders Association (AIA; 2016) in specialized Italian Holstein (31.3 kg/d), Italian Brown Swiss breeds (23.6 kg/d), and dual-purpose Italian Simmental cows (22.0 kg/d). Different measures of milk somatic cell content in the Rendena breed have never been investigated before this study. In Italy, SCC is regularly collected during the official

Table 3. Estimates¹ of genetic correlations obtained from a bivariate animal model analysis between milk, fat, and protein yields and alternative SCC traits

Trait ²	Milk	Fat	Protein
SCS	0.122 (0.006; 0.244)	0.028 (-0.086; 0.149)	0.139 (0.016; 0.269)
LTSCC	0.379 (0.271; 0.484)	0.240 (0.133; 0.348)	0.370 (0.256; 0.482)
SCC80	0.068 (-0.055; 0.193)	0.008 (-0.109; 0.131)	0.088 (-0.040; 0.223)
SCC150	0.082 (-0.041; 0.207)	0.005 (-0.115; 0.130)	0.096 (-0.034; 0.229)
SCC400	0.205 (0.057; 0.362)	0.081 (-0.065; 0.233)	0.234 (0.077; 0.401)

¹Mean of marginal posterior densities of the parameters. Bounds of the 95% high posterior density interval are within parentheses.

²SCS = $3 + \log_2(\text{SCC}/100,000)$; LTSCC = log daily total SCC; SCC80 = test-day (TD) record of SCC $\geq 80,000$ cells/mL; SCC150 = TD record of SCC $\geq 150,000$ cells/mL; SCC400 = TD record of SCC $\geq 400,000$ cells/mL. For SCC80, SCC150, and SCC400 values, 0 was assigned for TD below the threshold and 1 for TD above the threshold; values are expressed on a liability scale.

milk recording system, and it is the most commonly assumed udder health indicator (Bobbo et al., 2017). Typically, the SCC trait in the genetic evaluation is log transformed as SCS because it is not normally distributed. This trait is currently included in breeding programs of the main Italian dairy (Bobbo et al., 2017) and dual-purpose (Sandri et al., 2015) cattle, despite the fact that its routine collection does not include data from unhealthy quarters in the target day of recording. The heritability value of SCS observed in this study, namely 0.088, was in agreement with the heritability reported in other countrywide spread dairy or dual-purpose breeds such as Canadian and Finnish Holstein, Finnish Ayrshire, and Italian Brown Swiss (Reents et al., 1995; Ikonen et al., 1999; Ikonen et al., 2004; Dal Zotto et al., 2007). However, higher heritability was reported when the trait was evaluated as a lactation-basis mean SCS (Kadarmideen, 2004; Samoré et al., 2010; Martin et al., 2013).

Our study on milk SCC, aimed at introducing a possible udder health indicator trait in the breeding of Rendena, has led to the exploration of other possible uses of the same phenotype (SCC). A trait rarely used but reported in the literature is the LTSCC, which was a measure of the amount of SCC present in daily milk

production and that was then log transformed, with the purpose of counteracting the possible effects of dilution. This trait was considered by Heuven et al. (1988), who reported heritability values ranging from 0.06 to 0.19 considering the first 3 lactations. Alternative traits derived from information present in TD SCC records were studied as indicator traits for mastitis, although the relationship with mastitis diagnosis was not considered in the present study but was derived from literature. For example, Green et al. (2004) considered the distribution characteristics of TD log-transformed SCC (mean, standard deviation, maximum, and minimum values) and reported that maximum and standard deviation of log SCC were the best indicators of clinical mastitis, compared with mean SCC. Other authors (de Haas et al., 2008; Urioste et al., 2010) used the average of TD SCC calculated over different lactation periods to compare the first versus the second parts of lactation. de Haas et al. (2008) reported greater genetic correlation between clinical mastitis and SCC in the first part than in the second part of lactation, confirming the results observed in previous studies (Emanuelson et al., 1988; Barkema et al., 1998), that showed that the frequency of cases of mastitis is much greater in the first part of lactation than in the second part. Urioste et al. (2010)

Figure 1. Estimated marginal posterior densities of genetic correlations between milk yield and alternative SCC traits of Rendena for SCS (continuous black line), log daily total SCC (LTSCC; dashed black line), SCC80 (continuous gray line), SCC150 (dashed gray line), and SCC400 (dotted gray line) traits. SCC80, SCC150, and SCC400 = test-day record of SCC $\geq 80,000$, $\geq 150,000$, and $\geq 400,000$ cells/mL, respectively.

used the measures of number of days sick during lactation as a trait to increase mastitis resistance in dairy cattle and found a high correlation between clinical mastitis and number of infectious peaks (i.e., period of increased SCC >150,000 cells/mL between 2 low ≤150,000-cells/mL TD observations).

An alternate way is to consider SCC as a threshold trait, as in the present study, in which 3 threshold traits (SCC80, SCC150, and SCC400) have been considered. These traits were treated as dummy variables; the residual variance was assumed equal to one, as in, for example, the studies by Arango et al. (2006), Negussie et al. (2008), and Urioste et al. (2012); and the heritability was reported on a liability scale.

The advantages of using a threshold model to estimate covariance components with a binary trait, including a better estimation of threshold traits, have been reported by others (Varona et al., 1999). However, in some other studies (e.g., de Haas et al., 2008) a bivariate linear model instead of a threshold model was used due to the small differences in the estimates obtained with these 2 methods. The heritability value estimated for the SCC150 trait in this study (0.06) was similar to the heritability reported by de Haas et al. (2008) for suspicion of the IMI trait (0.06), which used the same SCC threshold of the present study.

Almost zero genetic correlations were found in this study between yield traits (milk, fat, and protein) and the alternative somatic cell traits, except for LTSCC, which, as expected, was moderate and positive. In the literature, low, but slightly greater, genetic correlations than in this study have been reported for production traits and SCS, even if evaluated as an average SCS on a lactation basis. For example, Kadarmideen (2004) in Swiss Holstein observed genetic correlations of 0.13, 0.10, and 0.15 between lactation-mean SCS and milk, fat, and protein yields, respectively. On the other hand, Dechow et al. (2007) reported higher genetic correlation for milk, fat, and protein yields with lactation average SCS (0.53, 0.27, and 0.51, respectively) in Holstein, Brown cows and their crossbreds. In Swedish Holstein cows, Carlén et al. (2004) reported lower genetic correlations between production traits and SCS than the corresponding genetic correlations between mastitis and production traits. Moreover, the same study observed genetic correlations between mastitis and SCS ranging from 0.66 and 0.77, highlighting the positive relationships that exist between these traits.

In the present study, genetic correlations were different when comparing productive traits with SCS and LTSCC log-transformed TD records (null and the positive, respectively). A possible explanation for these differences could be linked to the different meanings of the traits. The SCS reflects the content of the

log-transformed cell count per milliliter of milk, and LTSCC represents the log-transformed yield of TD cell count. Therefore, the correlation expected for these traits with milk yield follows a similar pattern to that observed when milk is compared with content traits (e.g., protein or fat content) or to yield traits (i.e., kg of protein and fat in milk), which always exhibit an opposite genetic correlation (negative the contents and positive the yields; Van Vleck, 1978; Schutz et al., 1990). The SCC150 trait considered in this study showed close to zero genetic correlations with milk, fat, and protein yield. Nevertheless, de Haas et al. (2008), when considering this suspicion-of-IMI threshold trait, reported a high genetic correlation with clinical mastitis (0.68) and very strong correlations with subclinical mastitis (0.96). These results indicate that the trait threshold of SCC150 could be potentially considered in the genetic evaluation as an indicator of subclinical or clinical mastitis. The SCC80 and SCC400 thresholds also considered in present work showed almost null genetic correlations with milk, fat, and protein yields. The chosen threshold of 80,000 cells/mL could be, however, too low to make it possible to differentiate between healthy and infected cows. Bobbo et al. (2017) for example, have shown that milk with low SCC could be related to the inability of cows to respond to the mammary inflammation, and this can affect milk processed as the milk of unhealthy cows. However, the SCC400 threshold, which represents the legal limit of milk merchantability, could be compared with the threshold of TD >500,000 cells/mL (TD >500) considered in the research of Koeck et al. (2012) and Urioste et al. (2012). In these latter studies, high genetic correlations were obtained between TD >500 and clinical mastitis (0.83) and very strong correlations with subclinical mastitis (0.93), highlighting this threshold trait as being one of the best predictors of resistance to mastitis. Results from our study may be considered as a first step into the possible application of SCC in breeding goals of the Italian dual-purpose Rendena breed, as already carried out in specialized (Miglior et al., 2005) and in a few dual-purpose breeds (Fuerst-Waltl et al., 2016). All the SCC traits considered in the present study could be suitable for inclusion within breeding aims, because somatic cells are not directly selected in the Rendena population. All the genetic parameters considered have been efficiently estimated by applying the official method used for routine genetic evaluations of yield traits, as confirmed by the trace plot of the iterations (data not shown) and looking at the distributions of posterior means, almost symmetric especially for heritability values (see Figure 1 and HPD of estimates). The greater heritability of SCS with respect to the values obtained for threshold traits could suggest that it is preferable for breeding

purposes due to a faster selection response. In contrast, LTSCC is less preferable considering its strong connection with yield traits as suggested by the moderate but positive genetic correlations, higher than the estimates obtained for the other SCC traits with yield traits. The knowledge of genetic correlations among traits is a main point for properly including a new trait within a selection index (Hazel et al., 1994). A recent study from our group (Sartori et al., 2018) highlighted that the actual breeding goal for dual purpose in Rendena produces an increase (via indirect selection for beef traits, particularly ADG measured on young candidate bulls) in SCS. On the other hand, mammary correctness (e.g., udder depth, suspensory ligament, teat placement side view) is favorably linked to udder health, further indicating that more supported udders with strong suspensor ligaments are less productive but also less susceptible to mastitis. Further investigations could evaluate possible inclusion of other SCC traits within the current selection index. Similar evaluations could be carried out in several other local and dual-purpose cattle; breeding for these traits could produce possible advantages in these breeds.

CONCLUSIONS

The results obtained in this study demonstrated that SCC could be introduced as a breeding goal trait in the local Rendena breed, although it is not strictly necessary. The SCS and LTSCC traits have shown greater genetic variability and heritability compared with other threshold traits suggested in literature as possible reliable predictors of mastitis. In addition, the present selection goal based on milk in Rendena cattle is not conflicting with worsening of somatic cells traits. Further insights are therefore needed with regard to the threshold traits before their possible application in routine genetic evaluations of the Rendena breed.

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