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CICLO XXXI

GENETIC AND PHENOTYPIC ASPECTS OF PRODUCTION, CONFORMATION AND SOMATIC CELL COUNT TRAITS IN ITALIAN JERSEY CATTLE

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Abstract

Breeders appreciated Italian Jersey dairy cattle (IJ) for the efficiency and high quality of milk yield in the national dairy scenario.

The overall object of this PhD thesis is to investigate the phenotypic and genetic aspects of milk production, conformation and somatic cell score traits of IJ in order to lay the groundwork for an updating of selection index in IJ population (Jersey Quality Index).

The first chapter aimed to highlight the phenotypic peculiarities of IJ milk and confirmed that high content of fat (5.18%), protein (4.08%) and casein (3.16%) made IJ milk suitable for cheese manufacture. Moreover, somatic cell score (SCS), one of the best indicator of both clinical and subclinical mastitis, was investigated in IJ. The SCS average of 3.35 units should be lowered through specific managerial actions in order to reduce the IJ susceptibility to one of the most prominent and economically significant disease impacting on the dairy industry. Also milk urea nitrogen (MUN) content was assessed in order to verify if could be a valid indicator of feed efficiency; this was confirmed by the phenotypic variance of this trait, mainly due to the herd management.

In the second chapter, heritability estimates of 0.14, 0.21, 0.26, 0.24, 0.20 and 0.10 for milk yield, content of fat, protein, casein, lactose and SCS, respectively, were assessed in 1902 Italian Jersey. Genetic correlations investigated between SCS and milk yield components were negative (ranging from -0.13 to -0.27), the most unfavourable was with lactose percentage (-0.30).

The third chapter updated estimates of genetic parameters of 20 type traits in first-lactation IJ, including novel traits of functional and economic relevance, as locomotion score. Despite IJ type traits heritabilities estimated were generally low or moderate (from 0.04 to 0.32), additive genetic variation suggested the possibility to further enhanced

functionality in IJ. The strongest correlations were estimated between locomotion and other feet and legs traits, but also between locomotion and front teat placement (0.97) and rear teat placement (0.88), suggesting that improved udder conformation was also associated with better mobility.

Four alternative somatic cell count (SCC) traits, derived from routine test-day (TD) recording system, were defined in the fourth chapter as: 1) TD SCS averaged over early lactation (SCS_150); 2) standard deviation of SCS of the entire lactation (SCS_SD); 3) a binary trait indicating absence (0) or presence (1) of at least one TD SCC >400 000 cells/mL in the lactation (Infection); and 4) the ratio of the number of TD SCC >400 000 cells/mL to total number of TD in the lactation (Severity). Genetic and phenotypic parameters between alternative SCS traits and milk yield, composition and udder type traits in IJ were estimated. Results showed exploitable genetic variation and heritability, suggesting that alternative SCS traits might be suitable candidates to update Jersey Quality Index and improve mastitis resistance in IJ.

Finally, to ensure maximal benefit for IJ farmers, not only genetic parameters, but also economic values (EV) of milk production and quality traits are required. Economic values of SCS based on its relationship to price payment system in IJ were assessed in the final chapter, comparing two different methods in two different Italian dairy plants which produced Grana Padano cheese. The second method (method 2), that defined SCS costs as the sum of frequency of each level of SCS multiplied by its penalty, was more penalizing than method 1, which was based on a non-linear function of the penalty applied in the milk price respect to the average of SCS. Penalties for high SCS are intended to include SCS in IJ breeding goal with the final purpose of reducing mastitis susceptibility in the next generations of IJ cows.

Riassunto

La razza Jersey Italiana (IJ) è apprezzata per la sua efficienza e l'alta qualità del suo latte all'interno del contesto lattiero-caseario nazionale. L'obiettivo generale della presente tesi è la caratterizzazione fenotipica e genetica della produzione di latte, della morfologia e della conta di cellule somatiche della JI al fine di fornire alcuni strumenti utili per migliorare l'attuale indice di selezione della popolazione (Indice Qualità Jersey, IQJ).

Nel primo capitolo si confermano le peculiarità fenotipiche del latte di JI, ovvero un alto contenuto di grasso (5.18%), proteina (4.08%) e caseina (3.16%), che lo rendono adatto alla trasformazione casearia. Il valore medio di punteggio di cellule somatiche (SCS) è risultato piuttosto alto (3.35), il che suggerisce l'importanza di indirizzare gli sforzi verso una riduzione di questo valore attraverso il miglioramento del *management* aziendale e la selezione, diminuendo indirettamente la suscettibilità della JI alla mastite. In questo studio è stato investigato anche il contenuto di urea del latte di JI quale indicatore di efficienza alimentare.

Nel secondo capitolo sono state stimate ereditabilità pari a 0.14, 0.21, 0.26, 0.24, 0.20 e 0.10 rispettivamente per la produzione di latte, il contenuto di grasso, proteina, caseina, lattosio e SCS nel latte di bovine IJ. Le correlazioni genetiche tra SCS e i costituenti del latte sono risultate negative, e la più forte è stata stimata tra SCS e la percentuale di lattosio (-0.30).

Il terzo capitolo ha stimato i parametri genetici di 20 caratteri morfologici in primipare di JI, includendo nuovi caratteri di rilievo funzionale ed economico, come la locomozione. Anche se le ereditabilità stimate per i caratteri morfologici sono risultate generalmente basse o moderate (da 0.04 a 0.32), la variabilità genetico-additiva ha suggerito la possibilità di intervenire con la selezione per migliorare geneticamente alcuni aspetti funzionali della razza. Le correlazioni più forti sono state stimate tra il

punteggio di locomozione e i caratteri legati ad arti e piedi, ma anche tra punteggio di locomozione e la posizione dei capezzoli anteriori (0.97) e posteriori (0.88), suggerendo che un miglioramento della conformazione della mammella è associato a un potenziale perfezionamento della locomozione.

Nel quarto capitolo sono stati definiti quattro caratteri alternativi derivati dalla conta di cellule somatiche (SCC) nel latte di JI rilevata nel corso dei controlli funzionali routinari (*test-day*, TD): 1) la media di TD SCS nei primi 150 giorni di lattazione; 2) la deviazione standard delle SCS nell'intera lattazione; 3) un carattere binario che indica l'assenza (0) o la presenza (1) di almeno un valore di TD SCC >400.000 cellule/mL nell'intera lattazione (Infezione); e 4) il rapporto tra il numero di TD SCC >400.000 cellule/mL e il numero totale di TD nell'intera lattazione (Severità). Sono stai stimati i parametri genetici di questi 4 caratteri alternativi delle SCC e le correlazioni genetiche gli aspetti produttivi e la morfologia della mammella. I risultati hanno mostrato la presenza di varianze genetiche ed ereditabilità dei caratteri alternativi delle SCC potenzialmente sfruttabili per migliorare la resistenza alla mastite.

Infine, nel quinto capitolo sono stati stimati i valori economici (VE) delle SCS con due metodi differenti e in base al sistema pagamento latte-qualità di due caseifici italiani che producono Grana Padano. Tra i due metodi, quello basato sulla somma delle frequenze di ogni livello di SCS moltiplicato per la rispettiva penalità si è rivelato più penalizzante. Il sistema pagamento latte–qualità del caseificio 1 è risultato più rigido rispetto al caseificio 2. L'aumento delle penalità per livelli alti di SCS nel latte incentiva maggiormente ad includere SCS nell'indice di selezione della JI.

Declaration

I declare that the present thesis has not been previously submitted as an exercise for a degree at University of Padova, or any other University, and I further declare that work embodied is my own.

Chiara Roveglia

GENETIC SELECTION IN DAIRY CATTLE

Genetic selection is responsible for almost half of the observed variation in animal performance in a structured breeding program and has contributed to dairy cattle industry advance (Norman *et al.*, 2004). During decades, traits considered in dairy cattle selection programs have evolved as a response to producers, consumers, and society needs.

At the beginning of the 20th century, the increase of milk production was the main goal of dairy breeders. However, by the end of the last century, the aim of genetic selection evolved from being mainly production oriented toward a more balanced breeding goal. Indeed, health, fertility, longevity, and workability traits were included in breeding objectives and selection indices in several countries (Miglior *et al.*, 2005). The need to identify and select for additional traits other than milk yield emerged mainly from the recognition of the decline of cow fertility (Pryce *et al.*, 1998).

Breeding goals have changed and more balanced indices have been developed and implemented; hence, key traits related to milk quality, reproductive performance, health status, longevity, feed efficiency, easy management (i.e. easy calving, positive relation with human and herd, workability), conformation, low environmental footprint and resiliency to external perturbations should be considered in a comprehensive selection program.

In order to be included in a selection program, a potential trait must comply with several criteria (Shook, 1989). Firstly, it should have an economic value as commodity or its implementation should reduce production costs and/or increase benefits for dairy breeders. Secondly, the trait should be clearly defined, measurable at the lowest cost and reliably recorded. Moreover, the trait must have adequate genetic variation and suitable heritability (Lopez-Villalobos, 2013). Eventually, an indicator (alternative) trait may be preferred if it i) reduces even more recording costs, ii) has a higher heritability, iii) can be measured earlier in life, and iv) presents a reasonable correlation with the real target trait.

Once traits have been defined, the extent of genetic variation and the genetic relationship with other traits have to be quantified (Berry, 2015). A trait may be more or less heritable, with phenotypic and genetic correlation to one another either positive or negative, either strong or weak. Finally, the definition of the best strategy (phenotyping, genetic evaluations, exploitation of genomic information) to achieve the desired gains is the final step.

Some of the main requirements for the genetic selection are a valid recording scheme, and easy access to defined, accurate, and cost-effective phenotypes. Traits included in selection programs vary among countries due to differences in milk price, costs of inputs and services, production environments, availability of phenotypes, as well as local traditions and culture (Miglior *et al.*, 2005). The identification of traits that are currently important for genetic selection and those that will be essential in the future is a fundamental aspect of selection research. Acquisition of phenotypic data remains one of the key components for achieving high accuracy of selection and thus genetic gain, even in the genomics era.

Variance components determination is an integral part of animal breeding, considering that genetic gain for a trait strictly depends on its heritability as reported by Rendel and Robertson (1950):

$$\Delta \mathrm{G} = \frac{\mathrm{i} \times \mathrm{r} \times \sigma_{\mathrm{g}}}{\mathrm{L}}$$

where ΔG is the annual genetic gain for a given trait, i is the selection intensity, r is the accuracy of breeding values, σg is the genetic standard deviation of the trait and L is the generation interval. The accuracy of selection is affected by both the heritability of the trait and the information available on the animal itself and its relatives (Berry, 2015).

Breeders are commonly concerned with the narrow sense heritability, which is the proportion of phenotypic variation attributed to additive genetic variation, i.e. the allelic effects transmitted from one generation to the next (Berry, 2015). Heritability varies from 0 (not heritable) to 1 (fully heritable); heritability estimates for several traits in dairy cattle are given in Figure 1. In general, traits associated with viability and fitness are lowly heritable, while those associated with animal morphological characteristics show greater heritability (Visscher *et al.*, 2008).

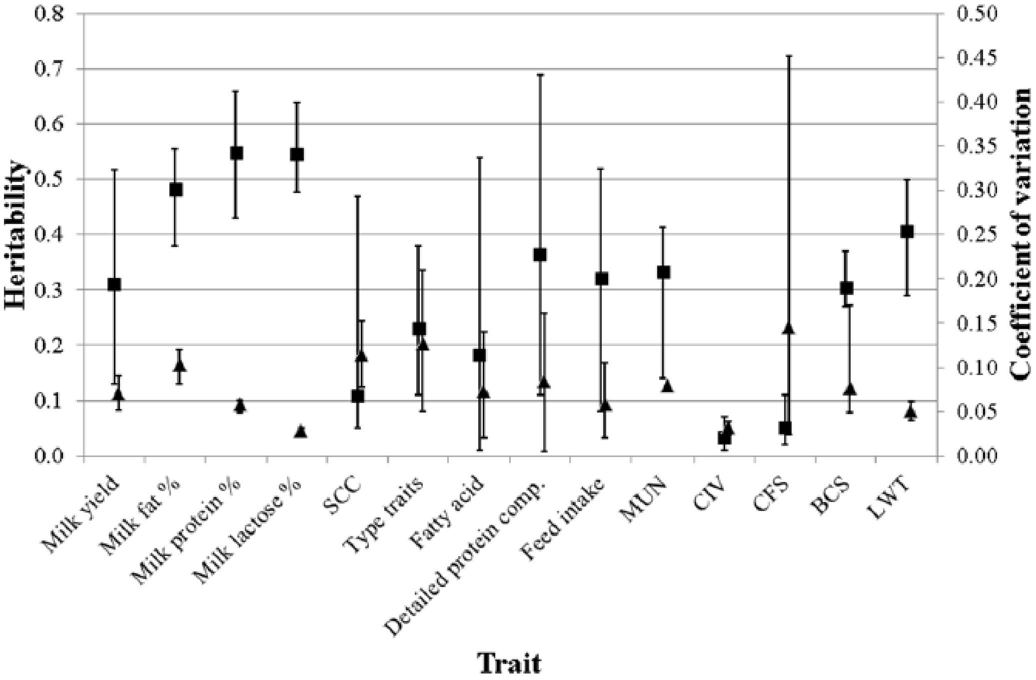

Figure 1. Mean heritability (■) and coefficient of genetic variation (▲) for performance traits including: somatic cell count (SCC), milk urea nitrogen (MUN), calving interval (CIV), calving to first service interval (CFS), body condition score (BCS) and live-weight (LWT) (source: Berry, 2015).

The coefficient of genetic variation is unit-less, allowing comparisons between traits with different units of measurement. The existence of significant genetic variation in all traits implies that once high accuracy of selection is achievable, genetic gain in each of these traits is feasible.

Milk quality traits

Milk and dairy products are important in human nutrition, since they are source of energy, important fatty acids, amino acids, mineral elements including calcium, magnesium, selenium, and vitamins such as riboflavin, vitamins B5 and B12 (FAO, 2018). For many years, milk has been considered a versatile food, i.e. usually added in different types of products thank to the high amount of important nutrients per unit of energy. Milk contributes on average 134 kcal of energy, 8.3 g of protein and 7.6 g of fat per capita per day (FAO, 2018). At global level, bovine milk production has increased constantly between 2013 and 2018, from 467 million tons in 2013 to 510 million tons in 2018 (USDA, 2018), and it is supposed to increase by 177 million tons by 2025, at an average growth rate of 1.8% per year (OECD-FAO, 2016). Until 2015 milk production in the European Union remained constant at about 150 million tons due to the milk quota regime (EEC Regulation 856/1984). After the abolition of the quota regime in March 2015, milk production increased in the EU-28 and it reached 168.3 million tons in 2016. The main part was delivered to the dairies (157.1 million tons) and the remaining amount was directly processed, own-consumed, sold directly to consumers, or used as feed in the farms (EUROSTAT, 2018).

Additionally, in order to make a farm financially sustainable, milk production should be improved by i) increasing production per cow, without compromising the health status of animals, ii) increasing the number of heads, or iii) improving cow feed conversion efficiency and feed utilization without increasing the amount of land utilized (van Zanten *et al.*, 2016).

According to the history of genetic parameters estimation, since first estimates of milk components were assessed and reported by Fisher (1925), the interest in genetic analysis of milk components began to take credit. Twenty years later, Lush (1943) established the tenets of breeding programs based on breeding values estimated from adjusted phenotypic records; the aim of any animal breeding program was to use genetics by selective breeding in order to obtain desired phenotypes. Currently, there are several studies reporting estimates of phenotypic and genetic parameters for milk, fat and protein content (Cassandro *et al.,* 2008; Visentin *et al.,* 2017), which are part of almost all dairy cow breeding goals at international level (Berry *et al.,* 2014). Conversely, even if moderately to highly heritable (Costa *et al.,* 2018), lactose yield and percentage have been scarcely studied because the economic value of lactose has been neglected by dairy industry (Sneddon *et al.,* 2012). However, the genetic correlation between milk yield and lactose yield is close to unity (Costa *et al.,* 2018) and the genetic correlation between lactose percentage and SCS is negative and moderate, suggesting that lactose could be exploited at genetic level. Also, selection for fatty acids and milk proteins profiles is limited (Lopez-Villalobos *et al.,* 2014), partly due to the worldwide payment systems of milk supply, which is based on total fat and protein, but mostly to the high cost of laboratory analysis for the determination of detailed fatty acids and protein fraction composition. Mid-infrared spectroscopy has been recently proposed as a useful tool to predict unconventional milk traits such as minerals, fatty acids, protein fractions and antioxidant activity (Lopez-Villalobos *et al.,* 2014; Niero *et al.,* 2016; Visentin *et al.,* 2016). Also, milk coagulation properties, proposed as technological traits to increase the efficiency of dairy industry (Pretto *et al.,* 2013), can be cheaply predicted at population level using mid-infrared spectroscopy (De Marchi *et al.,* 2014). One of the major benefits of the development of mid-infrared spectroscopy prediction equations is the negligible marginal cost of implementing further prediction equations for other milk characteristics (De Marchi *et al.,* 2014).

Conformation traits

As soon as dairy cattle started to be bred, conformation traits were the most important criteria for breeders to select the best animals. In the past, a standard of beauty of the animal has been the main reason for selection, and morphological evaluation was one of the bases of cattle selection because it enabled an immediate valuation of the animal conformation and a relatively simple classification (Forabosco *et al.,* 2005). The standards for conformation and beauty in dairy cattle have been passed down through time and broadcast from generations of breeders (Copeland, 1941).

Associations of breeders started evaluation programs to assess conformation of animals based on score scale. In the 1930s, United States began to classify Holstein cattle according to 4 major categories: general appearance, dairy character, body capacity and mammary system. Also, in 1932 an analogous classification program was adopted by the American Jersey Cattle Club. Moreover, a moderate relationship between conformation and producing ability was confirmed, highlighting the fact that both morphology and production should be considered in selection programs (Copeland, 1938).

Interest in including conformation traits other than milk yield in dairy cattle selection indices has increased during the years (Figure 2). In fact, the past exclusive selection for milk yield is supposed to have led to the increase of diseases susceptibility (Oltenacu and Broom, 2010; Egger Danner *et al.*, 2015).

Heritabilities estimated for type traits are generally low to moderate; in particular, frame traits are usually the most heritable, followed by udder, and feet and legs traits (Brotherstone, 1994). Indeed, heritabilities of 27 different morphology traits in Holstein-Friesian were investigated by O’Bleness *et al.* (1960), ranging from 0.00 to 0.33. After more than half a century, Cassandro *et al.* (2015) reported heritabilities of 20 linear type traits in Italian Holstein-Friesian from 0.02 to 0.20.

Pryce *et al.* (1998) demonstrated the potential of linear type traits as predictors of body weight, health and fertility in dairy cattle; moreover, the same authors demonstrated that only chest width was genetically correlated with fertility, and that narrower chest was associated with longer calving interval and lower conception rate at first service.

Several studies reported the predictive ability of morphology traits for alternative traits of interest, other than production or longevity. For example, udder conformation traits are genetically correlated with milking ability (Blake and McDaniel, 1979), udder health and fertility (Dadati *et al.*, 1986).

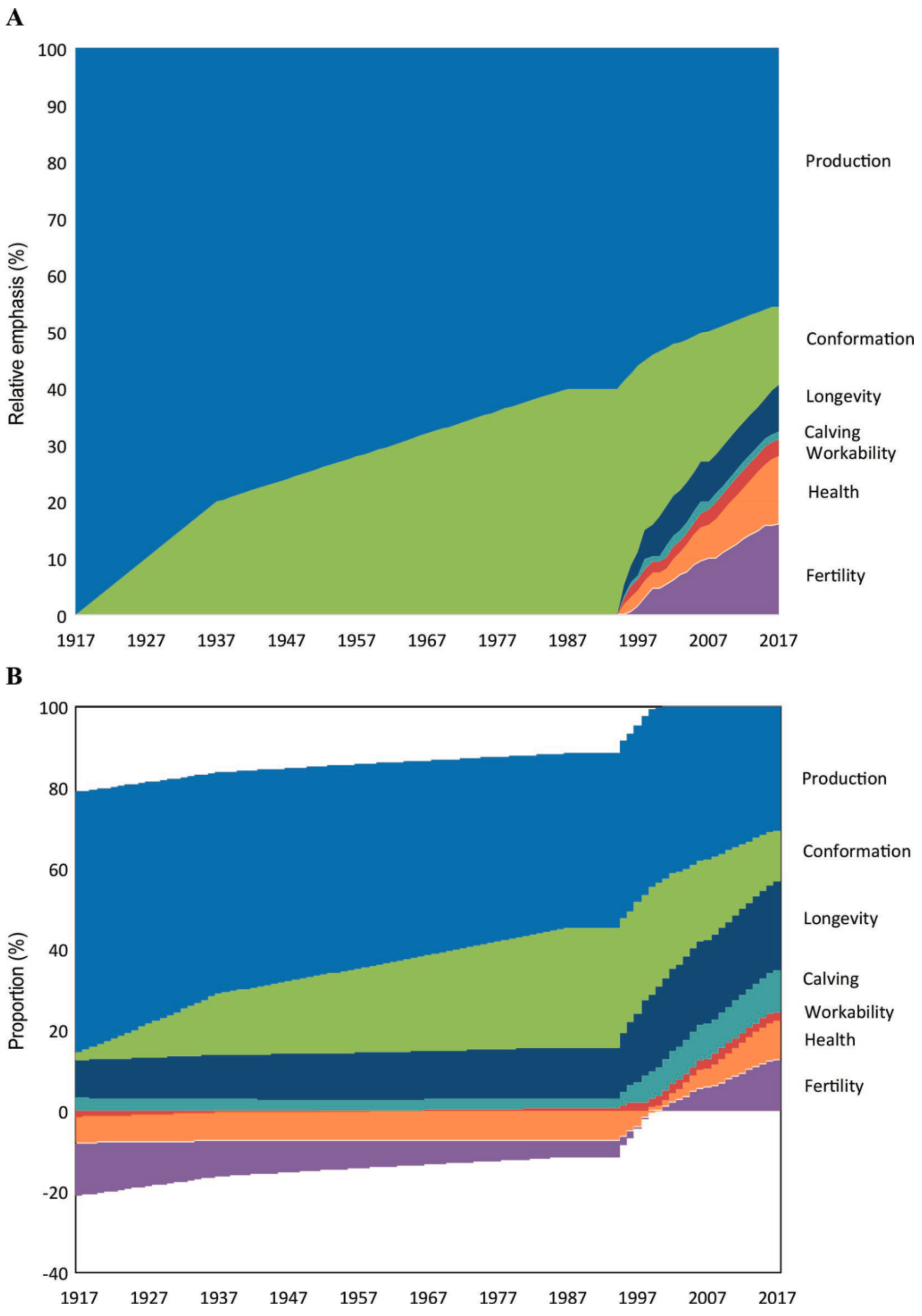

Figure 2. (A) relative emphasis of traits included in an average selection index over time and (B) proportion of estimated selection response for various trait categories over time (summing to 100%) (source: Miglior *et al.*, 2017).

Moreover, Cue *et al.* (1990) reported that on one hand the relationship between conformation and calving ease was positive, considering the conformation of the dam, on the other hand was negative, considering the conformation of the calf.

Health traits

Decrease of production, early death or culling, veterinary interventions, worsening of milk quality due to antibiotic use, delayed conception and increased susceptibility to other diseases are possible consequences of a disease condition in dairy cattle (Oltenacu and Broom, 2010). Recently, interest of including health traits in animal breeding programs has increased due to the concerns about the antibiotic abuse, animal welfare and ethics. Management and environmental aspects are the first factors involved in disease occurrence, however, genetic variation for health traits exists (Egger Danner *et al.,* 2015).

The most common, prominent and expensive disease in the dairy herd is mastitis, an inflammatory status of mammary tissue affecting one or more udder quarters caused by different pathogens (de Haas *et al.*, 2002; Bobbo *et al.*, 2017). The possible inheritance of mastitis resistance was firstly studied by Lush (1950), who examined cows that developed mastitis at any age and those that had not developed mastitis by the age of 8 years. Genetic background of susceptibility to mastitis was found to be unclear and gloom, so the author concluded that the incidence of mastitis could be reduced by selecting against severely affected cows or those with severely affected sisters or daughters. These primary results highlighted the need to improve phenotypes and methods for earlier evaluation. Somatic cell count (SCC) was introduced into many milk recording programs in Europe and North America at the end of the 1970s. Ali and Shook (1980) demonstrated that a log-transformation of SCC produced a score (somatic cell score, SCS) which resulted in a nigh-normal distribution and greater heritability. An average heritability of 0.08 for SCS and weak genetic correlations of SCS with yield traits were estimated by Kennedy *et al.* (1982), and Coffey *et al.* (1985) reported a range of heritability for SCS from 0.09 to 0.29 depending on parity. Moderate genetic correlations in the range from 0.36 to 0.67 between SCS and measures of infection were assessed by Coffey *et al.* (1986), supporting the potentiality of genetics in reducing mastitis incidence. One of the concerns in the implementation of selection for mastitis resistance was the antagonistic genetic relationship between mastitis and yield traits (Kennedy *et al.*, 1982; Coffey *et al.*, 1986). However, the decreasing genetic trend in cow health due to selection for milk yield was the problem to be solved; therefore mastitis resistance or indirectly SCS were considered in breeding programs (Shook, 1989). Somatic cell score became the main trait for improving udder health and mastitis resistance in selection indices (Koeck *et al.*, 2012a). Since disease-recording systems were not widely implemented, lactation-mean SCS or test-day SCS were the most commonly used as mastitis indicators; quite recently, alternative traits, derived from SCC, have been suggested to improve genetic evaluations for mastitis resistance (Koeck *et al.*, 2012b).

Some countries also included udder conformation traits, milking speed, clinical mastitis and dairy attitude (Miglior *et al.*, 2005).

Genetic evaluations of metabolic diseases in dairy cattle and other health indicators have been recently dealt with (Pryce *et al.*, 2016). At first, milk acetone was considered to be an indicator for clinical ketosis, a frequent disease caused by negative energy balance in early lactation, but its low heritability implied scarce genetic control (Koeck *et al.*, 2014). Subsequently, milk beta-hydroxybutyrate, rapidly and cheaply predicted by mid-infrared spectroscopy, showed genetic correlation with clinical ketosis and displaced abomasum, as well as fat-to-protein ratio and body condition score (Jamrozik *et al.*, 2016). Moreover, energy balance in dairy cattle, predicted directly using mid-infrared spectroscopy (McParland *et al.*, 2014) or indirectly from milk fatty acid content (Berry *et al.*, 2013), has been genetically correlated with many metabolic diseases, which also affected variation of body condition score (Roche *et al.*, 2009; Jamrozik *et al.*, 2016).

Novel traits

For several years, selection in dairy cattle has been focused on production and partly on conformation traits (Figure 2). To reduce the deteriorating trend on health and fertility, some target traits have been included in selection indices, whose emphasis has increased gradually. Since the inclusion of functional traits in selection indices, more balanced breeding programs have been proposed and the negative effects of pure selection for production have been reduced; nowadays making genetic progress in all traits of economic interest is the main purpose.

To guarantee progress and to develop breeding goals in accordance with producer and consumer, the inclusion of novel traits can be considered. For instance, the combination between residual feed intake in growing calves and lactating cows with feed required for maintenance predicted from body weight as a new indicator of feed efficiency in dairy cows was proposed by Pryce *et al.* (2015). Since April 2015, this novel trait has been included as part of the Australian national selection index. As well, several authors reported heritability for predicted methane emission that ranged from 0.21 to 0.35 (de Haas *et al.*, 2011; Lassen and Løvendahl, 2016). Recently, implementation of genetic selection for heat tolerance in tropical countries is under discussion and has been shown to be heritable, with heritability in the range from 0.17 to 0.33 (Nguyen *et al.*, 2016). Moreover, de Mol *et al.* (2013) analysed the possibility to implement a lameness detection model based on daily activity data, reporting that automated lameness detection based on day-to-day variation in behaviour could be a useful tool for dairy management. Still more recently, Denholm *et al.* (2017) showed phenotypic and genetic parameters for alternative traits indicators of immune response of dairy cows to be included in a futuristic selection index.

The estimates of heritability (ranging from 0.17 to 0.41) obtained by Lopez-Villalobos *et al.* (2014) confirmed the existence of genetic variability of milk fatty acids, which could be used to improve the nutritional and textural properties of milk fat by selective breeding and to meet the needs of consumer, market and industry. Also milk minerals are important for both consumers and processors, and they can concur to increase milk added value, however, monitoring of these traits was disadvantaged by expensive and time-consuming reference analyses (Soyeurt *et al.,* 2009). Visentin *et al.* (2016) developed mid-infrared spectroscopy prediction models for major milk minerals (Ca, K, Mg, Na and P), which allows collection of phenotypes at population level.

In those countries producing relevant amount of cheese such as Italy (CLAL, 2018), milk coagulation properties should be considered in selection indices. In fact, cheese-making related traits, such as rennet coagulation time, curd firmness and curd firming time should be routinely predicted through milk spectra, since reliable prediction equations exist (Cassandro *et al.,* 2008; De Marchi *et al.,* 2014; Visentin *et al.,* 2017). The exploitable genetic variation for all milk coagulation traits suggested that breeding for improved cheese-making efficiency is achievable (Cassandro *et al.,* 2016; Vistentin *et al.,* 2017).

Other innovative traits that can be derived from SCC have been suggested as alternatives to improve genetic evaluations for mastitis resistance (de Haas *et al.,* 2008; Koeck *et al.,* 2012; Urioste *et al.,* 2012; Bobbo *et al.,* 2018).

The traits included in selection of dairy cattle continue to evolve; lot of novel traits are at various stages of development to improve breeding goals in different productive scenarios.

Economic value of traits

Animal breeding is an economic system aiming to improve the profit from one animal generation to another.

To implement any animal breeding program, it is important to define which traits aim at improving the profit of the production system and which ones will be measured, basing on genetic variation and heritability. Once the desired characteristics to be considered in the breeding goal have been defined, the relative economic emphasis of each trait should be estimated (Berry, 2015).

The economic value (EV) of a trait can be defined as the change in profit of the farm expressed per lactating cow per year, as a consequence of one unit of change in the genetic merit of the trait considered, holding the other traits constant (Groen, 1989), and it has historically been the driver for genetic selection. In fact, the selection-index theory (Hazel, 1943), which allows multiple-trait selection of animals, uses economically important trait information or other correlated traits, weighted by their EV. The relative emphasis on an individual trait in a breeding scheme is usually depicted as the product of the genetic standard deviation times the economic weight of that trait divided by the sum of the same calculation for all traits in the breeding goal (Berry, 2015):

$$\mathrm{Emphasis_i} = \frac{|\mathrm{a_i} \cdot \sigma_\mathrm{i}|}{\sum_{\mathrm{j=1}}^{\mathrm{n}} |\mathrm{a_j} \cdot \sigma_\mathrm{j}|}$$

where a_i and a_j are the EVs for trait *i* and *j*, respectively, and σ_i and σ_j are the genetic standard deviations for trait *i* and *j*, respectively.

The actual rate of genetic gain achievable for a trait is a function of the relative (economic) weight on the trait within the overall breeding goal, but it also depends on the genetic correlations between that trait and the other traits included in the breeding goal.

JERSEY DAIRY CATTLE BREED

Jersey breed derives its name from the homonymous island, protectorate of the English crown located in the English Channel, close to the French coast of Normandy. In ancient times it was a peninsula, so it is assumed that the origin of the livestock derives from a Neolithic settlement of animals, later crossed with animals of the provinces of Brittany and Normandy. The conditions of the island, with rocky terrain, mild climate and windy pastures, have contributed to the development of the morphological type of small size, as well as a local policy of selection in consanguinity, as a result of the overwhelming superiority of the island's cattle on French cattle (ANAFI, 2018).

In the 1850s Jersey cows were brought to the United States and have spread across the globe because of their adaptation to many climates, especially in countries where extensive grazing is practised. Nowadays, there are large populations of Jersey cows in New Zealand, United Kingdom, United States, Canada, South Africa, and Zimbabwe. Currently, New Zealand has the largest population of Jerseys of the world (900 000 milking cows; Garcia *et al.*, 2015).

Jersey cows have been always appreciated for the creamy milk, used for the production of excellent butter (Hickson *et al.,* 2006; ANAFI, 2018). In fact, the name Jersey derives from a contraction of *Caesarea,* which was attributed to the name that the Romans used to call the Jersey's island. From other historian's hypothesis, the term Jersey could be related to the name Caesar, linked also to the Latin name of cheese, *Caseum*. The quality of Jersey milk has gained fame all over the world, allowing Jersey to become the second dairy breed worldwide, after Holstein (ANAFI, 2018).

The average size of Jersey cows is small, if compared to other breeds such as Holstein or Brown Swiss; in fact, animals are 120 cm tall, with a mature weight ranging from 400 to 600 kg according to the gender. Although Jersey cows are characterized by a relatively low milk yield, if compared to other dairy cattle breeds, they are appreciated for the great milk solids concentration and production per unit of feed, the excellent feed conversion efficiency per kilogram of liveweight and good reproduction performances (Hickson *et al.,* 2006). Besides, Jerseys are worth as regard some management aspects, since their low productivity and their udder conformation are suitable for a low environmental impact breeding (Dalla Riva *et al.*, 2014) and for once-a-day milking (Rocha *et al.,* 2018). Therefore, Jersey cows produce high quality milk, efficiently enduring loads of high stress (Smith *et al.*, 2013).

Jersey cows were introduced in Italy in the early 1980s, whereas the Italian Jersey herd book was established ten years later. Since 1999, the Italian Holstein Association (ANAFI) is responsible for the Italian Jersey genetic evaluation and herd book maintenance. Since 2008 and up to 2017 the number of Jersey cows registered in Italy changed from 6488 (718 herds) to 6730 (727 herds). Milk production increased from 5901 to 6514 kg/lactation, whereas fat and protein content slightly decreased from 5.10% to 4.87% and from 4.02% to 3.93%, respectively (ANAFI, 2018). As a result of the growing interest of the breeders for Jersey cows, a selection index named IQJ (Jersey Quality Index) was developed. The introduction of IQJ has been the first selection tool for Italian Jersey breeders, including at that time milk and protein yields (Biffani *et al.,* 2003). Soon after Biscarini *et al.* (2003) estimated genetic parameters for 16 type traits of Italian Jersey in order to develop a wider selection index. Currently, IQJ index of Italian Jersey includes milk yield (with a negative weight), protein yield, fore udder attachment, udder support and udder depth (ANAFI, 2018). In Italy, Jersey breed is often reared in mixed-herds with Holstein, which is characterized by greater milk yield but lower milk fat and protein content (Biffani *et al.,* 2003). Indeed, Bland *et al.* (2015) demonstrated that by blending Jersey and Holstein Friesian milk, the composition of milk was enhanced as well as Cheddar cheese yield and sensory properties. In the Italian dairy scenario, where more than 70% of milk is used to produce cheese (Pretto *et al.,* 2013; CLAL, 2018), the quality of milk used for cheese production is an essential aspect (Cassandro *et al.,* 2008) and Jersey cows could be suitable for this purpose due to the great amount of milk solids.

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Aim of the thesis

The general aim of the thesis was to characterize both phenotypically and genetically Italian Jersey breed in order to provide tools for planning future breeding strategies and facilitate progress for traits of economic interest for this breed. The specific aims were:

1. to investigate sources of variation of milk yield, composition traits, milk urea nitrogen and somatic cell score (SCS) in Italian Jersey breed;
2. to evaluate genetic parameters for milk yields, composition traits and SCS in the Italian Jersey cattle population;
3. to assess sources of variation of type traits, including locomotion and final score, and to estimate their genetic parameters in Italian Jersey cows;
4. to characterize four alternative SCS traits, derived from routine test-day recording system, in Italian Jersey cows and to estimate their genetic and phenotypic relationships with milk yield, composition and udder type traits;
5. to estimate the economic values (EV) of production traits and SCS in Italian Jersey dairy cattle for milk destined to produce Grana Padano cheese.

Chapter 1

Phenotypic analysis of milk composition, milk urea nitrogen and somatic cell score of Italian Jersey cattle breed

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Abstract

The present study aimed to assess the phenotypic variation of milk yield (MY) and quality traits in Italian Jersey (IJ) breed. Sources of variation were investigated through a linear mixed model, including the fixed effects of days in milk (DIM), parity, calving season, milking frequency, recording type, the interaction between DIM and parity, and the random effects of herd-test-day (HTD), cow and the residual. Results highlighted the high contents of milk fat (5.18%), protein (4.08%) and casein (3.16%) of IJ cows. Somatic cell score (SCS), averaging 3.35 units, should be lowered through specific managerial actions. Phenotypic variances of MY and milk quality traits were mainly due to cow effect, whereas phenotypic variance of milk urea nitrogen (MUN) content was mainly due to HTD effect, meaning that managerial conditions, especially feeding, are very important to explain the variation of MUN. In conclusion, the present study allowed to characterize milk of IJ cows at population level and to identify environmental factors associated with variation of milk yield and quality traits, which will be useful to adjust phenotypic records in genetic evaluation of Jersey breed.

Keywords: Jersey cow; Italian dairy sector; milk composition.

Introduction

Among dairy cow breeds, Jersey is characterized by relatively low milk yield (MY). Nevertheless Jerseys are endowed with a number of favourable production related traits, such as high milk solids production per unit of feed, high feed conversion efficiency per kilogram of liveweight and high reproductive performance (Hickson *et al.*, 2006). Jerseys are worthy also with regard to management aspects, since their productivity and udder conformation are suitable for grazing systems (Lopez-Villalobos *et al.*, 2014) and once a day milking (Rocha *et al.*, 2018). Furthermore, Jerseys experiment less heat stress load compared with other cattle breeds (Smith *et al.*, 2013).

Jersey cows were introduced in Italy in the early 1980’s and the Italian Jersey (IJ) herd book was established ten years later. Since 1999, the Italian Holstein Association (ANAFI, Cremona, Italy) is responsible of the IJ genetic evaluation and herd book maintenance. From 2007 to 2016 the number of Jersey cows farmed in Italy increased from 6391 to 7009 (ANAFI, 2016), milk production increased from 5953 to 6521 kg/lactation, but fat and protein content decreased from 5.20% to 4.93%, and from 4.00% to 3.94%, respectively (ANAFI, 2016). Giving the high milk solids content, Bland *et al.* (2015) investigated the effect of blending Jersey and Holstein milk, showing enhanced milk composition, as well as improved Cheddar cheese yield and sensory properties.

There is a lack of studies that characterize milk quality traits of IJ at population level. A study is required to provide a comprehensive insight into IJ milk quality traits in the context of Italian dairy industry, where 70% of milk is used to produce cheese. Therefore, the aim of the present study was to investigate sources of variation of MY, composition traits, milk urea nitrogen (MUN) and somatic cell score (SCS) in IJ breed.

Materials and methods

Data collection and editing

The initial dataset was provided by ANAFI and included 527 585 test-day records from 24 447 IJ cows in 1625 herds, recorded from 1994 to 2016. Milk samples were alternatively collected during morning or evening milking, every four (AT4) or five weeks (AT5) and analysed for fat, protein, casein, and lactose percentages, and MUN content (mg/dL) using mid-infrared spectroscopy. Somatic cell count (SCC, cells/mL) was determined using a Fossomatic (Foss Electric A/S, Hillerød, Denmark), and values of SCC were transformed to SCS to achieve normality and homogeneity of variances through the formula $SCS = 3 + \log_2 (SCC/100\ 000)$.

Data from 2005 to 2016 were selected because few observations were available from previous years. Days in milk (DIM) were restricted to be between 5 and 480 d, and parity between 1 and 6. Records with milk yield < 2 kg/d were discarded. Lactations with at least 3 test-day records and herd-test-day (HTD) with at least 3 cows were considered. Samples exceeding 4 standard deviations from the mean of each trait were considered as missing values. After editing, 417 006 test-day records from 20 434 cows and 600 herds were available for analysis. In the dataset, the DIM and parity averaged 171 d and 2.50, respectively.

Statistical analysis

Descriptive statistics were obtained using the MEAN procedure of SAS version 9.4 (SAS Institute Inc., Cary, NC) and analysis of variance was carried out on a subset extracted from the previously edited dataset considering a herd random sampling approach within records collected between 2014 and 2016. The subset accounted for 13 476 test-day records from 1152 cows and 36 herds, and reflected the variability of the edited data for all the studied traits. Preliminary Shapiro-Wilk's test showed that all traits were normally distributed. The following linear mixed model was used (MIXED procedure of SAS):

$$y_{ijklmno} = \mu + \mathrm{DIM}_i + \mathrm{P}_j + \mathrm{S}_k + \mathrm{N}_l + \mathrm{T}_m + (\mathrm{DIM} \times \mathrm{P})_{ij} + \mathrm{HTD}_n + \mathrm{cow}_o + e_{ijklmno},$$

where $y_{ijklmno}$ is the dependent variable; μ is the overall mean of the population; DIM_i is the fixed effect of the *i*th class of stage of lactation of the cow (i = 1 to 13, the first being a class from 5 to 30 d, followed by classes of 30 d each, and the last being a class from 360 to 480 d); P_j is the fixed effect of the *j*th parity of the cow (j = 1 to 6); S_k is the fixed effect of the *k*th season of calving (k = winter, spring, summer or autumn); N_l is the fixed effect of the *l*th number of milkings per day (l = 2 or 3); T_m is the fixed effect of the *m*th milk recording type (m = AT4 or AT5); $(\mathrm{DIM} \times \mathrm{P})_{ij}$ is the fixed effect of the interaction between DIM and parity; HTD_n is the random effect of the *n*th HTD (n = 1 to 1150) $\sim N(0, \sigma^2_{\mathrm{HTD}})$; cow_o is the random effect of the *o*th cow (o = 1 to 1152) $\sim N(0, \sigma^2_{\mathrm{cow}})$; and $e_{ijklmno}$ is the random residual $\sim N(0, \sigma^2_e)$.

Pearson correlations between the traits were computed on the subset using the CORR procedure of SAS.

Results and Discussion

Descriptive statistics of MY, composition, MUN and SCS

Milk yield averaged 20.11 kg/d (Table 1) which was lower than the average MY of IJ cows reported by Moioli *et al.* (2007), probably because of the longer DIM period considered in the present study. Lopez-Villalobos *et al.* (2014) and Coffey *et al.* (2016) reported lower MY of Jersey cows in New Zealand and Ireland, respectively, which is likely attributable to the lower feeding level of grazing cows in these two pasture-based systems. Milk yield of IJ followed the typical pattern during the lactation, with a peak between 30 and 50 d after calving, followed by a progressive decrease up to the end of lactation (Figure 1). Means of fat, protein and casein were 5.18%, 4.08% and 3.16%, respectively (Table 1), which were greater than averages reported by Capper and Cady (2012) in US Jersey cows and Penasa *et al.* (2014) in Italian Brown Swiss, Holstein Friesian and Simmental cows. Milk of IJ cows had lower fat content, and similar protein and casein contents than milk of New Zealand Jerseys (Auldist *et al.*, 2004). Casein is the only milk constituent reacting to rennet addition and curd formation occurs because of the aggregation of casein micelles, which consequently enclose milk fat and proteins. For this reason the high contents of protein and casein of IJ milk may be of interest for Italian dairy industry, since more than 70% of milk is used for cheese manufacturing (Pretto *et al.*, 2012). In addition, fat, protein and casein ratios are crucial for milk coagulation properties and cheese yield (Auldist *et al.*, 2004; Pretto *et al.*, 2013). All the major milk constituents, including fat, protein and casein with the exception of lactose, were less concentrated between 30 and 50 DIM (Figure 1), as a result of a dilution effect.

The average content of MUN observed in the present study was 23.51 mg/dL (Table 1). This result was consistent with findings of Penasa *et al.* (2014) and Niero *et al.* (2015) in milk of different Italian dairy cattle breeds, and slightly lower than the value reported by Bobbo *et al.* (2014) in milk of IJ cows reared in multi-breed herds. Conversely, MUN content was approximately twofold than MUN content reported by Miglior *et al.* (2007) in Ayrshire and Holstein cows. The great variability of MUN across different studies and conditions was expected, since this compound is closely linked to the herd management and to the feeding strategies, as well as to the breed and the physiological status of animals, including DIM, parity and the efficiency of nitrogen utilization (Miglior *et al.*, 2007). Milk urea nitrogen showed a slight increasing trend up to 150 DIM and was almost stable during the remaining part of lactation (Figure 1). This pattern was partially in agreement with findings of Miglior *et al.* (2007) who observed a nadir around 30 DIM and a peak around the middle of lactation followed by a slight increase over the remaining part of the lactation.

Somatic cell score averaged 3.35 units (Table 1). This value was slightly greater than SCS reported by Bobbo *et al.* (2014) in milk of IJ cows, but considerably lower than that reported by Sneddon *et al.* (2016) in New Zealand Jerseys. In a comparison with other dairy breeds reared in Italy, SCS of IJ cows was close to the SCS reported in Holstein Friesian, but greater than that of Brown Swiss and Simmental breeds (Penasa *et al.,* 2014). A decrease of SCS in IJ milk would be desirable in order to enhance and stand out its notable protein, casein and fat content that might be of great interest especially for the Italian dairy sector (Pretto *et al.,* 2013; Niero *et al.,* 2016). The curve of SCS across lactation was opposite to that of MY and lactose percentage (Figure 1), with a nadir in early lactation, followed by a gradual increase up to the end of lactation, in agreement with Hagnestam-Nielsen *et al.* (2009). The increase of SCS could be due to a greater incidence of mammary inflammation in cows at the end of lactation, when animals are more susceptible to pathogen infections (Green *et al.*, 2004).

Analysis of variance

F-values and significance of fixed effects included in the analysis of MY, composition traits, MUN and SCS of IJ cows are reported in Table 2. Days in milk, parity and their interaction were significant in explaining the variation of all studied traits ($P < 0.05$). Milking frequency and calving season were significant for all traits ($P < 0.05$), with the exception of lactose content in the case of milking frequency, and lactose content and SCS in the case of calving season. Recording type was significant only for MY, lactose and MUN content ($P < 0.05$).

Herd-test-day accounted for 5.99% (SCS) to 53.09% (MUN) of the phenotypic variance of the studied traits. On the other hand, the proportion of phenotypic variance explained by the effect of cow ranged from 6.28% (MUN) to 33.26% (MY; Table 2). Overall, variance explained by cow effect was greater for MY, protein, casein, and lactose percentages, and SCS, whereas HTD variance was greater for fat percentage and especially for MUN content. The latter result supports that management strategies have a strong influence on MUN content. Accordingly, Rajala-Schultz and Saville (2003) observed that the proportion of MUN variance explained by herd and test-day was much more relevant than the proportion of variance explained by cow effect. Once again, results of the present study are in agreement with Miglior *et al.* (2007) who reported that MUN is tightly connected to herd management, and are a further confirmation that MUN is a valid tool to monitor the efficiency of protein utilization of the diet, also in IJ herds.

Correlations

Pearson correlation coefficients (r) between the studied traits are presented in Table 3. All correlations were significant ($P < 0.001$). Milk yield was weakly negatively correlated with fat, protein, casein, and SCS (r between -0.26 and -0.20), in agreement with the opposite trend of MY and milk quality traits throughout the lactation, confirming a dilution effect as observed in other dairy breeds (Visentin *et al.,* 2017). Fat was moderately positively correlated with protein (r = 0.50) and casein (r = 0.52), and the correlation between protein and casein was close to unity, in agreement with previous studies (e.g. Visentin *et al.,* 2018). Somatic cell score was moderately negatively correlated with lactose, confirming the previously discussed opposite trends across lactation (Figure 1), and in agreement with previous phenotypic studies (e.g. Lindmark-Månsson *et al.,* 2006). Accordingly, Pyörälä (2003) reported that clinical and subclinical mastitis, that are often associated with an increased SCS, lead to a reduced synthetic ability of the enzyme systems of the milk secretory cells, with particular concern to a decrease in lactose percentage.

Conclusions

The IJ milk showed desirable fat, protein and casein contents for cheese production. Phenotypic variances of MY and composition traits were mainly driven by cow effect, whereas more than 50% of the phenotypic variance of MUN content was due to HTD effect, underlying the important role of farm and thus feeding management on MUN. Environmental factors associated with variation of the studied traits will be used to adjust phenotypic records when estimating genetic parameters and predicting breeding values for these traits at the population level.

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Disclosure statement

The authors declare that there is no conflict of interest associated with the paper. The authors alone are responsible for the content and writing of this article.

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Table 1. Descriptive statistics of milk yield, composition traits, milk urea nitrogen (MUN) and somatic cell score (SCS) of Italian Jersey cows.

Trait	No of records	Mean	SD	Minimum	Maximum
Milk yield, kg/d	416 846	20.11	6.61	2.00	46.50
Fat, %	415 849	5.18	1.13	0.50	9.86
Protein, %	416 547	4.08	0.49	2.04	6.11
Casein, %	198 713	3.16	0.39	1.04	5.26
Lactose, %	324 233	4.77	0.23	3.68	5.69
MUN, mg/dL	188 294	23.51	8.00	0.09	55.80
SCS, units	415 794	3.35	1.85	-3.64	10.84

Table 2. F-values and significance of fixed effects, and variance accounted by herd-test-day (σ^2_{HTD}, %) and cow (σ^2_{cow}, %) effects for milk yield, composition traits, milk urea nitrogen (MUN) and somatic cell score (SCS) (*n* = 13 476).

Trait	Fixed effects						Random effects		RSD[1]
	Days in milk (DIM)	Parity (P)	Calving season	Milking frequency	Recording type	DIM × P	σ^2_{HTD}, %	σ^2_{cow}, %	
Milk yield, kg/d	337.55***	19.41***	5.64***	39.24***	134.77***	7.64***	10.94	33.26	4.57
Fat, %	37.01***	4.12**	6.32***	26.32***	1.01	1.56**	18.27	14.73	0.88
Protein, %	166.38***	7.52***	4.29**	50.61***	3.42	1.64**	11.31	21.51	0.36
Casein, %	106.43***	4.94***	4.82**	23.28***	0.08	1.89***	9.77	18.46	0.31
Lactose, %	59.42***	47.86***	0.90	3.69	5.26*	3.05***	11.92	17.84	0.19
MUN, mg/dL	4.63***	4.32***	5.78***	21.97***	4.06*	1.41*	53.09	6.28	4.95
SCS, units	11.13***	33.05***	2.00	34.91***	0.20	2.26***	5.99	22.36	1.49

[1] RSD = residual standard deviation.

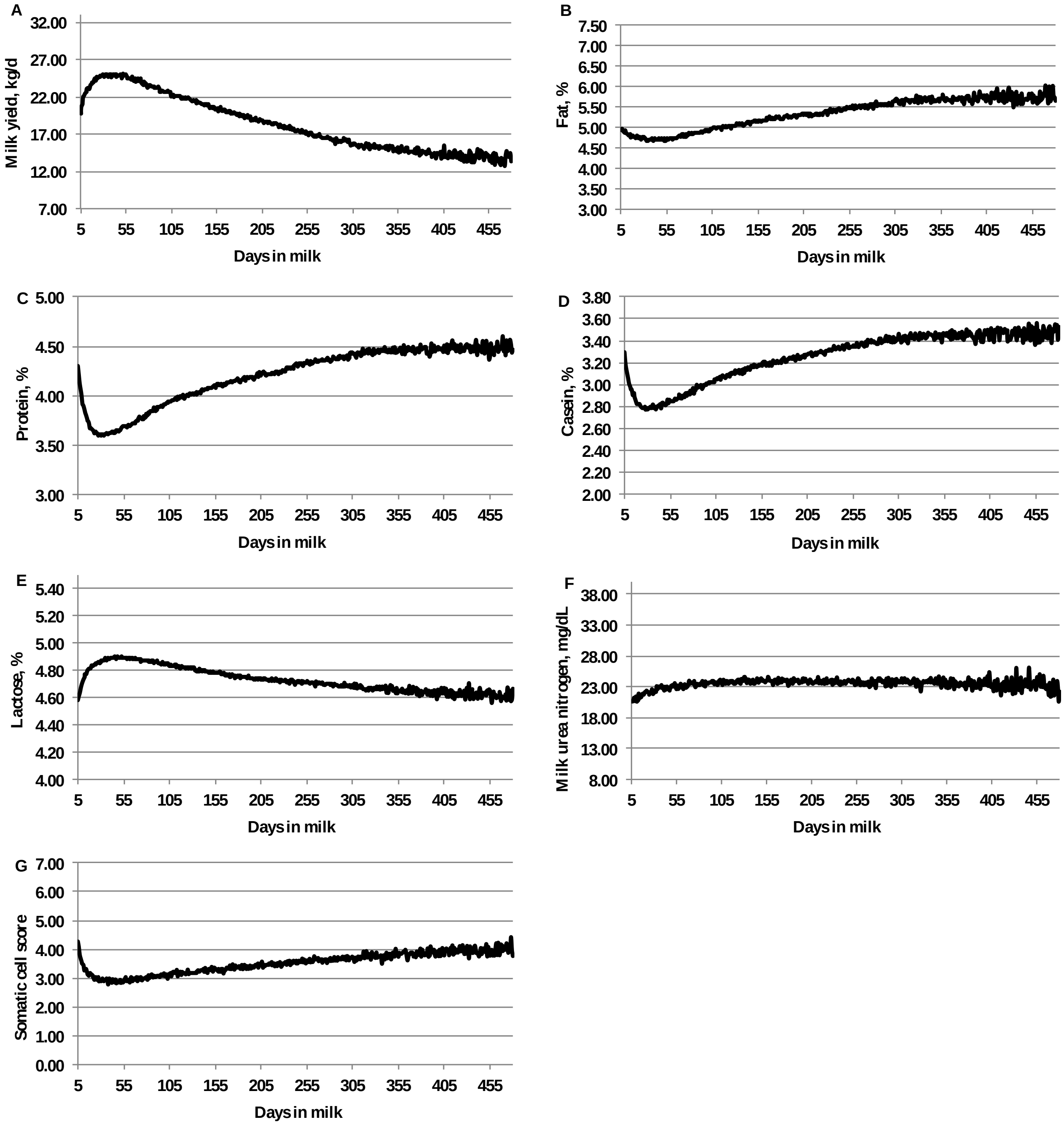
*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$

Table 3. Pearson correlations coefficients between milk yield, composition traits, milk urea nitrogen (MUN) and somatic cell score (SCS) (*n* = 13 476).

Trait	Fat	Protein	Casein	Lactose	MUN	SCS
Milk yield	-0.25	-0.26	-0.24	0.23	0.07	-0.20
Fat		0.50	0.52	-0.31	-0.09	0.10
Protein			0.98	-0.35	-0.02	0.11
Casein				-0.32	-0.03	0.09
Lactose					0.06	-0.39
MUN						-0.11

$P < 0.001$ for all correlations

Figure 1. Lactation curves of (A) milk yield, (B) fat, (C) protein, (D) casein, and (E) lactose percentage, (F) milk urea nitrogen content and (G) somatic cell score (n = 417 006).



Genetics of milk traits including lactose and somatic cell score in Italian Jersey cows

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Abstract

The objective of this study was to estimate phenotypic and genetic parameters for milk traits including lactose and somatic cell score (SCS) over lactation of Italian Jersey dairy cattle. A total of 38 831 test-day records from 1902 cows were collected from 2005 to 2016 in 20 dairy herds located in Italy. Days in milk were between 5 and 480 and thirteen classes of days in milk were defined. Analysis of variance was performed with a mixed linear model that included the fixed effects of herd-test day (n = 920), parity (5 classes), stage of lactation, calving season and interaction between parity and stage of lactation, and the random effects of animal and cow permanent environment. Heritabilities were estimated using a single-trait repeatability animal model, and genetic correlations were assessed through bivariate analyses. Mean milk yield was 18.76 kg/d, containing 5.29% fat, 4.09% protein, 3.20% casein, 4.80% lactose and 3.02 units of SCS. During lactation solids content and SCS increased, while solids yield decreased. Heritability estimates were 0.14, 0.21, 0.26, 0.24, 0.20 and 0.10 for milk yield, fat, protein, casein, lactose percentage and SCS, respectively. Genetic correlations between SCS and solids yield were negative, with the strongest estimate with lactose percentage (-0.30). Results of the present study emphasize quality of milk yield and composition of Italian Jersey cows and the possibility to develop new selective strategies for this breed.

Keywords: genetic parameter; milk yield; milk composition; somatic cell count; Jersey breed.

Introduction

Jersey dairy cows were introduced in Italy in the early 1980's and in 1991 the Italian Jersey herd book was established. Since then, number of registered cows has more than doubled and nowadays there are more than 7000 registered cows in 751 herds. The Italian Holstein Association (ANAFI) is in charge of Jersey cattle genetic evaluation and of maintaining the herd book. Until now, the Jersey breed has been appreciated by Italian breeders for the efficiency and high quality of milk yield (ANAFI, 2016). As a result of the growing interest of the breeders for Jersey cows, national genetic breeding value estimation and a selection index named IQJ (Jersey Quality Index) were developed. The introduction of the IQJ is a first tool for Italian Jersey breeders aiming to select IJ in the national scenario (Biffani *et al.,* 2003). The current model used to analyse data from Italian Jersey breed is a lactation model, whereas a novel aspect of the present study is to propose a test-day model.

Estimates of genetic and phenotypic parameters are necessary to determine the degree of variation due to genetics and environment, and also to predict genetic associations between two or more variables. These parameters are commonly required to construct selection indexes and predict correlated responses and to perform more efficient genetic evaluations (Rincòn *et al.,* 2015). Milk quality traits play an important role in genetic selection programs due to their economic impact on the dairy industry (Miglior *et al.,* 2005). Additionally, somatic cell score (SCS) and lactose are considered as variables of milk quality, also considered as indicators of subclinical mastitis, which is one of the most common and costly disease in dairy cattle population (Petzer *et al.,* 2017).

The aim of this study was to estimate genetic parameters for milk yields, SCS and milk composition traits in the Italian Jersey cattle population.

Material and methods

Data editing and analysis of variance

In the present study, 38 831 test-day records from 1902 cows collected between 2005 and 2016 in 20 dairy herds were available for investigation. Data were provided by the Italian Holstein Association (ANAFI). Herd-tests between 5 and 480 days in milk and from cows of parity 1 to 6 were retained in the dataset. Somatic cell count (SCC, cells/mL) was converted to somatic cell score (SCS) by applying the equation of Wiggans and Shook (1987): $SCS = 3 + \log_2(SCC/100\ 000)$. Values of milk yield, fat, protein, casein, and lactose percentages, and SCS outside mean ± 3 standard deviations (SD) were treated as missing data. Fat, protein, casein and lactose yields were calculated by multiplying milk yield by the respective content (%). Only cows with at least 3 test-day records within lactation and with known sire and dam were retained. Also, the minimum number of cows per herd-test day (HTD) was set to 3.

Analysis of variance were performed using SAS version 9.4 (SAS Institute Inc., Cary, NC, USA) with a mixed linear model that included fixed effects of HTD (*n* = 920), parity (5 classes; first, second, third, fourth, and fifth and six parities), stage of lactation (13 classes of 30 d each, except for the first class, which was between 5 and 30 d, and the last four which were classes of 40, 40, 50, 80 d, respectively), calving season [4 classes: winter (December to February), spring (March to May), summer (June to August) and autumn (September to November)], and first-order interaction between parity and stage of lactation. Cow effect was considered as random.

Genetic parameters

A repeatability animal model was used to estimate variance and covariance components for each of the traits considered in this study using the package VCE version 6 (Groeneveld *et al.*, 2010), with a linear mixed model that considered the fixed effects of HTD, parity, stage of lactation, season of calving, interaction between parity and stage of lactation, and the random effects of additive genetic animal, cow permanent environment and residual. The pedigree (*n* = 6 300; 6 generations) was provided by ANAFI. Heritability (h^2) and repeatability (rep) were defined according to the ratios:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_p^2 + \sigma_e^2} \qquad \text{and} \qquad rep = \frac{\sigma_g^2 + \sigma_p^2}{\sigma_g^2 + \sigma_p^2 + \sigma_e^2}$$

where σ^2_g, σ^2_p and σ^2_e are the additive genetic, cow permanent environmental and residual variances, respectively. Genetic correlations between traits were estimated through bivariate repeatability animal models considering the same fixed and random effects described for the single-trait analysis.

Results and Discussion

Descriptive statistics

Milk yield, fat percentage and protein percentage averaged 18.76 kg/d, 5.29% and 4.09%, respectively (Table 1). These means were similar to the values reported by Sneddon *et al.* (2012) in a New Zealand Jersey herd under grazing conditions. Lactose percentage of this study was 4.80%, which is higher than 4.45% in Brazilian (Ramos Garcia *et al.*, 2015), but lower than 5.09% in New Zealand (Sneddon *et al.,* 2012) Jersey cows.

The mean of SCS in this study was 3.02, which is lower than the value reported in Brazil (Ramos Garcia *et al.,* 2015). Comparison of SCS with the New Zealand Jersey study (Sneddon *et al.,* 2012) is not possible because the transformation from SCC to SCS was not the same. Least squares means of milk and solids yield, solids content, and SCS over the lactation of Italian Jersey cows are shown in Figure 1. Lactation curves of these traits were similar to the lactation curves of first-lactation Jersey cows in New Zealand (Sneddon *et al.,* 2016).

Heritability

The estimate of heritability for milk yield in this study was 0.14 (Table 1), which agrees with the values reported by Rincón *et al.* (2015) in Holstein Friesian (0.16) and Jersey (0.15) in Colombia. However, estimates varies from 0.19 (Sneddon *et al.,* 2015) to 0.50 (Sneddon *et al.*, 2012) in the New Zealand Jersey population, suggesting an important influence of environmental factors and sample size.

The estimates of heritabilities for yields of milk components were generally low, but comparable to those reported by Sneddon *et al.* (2015), who showed the same estimate of heritability for fat yield (0.12). Heritabilities for contents of milk components were slightly lower than those reported by Sneddon *et al.* (2015). Heritability of SCS was low (0.10) but similar to the value (0.08) reported by Sneddon *et al.* (2015), suggesting that this trait is more affected by environmental rather than genetic factors. This trait is associated with udder health, which also is not highly inheritable.

Correlations

The estimates of genetic correlations between SCS and yields of milk components were slightly negative (-0.25, -0.25, -0.27, -0.26 between SCS and milk yield, fat yield, protein yield and lactose yield, respectively; Table 2). Furthermore, as confirmed by New Zealand studies (Sneddon *et al.,* 2012, 2015) the genetic and phenotypic correlations between lactose yield and milk yield was almost 1, and between lactose yield and protein yield was strong and positive (Table 2), which indicates that an increase in milk yield will be accompanied with an increase in lactose yield. Selection for increased yields may decrease SCS as the estimated genetic correlation between yields and SCS were negative. However, selection for increased concentration of milk components may increase the SCS in cows due to positive estimated genetic correlations between concentrations and SCS (Sneddon *et al.,* 2012). The estimated phenotypic correlations were generally weak, which agree with estimates reported in the literature (Rincón *et al.,* 2015). However, the estimates of these correlations are very variable, according to the environment where they were estimated, so that it is common to find higher values in highly controlled production conditions.

Conclusion

The estimates of phenotypic and genetic parameters obtained in this study are within the ranges previously reported in other Jersey dairy cattle populations. These estimates of genetic parameters can be used in simulation studies to evaluate the genetic responses for individual traits of alternative selection indices and breeding objective that may be implemented in the Italian Jersey population, that ensure genetic in the right magnitude and direction.

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Table 1. Mean, standard deviation (SD), heritability (standard errors within parentheses), and repeatability of studied traits in Italian Jersey cows.

Trait	Mean	SD	Heritability	Repeatability
Solids yield, kg/d				
Milk	18.76	6.96	0.14 (0.02)	0.37
Fat	0.98	0.38	0.12 (0.08)	0.26
Protein	0.76	0.28	0.14 (0.02)	0.33
Casein	0.59	0.24	0.08 (0.02)	0.26
Lactose	0.91	0.35	0.13 (0.03)	0.37
Solids content, %				
Fat	5.29	1.04	0.21 (0.01)	0.28
Protein	4.09	0.48	0.26 (0.03)	0.39
Casein	3.20	0.39	0.24 (0.03)	0.33
Lactose	4.80	0.21	0.20 (0.02)	0.35
SCS[1], units	3.02	1.69	0.10 (0.02)	0.31

[1] SCS = somatic cell score, calculated as 3 + $\log_2$(SCC/100 000), where SCC is somatic cell count.

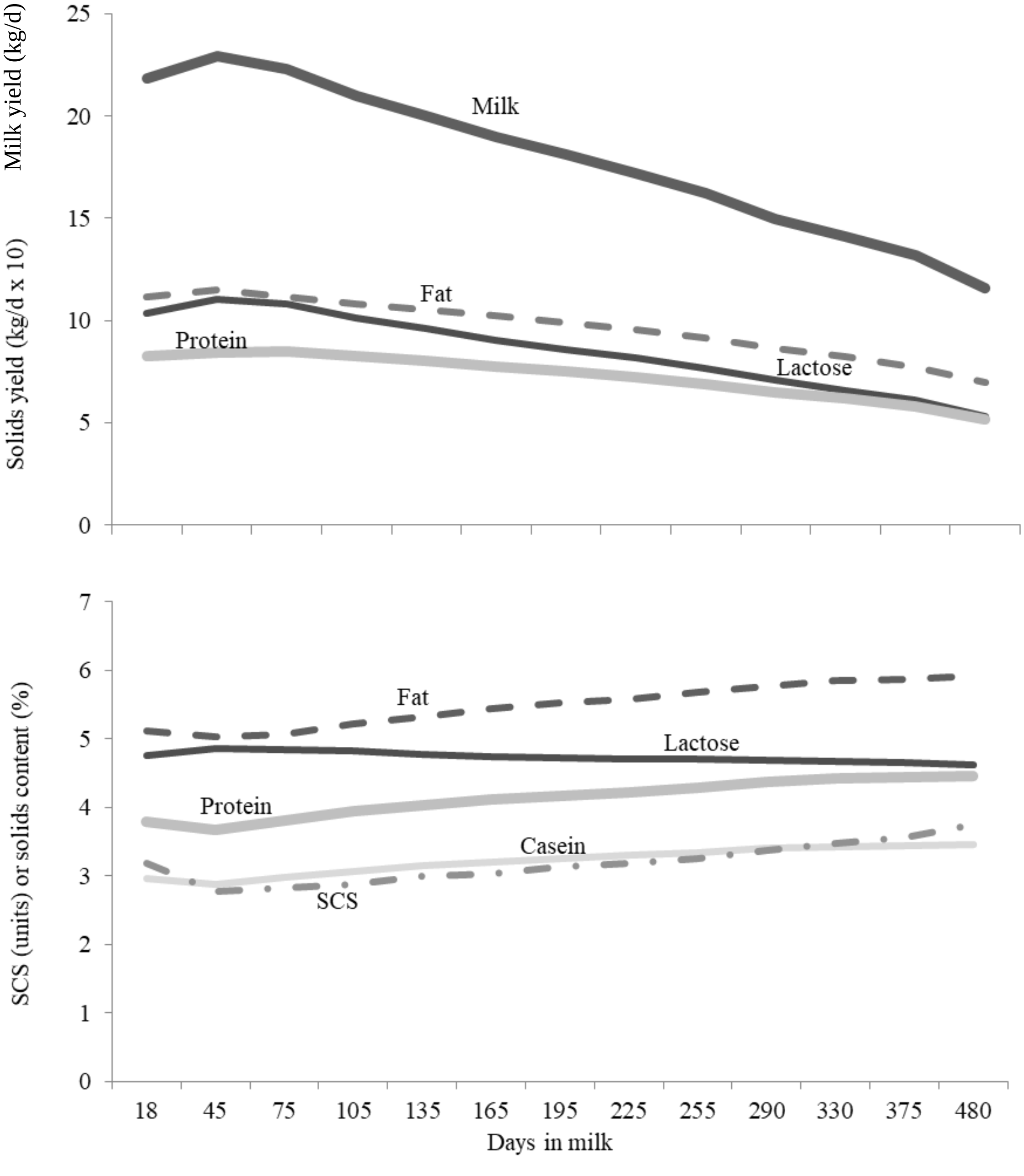
Table 2. Genetic (below the diagonal) and phenotypic (above the diagonal) correlations[1] between studied traits in Italian Jersey cows.

Trait[2]	MY	FP	PP	CP	LP	FY	PY	CY	LY	SCS
MY		-0.21	-0.20	-0.13	0.21	0.84	0.94	0.94	0.99	-0.24
FP	-0.37		0.50	0.52	-0.29	0.29	-0.06	-0.03	-0.24	0.04
PP	-0.43	0.82		0.98	-0.33	0.05	0.10	0.14	-0.20	0.11
CP	-0.43	0.82	0.99		-0.34	0.12	0.16	0.16	-0.14	0.09
LP	-0.02	-0.28	-0.21	-0.22		0.05	0.11	0.05	0.31	-0.38
FY	0.72	0.36	0.16	0.14	-0.14		0.88	0.89	0.82	-0.22
PY	0.91	-0.03	-0.04	-0.01	-0.07	0.88		0.99	0.93	-0.21
CY	0.91	-0.02	-0.06	-0.02	0.01	0.83	0.99		0.93	0.20
LY	0.99	-0.42	-0.43	-0.43	0.17	0.67	0.88	0.89		-0.25
SCS	-0.25	0.11	0.18	0.29	-0.30	-0.25	-0.27	-0.13	-0.26	

[1] Standard errors of genetic correlations ranged from 0.001 to 0.17.

[2] MY = milk yield; FP = fat percentage; PP = protein percentage; CP = casein percentage; LP = lactose percentage; FY = fat yield; PY = protein yield; CY = casein yield; LY = lactose yield; SCS = somatic cell score calculated as 3 + $\log_2$(SCC/100 000), where SCC is somatic cell count.

Figure 1. Least squares means of milk and solids yield, solids content, and somatic cell score (SCS) over the lactation in Italian Jersey cows.



Chapter 3

Genetic parameters for linear type traits including locomotion in Jersey cattle breed

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Abstract

This study aimed to estimate genetic parameters for 20 linear type traits and final score of 10 305 first-parity Jersey cows evaluated between 2004 and 2016. Since scoring of locomotion in Jersey breed started in 2009, a subset of 6853 animals was extracted from the original data and used to investigate sources of variation and heritability of locomotion, and its associations with the other traits. Univariate animal models were used to estimate variance components of type traits and bivariate analyses were implemented to obtain genetic correlations between traits. Fixed effects were herd-year-classifier, season of evaluation, stage of lactation at scoring and age at calving, and the random effects were additive genetic animal and the residual. Herd-year-classifier was the major source of variation affecting the traits. Heritabilities were low with the only exception of a moderate heritability (0.32) for stature. The lowest heritabilities were estimated for feet and legs traits with values between 0.04 (rear leg set side view, rear leg set rear view and locomotion) and 0.07 (foot angle). The final score had heritability of 0.20. Genetic correlations were generally stronger than their phenotypic counterparts. Overall, frame traits were weakly correlated with feet and legs, and udder traits, except for rump width, which showed moderate correlations with almost all traits, and angularity which showed the greatest correlations with rear udder height (0.61 ± 0.10) and rear udder width (0.62 ± 0.11). Genetic correlations between locomotion and frame traits ranged from 0.08 ± 0.22 (angularity) to 0.32 ± 0.16 (stature). The strongest correlations were estimated between locomotion and other feet and legs traits, but also with front teat placement (0.97 ± 0.19) and with rear teat placement (0.88 ± 0.17). Results of the present study will be used to enhance genetic evaluation of linear type traits in Jersey cattle breed.

Keywords: conformation; udder; heritability; genetic correlation; dairy cow.

Implications

The present study estimated the genetic parameters for type traits in Jersey cattle breed. Genetic selection towards increased milk production alone has reduced the genetic merit for health and fertility in dairy cattle. Given the increased concern on animal welfare, a greater emphasis on functional aspects, including type traits, should be considered in the selection index of Italian Jersey. Genetic parameters estimated in this study provided new insights on the genetic background of Jersey cow to be exploited for breeding purposes.

Introduction

The Jersey cattle breed is characterized by smaller body size, lower production and milk with higher fat and protein percentages, compared with other cosmopolitan dairy breeds. These features make Jersey cows suitable for both intensive and non-intensive farming systems, such as grazing and once-a-day milking (Lembeye *et al.,* 2016). Also, Jerseys are generally appreciated for their longevity, fertility and biological feed efficiency, expressed as kilograms of fat and protein per kilogram of body weight (Lopez-Villalobos *et al.,* 2014). These aspects are translated into greater incomes for farmers inserted in quality-based payment systems. Milk of Jerseys has better coagulation properties and results in greater cheese yield than milk of Holstein cows (Auldist *et al.,* 2004; Visentin *et al.,* 2017); this might have particular interest in the Italian dairy industry where more than 70% of milk is used for cheese making, and almost 50% of this percentage is destined to manufacture Protected Designation of Origin products (Pretto *et al.,* 2013).

Type traits have attracted the attention of farmers and scientific community due to the increasing awareness about animal welfare and consumer demands for healthy and welfare-friendly animal products (Egger-Danner *et al.*, 2015). An example is locomotion which is directly associated with animal welfare, with particular regard to lameness (Jabbar *et al.,* 2016). For these reasons, great emphasis has been placed on the inclusion of functional traits into selection programmes over the past years (Miglior *et al.,* 2005; Egger-Danner *et al.,* 2015). Selection for type traits has been commonly carried out in several genetic programs of cattle populations worldwide due to the economic importance of some conformation features (Miglior *et al.,* 2012). Indeed, udder type traits have shown strong associations with longevity in US Jersey cattle (Caraviello *et al.,* 2003) and Canadian Jerseys (Sewalem *et al.,* 2005). Favourable genetic correlations of type traits with milk yield, body weight, fertility and somatic cells of primiparous Holstein-Friesian cows have been reported by Berry *et al*. (2004), supporting the feasibility of indirectly selecting for improved fertility and health of animals.

While phenotypic and genetic aspects of linear type traits have been widely documented in Holstein and other cattle breeds (e.g. Battagin *et al.,* 2013; Gibson and Dechow, 2018), a paucity of information has been reported for Jersey (e.g. Cue *et al.,* 1996; Biscarini *et al.,* 2003; du Toit *et al.,* 2012). In particular, Biscarini *et al.* (2003) estimated genetic parameters for 16 type traits in first-lactation Italian Jerseys; results led to a subsequent inclusion of three udder type traits, namely udder depth, udder support and fore udder attachment in the current selection index of Italian Jersey breed (IQJ), which at the beginning considered only production traits (Biffani *et al.*, 2003). The study of Biscarini *et al.* (2003) is quite dated and there is need to update estimates of genetic parameters of type traits on a larger dataset and including locomotion, which is a novel trait of economic relevance in the dairy herd. Therefore, the aims of the present study were to (i) assess sources of variation of 20 type traits, including locomotion and final score, and (ii) estimate their genetic parameters in Italian Jersey cows.

Materials and methods

Dataset and editing

Data were provided by the Italian Holstein Association (ANAFI, Cremona, Italy), which is officially in charge of maintaining the Italian Jersey herd book and performing genetic evaluation. The dataset consisted of 15 816 linear type trait records of first-lactation cows (one record per cow) in 1055 herds. All the descriptors were evaluated by trained classifiers according to a linear scale ranging from 1 to 50 points, with 1-unit increments. In the present study, traits were divided in 3 groups, namely the “frame” group, which included 6 descriptors: stature, chest width, body depth, angularity, rump angle and rump width; the “feet and legs” group, which included 5 descriptors: rear leg set side view, rear leg set rear view, foot angle, feet and legs functionality and locomotion; and the “udder” group, which included 8 descriptors: fore udder attachment, rear udder height, rear udder width, udder support, udder depth, front teat placement, front teat length and rear teat placement. In addition, the final score, which is a weighted combination of structure traits (20%), dairy strength traits (20%), feet and legs traits (20%) and udder traits (40%), was available. This overall trait is assessed using a linear scale from 50 to 100 points, with 1-unit increments.

First-lactation cows were required to have age at calving between 18 and 42 months and to have been evaluated between 5 and 305 days after calving. Contemporary groups were defined as cows scored in the same herd-year by the same classifier, and contemporary groups with less than 3 observations were discarded from the dataset. Following these edits, the final dataset used for statistical analysis consisted of 10 305 cows scored by 42 classifiers in 231 herds from 2004 to 2016. Because the recording of locomotion started in 2009, i.e. 5 years later than other type traits, fewer observations were available for this trait. Therefore, a subset of 6853 cows scored by 35 classifiers in 154 herds from 2009 to 2016 was extracted from the previous dataset and used to investigate sources of variation and heritability of locomotion, and its associations with other traits.

Statistical analysis

Preliminary analysis showed that all traits were normally distributed. Sources of variation of linear type traits and final score were investigated using the GLM procedure of SAS version 9.4 (SAS Institute Inc., Cary, NC) according to the following linear model:

$$Y_{ijkl} = \mu + \text{hyc}_i + \text{stage}_j + \text{age}_k + \text{season}_l + e_{\text{ijkl}},$$

where Y_{ijkl} is the dependent variable (a linear type trait or final score); μ the overall mean; hyc_i the fixed effect of the i^{th} herd-year-classifier (i = 1 to 731; for the subset, i = 1 to 438); stage_j the fixed effect of the j^{th} class of stage of lactation at scoring (j = 1 to 10, with classes of 30 d each); age_k the fixed effect of the k^{th} class of age at calving (k = 1 to 9, the first being a class from 18 to 22 months, followed by 7 classes of 2 months each, and the last being a class from 36 to 42 months); $season_l$ the fixed effect of the l^{th} season of evaluation (l = winter: December, January, February; spring: March, April, May; summer: June, July, August; autumn: September, October, November); and e_{ijkl} the random residual $\sim N(0, \sigma^2_e)$.

Variance and covariance components of type traits were estimated through univariate and bivariate animal models, respectively, using the package VCE6 (Neumaier and Groeneveld, 1998; Groeneveld *et al.*, 2010). Fixed effects considered in the animal models were the same described above. The pedigree file was provided by ANAFI and included cows with phenotypic records and their ancestors up to 6 generations back, for a total of 22 577 animals (18 290 for the subset). Heritability (h^2), genetic correlations (r_a) and phenotypic correlations (r_p) were calculated as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2} \quad , \quad r_a = \frac{\sigma_{a1,a2}}{\sigma_{a1} \times \sigma_{a2}} \quad \text{and} \quad r_p = \frac{\sigma_{p1,p2}}{\sigma_{p1} \times \sigma_{p2}}$$

where σ^2_a and σ^2_e are the animal additive genetic and residual variances, respectively, $\sigma_{a1,a2}$ ($\sigma_{p1,p2}$) is the additive genetic (phenotypic) covariance between traits 1 and 2, respectively, and σ_{a1} (σ_{p1}) and σ_{a2} (σ_{p2}) are the additive genetic (phenotypic) SD of traits 1 and 2, respectively.

Results

Descriptive statistics and significance of fixed effects

The final score averaged 80.27 and means of linear type traits ranged from 22.30 (front teat length) to 30.13 (rear udder width), denoting cows with favourable dairy attitude, slightly shorter-looking teats and wide udder (Table 1). Rear teat placement had the greatest SD (8.36) and the SD for the other traits ranged from 2.34 (final score) to 8.18 (stature). Within the frame group, body depth had the greatest average score (28.92), followed by angularity (28.72). As regard feet and legs group, locomotion averaged 25.05 with a SD of 5.74, meaning that most animals had a medium stride length. Finally, within udder traits group, rear udder width showed the greatest mean (30.13) followed by udder support (27.47) and rear udder height (26.20) (Table 1)

Herd-year-classifier and stage of lactation were the most important sources of variation for all studied traits ($P < 0.05$), with the exception of fore udder attachment which was not affected by stage of lactation (Table 2). Age at calving was significant ($P < 0.05$) in explaining the variation of final score, and frame and udder traits, except for rump angle and rear udder height, and among feet and legs traits, it was important for foot angle and feet and legs functionality. Season of evaluation was an important source of variation for final score and frame traits, with the exception of chest width; with regard to feet and legs, and udder traits season of evaluation was important only for rear leg set side view, foot angle, fore udder attachment, udder support and udder depth. The coefficient of determination of the model for each linear type trait ranged from 0.17 (udder support and front teat placement) to 0.55 (stature).

Genetic parameters of type traits

Overall, heritability estimates of the investigated traits were low, with the only exception of a moderate heritability (0.32) for stature (Table 1). For all studied traits, standard error of heritability was 0.02. Among other frame traits, estimates ranged from 0.06 (rump width) to 0.14 (rump angle), and for udder traits they ranged from 0.07 (rear udder width) to 0.22 (udder depth). The lowest heritabilities were estimated for feet and legs traits, with values between 0.04 (rear leg set side view, rear leg set rear view and locomotion) and 0.07 (foot angle). The final score had heritability of 0.20. The coefficient of genetic variation for linear type traits ranged from 4.01% (locomotion) to 13.52% (stature), and it was 1.19% for final score.

The strongest phenotypic correlations were observed between locomotion and feet and legs functionality (0.65), chest width and body depth (0.61), and foot angle and feet and legs functionality (0.60) (Table 3). All other phenotypic relationships between linear type traits were moderate to low, with the overall strongest associations estimated within group. In particular, correlations within the frame traits were stronger than 0.20, except for the relationships involving rump angle. Phenotypic correlations within feet and legs traits ranged from 0.43 to 0.65, except for rear leg set side view which was negatively associated with other traits (from -0.35 with rear leg set rear view to -0.18 with locomotion). These negative values were likely due to the way rear leg set side view is scored on the linear scale: low scores are desirable for this trait, whereas high scores are desirable for all other descriptors (Table 1). Phenotypic correlations within udder traits were >0.10, except for the associations involving front teat length, and the relationship between rear udder width and udder depth. Phenotypic association between linear type traits of different groups were low and comprised between -0.07 (body depth and udder depth) and 0.29 (angularity and rear udder width). The final score showed positive phenotypic correlations with all linear type traits (0.12 to 0.58), except for a negative association with rear leg set side view (-0.14), and it was uncorrelated with rump angle (Table 3).

Genetic correlations were generally stronger than their phenotypic counterparts (Table 3). Within the frame group, genetic associations varied from 0.41 ± 0.14 (rump width and angularity) to 0.98 ± 0.03 (body depth and chest width), except for the genetic correlations between rump angle and other traits which were ≤0.28. Strong genetic correlations were assessed within feet and legs traits, with estimates from 0.72 ± 0.17 (locomotion and foot angle) to 1.00 ± 0.03 (rear leg set rear view with locomotion, and with feet and legs functionality), and -0.96 ± 0.11 to -0.68 ± 0.14 between rear leg set side view and other traits. Locomotion was also strongly associated with feet and legs functionality (0.97 ± 0.05) and rear leg set side view (-0.85 ± 0.16). Within the udder group, front teat length and rear udder width were generally weakly correlated with other traits, except for a strong association between rear udder width and rear udder height (0.81 ± 0.08). All other udder traits were moderately to strongly correlated to each other, with estimates that ranged from 0.33 ± 0.11 (rear teat placement and udder depth) to 0.93 ± 0.05 (rear teat placement and front teat placement). In particular, fore udder attachment strongly correlated with udder depth (0.86 ± 0.04), rear udder height (0.76 ± 0.06) and front teat placement (0.75 ± 0.07); udder support was strongly associated with front teat placement (0.77 ± 0.08) and rear teat placement (0.75 ± 0.10); and udder depth was strongly associated with front teat placement (0.70 ± 0.09). Considering genetic correlations between traits belonging to different groups, a wide range of estimates was obtained. Overall, frame traits were weakly correlated with feet and legs, and udder traits, except for rump width which showed moderate correlations with almost all features, and angularity which showed the greatest correlations with rear udder height (0.61 ± 0.10) and rear udder width (0.62 ± 0.11). Genetic associations between locomotion and frame traits ranged from 0.08 ± 0.22 (angularity) to 0.32 ± 0.16 (stature). The correlations between feet and legs, and udder type traits were generally moderate to strong, except for rear leg set side view which correlated moderately only with front teat placement (-0.40 ± 0.17) and front teat length (-0.46 ± 0.15). The strongest associations were estimated between locomotion and front teat placement (0.97 ± 0.19), and locomotion and rear teat placement (0.88 ± 0.17). The final score was almost uncorrelated with rump angle and front teat length, and moderately to strongly positively correlated with other traits (0.30 ± 0.11 to 0.91 ± 0.03), except for a negative relationship with rear leg set side view (-0.45 ± 0.02). Locomotion strongly correlated with final score (0.75 ± 0.12).

Discussion

Genetic and phenotypic variation of linear type traits have been extensively documented in Holstein (e.g. Battagin *et al.,* 2013; Cassandro *et al.,* 2015; Bilal *et al.,* 2016), as well as in Brown Swiss (e.g. de Haas *et al.,* 2007; Dal Zotto *et al.,* 2007; Gibson and Dechow, 2018), whereas less information is available for Jersey breed (Cue *et al.,* 1996; Biscarini *et al.,* 2003; du Toit *et al.,* 2012). In the present study, the average score of each linear type trait (except for final score) was close to 25, which was somewhat expected, since type evaluations are recorded on 1- to 50-point scale. On a scale ratio, findings of the present study were comparable with those reported by Cue *et al. (*1996), Caraviello *et al.* (2003) and du Toit *et al.* (2012), who evaluated type traits in New Zealand, American and South African Jersey cows, respectively, using a 1- to 9-point scale. Also, our results agreed with findings of Cassandro *et al.* (2015) in first-parity Holstein cows, who reported means of type traits that ranged from 21.0 (front teat length) to 31.6 (rear udder width). The average locomotion score was slightly greater than the value (23.48) reported by Battagin *et al.* (2013) in first-lactation Holsteins. Since locomotion evaluates the walking ability of the cow, high scores are desirable because they are associated with feet and legs functionality and long strides without abduction. One of the major factors affecting locomotion is the herd. Onyiro and Brotherstone (2008) reported that different housing systems explained a significant variability of locomotion (e.g. cows on pasture had favourable type trait scores compared with cows in other housing systems). In our study, HYC effect was very important in determining the variability of locomotion and results from an additional analysis of variance that included herd, year of scoring and classifier as separate effects, revealed that herd explained a larger proportion of locomotion variation than year of scoring and classifier.

Heritability

Overall, heritabilities for type traits in the present study were low; however, coefficients of genetic variation suggest that there is room to select for type traits in Italian Jersey cows. The greatest heritabilities were estimated for frame and udder traits, whereas feet and legs features showed the lowest values. These results agreed with those reported by several authors in different cattle breeds (Dal Zotto *et al.,* 2007; du Toit *et al.,* 2012; Cassandro *et al.,* 2015). Stature was the most heritable trait (0.32), in accordance with the estimate reported by Dal Zotto *et al.* (2007) in first-parity Italian Brown Swiss cows, whereas du Toit *et al.* (2012) and Cassandro *et al.* (2015) estimated lower heritability (0.20) for this trait in multiparous South African Jersey and first-parity Italian Holstein cows, respectively. Using a repeatability animal model, Gengler *et al.* (1997) obtained heritabilities of linear type traits for first- and second-lactation US Jersey cows that were higher compared with those reported in the present study. Heritability of locomotion was intermediate between estimates of 0.03 and 0.05 reported by Zink *et al.* (2011) and Battagin *et al.* (2013) in first-parity Czech and Italian Holsteins, respectively. Conversely, Onyiro and Brotherstone (2008) and Berry *et al.* (2004) estimated higher heritability (0.11 and 0.14) in first-lactation UK and Irish Holstein-Friesian cows, respectively. In general, the discrepancies between heritability estimates for type traits in the literature may be the result of differences in scale used for scoring the trait, editing procedure, statistical model, breed and parity. Also, the classifier may have an impact on the magnitude of heritability (Veerkamp *et al.*, 2002).

Correlations

The selection index of Italian Jersey (IQJ) includes two production traits (milk yield and protein yield) and three udder type traits (fore udder attachment, udder support and udder depth); the latter were added to the selection index in 2005 to improve cow's functionality, in particular udder health. The IQJ gives great emphasis to protein yield, which has a weight of 64.7% in the index, followed by milk yield (-19.3%), and less emphasis to type traits: 12.8% udder depth, 1.6% udder support and 1.6% fore udder attachment. Genetic parameters estimated in the present study might be a starting point to explore if additional type traits, including locomotion, are of potential interest to be considered in the IQJ to further enhance functionality of the breed.

Correlations between type traits of the same group. All genetic and phenotypic correlations within frame group were positive, differently from Biscarini *et al.* (2003), who presented negative genetic correlations of angularity with body depth (-0.06), rump with (-0.15) and chest width (-0.36). In the present study, the genetic correlation between chest width and body depth (0.98) was stronger than genetic relationships of 0.90 and 0.80 assessed by Biscarini *et al.* (2003) and Berry *et al.* (2004) in first-lactation Italian Jersey and Irish Holstein-Friesian cows, respectively. Genetic associations between stature, body depth and rump width were stronger than those reported by de Haas *et al.* (2007) in primiparous cows of three Swiss dairy cattle breeds. Brotherstone (1994) and Berry *et al.* (2004) reported a genetic correlation of 0.41 between stature and angularity in first-lactation Holstein-Friesians (0.41), which is very close to our estimate (0.44). Genetic correlations of final score with traits included in frame group were moderately favourable, except for the null correlation with rump angle. These findings agreed with Brotherstone (1994), except for rump angle, which was unfavourably correlated with final score (-0.37).

Strong and positive genetic correlations were estimated between feet and legs traits, suggesting that they reflect similar characteristics of the legs. This is particularly true for the genetic correlations of rear leg set rear view with locomotion, feet and legs functionality and rear leg set side view, and the genetic correlation between locomotion and feet and legs functionality, which were all greater than 0.90 in absolute value. These findings suggest that the number of traits to be included in the genetic evaluation could be reduced to avoid redundancy and increase selection efficiency. Strong and favourable correlations were found between feet and legs traits and final score, with the exception of rear leg set side view. Moreover, Van Dorp *et al.* (2004) concluded that cows with high locomotion score also had better body condition score. Unfortunately, a comparison is not possible since body condition score is not currently recorded in Italian Jersey breed.

Within udder group, fore udder attachment and udder depth were strongly genetically correlated, as previously reported by Biscarini *et al.* (2003) and Brotherstone (1994), followed by moderate correlations between fore udder attachment and udder support, and udder depth and udder support. Also in this case, the strong positive genetic correlation between fore udder attachment and udder depth were comparable with results obtained in US Brown Swiss (Gibson and Dechow, 2018). The genetic association between front teat placement and rear teat placement estimated in the present study was stronger than that reported by Cue *et al.* (1996) in New Zealand Jersey. Front teat length had a negative association with the majority of udder traits, similarly to previous findings on Italian Jersey (Biscarini *et al.,* 2003). Overall, udder traits were moderately to strongly associated with final score (0.40 to 0.91), except for front teat length, in agreement with findings of Brotherstone (1994) in Holstein-Friesian.

Correlations between type traits of different groups. Opposite to our study, Berry *et al.* (2004) estimated a stronger genetic and a null phenotypic correlation between angularity and locomotion in Irish Holsteins. The favourable genetic correlations between angularity, rear udder width and rear udder height agreed with previous findings on Jersey cows (Gengler *et al.,* 1997; Biscarini *et al.,* 2003), suggesting that increased animal sharpness is associated with improvement of udder conformation. Similarly to results of the current study, Gibson and Dechow (2018) reported a favourable relationship between udder traits and mobility score, suggesting that improved udder conformation was also associated with improved locomotion. Indeed, in the present study, the genetic correlations between locomotion and udder traits group were moderate to high; the negative association between front teat length and locomotion was the exception, as confirmed also by Berry *et al.* (2004) in primiparous Holstein-Friesians. Conversely, Boelling and Pollott (1998) justified the negative correlation between locomotion and udder depth in their study by the fact that an udder with less depth could be a smaller obstacle to the rear legs, therefore could improve walking ability.

Conclusions

Heritability estimates for type traits in Italian Jersey were generally low, but additive genetic variation suggested that there is room to select for improved functionality in this breed. Heritabilities were greater for the frame traits, followed by udder traits and feet and legs. Genetic correlations between linear type traits were greater than their phenotypic counterparts. Some strong genetic correlations between linear type traits underlined redundancy, meaning that the number of evaluated traits might be reduced by losing minor information on type traits, and increasing genetic selection efficiency at the same time. Genetic parameters estimated in the present provided some new insights, especially with regard to locomotion, which could be potentially included in the IQJ to further enhance functionality of the breed.

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Declaration of interest

The authors declare that they do not have conflicts of interest.

Ethics statement

Procedures used in this study are excluded from the authorisation of the animal welfare committee.

Software and data repository resources

None of the data were deposited in an official repository.

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Table 1 Descriptive statistics, coefficient of genetic variation (CV_g), heritability (h^2; standard error in parentheses) for linear type traits and final score[1] of first-parity Jersey cows (*n* = 10 305)[2].

Trait	Mean	SD	CV_g, %	h^2	Descriptor Minimum (1)	Descriptor Maximum (50)
Frame						
Stature	24.14	8.18	13.52	0.32 (0.02)	Short	Tall
Chest width	25.28	5.47	6.33	0.12 (0.02)	Narrow	Wide
Body depth	28.92	4.79	5.14	0.12 (0.02)	Shallow	Deep
Angularity	28.72	4.78	4.36	0.08 (0.02)	Coarse	Angular
Rump angle	24.84	6.03	8.62	0.14 (0.02)	High pins	Low pins
Rump width	25.01	6.35	5.35	0.06 (0.02)	Narrow	Wide
Feet and Legs						
Rear leg set side view	26.98	5.03	3.60	0.04 (0.02)	Straight	Sickle
Rear leg set rear view	26.69	5.94	4.05	0.04 (0.02)	Hocked in	Correctly straight
Foot angle	24.85	5.84	5.71	0.07 (0.02)	Low	High
Feet and legs functionality	24.33	5.71	5.34	0.06 (0.02)	Low	High
Locomotion	25.05	5.74	4.01	0.04 (0.02)	Short stride	Long stride
Udder						
Fore udder attachment	23.56	6.38	10.13	0.16 (0.02)	Loose	Tight
Rear udder height	26.20	6.01	6.70	0.10 (0.02)	Low	High
Rear udder width	30.13	5.91	4.57	0.07 (0.02)	Narrow	Wide
Udder support	27.47	5.94	6.37	0.10 (0.02)	Weak	Strong
Udder depth	25.59	6.83	11.40	0.22 (0.02)	Deep	Shallow
Front teat placement	23.43	5.34	5.98	0.08 (0.02)	Wide	Close
Front teat length	22.30	6.05	7.55	0.10 (0.02)	Short	Long
Rear teat placement	24.18	8.36	9.90	0.09 (0.02)	Wide	Close
Final score	80.27	2.34	1.19	0.20 (0.02)	-	-

[1] Linear type traits and final score evaluated on a 1- to 50-point and 50- to 100-point scale, respectively.

[2] *n* = 6853 for locomotion.

Table 2. F-value and significance of fixed effects included in the analysis for linear type traits and final score of first-parity Jersey cows.

Trait	Herd-year-classifier	Season of evaluation	Stage of lactation	Age at calving	R^2	RMSE
Frame						
Stature	13.76***	3.45*	11.20***	20.37***	0.55	5.69
Chest width	5.50***	0.23	19.51***	22.82***	0.33	4.65
Body depth	4.15***	7.24***	27.86***	22.71***	0.27	4.26
Angularity	3.32***	16.06***	6.93***	3.32***	0.21	4.41
Rump angle	2.99***	5.64***	4.71***	1.46	0.19	5.63
Rump width	4.45***	9.37***	6.13***	11.23***	0.26	5.68
Feet and Legs						
Rear leg set side view	2.87***	7.18***	7.74***	1.24	0.19	4.70
Rear leg set rear view	3.53***	1.33	4.13***	0.88	0.22	5.45
Foot angle	3.05***	5.81***	3.37***	1.77*	0.20	5.43
Feet and legs functionality	3.35***	0.55	4.50***	1.68**	0.21	5.27
Locomotion	3.50***	0.08	2.44**	0.44	0.20	5.35
Udder						
Fore udder attachment	3.33***	6.00**	1.28	1.99*	0.21	5.90
Rear udder height	3.28***	0.42	5.30***	1.75	0.21	5.54
Rear udder width	5.11***	1.18	3.41***	1.95**	0.30	5.14
Udder support	2.49***	5.31**	3.70***	13.73***	0.17	5.61
Udder depth	3.93***	10.30***	4.50***	12.41***	0.25	6.16
Front teat placement	2.56***	0.53	3.27***	4.16***	0.17	5.05
Front teat length	4.06***	1.12	3.03**	3.12**	0.26	5.39
Rear teat placement	3.02***	0.50	9.27***	6.67***	0.20	7.74
Final score	4.32***	4.61**	2.21*	1.95*	0.26	2.10

*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$

Table 3 Genetic (below the diagonal) and phenotypic (above the diagonal) correlations for linear type traits and final score of first-parity Jersey cows. Standard error of genetic correlations ranged from 0.02 to 0.22.

Trait	STA	CWD	BD	ANG	RAN	RW	RLS	RLR	FAN	FL	LOC	FU	RUH	RUW	US	UDT	FTP	FTL	RTP	FS
Frame																				
Stature (STA)		0.43	0.43	0.22	0.12	0.26	-0.03	0.11	0.16	0.16	0.16	0.05	0.09	0.12	0.05	0.05	0.03	0.13	0.02	0.25
Chest width (CWD)	0.81		0.61	0.25	0.06	0.32	-0.04	0.18	0.19	0.22	0.21	0.11	0.11	0.19	0.07	-0.02	0.06	0.13	0.04	0.29
Body depth (BD)	0.71	0.98		0.42	0.05	0.33	-0.02	0.18	0.20	0.24	0.26	0.10	0.15	0.26	0.09	-0.07	0.07	0.14	0.07	0.33
Angularity (ANG)	0.44	0.43	0.63		0.07	0.22	0.01	0.14	0.17	0.20	0.24	0.13	0.24	0.29	0.14	0.00	0.09	0.09	0.07	0.37
Rump angle (RAN)	0.26	0.28	0.14	0.08		0.00	0.02	0.01	0.01	0.01	0.02	-0.05	-0.02	0.04	0.01	-0.02	0.02	0.03	0.02	0.01
Rump width (RW)	0.75	0.77	0.65	0.41	0.10		-0.06	0.18	0.20	0.22	0.23	0.18	0.16	0.20	0.14	0.06	0.09	0.12	0.08	0.33
Feet and Legs																				
Rear leg set side view (RLS)	-0.01	-0.10	0.12	0.01	0.02	-0.20		-0.35	-0.27	-0.28	-0.18	-0.05	-0.04	-0.03	0.01	-0.03	-0.01	-0.04	0.06	-0.14
Rear leg set rear view (RLR)	0.22	0.18	0.05	0.04	0.04	0.50	-0.92		0.43	0.49	0.43	0.14	0.13	0.17	0.09	0.05	0.06	0.10	0.01	0.36
Foot angle (FAN)	0.30	0.23	0.16	0.27	0.04	0.43	-0.68	0.79		0.60	0.47	0.20	0.23	0.17	0.12	0.10	0.09	0.13	0.06	0.44
Feet and legs functionality (FL)	0.31	0.18	0.24	0.14	0.03	0.48	-0.96	1.00	0.92		0.65	0.21	0.21	0.20	0.15	0.11	0.11	0.12	0.06	0.52
Locomotion (LOC)	0.32	0.25	0.21	0.08	0.11	0.29	-0.85	1.00	0.72	0.97		0.23	0.23	0.22	0.16	0.12	0.12	0.10	0.08	0.52
Udder																				
Fore udder attachment (FU)	0.07	0.25	0.10	0.11	-0.25	0.47	-0.24	0.57	0.63	0.63	0.67		0.41	0.23	0.34	0.47	0.31	0.05	0.21	0.58
Rear udder height (RUH)	0.21	0.07	0.15	0.61	-0.05	0.35	-0.12	0.53	0.57	0.54	0.63	0.76		0.42	0.30	0.18	0.22	0.08	0.16	0.48
Rear udder width (RUW)	0.16	0.05	0.20	0.62	0.24	0.13	0.03	0.35	0.26	0.54	0.27	0.28	0.81		0.27	-0.01	0.13	0.07	0.12	0.38
Udder support (US)	0.14	0.11	0.12	0.13	0.04	0.33	-0.24	0.45	0.38	0.33	0.37	0.54	0.61	0.27		0.32	0.38	0.05	0.34	0.46
Udder depth (UDT)	0.10	0.08	0.11	-0.18	-0.18	0.31	-0.26	0.38	0.47	0.56	0.40	0.86	0.44	-0.12	0.48		0.26	-0.01	0.18	0.44
Front teat placement (FTP)	0.12	0.29	0.26	0.09	-0.15	0.36	-0.40	0.63	0.66	0.50	0.97	0.75	0.61	0.23	0.77	0.70		-0.09	0.45	0.39
Front teat length (FTL)	0.36	0.37	0.27	0.01	0.10	0.39	-0.46	0.38	0.36	0.19	-0.06	-0.05	-0.04	-0.29	-0.13	0.01	-0.10		-0.05	0.12
Rear teat placement (RTP)	0.12	0.24	0.27	0.21	0.02	0.45	0.05	0.46	0.24	0.32	0.88	0.50	0.50	0.34	0.75	0.33	0.93	-0.09		0.24
Final score (FS)	0.40	0.42	0.43	0.30	0.03	0.66	-0.45	0.80	0.78	0.82	0.75	0.91	0.78	0.40	0.49	0.72	0.77	0.01	0.59	

Chapter 4

Genetic relationships of alternative somatic cell count traits with milk yield, composition and udder type traits in Italian Jersey cows

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Abstract

The aim of this study was to characterize novel somatic cell count (SCC) traits, derived from routine test-day (TD) recording system, and to estimate their genetic and phenotypic relationships with milk yield, composition and udder type traits in Italian Jersey cows. Alternative SCC traits were: TD somatic cell score (SCS) averaged over early lactation (SCS_150); standard deviation of SCS of the entire lactation (SCS_SD); a binary trait indicating absence (0) or presence (1) of at least one TD SCC >400 000 cells/mL in the lactation (Infection); and the ratio of the number of TD SCC >400 000 cells/mL to total number of TD in the lactation (Severity). After editing, 101 420 TD SCC, milk yield and composition records of 12 754 first-lactation Jersey cows in 428 herds were available for statistical analysis, as well as 9482 udder type traits evaluations. A 5-trait animal model was employed to estimate heritability of and genetic correlations between SCC traits, including lactation-mean SCS (SCS_LM), and bivariate analyses were run to estimate heritability of milk composition and udder type traits, and their genetic correlations with SCC traits. Heritabilities of SCC traits ranged from 0.038 ± 0.015 (SCS_SD) to 0.136 ± 0.022 (SCS_LM), and they were comparable to heritabilities of udder type traits but smaller than those of milk production and composition. Moderate to strong genetic correlations were obtained between SCC traits (0.521 ± 0.171 between SCS_SD and Severity to 0.989 ± 0.014 between Infection and Severity), except for the null genetic associations of SCS_SD with SCS_LM and SCS_150. Unfavorable genetic correlations between milk yield and both SCS_SD (0.566 ± 0.246) and Infection (0.374 ± 0.213) suggested that high-producing cows were more susceptible to variation of SCC than low-producing animals. Lactose exhibited low or moderate negative correlations with SCC traits. Our findings highlighted that cows with deep udders, loose attachments, weak ligaments and long teats were more susceptible to an increase of SCC in milk. Alternative SCC traits showed exploitable genetic variation and heritability, and thus they are candidate traits to be included in the selection index of the Jersey breed to select cows with improved resistance to mastitis.

Keywords: somatic cell score; mastitis; udder conformation; genetic selection; dairy cattle.

Implications

Our analysis revealed genetic variation and heritability of alternative somatic cell count (SCC) traits exploitable for breeding purposes in Italian Jersey cows. Estimated genetic correlations between novel SCC traits and traits currently included in the selection index of Jersey breed would be beneficial to increase effectiveness of selection for mastitis resistance, by combining udder type and SCC traits into an udder health index.

Introduction

Since a rapid implementation of on-farm disease-recording systems is not feasible worldwide, a possible way to improve genetic selection for disease resistance is to exploit the information routinely collected during milk recording procedures. A clear example is given by somatic cell count (SCC), which is routinely recorded in many countries all over the world and is the most common indicator of udder health. Indeed, log-transformed SCC (SCS) is known to be strongly genetically associated with clinical mastitis, thus explaining why test-day (TD) SCS and lactation-mean SCS have been historically included in selection programs to improve mastitis resistance (Martin *et al.*, 2018). However, TD SCS and lactation-mean SCS are not very informative on the dynamic of the infection. Therefore, alternative traits derived from TD SCC data have been explored to better describe SCC variation during the lactation and to genetically improve resistance to mastitis (de Haas *et al.*, 2008; Urioste *et al.*, 2010; Koeck *et al.*, 2012a). Recently, Bobbo *et al.* (2018) have investigated phenotypic and genetic aspects of four alternative SCC traits and concluded that a combination of those traits was a better predictor of SCC variation during lactation in Holstein cows. Results of the above-mentioned study contributed to define a novel udder health index in the Italian Holstein breed (Finocchiaro *et al.*, 2018), in support of the current one which is based on TD SCS.

Among its responsibilities, the Italian Holstein Association (ANAFI, Cremona, Italy) is in charge of the genetic evaluation of the Italian Jersey, a dairy breed characterized by lower milk production than Holstein, but with optimal milk composition and coagulation ability (Stocco *et al.,* 2017; Visentin *et al.,* 2017a; Roveglia *et al.,* 2018). Given the favourable milk composition and technological properties, Jersey cows are often reared in mixed herds with Holsteins. At first, the national selection index of the Jersey breed included only production traits (Biffani *et al.,* 2003). In 2005, three udder type traits were added to the index, namely fore udder attachment, udder support and udder depth. However, no selection for somatic cell traits in milk has been performed so far.

Therefore, the aim of the present study was to characterize four alternative SCC traits, derived from routine TD recording system, in Italian Jersey cows and to estimate their genetic and phenotypic relationships with milk yield, composition and udder type traits. Findings of this work will provide additional information to develop a health index aimed to improve udder resistance to mastitis in Italian Jersey breed.

Materials and methods

Data editing

The original database of TD records of Jersey cows provided by ANAFI was edited to include only first-parity cows between 5 and 305 days in milk, sampled between 2005 and 2016. Following Bobbo *et al.* (2018), cows with at least 5 TD records (of which at least 3 collected from 5 to 150 days in milk) were considered. In addition, only cows with the first TD within 60 d after calving and with an interval between two consecutive TD lower than 70 d were retained. After editing, 101 420 TD SCC (cells/mL), milk yield (kg/d) and composition records of 12 754 Jersey cows in 428 herds were available for statistical analysis. As reported in Bobbo *et al.* (2018), for each animal TD SCC data were log-transformed to TD SCS (Ali and Shook, 1980), and lactation-mean SCS (SCS_LM) was calculated. Alternative SCC traits were: TD SCS averaged over early lactation, i.e. from 5 to 150 days in milk (SCS_150); standard deviation of SCS of the entire lactation (SCS_SD); a binary trait indicating absence (0) or presence (1) of at least one TD SCC >400 000 cells/mL in the lactation (Infection); and the ratio of the number of TD SCC >400 000 cells/mL to total number of TD in the lactation (Severity). Milk composition traits included fat, protein, casein and lactose percentages, and milk urea nitrogen (mg/dL), which were determined using mid-infrared spectroscopy. Furthermore, information on the following udder type traits scored on a 1 to 50-point linear scale was provided by ANAFI:

- fore udder attachment: strength of the attachment of the fore udder to the body wall (1 = loose, 50 = tight);
- rear udder height: distance between the bottom of the vulva and the milk secreting tissue (1 = low, 50 = high);
- rear udder width: width of the high part of udder (1 = narrow, 50 = wide);
- udder support: depth of cleft of the udder, measured at the base of the rear udder (1 = weak, 50 = strong);
- udder depth, measure of the depth of udder floor relative to the hock (1 = deep, 50 = shallow);
- front teat placement: position of the front teats from center of quarter, viewed from the rear (1 = wide, 50 = close);
- front teat length: length of the front teats from the base to the end of the teat (1 = short, 50 = long).

Only evaluations performed between 5 and 305 days *postpartum* on cows from 18 to 42 months of age at calving were considered (*n* = 9482).

Statistical analysis

A preliminary investigation of the non-genetic sources of variation of SCS_LM and alternative SCC traits was conducted by fitting linear mixed or logistic regression models in SAS (SAS Institute Inc., Cary, NC) depending on the type of traits considered (binary or continuous), including year of calving (13 levels, from 2004 to 2016), season of calving (4 levels, winter: December, January, February; spring: March, April, May; summer: June, July, August; autumn: September, October, November), number of TD (6 levels, from 5 to 10) and milk yield (3 levels, based on mean ± 1 SD) as fixed effects, and herd (428 levels) as random effect.

A 5-trait animal model was then applied to a subset of 8124 Jersey cows to estimate heritability of and genetic correlations between SCC traits. Herd-year-season of calving (HYS; 650 levels) and number of TD (6 levels) were included as fixed effects, and additive genetic animal (25 889 individuals) as random term.

Bivariate animal models were run using a subset of 5601 cows to estimate heritability of lactation-mean composition traits, and genetic correlations between SCC traits and milk composition. The effects described above were included in the model: HYS (381 levels) and number of TD (6 levels) as fixed effects, and additive genetic animal (18 612 individuals) as random effect.

Similarly, bivariate animal models were performed using a subset of 6195 cows to estimate heritability of udder type traits, and genetic correlations between SCC traits and udder type traits. The model for SCC traits included the fixed effects of HYS (489 levels) and number of TD (6 levels), and the random effect of additive genetic animal (20 145 individuals). The model for udder type traits accounted for the fixed effects of herd-year-classifier (241 levels), season of evaluation (4 levels, winter: December, January, February; spring: March, April, May; summer: June, July, August; autumn: September, October, November), days in milk at scoring (10 levels of 30 d each) and age at calving (9 levels, the first being a class from 18 to 22 months, followed by 7 classes of 2 months each, and the last being a class from 36 to 42 months), and for the random effect of additive genetic animal (20 145 individuals).

The same selection criteria (inclusion of cows with known sire and dam and at least 5 observations for each HYS level) were adopted for the extraction of the three subsets described above and used to estimate genetic parameters. Moreover, at least 3 observations for each HYC level were required for udder type traits. Variance components and heritability of milk yield, composition and udder type traits were the average of the values obtained from the bivariate analyses. All the genetic analyses were performed using the software VCE6 (Neumaier and Groeneveld, 1998).

Results

Descriptive statistics

Lactation-mean SCS and SCS_150 averaged 3.09 and 3.01, respectively (Table 1). Standard deviation of SCS ranged from 0.11 to 4.26, with a mean of 1.10. About 43% of the cows had at least one TD SCC >400 000 cells/mL during the lactation (Infection) and the ratio of the number of TD SCC >400 000 cells/mL to total number of TD (Severity) averaged 0.11. Jersey cows had an average milk production of 19.46 kg/d (Table 1). Means of concentration of fat, protein, casein and lactose were 5.03%, 3.97%, 3.08% and 4.85%, respectively, and milk urea nitrogen averaged 23.56 mg/dL. Udder type traits averaged from 22.38 (front teat length) to 30.16 (rear udder width) and their coefficient of variation ranged from 20% (rear udder width) to 27% (fore udder attachment, udder depth and front teat length) (Table 1).

Genetic variation and heritability

Fixed effects (year and season of calving, number of TD and milk production) included in the models for phenotypic analysis of alternative SCC traits were significant in explaining the variation of these traits. A remarkable result was that SCS_LM increased across years of calving (Figure 1). Variance components and heritability of SCC traits, milk yield, composition and udder type traits are reported in Table 2. The subsets used for the genetic analysis were representative of the edited dataset, as the descriptive statistics of the analysed traits were comparable with those reported in Table 1. All traits had coefficients of additive genetic variation below 13%, with the only exception of Infection (26.5%) and Severity (38.2%). Medium to high heritability was estimated for milk yield and composition traits, ranging from 0.271 ± 0.035 (milk urea nitrogen) to 0.610 ± 0.034 (fat percentage). Heritability of SCC traits and udder type traits was smaller than that of milk production and composition, ranging from 0.038 ± 0.015 (SCS_SD) to 0.136 ± 0.022 (SCS_LM) for SCC traits and from 0.073 ± 0.022 (rear udder width) to 0.190 ± 0.028 (udder depth) for udder type traits.

Correlations

Correlations between SCC traits. Genetic and phenotypic correlations between SCC traits were estimated using a 5-trait analysis (Table 3). Strong genetic correlations were obtained between SCS_LM and SCS_150 (0.986 ± 0.014), and between Infection and Severity (0.989 ± 0.014). Genetic correlations between other SCC traits ranged from 0.521 ± 0.171 (SCS_SD and Severity) to 0.846 ± 0.055 (SCS_LM and Severity), except for the null genetic association of SCS_SD with SCS_LM and SCS_150. Overall, phenotypic correlations between SCC traits were lower than their genetic counterparts.

Correlations of SCC traits with milk yield and composition. Results from bivariate analyses demonstrated unfavorable genetic correlations between milk yield and both SCS_SD (0.566 ± 0.246) and Infection (0.374 ± 0.213) (Table 4). Phenotypic and genetic correlations between SCC traits and fat, protein and casein percentages were generally very weak (0.004 to 0.200, in absolute value). Lactose percentage was lowly or moderately negatively correlated with all SCC traits, both at genetic and phenotypic level (-0.360 ± 0.181 to -0.064 ± 0.166). Milk urea nitrogen was positively genetically associated with SCS_LM (0.184 ± 0.125), SCS_150 (0.221 ± 0.132) and Severity (0.186 ± 0.176), and negatively genetically associated with SCS_SD (-0.278 ± 0.182) and Infection (-0.232 ± 0.208).

Correlations between SCC traits and udder type traits. Weak genetic correlations were estimated between SCC traits and udder type traits (Table 5). Fore udder attachment was negatively associated with SCS_150 (-0.209 ± 0.152) and SCS_SD (-0.190 ± 0.198), and udder support was negatively correlated with SCS_LM (-0.164 ± 0.187) and SCS_150 (-0.145 ± 0.202). Negative genetic correlations were assessed between udder depth and SCC traits, ranging from -0.304 ± 0.176 (udder depth and SCS_SD) to -0.189 ± 0.143 (udder depth and Severity). Positive genetic correlations were estimated between front teat length and SCS_SD (0.306 ± 0.210), Infection (0.233 ± 0.199) and Severity (0.267 ± 0.182). Moreover, positive genetic associations were obtained between rear udder height and Infection (0.206 ± 0.220), and rear udder width and Infection (0.143 ± 0.233).

Discussion

A strategy to decrease the incidence of mastitis in the farm is to breed for resistance to the disease (Ruegg, 2017). To this purpose, exploiting all information currently recorded in the framework of routine milk recording system is of great importance, given the difficulty of implementing direct recording of disease. In the present study we defined four alternative SCC traits, derived from TD data routinely collected at monthly intervals, and estimated their phenotypic and genetic relationships with milk yield, composition and udder type traits in Jersey cows. Alternative SCC traits, currently included in a novel udder health index of Italian Holsteins (Finocchiaro *et al.*, 2018), could possibly be considered in the national selection index of the Jersey breed, to select cows with improved resistance to mastitis. Figure 1 provides further evidence for the need of inclusion of SCC in the selection index. In fact, in the last years there has been an increase of SCS_LM, suggesting that current selection for udder type traits alone is not sufficient.

Heritability

Alternative SCC traits. To the best of our knowledge, this is the first study dealing with alternative SCC traits in Jersey breed. Thus, our results could be compared only with the existing literature on Holsteins. In the present study, novel SCC traits were heritable and expressed exploitable additive genetic variation (Table 2), implying the feasibility of their inclusion in genetic selection programs for mastitis resistance. Estimates of heritability of average SCS in early lactation (from 5 to 150 days in milk) were comparable with those (0.08 to 0.11) reported for Holstein cows (de Haas *et al.*, 2008; Windig *et al.*, 2010; Bobbo et al., 2018). Heritability of SCS_SD, a trait which describes SCC distribution during lactation and identified by Green *et al.* (2004) as a good predictor of clinical mastitis, was in agreement with estimates of 0.03 and 0.04 reported by Koeck *et al.* (2012a) and Bobbo *et al.* (2018), respectively. According to de Haas *et al.* (2008), Urioste *et al.* (2010) and Koeck *et al.* (2012a), traits that express excess of TD SCC above a predefined threshold are potential indicators of udder infection and thus interesting for indirect selection against mastitis. Infection and Severity, both associated with TD SCC greater than 400 000 cells/mL, showed heritability of about 0.06 (Table 2), similar to the results of Bobbo *et al.* (2018) for Italian Holsteins (0.057 and 0.047 for Infection and Severity, respectively).

Milk yield, composition and udder type traits. In the present study, heritabilities of milk yield and composition traits were moderate to high (Table 2), and generally in agreement with previous results in the same breed. For instance, Campos *et al.* (1994) reported heritability estimates of 0.327, 0.526 and 0.662 for milk yield, fat percentage and protein percentage, respectively. Roman *et al.* (2000) estimated heritabilities of 0.26 for milk yield and 0.53 for fat and protein percentages in first-parity Jerseys, and Missanjo *et al.* (2013) reported heritabilities of 0.38, 0.47 and 0.49 for milk yield, fat percentage and protein percentage, respectively. Sneddon *et al.* (2012) assessed heritabilities of 0.50 for milk yield, and 0.33, 0.58 and 0.64, for fat, protein and lactose percentages, respectively. Heritabilities of udder type traits agreed with findings of du Toit *et al.* (2012) for South African Jersey breed and were slightly lower than estimates of Gengler *et al.* (1997), who reported heritabilities of udder traits in the range from 0.20 to 0.30. Moreover, heritability estimates of udder type traits of the present study were consistent with those reported by Cassandro *et al.* (2015) for Holstein Friesian and Dal Zotto *et al.* (2007) for Brown Swiss cows.

Correlations

Correlations between SCC traits. Genetic correlations between alternative SCC traits have been reported only for Holstein cows (Windig *et al.*, 2010; Urioste *et al.*, 2012; Bobbo *et al.*, 2018) and thus findings of the current study could be compared only with the existing literature. Overall, our results demonstrated strong genetic correlations between SCC traits, with the only exception of SCS_SD, which was moderately correlated with traits indicating the presence of SCC peaks in the lactation (Infection and Severity) and uncorrelated with traits expressing mean values (SCS_LM and SCS_150). Similar results were obtained by Koeck *et al.* (2012a) and Bobbo *et al.* (2018) in Holsteins. Genetic correlations between SCS_LM and alternative SCC traits of the present study confirmed the strong associations reported by de Haas *et al.* (2008) between lactation average SCS and new SCC traits (i.e. SCS in early lactation, presence of at least one TD SCC >150 000 cells/mL and proportion of TD SCC >150 000 cells/mL).

Correlations of SCC traits with milk yield and composition. To the best of our knowledge, genetic correlations between alternative SCC traits and milk production and composition traits on Jersey cattle have been reported for the first time in the present study (Table 4). Thus, comparisons with the existing literature can be made considering the standard TD or lactation-average SCC or SCS. Our findings confirmed the association between high milk SCC and reduced milk production (weak negative phenotypic correlation with all SCC traits) and may suggest that high-producing cows are more susceptible to variation of SCC than cows with intermediate or low production (positive genetic correlation with SCS_SD and Infection). This hypothesis was supported also by Haile-Mariam *et al.* (2001) and Koivula *et al.* (2005), who observed unfavorable genetic correlations between SCC and milk production in first-parity Australian Holsteins and Finnish Ayrshires, respectively. Positive genetic correlations of SCS with milk yield and composition traits were estimated by Carlen *et al.* (2004) in Swedish Holstein cows; those authors reported genetic correlations of 0.22, 0.17 and 0.23 between lactation-average SCS, calculated as the arithmetic mean of monthly TD SCC from 5 to 150 d after calving, and 305-d milk, fat and protein yield, respectively. In the present study, lactose percentage showed the strongest correlations with SCC traits, negative both at phenotypic and genetic level. Therefore, as expected, increased milk SCC was associated with a reduction of lactose content. Negative genetic (phenotypic) correlations of -0.20 (-0.23) and -0.44 (-0.24) between lactose percentage and SCS were reported also by Miglior *et* *al.* (2007) in Canadian Holsteins and Stoop *et al.* (2007) in Dutch Holstein-Friesians, respectively. Moreover, Visentin *et al.* (2017b) estimated an average genetic correlation of -0.28 between lactose percentage and SCS in Irish dairy cows from several breeds, including Jersey, and crossbreds.

Correlations between SCC traits and udder type traits. Our estimates highlighted that cows with deep udders, loose attachments, weak ligaments and long teats were more susceptible to have an increase of SCC in milk, as suggested by the negative genetic correlations of alternative SCC traits with udder depth, fore udder attachment and udder support, and the positive genetic correlations with front teat length (Table 5). Interestingly, our findings confirmed previous results of Koeck *et al.* (2012b) on alternative SCC traits in Canadian Holsteins. In fact, those authors reported moderate negative genetic correlations between alternative SCC traits (i.e. mean SCS in early lactation, standard deviation of SCS and presence of at least one TD SCC above 500 000 cells/mL) and udder type traits (udder depth and fore udder attachment), in the range from -0.31 (standard deviation of SCS and udder depth) to -0.15 (standard deviation of SCS and fore udder attachment). Results of the present study agreed with previous findings of Dube *et al.* (2009) in Jersey cattle; those authors suggested that deep, loosely attached udders were associated with high SCS, as they are possibly at greater risk of injury and contamination due to closeness to the ground. Moreover, Rogers *et al.* (1991) reported that longer teats were more prone to injury during handling and milking. An increased risk of subclinical mastitis in Jersey cows with udders close to the ground and long front teats have been observed also by Akdag *et al.* (2017).

Conclusions

Alternative SCC traits analysed in the present study showed genetic variation which is exploitable for breeding purposes. Estimated genetic correlations between novel SCC traits and traits currently included in the selection index (i.e. milk yield, protein percentage, fore udder attachment, udder support and udder depth) would help to identify the best SCC traits to be used as indicators of intramammary infection and thus for selection to improve udder health in the Italian Jersey breed.

Also, selection accuracy for mastitis resistance may be increased by combining udder type and SCC traits into an udder health index, using genetic parameters estimated in the current study. Further work is required to assess the association between the new SCC traits and clinical mastitis events.

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Table 1. Number of records (N), mean, standard deviation (SD), minimum and maximum of lactation-mean somatic cell score (SCS_LM), alternative somatic cell count (SCC) traits, lactation-mean milk yield and composition, and udder type traits of first-parity Jersey cows.

Trait	N	Mean	SD	Minimum	Maximum
SCS_LM, units	12 754	3.09	1.12	-0.96	8.42
Alternative SCC traits					
SCS_150, units	12 732	3.01	1.22	-1.22	9.03
SCS_SD, units	12 754	1.10	0.59	0.11	4.26
Infection	12 754	0.43	0.49	0	1
Severity	12 754	0.11	0.18	0	1
Milk yield, kg/d	12 754	19.46	4.15	4.32	40.55
Milk composition					
Fat, %	12 754	5.03	0.65	2.46	7.71
Protein, %	12 754	3.97	0.28	2.91	4.95
Casein, %	8259	3.08	0.25	2.18	5.00
Lactose, %	10 781	4.85	0.13	3.96	5.28
Milk urea nitrogen, mg/dL	8135	23.56	6.30	2.00	45.42
Udder type traits, score					
Fore udder attachment	9482	23.66	6.39	1.00	45.00
Rear udder height	9482	26.38	6.04	2.00	48.00
Rear udder width	9482	30.16	5.93	2.00	49.00
Udder support	9482	27.47	5.98	1.00	49.00
Udder depth	9482	25.59	6.82	2.00	50.00
Front teat placement	9482	23.37	5.29	1.00	45.00
Front teat length	9482	22.38	6.03	2.00	48.00

SCS_150 = average SCS in early lactation; SCS_SD = standard deviation of SCS; Infection = a binary trait indicating absence (0) or presence (1) of at least one test-day SCC above 400 000 cells/mL; Severity = ratio of the number of test-day SCC above 400 000 cells/mL to total number of test-days in the lactation.

Table 2. Additive genetic variance (σ^2_a), residual variance (σ^2_e), coefficient of additive genetic variation (CV_a) and heritability (h^2; SE within parentheses) of lactation-mean somatic cell score (SCS_LM), alternative somatic cell count (SCC) traits, lactation-mean milk yield and composition, and udder type traits of first-parity Jersey cows.

Trait	σ^2_a	σ^2_e	CV_a, %	h^2 (SE)
SCS_LM, units	0.135	0.857	11.8	0.136 (0.022)
Alternative SCC traits				
SCS_150, units	0.136	1.068	12.1	0.113 (0.021)
SCS_SD, units	0.011	0.272	9.4	0.038 (0.015)
Infection	0.013	0.208	26.5	0.058 (0.017)
Severity	0.002	0.024	38.2	0.066 (0.017)
Milk yield, kg/d	3.170	5.414	9.1	0.369 (0.038)
Milk composition				
Fat, %	0.160	0.102	8.2	0.610 (0.034)
Protein, %	0.034	0.022	4.6	0.604 (0.034)
Casein, %	0.018	0.022	4.3	0.444 (0.036)
Lactose, %	0.007	0.007	1.7	0.486 (0.037)
Milk urea nitrogen, mg/dL	2.585	6.961	6.6	0.271 (0.035)
Udder type traits, score				
Fore udder attachment	5.666	31.181	10.2	0.154 (0.027)
Rear udder height	2.823	29.994	6.5	0.086 (0.023)
Rear udder width	1.905	24.175	4.5	0.073 (0.022)
Udder support	2.824	27.219	6.1	0.094 (0.027)
Udder depth	7.216	30.688	10.4	0.190 (0.028)
Front teat placement	2.206	24.448	6.3	0.083 (0.021)
Front teat length	2.847	28.141	7.7	0.092 (0.022)

SCS_150 = average SCS in early lactation; SCS_SD = standard deviation of SCS; Infection = a binary trait indicating absence (0) or presence (1) of at least one test-day SCC above 400 000 cells/mL; Severity = ratio of the number of test-day SCC above 400 000 cells/mL to total number of test-days in the lactation.

Table 3. Genetic correlations (above diagonal; SE within parentheses) and phenotypic correlations (below diagonal) of lactation-mean somatic cell score (SCS_LM) and alternative somatic cell count traits of first-parity Jersey cows (*n* = 8124).

Trait	SCS_LM	SCS_150	SCS_SD	Infection	Severity
SCS_LM	-	0.986 (0.014)	0.000 (0.207)	0.808 (0.074)	0.846 (0.055)
SCS_150	0.894	-	-0.027 (0.222)	0.783 (0.098)	0.802 (0.083)
SCS_SD	0.215	0.186	-	0.589 (0.149)	0.521 (0.171)
Infection	0.565	0.519	0.610	-	0.989 (0.014)
Severity	0.704	0.628	0.454	0.702	-

SCS_150 = average SCS in early lactation; SCS_SD = standard deviation of SCS; Infection = a binary trait indicating absence (0) or presence (1) of at least one test-day somatic cell count above 400 000 cells/mL; Severity = ratio of the number of test-day somatic cell count above 400 000 cells/mL to total number of test-days in the lactation.

Table 4. Genetic (r_a; SE within parentheses) and phenotypic (r_p) correlations of lactation-mean somatic cell score (SCS_LM) and alternative somatic cell count traits with lactation-mean milk yield and composition traits of first-parity Jersey cows (*n* = 5601).

Trait	SCS_LM		SCS_150		SCS_SD		Infection		Severity	
	r_a (SE)	r_p	r_a (SE)	r_p	r_a (SE)	r_p	r_a (SE)	r_p	r_a (SE)	r_p
Milk yield	-0.052 (0.117)	-0.100	0.004 (0.128)	-0.084	0.566 (0.246)	-0.028	0.374 (0.213)	-0.056	0.122 (0.176)	-0.055
Milk composition										
Fat	0.073 (0.099)	0.025	0.053 (0.108)	0.024	-0.109 (0.168)	-0.020	-0.062 (0.173)	0.004	0.200 (0.163)	0.013
Protein	0.030 (0.101)	0.084	-0.025 (0.110)	0.064	-0.083 (0.161)	0.033	-0.055 (0.172)	0.044	0.084 (0.151)	0.063
Casein	-0.053 (0.111)	0.033	-0.111 (0.121)	0.019	-0.032 (0.181)	0.019	-0.072 (0.197)	0.011	0.087 (0.174)	0.021
Lactose	-0.277 (0.102)	-0.347	-0.287 (0.113)	-0.295	-0.064 (0.166)	-0.099	-0.360 (0.181)	-0.227	-0.339 (0.152)	-0.279
Milk urea nitrogen	0.184 (0.125)	-0.080	0.221 (0.132)	-0.076	-0.278 (0.182)	-0.056	-0.232 (0.208)	-0.067	0.186 (0.176)	-0.074

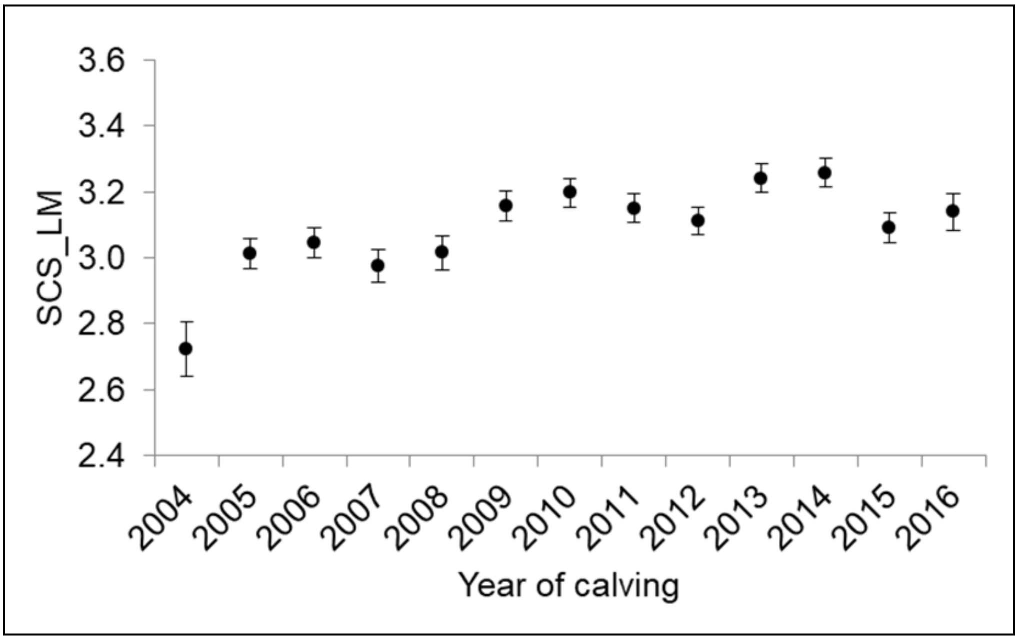
SCS_150 = average SCS in early lactation; SCS_SD = standard deviation of SCS; Infection = a binary trait indicating absence (0) or presence (1) of at least one test-day somatic cell count above 400 000 cells/mL; Severity = ratio of the number of test-day somatic cell count above 400 000 cells/mL to total number of test-days in the lactation.

Table 5. Genetic (r_a; SE within parentheses) and phenotypic (r_p) correlations of lactation-mean somatic cell score (SCS_LM) and alternative somatic cell count traits with udder type traits of first-parity Jersey cows (*n* = 6195).

Trait	SCS_LM		SCS_150		SCS_SD		Infection		Severity	
	r_a (SE)	r_p	r_a (SE)	r_p	r_a (SE)	r_p	r_a (SE)	r_p	r_a (SE)	r_p
Fore udder attachment	-0.114 (0.148)	-0.047	-0.209 (0.152)	-0.058	-0.190 (0.198)	-0.070	-0.105 (0.184)	-0.047	-0.151 (0.157)	-0.055
Rear udder height	0.072 (0.181)	-0.028	0.064 (0.190)	-0.040	0.086 (0.238)	-0.029	0.206 (0.220)	-0.006	0.081 (0.193)	-0.003
Rear udder width	0.007 (0.182)	-0.003	0.091 (0.206)	-0.014	0.053 (0.254)	-0.029	0.143 (0.233)	-0.004	-0.108 (0.207)	-0.007
Udder support	-0.164 (0.187)	-0.054	-0.145 (0.202)	-0.064	0.171 (0.253)	-0.042	-0.096 (0.222)	-0.042	-0.107 (0.199)	-0.048
Udder depth	-0.228 (0.041)	-0.061	-0.215 (0.138)	-0.052	-0.304 (0.176)	-0.075	-0.196 (0.162)	-0.076	-0.189 (0.143)	-0.075
Front teat placement	-0.019 (0.173)	-0.028	-0.063 (0.194)	-0.035	-0.018 (0.257)	-0.019	0.083 (0.216)	-0.010	0.026 (0.198)	-0.026
Front teat length	0.074 (0.171)	0.022	0.042 (0.189)	0.018	0.306 (0.210)	0.006	0.233 (0.199)	0.031	0.267 (0.182)	0.024

SCS_150 = average SCS in early lactation; SCS_SD = standard deviation of SCS; Infection = a binary trait indicating absence (0) or presence (1) of at least one test-day somatic cell count above 400 000 cells/mL; Severity = ratio of the number of test-day somatic cell count above 400 000 cells/mL to total number of test-days in the lactation.

Figure 1. Least squares means of lactation-mean somatic cell score (SCS_LM) across years of calving of first-parity Jersey cows (*n* = 12 754).



Chapter 5

Estimation of economic values for milk production traits and somatic cell score in Italian Jersey cattle breed

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Abstract

Economic values (EV) of milk production traits and somatic cell score (SCS) were reported for Italian Jersey cattle (IJ). Two different methods were compared; the first used a non-linear function of the penalty applied in the milk price respect to the average of SCS, the second defined SCS costs as the sum of frequency of each level of SCS multiplied by its penalty. Economic values were estimated to simulate the transformation of milk into Grana Padano cheese, one of the most popular dairy products in Italy, in two different dairy plants. At 5 SCS units no penalties/premium were assessed. In both dairy plants at ≤ 3 SCS units premium was constantly at €0.012/kg; differences in penalty trends were present after 5 SCS units. Economic values for 305-d fat, protein and milk carrier production of both dairy plants were €2.173/kg, €8.664/kg and €-0.042/kg, respectively. Economic values for SCS level in dairy plant 1 were €21.519 and €37.093 with method 1 and 2, respectively; in dairy plant 2 were €8.126 and €16.274, respectively. Method 2 showed a double economic weight respect to Method 1. In conclusion, the relative weight of SCS, should be range from 2% to 8% in an aggregate index for a milk production of Jersey cattle.

Keywords: economic value; milk production; somatic cell score; Jersey breed; Grana Padano cheese.

Introduction

Breeding program starts with the definition of the breeding goal, which generally is to improve the profit of the livestock production system (Harris *et al.*, 1994). Once the breeding goal is defined, the breeding objective is formulated as a combination of breeding values and economic values of important traits affecting profitability. Moreover, to implement any animal breeding program, it is important to delineate the production context of the animals of interest to determine which traits are of economic interest and which will be measured (Hazel, 1943).

In Italy more than 70% of milk produced is used for cheese making, and approximately 50% of this fraction is used for Protected Designation of Origin (PDO) products like Grana Padano cheese (GP; Pretto *et al.,* 2013). Grana Padano is an extra-hard cheese with a long ripening period (from a minimum of 9 months up to 20 and more, depending on product category). It is produced in a defined area in Northern Italy, using partly skimmed raw milk, calf rennet and natural whey cultures of thermophilic lactic acid bacteria as a starter (European Commission, 2011). The GP production represents 24% of the volume of total milk produced in Italy, and 38% of the total Italian PDO cheese production (CLAL, 2018). The production of GP has increased by 2.41% from 2016 to 2017, reaching 190 353 tons of cheese; cheese wheels recorded in July 2018 were 353 587, up 4.75% compared to 2017 (CLAL, 2018). More than one third of this production is exported to Germany, US, France and to the rest of the world (CLAL, 2018).

In countries where there is differentiated payment for milk due to its quality, one of the breeding objectives is to select animals of high merit for milk, fat and protein production (Cassandro *et al.,* 2016) and low genetic merit for somatic cell count (SCC; Kadarmideen and Pryce, 2001). Progeny test and a selection index giving large emphasis on milk and protein production per cow were defined in Italian Jersey cattle breed (IJ), such as Index of Quality in Jersey cows (IQJ). In IQJ only three udder traits (i.e. fore udder attachment, udder support, udder depth) other than production traits (i.e. milk and protein production) are included (ANAFI, 2018). The development of breeding programs involving IJ is necessary to improve quantity and quality of milk production to insure the profitability of this breed introduced in Italy in the early 1980s. Italian farmers appreciate Jersey cows for their higher contents of fat and protein (Biffani *et al.,* 2003), superior milk coagulation properties and cheese yield (Visentin *et al.,* 2017) compared to Holstein Friesian (HF) cows. Despite this, mastitis in Jersey cows is one of the most critical disease, as well as in Holsteins (Prendiville *et al.,* 2010). In 1991 the IJ herd book was established; since then, the number of registered cows has increased and nowadays there are almost 7000 IJ registered in 727 herds (ANAFI, 2018).

The quality of milk is the key factor for the optimal cheese production, and it is mainly driven by its composition, level of SCC and milk coagulation properties (Cassandro *et al.*, 2008). Moreover, SCC has been considered as indicator of both clinical and subclinical mastitis, that worldwide causes serious economic impact in the dairy industry (Halasa *et al.*, 2007). Decrease in milk yield and quality, reduced lactation persistency, early culling, veterinary treatments, increased labour and replacement costs are consequences of mastitis to be added to the suffering of the animal (Seegers *et al.*, 2003). Still, milk from infected or treated cows can cause problems during milk processing, e.g. in cheese manufacturing (Le Maréchal *et al.*, 2011). Somatic cell count has been included in the selection index of most countries with a negative economic value in an attempt to improve genetic resistance to intramammary infections (Sadeghi-Sefidmazgi *et al.*, 2011). Currently, SCC is widely, easily and cheaply recorded in many countries as part of the milk recording routine in dairy herd improvement programs; it is measured on a continuous scale and rather normally distributed once the values have been log-transformed. The log-transformed SCC, i.e. somatic cell score (SCS) (Schutz and Powell, 1993), has a proper economic value (EV) in those industries where there are penalties for high SCS in supplied milk.

To ensure maximal benefit for dairy cattle farmers, not only genetic parameters, but also economic values (EVs) of production and quality traits are required. Indeed, EV for SCS is needed to determine the optimal emphasis on SCS trait in selection relative to other traits and to quantify economic benefits including SCS in breeding programs. Due to their importance, there are even more interests to include production traits and level of SCS (LSCS) in milk payment systems and in breeding selection index (Sadeghi-Sefidmazgi *et al.*, 2011).

Few studies (Charfeddine *et al.*, 1997; Sadeghi-Sefidmazgi *et al.*, 2011) have derived EVs for LSCS based on its relationship to price payment systems. In particular, the effect on payment system of these traits has been rarely investigated in Jersey cows. Therefore, the aim of this study was to estimate the EVs for milk production traits and LSCS in IJ dairy cattle for destination of milk into GP manufacture.

Materials and Methods

Production parameters

Table 1 presents representative values of quantity and quality of milk production of Jersey cows in Italy. In 2017 the Italian Jersey cow produced 6521 kg milk in 305 d with 4.93% fat and 3.94% protein. Casein content was calculated to be equal to 3.07%, assuming a protein-to-casein ratio of 0.78 (Norman *et al.,* 1991). Average 305-d milk carrier production, equal to 5942.59 kg, was calculated as milk production – (fat production + protein production). Means of SCC (234 cellsmL10^{-3}) and SCS (3.02 units) of IJ reported in Table 1 were retrieved from Roveglia *et al.* (2018). Average body weight (BW) was assumed at 454 kg (Dalla Riva *et al.*, 2014).

Grana Padano cheese industry parameters, costs, and prices considered in this study are reported in Table 2. In this study, the 9 months ripened GP was considered, made with partially skimmed milk, with contents of fat, protein and casein of 3.32%, 4.26% and 3.32%, respectively.

Costs of GP production included prices paid for electricity, commercialization, labour, depreciation charge, raw materials, and other general costs. In particular, expense for milk collection, obtained from Centro di Ricerche Produzioni Animali (CRPA, 2015) and included as a function of milk production, was equal to €0.005/kg of milk. Cheese processing cost provided by the standard GP was estimated at €1.77/kg of cheese, i.e. around 25% of the price of 1 kg of cheese.

Average of GP price was valued €7.08/kg, retrieved from Italian dairy market (CLAL, 2015-2016-2017), as well as prices of whey (€0.013/kg) and butter (€2.73/kg). Revenues per kg of whey and butter were estimated 0.18% and 38.6% of the price of 1 kg of cheese, respectively.

Different cheese-making processes for different type of cheese were developed in Italy; in particular the GP production follows a strict manufacture protocol according to European regulations (no. 2081/92 and no. 1170/96) and the GP Consortium. Basically raw milk must be obtained from cows milked twice a day in dairy farms located in the defined GP production area in Northern Italy (European Commission, 2011). To summarize, milk is stored in shallow settling tanks for about 12 h so that the fat can naturally rise to the surface (natural creaming). This process is driven to obtain a partially skim milk with fat-to-casein ratio (F:C) of about 1. The cream resulting from the natural creaming is usually destined for the production of butter. Partially skim milk is then transferred to copper bell-shaped vats that contain 1000 kg of milk and processed according to the following steps: (1) addition of natural whey starter, (2) heating of milk to 30°C; (3) addition of powder calf rennet, (4) breaking up of the curd, and (5) cooking of the curd until temperature reaches 53.5°C. Two wheels are obtained for each vat. After 2 d of drainage, the wheels are placed into brine for approximately 3 weeks and then transferred to the warehouse. The product cannot be labelled as PDO GP until a minimum ripening period of 9 months, under controlled conditions of temperature and humidity, and has passed the official quality control steps (D'Incecco *et al.*, 2016). Cow feeding ration is based on fresh or preserved (as hay or silage) forages, and concentrates; the ratio between forage and concentrate, on dry matter (DM) basis, has to be lower than 1 in the daily ration. The typical ration in terms of DM is based on 60% forages and 40% concentrates (Cassandro *et al.*, 2016). At least 50% DM of the whole daily ration must be produced within the defined production area. Addition of lysozyme to milk is accepted up to a maximum of 25 g/t milk.

Inputs for the profit function

The profit function (Π) was calculated as:

$$\Pi = R - C,$$

where R are revenues and C are costs per cow per year. Revenues assumed in this study derived from selling of GP, butter and whey and only costs for milk collection, cheese processing and feed related to milk production were considered.

Revenues from milk products were calculated in a nonquota restriction and nonsaturated market as follows (Wolfová *et al.*, 2007):

$$R = (P_{cheese} \times Y_{cheese} \times MY) + (P_{butter} \times Y_{butter} \times MY) + (P_{whey} \times Y_{whey} \times MY),$$

And costs were calculated as:

$$C = (C_{cheese} \times Y_{cheese} \times MY) + (C_{collection} \times MY) + C_{maintenance} + C_{carrier} + C_{fat} + C_{protein},$$

where P_{cheese}, P_{butter}, and P_{whey} are prices (€) per kilogram of cheese, butter, and whey, respectively; Y_{cheese}, Y_{butter}, and Y_{whey} are yields of cheese, butter, and whey, respectively, expressed as kilogram of product per 1 kg of milk processed; MY is the annual milk production (kg) per cow; C_{cheese} are costs (€/kg of cheese) for cheese processing; $C_{collection}$ are costs for milk collection from dairy farm to dairy plant (€/kg of milk); and $C_{maintenance,}$ $C_{carrier}$, C_{fat} and $C_{protein}$ are annual feed costs (€/cow) for maintenance, milk carrier, milk fat, and milk protein, respectively.

Cheese yield was estimated according to Aleandri *et al.* (1989), corrected for a coefficient to calculate Y_{cheese} on full milk:

$$Y_{cheese} = [2.83329 + 0.9877 \times \%Fat_{SM} + 0.179 \times (\%Protein_{SM})^2] \times (100 - Y_{cream}),$$

where $\%Fat_{SM}$ and $\%Protein_{SM}$ are fat and protein contents in partially skim milk, respectively; and Y_{cream} is the amount of cream obtained from natural creaming of full milk. The Y_{cream} was calculated as follows:

$$Y_{cream} = [\%Fat_{FM} - (\%Casein_{FM} \times F{:}C)] / (\%Fat_{cream}/100),$$

where $\%Fat_{FM}$ and $\%Casein_{FM}$ are fat and casein content of full milk, respectively (Table 1); $\%Fat_{cream}$ is the percentage of fat in the cream, assumed as 25%; and F:C was assumed to be 1.00, following parametrs of GP Consortium (2011). The amount of butter (Y_{butter}) from full milk was estimated using the following equation:

$$Y_{butter} = Y_{cream} \times (\%Fat_{cream}/\%Fat_{butter}),$$

where $\%Fat_{butter}$ is the percentage of fat in the butter, which was set to 82%. The amount of whey (Y_{whey}) from full milk was estimated as:

$$Y_{whey} = 1 - Y_{cheese} - Y_{butter}.$$

Feed costs for maintenance were calculated as:

$$C_{maintenance} = 365 \times [(Fm + Ac) / k_m] \times C_{MJME},$$

where Fm is the fasting metabolism energy requirements per day calculated as $Fm = 0.53 \times (BW/1.08)^{0.67}$; Ac is the metabolic energy (ME) required for activity calculated as $Ac = 0.016 \times BW$; k_m = is the efficiency of ME used for maintenance assumed as $k_m = 0.71$; and C_{MJME} is the cost per MJ of ME. The energy level of the ration was 11.06 MJ of ME/kg of DM.

The costs of milk carrier, fat, and protein were calculated as:

$$C_{carrier} = [(MCY \times 0.948) / k_l] \times C_{MJME},$$

$$C_{fat} = [(FY \times 37.60) / k_l] \times C_{MJME},$$

$$C_{protein} = [(PY \times 20.90) / k_l] \times C_{MJME},$$

where MCY, FY, and PY are the annual productions per cow of milk carrier, fat, and protein; k_l is the efficiency of ME used for milk production assumed as $k_l = 0.63$ (Cassandro *et al.,* 2016).

Estimation of Economic Value

Milk carrier, fat, and protein. The EV of trait I, the profit change per cow per year, for one unit of variation in the genetic merit of the trait i, keeping all other parameters constant. It was obtained according to (Wolfova *et al.,* 2007):

$$EV_i = \Pi_{milk} / \Pi_i ,$$

where *i* is milk carrier, fat, or protein yield. The relative contribution of trait *i* to the breeding objective was calculated as the relative standardized economic weight (rEW) according to Komlosi *et al.* (2010):

$$rEW_i = 100 \times |EV_i \times \sigma_{gi}| / \sum_i |EV_i \times \sigma_{gi}|$$

where where *i* is milk carrier, fat, or protein yield, and σg_i is the genetic standard deviation of trait *i*.

Genetic standard deviations for fat, protein and milk carrier production of IJ were retrieved from the Italian National genetic Evaluation Forms of Interbull of Jersey breed (2017) and were equal to 24.913, 17.383 and 475.113 kg, respectively. Both genetic standard deviations of LSCS (0.526) were retrieved from Roveglia *et al.* (2018).

Somatic cell score. Costs associated with LSCS results from the penalty applied in the milk price according to the payment scheme for LSCS in two different italian dairy plants. The actual payment system gives discontinuous and different penalties in the payment for different classes of LSCS within dairy factory in Italy. This is an example of a typical Italian dairy scenario in which each dairy plant arranges a plan for milk quality payment system.

Two methods were defined to express LSCS costs from the discontinued penalty system of the milk, following the level of somatic cell concentration. In the method 1 (M1), similarly to Weller *et al.* (1996), the penalty applied in the milk price was defined as a non-linear function with respect to average SCS. The EVs of LSCS with M1 (a_{LSCS}) are given by the following expressions in dairy plant 1 and 2 considered in this study, respectively:

$$a_{\text{LSCS dairy plant 1}} = 0.0896 - 2 \times (0.0247) \times \text{SCS} + 3 \times (0.0023) \times (\text{SCS})^2$$

$$a_{\text{LSCS dairy plant 2}} = -1 \times (0.0655) + 2 \times (0.0165) \times \text{SCS} + 3 \times (-0.0012) \times (\text{SCS})^2$$

The second method (M2) follows a threshold methodology used by Meijering (1986), applied to LSCS by Charfeddine *et al.* (1997); it defined costs of LSCS as the sum of the frequency of each LSCS multiplied by its penalty. The EV was then defined by determining the effect of an increase in the herd LSCS on the proportion of cows producing milk in each SCS class.

The cost of LSCS (CL_{SCS}) was calculated as:

$$C_{LSCS} = \sum_{i=1}^{n} [\phi(z_i) - \phi(z_{i-1})]p_1$$

where:

n=number of thresholds (i=1, 2 and 3);

$$z_i = \frac{(t_i - \mu)}{\sigma}\text{; and}$$

$$z_i = \frac{(t_{i-1} - \mu)}{\sigma}.$$

ϕ (z_i) = the normal cumulative distribution function (probability of the variable LSCS has a value less than threshold value, z_i) is expressed as:

$$\phi(z) = Pr\ (Z < z) = \int_{-\infty}^{z} \frac{1}{\sqrt{2\pi}} e^{-z^2/2}\, \delta z$$

t_i= threshold that separates SCS class i from class i+1;

p_i= the penalty associated with LSCS;

μ = average SCS;

σ = standard deviation SCS;

e = base of the natural logarithms base e;

and

π = 3.14159365359.

The EV for LSCS (a_{LSCS}) based on M2 was calculated as:

$$a_{LSCS} = -\frac{1}{\sigma}\left[\sum_{i=1}^{n} \phi\,(Z) \times (p_i - p_{i-1})\right]$$

where:

p_i, σ = was defined before;

ϕ (Z) = is the standard normal density function that shows the vertical height on the normal distribution, and can be expressed as:

$$\phi(Z) = \frac{\delta\phi\,(Z)}{\delta Z} = \frac{1}{\sqrt{2\pi}}e^{-z^2/2}$$

where:

e = natural logarithm base e; and other terms were previously defined.

Results

In this study, the total revenue was €4383/cow per year, comprised of incomes from cheese (€3915), butter (€394) and whey (€74) with proportions shown in Figure 1a. The total cost was €2089/cow per year, in which feed, cheese processing and milk collection costs were €1079, €979 and €32, respectively, with proportions shown in Figure 1b. The net profit, therefore, was €2294/cow per year. The value of milk, milk revenue per kilogram of milk, was €0.67/kg. Two different dairy herds (input data) and payment systems (scenarios) were considered for simulating EVs and rEWs.

Economic values

Table 3 shows the EVs of milk production traits and LSCS at basic situation for free market under a non-quota restriction. Economic values for 305-d fat and protein production of both dairy plants considered in this study were positive and equal to €2.173/kg and €8.664/kg, respectively. Instead EV of milk carrier production was slightly negative and equal to €-0.042/kg.

Regarding dairy plant 1, EV of LSCS obtained with M1 was €21.519, accounting for 4.796% (rEW) on the total number of traits considered, whereas EV of LSCS obtained with M2 was €37.093, with a rEW of 7.99%. In dairy plant 1, rEWs relative to fat, protein and milk carrier production calculated with M1 were 22.937%, 63.812% and 8.455%, respectively; whereas rEWs relative to fat, protein and milk carrier production based on M2 were equal to 22.168%, 61.671% and 8.171%, respectively.

In dairy plant 2, EV of LSCS obtained with M1 was €8.126, with rEW of 1.867 % on the total number of traits considered, whereas EV of LSCS obtained with M2 was €16.274, with rEW of 3.670%. In dairy plant 2, rEWs relative to fat, protein and milk carrier production calculated with M1 were 23.643%, 65.775% and 8.715%, respectively; whereas rEWs relative to fat, protein and milk carrier production based on M2 were equal to 23.209%, 64.567% and 8.555%, respectively.

Figure 2 illustrates the penalty functions applied for the milk price in function of LSCS; in both cases the obtained function was non-linear. No penalties or premiums were found when LSCS was equal to 5 units. Despite the premium was constantly at €0.012/kg when LSCS was equal or less than 3 units in both dairy plants, differences in penalty trends were present after 5 units of LSCS. In particular, the penalty remained constant at €0.002 /kg for dairy plant 2, while increased exponentially up to more than 6 LSCS for dairy plant 1. The R-square of the model is equal to 0.9995 and 0.9906 in dairy plant 1 and 2, respectively.

Discussion

The total revenue calculated for a representative Italian Jersey cow was €4383/cow per year, which is lower than the value calculated of €5454/cow per year for a Holstein cow (Cassandro *et al.,* 2016), when milk was processed to same dairy products simulated in this study. This is expected because the volume of milk produced by the Holstein cow (9072 kg) simulated by Cassandro et al. (2016) was greater that the volume of milk simulated for the Jersey cow (6521 kg). However, the value of milk from the Holstein cow was €0.60/kg, which is smaller than €0.67/kg from the Jersey cow. This greater value of the Jersey milk reflects the higher concentration of fat, protein and casein in the Jersey cow, which better suitability for cheese manufacturing, if compared to Holstein (Pretto *et al.,* 2013; Visentin *et al.,* 2017).

In Italy, there is not a unique payment system for milk, indeed, several buyers having different criteria and traits considered for payment are present. Moreover, differences in milk price determination are also present between and within regions (CLAL, 2018).

Generally, the existing differences between rEWs of dairy plant 1 and 2 were related to both equations and EVs used for the milk payment calculation. The EVs in ascending order belonged to protein, fat, and milk carrier and they were assumed equal in the two dairy plants. In fact, the greatest rEW was computed for protein, confirming this component to have the greatest impact on milk revenue, as reported by Gwaza *et al.* (2018). Protein fraction is mainly composed by casein micelles, which are favourably related to coagulability of milk and cheese yield (Cassandro et al., 2008). In both dairy plants and with both methods, the EVs of fat just accounted on average for 25% of protein EVs and it was very similar to the value (24%) of Cassandro *et al.* (2016). Generally, in agreement with this finding, the rEW of fat was 36% of protein rEW, in an intermediate position between values reported by Cassandro *et al.* (2016) and Krupová *et al.* (2016b) in Holstein, who found fat rEW to be 30 and 47% of protein rEW, respectively. Moreover, a greater emphasis was attributed to protein rather than to fat content also in Pinzgau dual-purpose breed (Krupová *et al.*, 2016a), for which this ratio was 48%. The differences have to be attributed to the breed-specific breeding goals, the milk composition required by factories, and the final milk destination. In the present study, milk carrier EV was considered as negative, confirming that both the considered systems were penalizing milk volume, promoting milk quality. In fact, the milk carrier usually has EV equal or close to zero worldwide (Sneddon *et al.*, 2013), with values equal to 0.027, 0.103, and 0.124 in studies from Italy, Czech Republic and Slovak, respectively (Cassandro *et al.*, 2016; Krupová *et al.* 2016a, 2016b). A negative emphasis for milk carrier (referred to milk volume) is also used in payment system of Fonterra, the most important dairy company of New Zealand. This payment system is known as 'A+B-C', where A, B, and C are the values for fat, protein, and milk volume, respectively (Sneddon *et al.*, 2013).

Within-system EVs of LSCS differed, in particular, in dairy plant 1, the EV of LSCS calculated with M1 was 58% of that determinate with M2, and in dairy plant 2 the EV of LSCS estimated with M1 was 50% of that assessed with M2. Also rEWs of LSCS differed between methods and within-system, in both dairy plants rEWs differed of about 50%, using M1 or M2. The rEW was greater when M2 was used for LSCS in both dairy plants, suggesting that more emphasis is given to milk SCS when a threshold method, as M2, is used. However, rEWs of milk, fat, and protein were similar between dairy plants (Table 3). Comparisons with values reported in the literature are difficult, because there are breed differences, different milk uses and investigated traits. However, this evidences that, according to milk buyers' applied criteria for penalization of SCS/SCC, a relevant variability exists for the ex-farm milk price (Figure 2). Indeed, the penalty extent when LSCS > 5.00 was stronger in M2 rather than in M1, suggesting a more severe and less tolerant payment system for M2, when compared to M1 one. As stated by Charfedinne *et al.* (1997), an overall best profit function unique for all systems does not exist, indeed specific adjustments are required in order to better fit each country-, product-, and economic-systems.

Conclusions

In this study was to estimate, for the first time, the EVs of milk traits including SCS for Italian Jersey breed. Results showed that high LSCS milk is more penalized in threshold model system (M2), if compared to mean SCS-dependent system (M1). In fact, even if these results did not directly estimate the EV for mastitis, the futuristic purpose in Italian Jersey would be to include SCS in the breeding goal, in order to reduce susceptibility to mastitis in next generations of cows. Finally, a relative weight of SCS, should be range from 2% to 8% in an aggregate index for milk production of Jersey cattle.

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Table 1. Parameters of milk production and somatic cell count in Italian Jersey cattle breed.

Parameter	Mean
305-d milk production, kg	6521[a]
Fat, %	4.93[a]
Protein, %	3.94[a]
Casein, %	3.07[b]
305-d fat production, kg	321.5
305-d protein production, kg	257.0
305-d milk carrier production, kg	5942.6[c]
SCC, cellsmL 10^{-3}	234[d]
SCS, units	3.02[d]

[a] ANAFI (2018). http://www.anafi.it/jersey/Statistiche/MedieProduzioniNazionali2016.htm
[b] Assuming a protein to casein ratio of 0.78 (Norman *et al.*, 1991).
[c] Calculated as milk production – (fat production + protein production).
[d] Roveglia *et al.* (2018). SCS = somatic cell score, calculated as 3 + $\log_2$(SCC/100 000), where SCC is somatic cell count.

Table 2. Parameters of Grana Padano cheese industry.

Parameter		Value
Grana Padano cheese		
	Type of cheese	Hard
	Type of milk used	Partially skimmed
	Ripening, mo	9
	Fat in partially skim milk, %	3.32
	Protein in partially skim milk, %	4.26
	Casein in partially skim milk, %	3.32
	Fat-to-casein ratio for partially skim milk	1
	Fat in the cream, %	25
	Fat in the butter, %	82
	Cheese yield, kg/100 kg of milk	8.66
	Cream yield, kg/100 kg of milk	7.43
	Butter yield, kg/100 kg of milk	2.26
	Whey yield, kg/100 kg of milk	89.08
Costs		
	Milk collection, €/kg of milk	0.005[a]
	Cheese processing, €/kg of cheese	1.77[a]
Prices, €/kg		
	Cheese	7.08[b]
	Whey	0.013[b]
	Butter	2.73[b]

[a] CRPA(2015). Grana Padano (CRPA, 2015), http://www.crpa.it/media/documents/crpa_www/Pubblicazi/Opuscoli-C/Archivio_2015/CRPA_1_2015

[b] Average of prices retrieved from CLAL (2015-2016-2017).

Table 3. Economic values (EV, €/unit of the trait) and relative economic weight (rEW, %) of production traits and somatic cell score in Italian Jersey cattle breed in two different dairy factories, dairy plant 1 and dairy plant 2, using two different methods based on Charfeddine *et al.*, (1997). Relative economic weight calculated with Method 1 and Method 2 refers to rEW_1 and rEW_2, respectively.

Trait	σ_g	Dairy plant 1			Dairy plant 2		
		EV	rEW_1[a]	rEW_2[a]	EV	rEW_1[a]	rEW_2[a]
305-d fat production, kg	24.913[b]	2.173	22.937	22.168	2.173	23.643	23.209
305-d protein production, kg	17.383[b]	8.664	63.812	61.671	8.664	65.775	64.567
305-d milk carrier production, kg	475.11[b]	-0.042	8.455	8.171	-0.042	8.715	8.555
LSCS method 1, unit	0.526[c]	21.519	4.796	-	8.126	1.867	-
LSCS method 2, unit	0.526[c]	37.093	-	7.990	16.274	-	3.670

[a] Relative standardized economic weight for trait i calculated as rEWi= 100 ×EVi gi EV g i × σ /Σ i ×σ i (Komlósi *et al.*, 2010).

[b] Interbull. National Genetic Evaluation Forms. http://www.interbull.org/ib/geforms

[c] Roveglia *et al*. (2018) from WCGALP project. http://www.wcgalp.org/proceedings/2018/genetics-milk-traits-including-lactose-and-somatic-cell-score-italian-jersey-cows

Figure 1. Proportions of different sources of revenues (**a**) and costs (**b**).

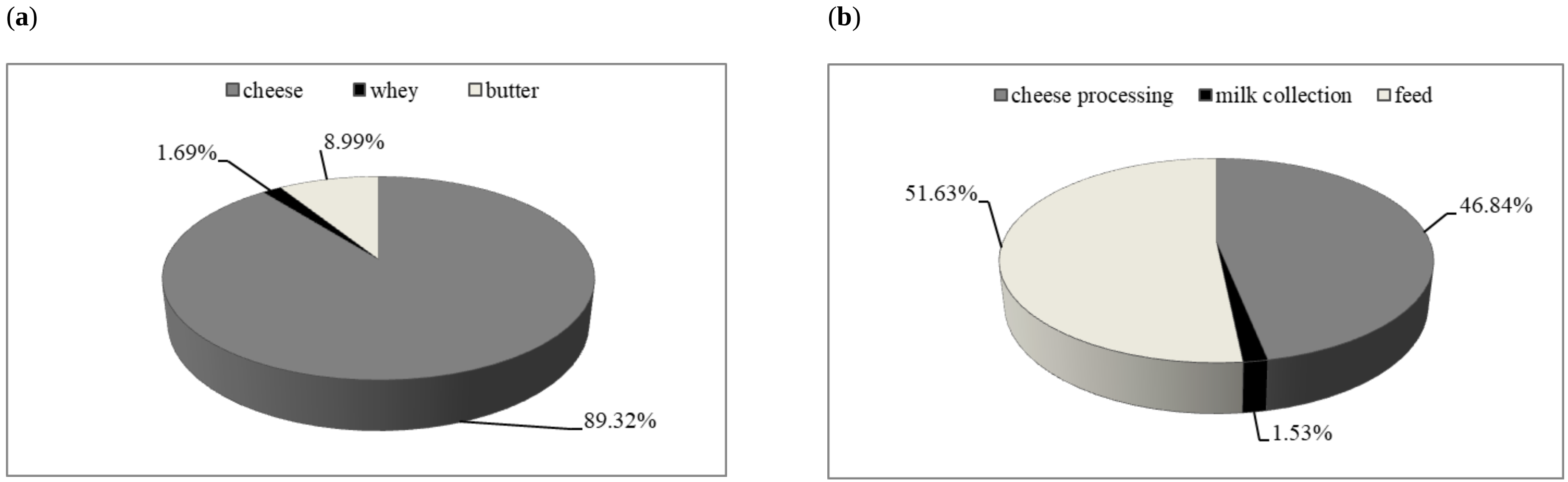
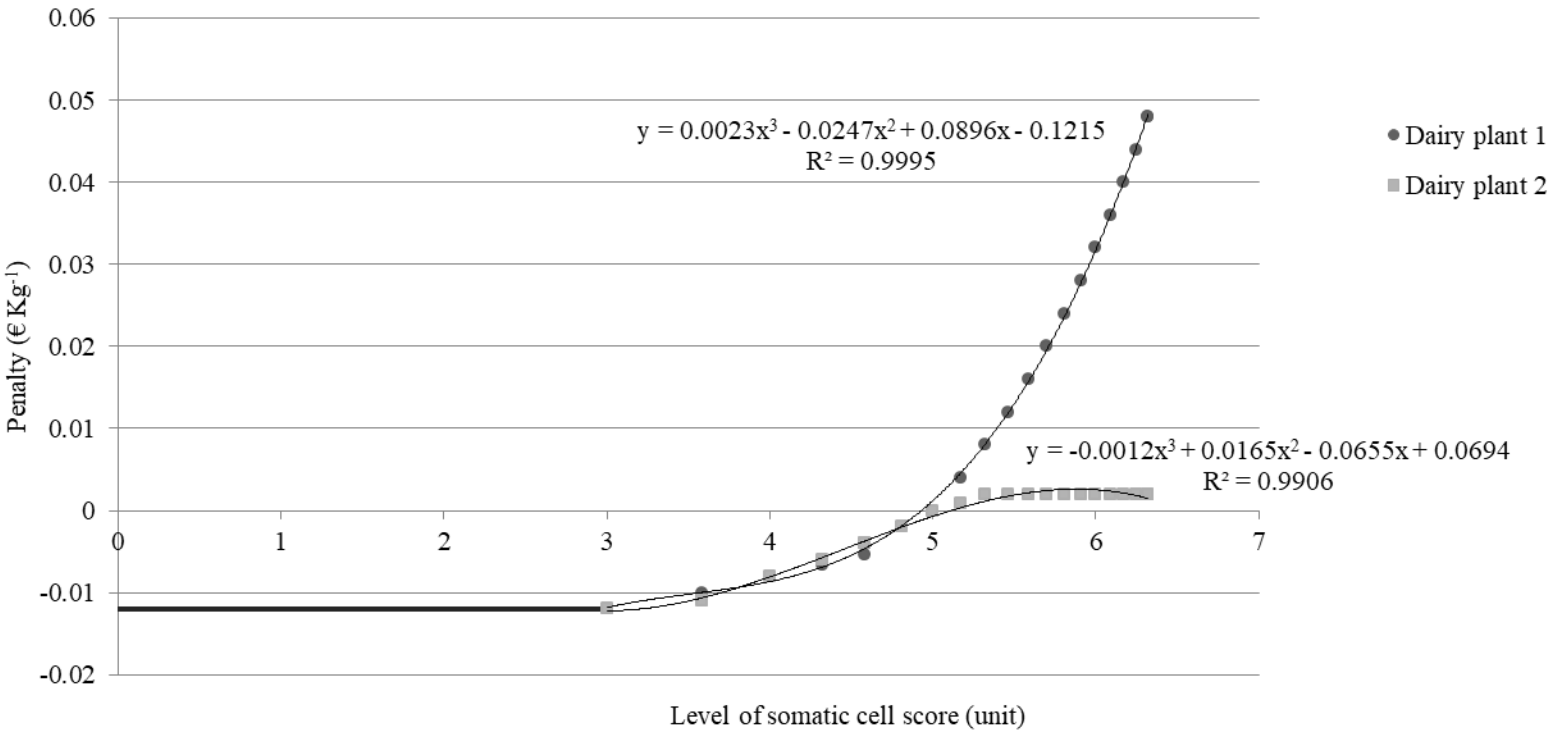


Figure 2. Penalty on milk price (€ Kg^{-1}) as a function of LSCS in dairy plant 1 and in dairy plan 2.



General conclusions

Findings of this PhD thesis contributed on gaining knowledge on the phenotypic and genetic aspects of traits of economic relevance in Italian Jersey breed. In particular:

1. eligible fat, protein and casein contents characterized the high quality of Italian Jersey milk, suitable for cheese production in Italian dairy industry scenario. Cow effect was the mainly source of variation of milk composition traits and milk yield, and farm and management were important in determining the phenotypic variance of milk urea nitrogen;
2. heritability estimates for yields of milk components were generally low, but comparable to those reported in other Jersey dairy cattle populations;
3. genetic parameters of type traits provided some new insights in Italian Jerseys, in particular locomotion score. Additive genetic variation suggested that functionality in Italian Jersey could be genetically improved;
4. alternative somatic cell count traits revealed exploitable genetic variation and heritability. These traits are candidate to be included in the selection index of the Jersey breed to select cows with improved resistance to mastitis;
5. penalties for high somatic cell score encourage the intent to adopt strategies to improve milk quality and udder health, including somatic cell score in the Italian Jersey selection index.

These results represent an initial step for future challenges:

1. the relatively high somatic cell score suggests that more efforts are needed to improve Italian Jersey rearing and management conditions;
2. improve breeding objectives and selection index in the Italian Jersey population, ensuring genetic in the right magnitude and direction.

3. some strong genetic correlations between linear type traits underlined redundancy, suggesting to reduce the number of evaluated traits avoiding loss of type traits information, and increasing genetic selection efficiency. Genetic correlations between type traits and production traits should be investigated to assess which type traits could be included in Italian Jersey selection index;
4. further investigation is required to assess the association between new somatic cell count traits and clinical mastitis events. Hence, selection accuracy for mastitis resistance may be increased by combining udder type and somatic cell count traits into an udder health index for Italian Jersey;
5. future research should focus on estimation of economic value for mastitis. Jersey farmers could be encouraged to improve milk quality and udder health, reducing susceptibility to mastitis in next generations of cows.

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