J. Dairy Sci. 101:1–9
https://doi.org/10.3168/jds.2017-14047

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 (≥80,000, ≥150,000, and ≥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 ≥150,000 cells/mL to 0.234 between protein yield and SCC ≥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 ≥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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Received October 25, 2017.
Accepted May 17, 2018.
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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 of 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, ×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

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