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GENETIC ANALYSIS OF MILK AND BEEF TRAITS IN THE AUTOCHTHONOUS RENDENA DUAL PURPOSE BREED

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ABSTRACT

The Rendena breed is an Italian small cattle population accounting for about 4,000 registered cows in the herd book, native of the homonymous Valley in Trento province and currently reared in the North-east of Italy. The selection objective in Rendena breed is the improvement of both quality and quantity of milk and meat with higher emphasis for milk, in tune with the maintenance of the fertility, longevity and rusticity in the breed, and with a special attention to the control of inbreeding, considering the reduced population size.

This thesis has aimed to deepen some aspects of genetic selection for the main productive aptitudes in the breed (milk and meat) investigating the possibility of implementing new breeding goals on the basis of new phenotypes such as udder health and milk technological properties considering carefully their genetic correlations with the quantity and quality of milk. Beside these objectives, the investigation on possible variance heterogeneity for milk yield traits and on the relationship between beef traits obtained in primiparous cows and young candidate bulls have been carried out. Therefore, the ultimate aim was a further improve of the knowledge on the genetic structure of the whole panel of traits accounting for the dual purpose attitude in the Rendena breed looking at possible additional improvement of the selection scheme. The first three steps of the study have been concerned different aspects of the milk production aptitude in the breed, using the currently repeatability test-day model applied in routinely genetic evaluation for milk. The first chapter of this thesis evaluated possible heterogeneity of variance for productive traits using average milk yield recorded in Rendena farms under functional control in years 2004-2013 (114 farms). Medium and high productive groups (average milk yield of 15.63 ± 4.96 and 19.95 ± 5.95, respectively) were identified via cluster analysis. Subsequently, the estimated heritability and genetic correlations between groups were obtained via bi-trait animal model using 73,916 test-day records of milk, fat and protein yield belonging to a sample of 49 herds with the same numerical proportion as in

medium and highly productive levels and considering yields in the two productive groups as different traits. The genetic components and heritability of milk, fat and protein yield were heterogeneous between the two productive groups, with higher values for the highly productive group (0.16 and 0.30, respectively). However, the genetic correlations for milk yield traits between productive groups resulted sufficiently great (≥ 0.88) to support the hypotheses of no heterogeneity between productive groups. Even the rank correlation between EBVs of bulls that had daughters in both groups confirmed this finding (0.98). The results suggested that genetic evaluation not accounting for the heterogeneous variance may be applied without producing biased estimates for the bulls EBVs. However, a more careful selection should be considered for bull dams.

In the second study genetic parameters for the content of milk somatic cells (SCC) were estimated using different and alternative methods. In particular, the SCC traits defined for genetic evaluation were: somatic cells score (SCS), log total somatic cell counts (LTSCC) and three different thresholds (80,000, 150,000 and 400,000 cells/ml) for somatic cells. A total of 69,796 TD records of milk, fat, protein yields and SCC belonging to 4,325 cows was used to analyse heritability and genetic correlations between SCC and yield traits using bi-trait animal model under Bayesian approach. The threshold traits showed heritability values expressed under a liability scale ranging from 0.04 to 0.07, lower than those obtained for SCS and LTSCC traits that were equal to 0.09 and 0.10, respectively. The genetic correlations between yield traits and the SCC traits were almost null (from -0.09 between fat yield and SCS, to 0.13 between protein yield and SCC400), with the only exception of LTSCC (0.29 for milk, 0.16 for fat and 0.28 for protein). These results indicated that the genetic selection for milk, fat and protein production does not negatively influence the content of somatic cells in milk. Nevertheless, the complete framework of genetic relationships of SCC with all traits under selection should be considered to decide for possible inclusion of SCC in the breeding program.

In the subsequent study, milk technological traits for cheese production were analysed using their Fourier Transform Infrared (FTIR) predictions (milk coagulation properties, MCP, curd firmness model parameters, cheese yields, the nutrient recoveries in the curd and the daily cheese yields), obtained from routinely functional controls carried out in the Trento province. A total of 9,947 FTIR predictions representing the test-day records of 997 Rendena cows, collected over a 5-yr period, were available for the study. The (co)variance components were estimated for the milk technological traits, milk production, and milk composition traits (fat, protein and lactose percentages, and SCS), via a bi-trait analysis by means of a Gibbs sampling algorithm. Milk of Rendena cows exhibited good aptitude for coagulation. In general the heritability obtained for all the predicted traits were comparable and in some case greater than those reported for milk production and composition. Heritability estimates for quality traits ranged from 0.11 for fat percentage to 0.39 for time of maximum curd firmness, whereas SCS showed the lowest heritability (0.01). The improvement of milk production favoured some of the traditional MCP traits, but did not promote cheese yield traits (average genetic correlation of -0.34). However, the relationships between milk production and the nutrients recovery traits were almost null. Conversely, favourable genetic correlations were obtained between milk composition and cheese yields and nutrient recoveries traits (average values of 0.57 and 0.34, respectively). These results suggested that it is possible to efficiently improve the technological properties of milk for cheese production and therefore the economic value of milk in the Rendena breed.

The improvement of beef aptitude together with the milk ability has played an important role for maintaining the dual attitude in the selection of the Rendena breed. Therefore, the last part of the study was aimed at estimating genetic relationships between muscularity type traits obtained in primiparous cows (front muscularity; back, loins, and rump; thigh, buttocks side and rear views) with the same types scored on candidate young bulls at the end of the performance test for beef aptitude, and the performance test traits (average daily gain, ADG; EUROP fleshiness evaluation and dressing percentage). Muscularity linear type traits recorded on 11,992 first parity cows and both performance test traits and the muscularity types scored on 957 candidate young bulls at the end of the performance test were used. Through a series of single-trait REML analyses, genetic parameters for both muscularity traits of cows and young bulls, and beef performance test traits of young bulls were obtained. The models for the two datasets of cows and bulls accounted for different fixed effects, i.e., herd-year-classifier, age at calving and days in milk for muscularity evaluated on primpiparous cows, and group of contemporary, parity order of mother for muscularity and performance test traits relative to young bulls. The only communality between data sets was the random additive genetic variance. All the previous effects were jointly retained for the AIREML bivariate analysis to assess the genetic correlations between beef traits. Heritability estimates were moderate for both groups of traits and ranged from 0.25 for front muscularity in primiparous cows, to 0.36 for both back, loins and rump and dressing percentage recorded in young bulls. Medium to high genetic correlations were found between performance test and muscularity type traits collected in young bulls (from 0.47 between thigh, buttocks side view and ADG to 0.97 between thigh, buttocks side view and *in vivo* EUROP score). Low genetic relationships were obtained between muscularity linear type traits of primiparous cows and performance test traits or the same types traits scored on young bulls , which showed genetic correlations ranging from 0.07 to 0.82. These results indicate a common way for the meat selection route in Rendena, suggesting the possibility to account for young bull muscularity traits in genetic improvement of the breed.

In conclusion, all the four studies suggested possible positive aspects, either methodological or related to productive or functional traits, likely to be used in the selection practice of Rendena breed.

RIASSUNTO

La razza Rendena è una piccola popolazione bovina Italina che conta circa 4,000 vacche registrate al libro genealogico, originaria dall'omonima Valle in provincia di Trento è allevata nel nord-est dell'Italia (nelle regioni del Trentino Alto Adige e del Veneto). L'obiettivo di selezione della razza Rendena è il miglioramento sia della quantità che della qualità di latte e carne con una maggiore enfasi per la produzione di latte, in sintonia con il mantenimento delle caratteristiche di fertilità, longevità e rusticità della razza e con una attenzione particolare per la consanguineità, considerando la ridotta dimensione della popolazione.

Questa tesi ha voluto approfondire alcuni aspetti della selezione genetica delle principali attitudini produttive della razza (latte e carne) e valutare la possibilità di implementare la selezione con altri fenotipi come per esempio la salute della mammella e le proprietà tecnologiche del latte, valutando le correlazioni con i caratteri quantitativi e qualitativi del latte. A partire da questi obbiettivi, sono stati condotti degli studi volti a valutare la possibile eterogeneità di varianza per i caratteri di produzione di latte e le relazioni tra i caratteri legati alla produzione di carne ottenuti da bovine primipare e giovani tori candidati. Lo scopo ultimo di questa tesi è stato quindi quello di ampliare la conoscenza della struttura genetica dell'insieme complessivo di caratteri volti al miglioramento della duplice attitudine nella razza Rendena, nell'ottica di un possibile sviluppo dello schema di selezione. I primi tre studi hanno quindi riguardato diversi aspetti dell'attitudine alla produzione di latte della razza, usando il modello a ripetibilità che è attualmente applicato alla valutazione genetica del latte.

Nel primo capitolo di questa tesi è stata valutata l'eventuale eterogeneità della varianza dei caratteri della produzione di latte utilizzando la media produttiva aziendale annua di tutte le aziende con bovini di razza Rendena sotto controllo funzionale negli anni 2004-2013 (114 aziende agricole).

Attraverso una analisi cluster sono stati individuati due gruppi produttivi di aziende: uno a media ed uno ad alta produzione (la media produttiva è rispettivamente di 15.63±4.96 e 19.95±5.95). Successivamente, usando 73,916 rilievi test day delle produzioni di latte, grasso e proteine appartenenti ad un campione di 49 aziende scelte in proporzione tra il medio e l'alto livello produttivo, sono state stimate le ereditabilità e le correlazioni genetiche tra i due livelli considerando i caratteri produttivi nei due gruppi come se fossero caratteri diversi. Le componenti di varianza e le ereditabilità delle produzioni di latte, grasso e proteine sono risultate essere eterogenee tra i due gruppi produttivi, con valori più alti nel gruppo ad alta produzione (rispettivamente 0.16 e 0.30). Tuttavia, le correlazioni genetiche dei caratteri produttivi tra i due gruppi sono risultate sufficientemente grandi (≥ 0.88) per sostenere l'ipotesi che non c'è eterogeneità della varianza tra i due gruppi produttivi e anche la correlazione dei rank tra i valori genetici (EBV) dei tori con figlie in entrambi i gruppi conferma questo risultato (0.98). I risultati hanno suggerito che la valutazione genetica per i caratteri produttivi può essere effettuata senza produrre stime pregiudizievoli per gli EBV dei tori anche senza tenere conto dell'eterogeneità della varianza. Tuttavia, sarebbe opportuno operare una selezione più attenta alla presenza di eterogeneità della varianza nell'ambito del miglioramento genetico delle vacche, in particolare delle madri di toro.

Nel secondo studio sono stati stimati i parametrici genetici per il contenuto di cellule somatiche del latte (SCC) utilizzando metodi diversi e alternativi. Nello specifico, sono stati definiti i seguenti caratteri di SCC per la valutazione genetica: il punteggio normalizzato di cellule somatiche (SCS), la conta totale delle cellule somatiche (LTSCC) e tre diversi caratteri soglia (80.000, 150.000 e 400.000 cellule / ml) della conta delle cellule somatiche. Per stimare le componenti genetiche sono stati usati 69,796 rilievi test day delle produzioni di latte, grasso e proteine (kg/d) e SCC appartenenti a 4,332 vacche, usando un bi-trait animal model con un approccio bayesiano. I caratteri soglia hanno mostrato valori di ereditabilità, espressi su scala liability, che variavano da 0.04 a 0.07, più bassi rispetto alle ereditabilità ottenute per i caratteri SCS e LTSCC, rispettivamente pari a 0.09 e 0.10. Le correlazioni genetiche tra i caratteri produttivi e i caratteri SCC erano quasi nulle (da -0.09 tra la produzione di grasso e le SCS, a 0.13 tra la produzione di proteina e la soglia SCC400), ad eccezione di LTSCC (0,29 per latte, 0,16 per il grasso e 0,28 per proteine). Questi risultati indicano che la selezione genetica per la prodizione di latte, grasso e proteina non influenza negativamente il contenuto delle cellule somatiche. Tuttavia, dovrebbe essere presa in considerazione una valutazione delle relazioni genetiche delle SCC con tutti i caratteri oggetto di selezione prima di decidere per un'eventuale inclusione del carattere nell'ambito delle programma di selezione della razza.

Nello studio successivo sono state analizzate le predizioni FTIR (Fourier Transform Infrared Spectroscopy) dei caratteri tecnologici del latte (proprietà coagulative del latte, MCP, i parametri del modello di rassodamento della cagliata, le rese in formaggio, i recuperi dei nutrienti nella cagliata e le rese in formaggio giornaliere) ottenute dai controlli funzionali periodici in provincia di Trento. Per lo studio erano disponibili 9,947 rilievi test day di predizioni FTIR appartenenti a 997 vacche di razza Rendena raccolti nell'arco di 5 anni. Con lo scopo di stimare le componenti di (co)varianza dei caratteri tecnologici del latte, la produzione di latte e le percentuali di grasso, proteine, lattosio e SCS sono state condotte analisi bi-trait con algoritmo Gibbs sampling. Complessivamente, il latte delle vacche di razza Rendena ha mostrato buona attitudine alla coagulazione. In generale, le ereditabilità ottenute da tutti i caratteri predetti erano simili e in alcuni casi più alte di quelle ottenute per la produzione e la composizione del latte. Le stime di ereditabilità variavano da 0.11 per la percentuale di grasso a 0.39 per il tempo massimo di rassodamento della cagliata, mentre le SCS ha mostrato i valori più bassi di ereditabilità (0,01). Il miglioramento della produzione di latte ha favorito i tradizionali caratteri MCP, ma non ha favorito i caratteri di resa del formaggio (correlazione genetica media di -0.34). Tuttavia, le correlazioni tra la produzione di latte e i caratteri di recupero dei nutrienti erano quasi nulle. Al contrario, sono state ottenute correlazioni genetiche favorevoli tra la composizione del latte e le rese in formaggio e il recupero dei nutrienti (valori medi rispettivamente di 0.57 and 0.34). Questi risultati suggeriscono che è possibile migliorare in modo efficace le proprietà tecnologiche del latte per la produzione di formaggio e quindi il valore economico del latte nella razza Rendena.

Il miglioramento della capacità di produrre carne insieme alla capacità di produrre latte svolge un ruolo importante nel mantenere la duplice attitudine nella selezione della razza Rendena. Pertanto, l'ultimo studio ha inteso valutare le relazioni genetiche dei caratteri di muscolosità rilevati con la valutazione morfologica lineare nelle primipare (muscolosità dell'anteriore, del dorso, lombi e groppa della coscia e natica visti di lato e da dietro) con gli stessi caratteri rilevati sui candidati giovani tori alla fine del performance test per l'attitudine alla produzione di carne, e per i caratteri performance test (accrescimento medio giornaliero, ADG, valutazione in vivo della conformazione EUROP e della resa percentuale). Nello studio sono stati usati i caratteri morfologici lineari di muscolosità valutati su 11,992 primipare e i caratteri di performance test e muscolosità rilevati su 957 giovani tori alla fine del performance test. Attraverso una serie di analisi REML single-trait, sono stati stimati i parametri genetici sia dei caratteri muscolosità delle primipare e dei giovani tori, sia dei caratteri carne del performance test. I modelli usati per vacche e tori differenti effetti fissi, riguardanti l'allevamento-anno-esperto, le classi di età al parto e quelle di giorni in lattazione al momento della valutazione per la muscolosità sulle primipare, e il gruppo di contemporanei, l'ordine di parto della madre per la muscolosità e i caratteri di performance test rilevati nei giovani tori. I due dataset avevano in comune solo l'effetto casuale della varianza genetica additiva. Tutti gli effetti sopra citati per i due differenti dataset sono stati poi uniti in un unico modello per analizzare le correlazioni genetiche tra i caratteri, attraverso una serie di analisi REML bi-trait.

Le stime di ereditabilità sono risultate moderate per entrambi i gruppi di caratteri e variavano da 0.25 per la muscolosità della spalla rilevata nelle primipare, a 0.36 sia per la muscolosità di dorso, lombi e groppo che per la resa percentuale rilevata sui giovani tori. Sono state stimate correlazioni genetiche medio alte nei giovani tori tra i caratteri di performance e i caratteri morfologici lineari di muscolosità (da 0.47 tra coscia e natica vista di lato e AMG, a 0.97 tra coscia e natica vista di lato e in vivo EUROP). Sono state ottenute correlazioni genetiche basse tra i caratteri morfologici lineari di muscolosità delle primipare e i caratteri di performance test e i lineari di muscolosità rilevati nei giovani tori alla fine del performance test e hanno riportato correlazioni che variavano da 0.07 a 0.82. Questi risultati indicano che la selezione della carne ha la stessa direzione del miglioramento della morfologia, suggerendo la possibilità di tenere conto dei caratteri muscolari dei giovani tori nel miglioramento genetico della razza.

In conclusione, tutti i quattro studi hanno suggerito possibili aspetti, sia metodologici che correlati a caratteri produttivi o funzionali, che potrebbero essere utilizzati nella pratica selettiva della razza Rendena.

INTRODUCTION

RENDENA BREED

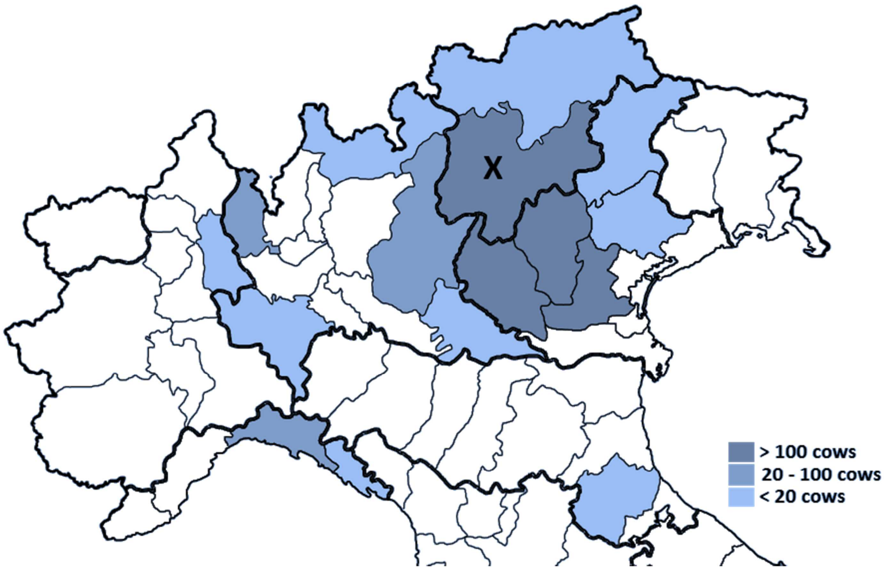
Rendena (Figure 1) is a small local breed of the alpine arch, native of the homonymous Valley in Trento province, Italy. A recent classification based on molecular data (Felius et al., 2011) accounted the breed in the group of central European brown cattle, including Italian Brown Swiss, Swiss Brown, and Cabannina. Rendena cattle was firstly mentioned in documents of early 1700s. After cattle plague the breed was crossed with local gray and brown breeds till 1870, when it increased in size and importance. Herds and animals were found in the original areas, and also in South Tyrol, in Veneto and in Lombardy. After a policy of massive crosses with more productive breeds started in early 1900s, and after the effects of two world wars, the situation of the breed became critical and required, in 1947, the creation of a local breeders association. The herd book was established in 1976, and the National Association of Breeders of Rendena cattle (A.N.A.RE) since 1981 deals with collecting and storing genealogical information, productive and reproductive data, morphological evaluations and genetic indexes (Mantovani et al., 1997; Del Bo et al., 2001; Mazza and Mantovani, 2012). Currently, Rendena breed accounts for about 7,000 registered animals in the herd book, 3985 of which are cows, reared in 199 farms mainly in Trentino Alto Adige and Veneto regions in provinces of Trento, Padova, Vicenza and Verona in the North-east of Italy (Bittante et al., 1993). The current distribution of the breed is reported in Table 2. The farms are of small-medium size, (around 20 heads each), and located both in mountain and in plain. In these two environments the management of farms and the feeding strategies are different and associated with the territory's resources. The farming systems are traditional in mountain (i.e., tied animals fed hay and concentrate) and based on the practice of the alpine pasture for the whole herds during the summer season, whereas in plain they are more intensive (i.e, feeding system mainly based on the use corn silage), with the summer alpine pasture that is common for young cattle only.

Typical of the Rendena cattle is the coat with different shades of dark brown with hairs of tuft and the dorsal line with lighter dorsal stripe, almost black in males, with a white ring around the black muzzle. As many other Alpine breeds, Rendena cattle is characterized by small to medium body size, dual purpose aptitude for milk and beef production, good fertility and longevity (Forabosco and Mantovani, 2011). The main characteristic of the breed is the rusticity, namely its ability to adapt itself to living and producing in harsh environments with low quality forages, as well as its suitability to graze during the summer season in the alpine high pastures (Mantovani et al. 1997). Indeed, almost all of the cows reared in Trentino and more than 50% of those reared in Veneto spend the four months in the summer period from early June to late September in the mountains of Val Rendena and in the Altopiano di Asiago (ANARE, 2017). As effect of the pasture, this breed maintains the seasonality of calving, with a maximum number of calving between October and February.

Figure 1. Cows of Rendena breed at pasture

The average milk yield registered in 2015 was about 5,200 kg per lactation with 3.47% fat and 3.24% protein (ANARE, 2017). Rendena cows calve for the first time at around 33 months of age and have on average 3.3 lactations with a mean days open of approximately 116 days (ANARE, 2016). The meat aptitude is evaluated in young bulls, which at the end of performance test, at around 11 months of age, weight between 350 and 400 kg with a mean of in vivo dressing percentage of 58% (Forabosco & Mantovani, 2011).

Figure 2. Current geographical distribution of Rendena breed. The X indicates the Rendena Valley.

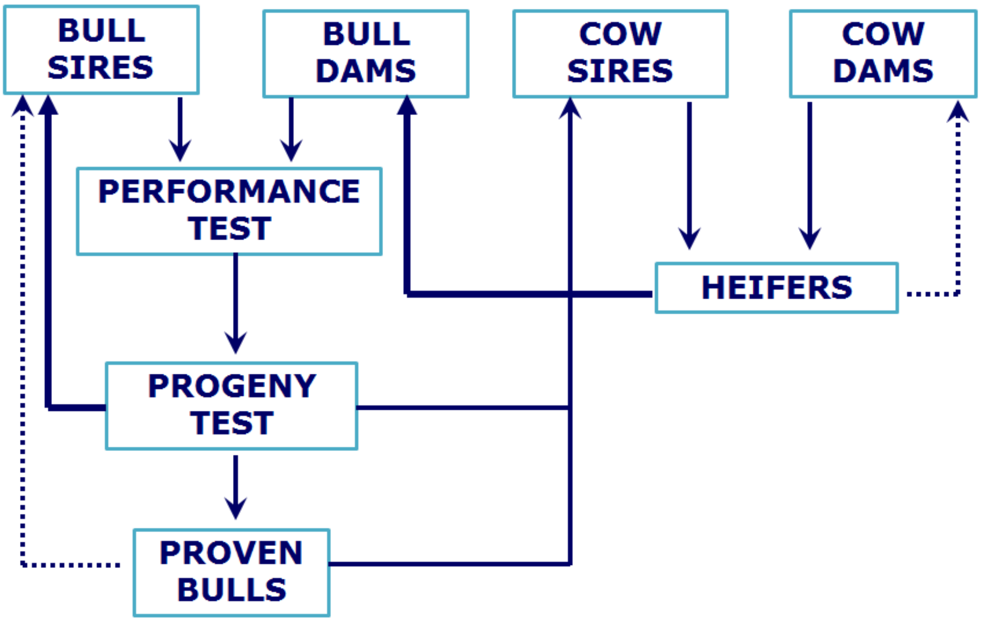


SELECTION SCHEDULE

The selection objective in Rendena breed is the improvement of milk yield and quality and the beef aptitude, in tune with the functional traits of fertility, longevity and rusticity, with a special attention for inbreeding. In Rendena cattle, the annual inbreeding increase is 0.16% per year (FAO, 2017) considering an average generation length of 4.48 years. This value is lower than the critical threshold of 1% per generation proposed by FAO. Rendena is labelled as “not-at-risk” (FAO, 2017), and reared following a selection program careful of the genetic relationships among selected animals to limit the inbreeding increase.

The selection set for the Rendena breed is an example of modern genetic improvement strategies applied to a population of limited numbers. In order to improve both milk and beef abilities, the Rendena breeders association (A.N.A.RE.), under the supervision of the former Department of Animal Science of the University of Padova (now Department of Agronomy Food Natural resources Animals and Environment, DAFNAE), has adopted a selection scheme (Figure 3) that involves the use of young bulls and heifers (animals without genetic evaluation), as bull sires and bull dams, bringing to an assortative matings phase that comes before the beginning of the actual progeny testing.

Figure 3. Selection schedule applied in Rendena breed (Mantovani et al., 1997)



This scheme, in detail described by Mantovani et al. (1997), allows a reduction in generation interval as respect to what generally observed in dual purpose cattle as it enters the denominator in the formula for calculating genetic progress (Van Vleck L.D. et al., 2003):

$$\Delta G = \frac{r \cdot i \cdot \sigma_a}{L}$$

Where:

ΔG = Genetic progress

r = accuracy of estimated genetic values

i = selection intensity

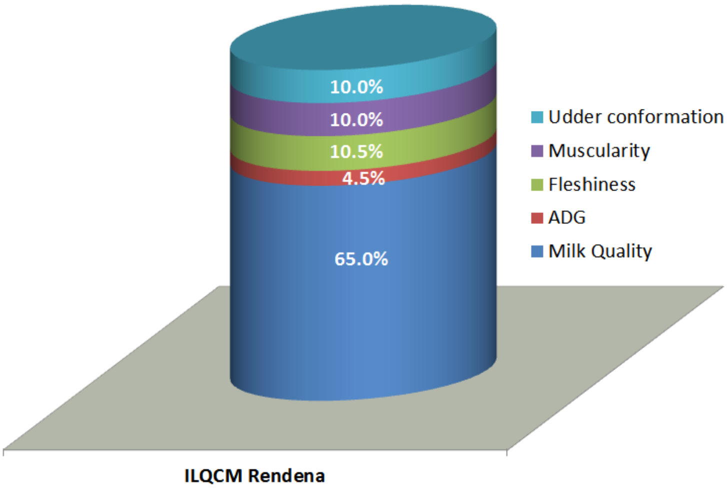
σ_a = genetic standard deviation of trait

L = generation interval

Furthermore, this method applied to Rendena is fundamental, because allows to differentiate the bloodlines of bull sires, avoiding the use few proven bulls that would cause high increases of inbreeding levels, thereby compromising the survival of the population.

The genetic improvement of quantity and quality of both milk and meat, in Rendena, is possible through selection global index (TSI; Figure 4) that provides an economic weight of 0.65 to protein and fat yields (kg), in proportion of 3:1 and corrected for the milk yield. Udder conformation and muscularity of cows have the same weight, that is 0.10 each. The other 0.15 of weight is for the beef traits measured at performance testing station on candidate young bulls, that is 0.045 for average daily gain (ADG) and 0.105 for the product of in vivo fleshiness and dressing percentage (Mantovani et al., 1997; Mazza et al., 2014). Milk productive traits have been evaluated using a test-day model since 2009, whereas linear type evaluation started in 1994. Candidate young bulls at performance testing stations have been valued since 1985, and a subsequent progeny testing for milk yield is routinely taken on candidate young bulls (Mantovani et al., 1997).

Figure 4. Milk Quality index in Rendena breed. ADG=Average Daily Gain



Milk Aptitude

From the early 1990s the genetic evaluation for milk production is largely carry out using single test day (TD) records (Ptak e Schaeffer, 1993). The more conservative and better adaptable model in small local breeds, with animals distributed in small herd sizes, is a repeatability test-day, because as reported by Dal Zotto (2000) the numbers of animals and farms implicated in the genetic evaluation systems were more high than those with the random regression models. In Italy, the repeatability test day model is applied in the Italian Brown (Dal Zotto, 2000), Italian Simmental (Degano et al., 2003), and local dual-purpose Valdostana breed (Mazza et al., 2016b).

In a preliminary study conducted in the Rendena breed, Guzzo et al. (2009) reported that the application of Test Day model as alternative to traditional lactation model was possible, so the genetic evaluation for milk, fat and protein production are currently evaluated using a repeatability test-day model as follows:

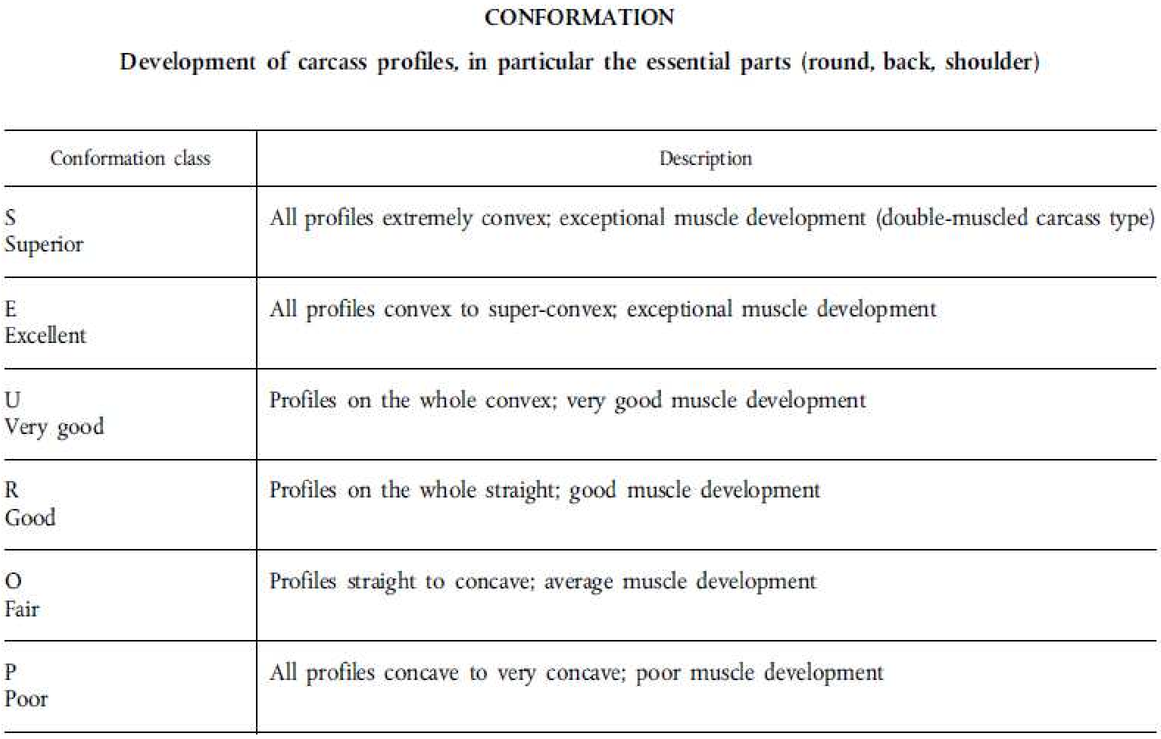
$$y_{ijklmn} = \mu + \text{HTD-LN}_i + \text{GEST}_j + \sum_{r=0}^{4} \varphi_r \text{AP-LN}_k + \sum_{r=0}^{4} \varphi_r \text{MP-LN}_l + \text{Pe}_m + a_n + e_{ijklmn},$$

The model considers: the fixed effect of herd-test-day within lactation number (HTD-LN), at least 4 test-day within lactation and at least 2 test-day within herd with the same lactation number, the fixed effect of the days of gestation class (GEST; 18 classes: the first class means no gestation; the further classes accounts for 15 d intervals from 1 to 240 d of gestation; and the last class considers ≥ 241 d of gestation), the fixed effect of age at parity within lactation (AP-LN; 42 classes in total), the fixed effect of the month of parity (MP-LN; 36 classes corresponding to single month of year within lactation number), the random permanent environmental component and the genetic additive component. The shape of the lactation curve is described by 4th order Legendre polynomials (Strabel and Misztal, 1999) for the fixed effects of AP-LN and MP-LN.

Meat Aptitude

Beef traits are routinely evaluated by performance test on young bulls, which measures average daily gain (ADG), in vivo dressing percentage estimates and in vivo fleshiness estimates according to SEUROP grading (European Community, 2006) as reported in Table 1. In Rendena breed about 50 male candidate calves per year, born through assortative mating, are grouped by month of birth and reared from 1 to 11 months of age at the performance testing station, where they are monthly weighted (Mantovani, 1997). The ADG (kg/d) is calculated by a linear regression of the weight on age. The in vivo SEUROP fleshiness and dressing percentage are evaluated at the end of the period of performance by three trained classifiers that provide separate scoring (percentage points), and then the mean are calculated within each traits. The value of 100% points is attributed at the R class (intermediate) with variations of ± 10% for each upper or lower class and introducing three subclasses for each class. Young bulls at the end of the performance test are evaluated morphologically. The linear type classification system consists in 13 linear traits and 4 composite traits. The individual type traits describe specific body regions of an animal, while composite traits resume specific aspects as the general score, frame size, the muscular development and the body shape. About 25 young bulls are yearly approved at the end of test and subsequently evaluated for milk attitude in progeny testing (Mantovani et al., 1997; ANARE, 2017).

Table 1. Europe SEUROP classification grid



CONFORMATION

Development of carcass profiles, in particular the essential parts (round, back, shoulder)

Conformation class	Description
S Superior	All profiles extremely convex; exceptional muscle development (double-muscled carcass type)
E Excellent	All profiles convex to super-convex; exceptional muscle development
U Very good	Profiles on the whole convex; very good muscle development
R Good	Profiles on the whole straight; good muscle development
O Fair	Profiles straight to concave; average muscle development
P Poor	All profiles concave to very concave; poor muscle development

The ADG and the product of in vivo fleshiness and dressing percentage obtained in performance test are routinely analysed in genetic evaluations through the following single-trait animal model:

$$y_{ijkl} = \mu + Gr_i + PO_j + a_l + e_{ijkl}$$

The model accounts for the fixed effect of group of conspecifics reared in the same pen at performance testing station, the parity order of the mother (4 levels: first parity, second parity, from third to seventh, and greater than seventh), and the random additive genetic effect.

Morphology

Morphological evaluation is an aspect important of cattle selection, because enables an immediate evaluation of the animal conformation and a relatively simple classification (Forabosco et al., 2005). Through the morphological evaluation, trained classifiers provide a description of the animal compared to a breed standard using points scale. In Rendena cattle, the morphological evaluation has been performed since 1993 on primiparous cows by trained classifiers considering a 1-5 point scale with biological meaning for extremes (Mazza et al., 2014). The linear type classification system consists in 20 linear description traits and five composite traits (Table 2). The individual type traits describe specific body regions of an animal including the thorax, rump, feet, legs, thigh and udder conformation. The composite traits summarize body size, fleshiness, body shape and udder as well as an overall animal conformation score. On the linear type traits related to muscularity (shoulder, fore view, back, loins and rump, thigh, buttocks side view, thigh, buttocks rear view) and the mammary correctness (i.e. udder depth, suspensory ligament, teat placement side view) a factor analyses is routinely performed, following the same approach applied and described in detail in a previous study in Rendena (Mazza et al., 2016a). This analysis allows to obtain two factor scores that are used in genetic evaluations. The advantage of this approach is to summarize the information of a number of genetically related traits all describing an aspect of interest of animal morphology, but, due to an high collinearity, these traits could not be included together in a selection index (Sieber et al. 1988).

Table 2. Descriptor of 20 linear type traits and 4 composite traits in Rendena breed. Traits included in the factor scores are highlighted in blue.

Traits	Descriptor	
	Minimum (1)	Maximum (5)
Composite traits		
Overall score	Poor	Excellent
Body size	Little	Large
Fleshiness	Poor	Excellent
Body shape	Fine	Heavy
Udder	Poor	Excellent
Linear type traits		
Body size		
Stature	Short	Tall
Body length	Short	Long
Thorax depth	Very thin	Very large
Thorax length	Short	Long
Fleshiness		
Shoulder, Fore view	Scarce	Developed
Back, Loins and Rump	Scarce	Developed
Thigh, Buttocks side view	Hollow	Rounded
Thigh, Buttocks rear view	Hollow	Rounded
Body shape and feet and legs		
Thinness	Heavy	Fine
Rump angle	Back-inclined	Counter-inclined
Rump width	Narrow	Broad
Rear legs side view	Straight	Sickle
Feet	Weak	Straight
Udder		
Fore udder attach	Loose	Tight
Rear udder attach	Short	Tall
Udder width	Narrow	Broad
Udder depth	Deep	Shallow
Suspensory ligament	Weak	Strong
Teat placement side view	Close	Far
Teat length	Short	Long

The factor scores obtained for the 10 type traits describing muscularity and udder are analysed ones per year through the following single-trait animal model (Mazza et al.,2014):

$$y_{ijkl} = \mu + HYC_i + AC_j + DIM_k + a_l + e_{ijkl}$$

The model considers the fixed effect of herd year classifier of evaluation (HYC) at least 2 primiparous within herd year classifier, the fixed effects of age of calving (AC; 9 classes: <24 months, from 25 to 38 using 2-months intervals, and ≥39 months for the last class), the fixed effects of days in milk (DIM; 8 classes from 10 to 30 days after calving and from 31 to 210 days after calving using 30-days intervals, or for later evaluation >210 days), and the random additive effect of cows.

REFERENCES

ANARE (2017). Homepage address: http://www.anare.it

ANARE (2016). Risultati controlli funzionali 2015. La Rendena, 1-2, 25–29.

Bittante G., Andrighetto I., & Ramanzin M. (1993). Tecniche Di Produzione Animale. Liviana, Padova, Italy.

Dal Zotto, R. (2000, May). Comparison of different test-day models for genetic evaluation of Italian Brown dairy cattle. In Proceedings of the international workshop on genetic improvement of functional traits in cattle (Vol. 25, pp. 95-98).

Degano, L., Marcomin, D., Vicario, D., Contiero, B., & Carnier, P. (2003). Applicability of different test day models and effect on time at first evaluation of Italian Simmental bulls. Italian Journal of Animal Science, 2(sup1), 43-45.

Del Bo, L., Polli, M., Longeri, M., Ceriotti, G., Looft, C., Barre-Dirie, A., & Zanotti, M. (2001). Genetic diversity among some cattle breeds in the Alpine area. Journal of Animal Breeding and Genetics, 118(5), 317-325.

European Community 2006. Council Regulation No 1183/2006 of 24 July 2006 concerning the Community scale for the classification of carcases of adult bovine animals (codified version). Official Journal of the European Communities, 214.

FAO 2017. DAD-IS, Domestic Animal Diversity Information System. FAO, Rome. Retrieved January 9, 2017, from http://dad.fao.org/.

Felius, M., Koolmees, P. A., Theunissen, B., Lenstra, J. A., & European Cattle Genetic Diversity Consortium. (2011). On the breeds of cattle-historic and current classifications. Diversity, 3(4), 660-692.

Forabosco, F., Rossetti, E., Sarti, F. M., Panella, F., Bittante, G., Mantovani, R., & Filippini, F. (2005, April). Morphological factorials for females of the Chianina, Marchigiana and Romagnola breeds. In Proceedings of the 4th World Italian Beef Cattle Congress. Gubbio (Italy), 29th April to 1st May.

Forabosco F., & Mantovani R. (2011) European and Indigenous Cattle Breeds in Italy. Schiel & Denver Publishing Limited. Houston, TX.

Guzzo, N., Sartori, C., & Mantovani, R. (2009). Test day-milk yields variance component estimation using repeatability or random regression models in the Rendena breed. Italian Journal of Animal Science, 8(sup3), 71-73.

Mantovani R., Gallo L., Carnier P., Cassandro M., & Bittante G. (1997) The use of a juvenile selection scheme for genetic improvement of small population: the example of Rendena breed. In: 48th Annual Meeting of the European Association of Animal Production, Vienna, Austria, 25–28 August 1997, 5 pp.

Mazza, S., & Mantovani, R. (2012). Heritability of linear type traits in the autochthonous rendena dual purpose breed. Acta Agriculturae Slovenica 100 (SUPPL.3), pp. 161-165

Mazza, S., Guzzo, N., Sartori, C., Berry, D. P., & Mantovani, R. (2014). Genetic parameters for linear type traits in the Rendena dual-purpose breed. Journal of Animal Breeding and Genetics, 131(1), 27-35.

Mazza, S., Guzzo, N., Sartori, C., & Mantovani, R. (2016a). Factor analysis for genetic evaluation of linear type traits in dual-purpose autochthonous breeds. animal, 10(03), 372-380.

Mazza, S., Guzzo, N., Sartori, C., & Mantovani, R. (2016b). Genetic correlations between type and test-day milk yield in small dual-purpose cattle populations: The Aosta Red Pied breed as a case study. Journal of Dairy Science, 99(10), 8127-8136.

Ptak, E., & Schaeffer, L. R. (1993). Use of test day yields for genetic evaluation of dairy sires and cows. Livestock Production Science, 34(1-2), 23-34.

Sieber, M., Freeman, A. E., & Hinz, P. N. (1988) Comparison between factor analysis from a phenotypic and genetic correlation matrix using linear type traits of Holstein dairy cows. *J. Dairy Sci.*, 71, 477.

Strabel, T., & Misztal, I. (1999). Genetic parameters for first and second lactation milk yields of Polish Black and White cattle with random regression test-day models. Journal of Dairy Science, 82(12), 2805-2810.

Van Vleck, L.D., Pollack, E.J., & Oltencu, E.A.B. (1993). Genetic for Animal Sciences. W.H. Freeman and Company, New York.

AIMS OF THIS THESIS

The present thesis has been carried out with intent to deepen further the procedures for calculating genetic parameters of the quantitative traits object of selection (milk and meat) in autochthonous dual purpose Rendena breed and evaluating the possibility of implementing selection with phenotypes related to udder health, as for example the somatic cells and new phenotypes related to the technological properties of the milk for the production of cheese and their relationship with the quantity and quality of milk. The studies have arisen from the collaboration between the University of Padua, Department of Agronomy, Food, Natural resources, Animals and Environment, the National Association of Rendena breeders and the Breeders Federation of Trento Province, based in Trento, Italy. In particular, the thesis is composed of four chapters with the following aims:

I. to estimate variance components, heritability and the genetic correlations for milk, fat and protein yields between different productive environments defined in Rendena breed. In addition, to evaluate rank correlations between EBV of bulls simultaneously estimated in different environments as possible fall-out of the variance heterogeneity problem in some cases evidenced by breeders;

II. to investigate different and alternative methods of using data of the content of milk somatic cells as udder health indicator and evaluate their relationships with the yield traits included in genetic selection for milk aptitude of the Rendena breed;

III. to estimate the variance component and heritability for Fourier-transform infrared (FTIR) predictions of the milk technological traits (MCP, CF, cheese yields, the nutrient recoveries in the curd and the daily cheese yields), and to evaluate their genetic relationships with the milk production and composition with the aim to analyse possible new selection criteria to be implemented, in addition to the present selection for the dual purpose, in the Rendena breed;

IV. to estimate genetic correlations between beef traits and the linear type traits related to muscularity evaluated in young bulls during performance test and muscularity linear type traits collected in first parity cows. This evaluation was performed to consider the possibility of selecting the morphological traits measured on young bulls instead that on cows.

CHAPTER 1

HETEROGENEITY OF VARIANCE FOR MILK, FAT AND PROTEIN YIELD IN SMALL CATTLE POPULATIONS: THE RENDENA BREED AS CASE STUDY

Under Submission

ABSTRACT

The aim of this study was to identify possible heterogeneity of variance for productive traits in a small cattle population. The Rendena breed, accounting for about 4,000 registered cows, was used as case study. At first, using average milk yield recorded in each Rendena farm under functional control in years 2004-2013 (114 farms) productive groups (low, medium and high levels) were identified via cluster analysis. Only the farms in medium and high productive levels were retained for the following analysis. Subsequently, a sample of 49 herds with the same numerical proportion as in medium and highly productive levels was obtained, and 73,916 test-day records for milk, fat and protein yields belonging to 4,582 cows were used to estimate heritability and genetic correlations between groups. The (co)variance components estimated for yields traits (kg) between productive groups were obtained via bi-trait repeatability test day model in which milk, fat and protein yields in two productive groups were considered as different traits using a bayesian approach. The estimated genetic (σ_a) and permanent environmental (σ_{pe}) variances resulted higher in highly than in medium productive level, i.e., σ_a was doubled and σ_{pe} was increased of about 60% for both milk, fat and protein yields. Heritabilities for milk, fat and protein yields in medium productive level were lower (0.16, 0.15 and 0.22, respectively) than in highly productive levels (0.30, 0.22 and 0.25). However, the genetic correlations between productive groups were 0.90 for milk and 0.88 both for fat and protein yield and the rank correlation between EBVs of bulls that had daughters in both groups resulted 0.98. This study suggests that a genetic evaluation not accounting for the heterogeneous variance may be applied without producing biased estimates, at least for bulls EBVs. On the other hand, a more careful selection should be considered for cows, i.e., for bull dams in particular.

Key Words: Heterogeneity of variance, yield traits, genetic parameters, Rendena breed

INTRODUCTION

Small local breeds have gained increasing interest in the maintenance of genetic diversity within the animal genetic resources (Ollivier and Foulley, 2005). The survival of the small local populations is mainly attributable to their diffusion in marginal areas and factors related to the traditional rural culture (Gandini and Villa, 2003). Native cattle breeds, especially dual purpose breed, have fewer productions than cosmopolitan breeds, and they are therefore economically less competitive, but they have important secondary characteristics of hardiness and adaptability to the environment, longevity, good fertility, and resistance both to the disease and to the stress that the cosmopolitan breeds have lost in the process of selection favouring a greater productivity (Biscarini et al. 2015). The main breeding goal in many small local populations deals with the control of the annual inbreeding rate that according to Meuwissen and Woolliams (1994) should be less than 1% per generation. However, selection goals of these small population is also based on the maintenance of a good compromise between the improvement of production performance (both milk and meat) and the preservation of the functional traits that distinguish them as compared to cosmopolitan breeds (Biscarini et al. 2015).

From a practical point of view, selection in small populations must take into account some technical problems linked to the population structure. Due to their adaptability to different environments, these populations may have different breeding areas, herd size, farming systems and feeding strategies, as well as production levels. In these situations, an effective genetic improvement must take into account both the small population size and the heterogeneity of breeding environments that may differ largely causing heterogeneity of variance between environments and/or farms (Brotherstone and Hill, 1986; Weigel et al., 1993; Ibanez et al., 1996; Costa, 1999; Fuerst-Waltl 2013). Numerous studies have indeed reported genetic, environmental and residual variances and, thus, the heritability of production traits heterogeneous between environments and farms (Hill et al., 1983; De Veer and Van Vleck, 1986; Boldman and Freeman, 1990; Dong and Mao, 1990). According to some authors, there is a positive connection between the increase in production levels and the increase in variance components and heritability; for this reason to cluster the herds on the mean yields could be considered an effective way to define environments potentially showing heterogeneity of variance (De Veer and Van Vleck, 1987; Dong and Mao, 1990; Boldman and Freeman, 1990). Falconer (1952) proposed to utilize genetic correlations to assess heterogeneity of variance, considering the same trait in different environments as different traits. Robertson (1959) suggested a genetic correlation of 0.80 between the same trait in different environments as threshold to discriminate between the presence and the absence of variance heterogeneity. Ignoring heterogeneous variances reduces indeed the accuracy of the estimated breeding values (EBV), resulting in inappropriate selective choices that could affect the genetic progress for a given trait (Hill, 1984; Vinson, 1987). To mitigate the problem of heterogeneous variance, different procedures have been suggested and implemented. Among suggested methods, the adjustment of production data before the genetic evaluation has been proposed by Wiggans and VanRaden (1991). Subsequently, others methods considering models accounting directly for the effect of the heterogeneity of variance have been suggested (Meuwissen et al., 1996).

Considering that the productive environments can be different both within and between breeds, detailed studies on heterogeneity of environments could be useful for a correct breeding plan to be adopted for any small cattle population. In the context of the Italian local breeds, the Rendena is a small dual purpose cattle breed selected for milk and meat productions (Mazza et al., 2014). This breed has the peculiarity of being raised both in mountain and in plain with similar amount of heads in the two environments, where the management of farms and the feeding strategies are different and associated with the area's resources; in mountain, for example, the farming system is traditional (i.e., tied animals fed hay and concentrate) and based on the practice of the alpine pasture for the whole herds during the summer season. However, in plain the rearing system of Rendena cattle is more intensive (i.e, feeding system mainly based on the use corn silage), with the summer alpine pasture that is common for young cattle only. Moreover, bull sires and bull dams yearly selected seems to come from a too limited group of farms, and breeders’ complain on this problem are well known to the breeders association that is charge for the selection program. Therefore, investigation on possible between-herd variance heterogeneity due to the small population size could be useful for the Rendena cattle breed, but it could be of general interest also for other small dual purpose breeds under selection. The objectives of this study were to estimate variance components, heritability and the genetic correlations for milk, fat and protein yields between different environments defined for the Rendena breed. Rank correlations between EBV of bulls simultaneously estimated in different environments were also analysed as possible fall-out of the variance heterogeneity problem.

MATERIALS AND METHODS

Subject of the study

The Rendena breed is a small cattle population accounting for about 4,000 registered cows in the herd book, reared in the North-east of Italy (i.e., Trentino Alto Adige and Veneto regions). Rendena cattle is characterized by small to medium body size, good fertility, i.e., a median days open period of about 116 days, and good longevity, accounting approximately 3.3 lactations per cow (ANARE, 2015). The main characteristic of the breed is the rusticity, namely its ability to adapt itself to difficult environments and marginal areas, as well as its suitability to graze during the summer season in the alpine high pastures (Mantovani et al. 1997). The selection objective in Rendena breed is the improvement of milk yield and quality without losing the beef aptitude. In 2015 the average milk yield was about 5,200 kg per lactation with 3.47% fat and 3.24% protein. As reported by Mazza et al. (2014), the 65% of the selection index currently applied to Rendena cattle includes protein and fat (3:1) corrected milk yield, while the remaining 35% account for beef traits measured at the performance testing station and with linear type evaluations. The traditional lactation model used for the genetic evaluation of the milk attitude in Rendena breed has been replaced in 2009 by a repeatability test day model (Guzzo et al, 2009).

Definition and characteristics of productive groups

A total of 963 conventional average lactation milk yields (i.e., 305 DIM) belonging to 114 Rendena farms under functional control between the years 2004 to 2013 was initially used to define possible within breed productive groups. Data were extracted from the whole national dataset collected by the Italian Animal Breeders Association. A weighted average herd milk yield per cow for each farm over the 10 years was calculated by weighting the yearly herd milk yield per cow for the number of cows under functional control. Three productive groups of farms were identified via cluster analysis performed using the CLUSTER procedure (SAS Institute Inc., 2009). The groups of farms were defined as low, medium and high level of production and they differed for number of herds (13, 80 and 21 respectively) and average lactation milk yield (2,797, 4,464 and 6,142 kg, respectively). The group of low production contained only marginal farms, and had few farms, thus it was not considered in subsequent analyses. Factors such as geographical location, management practices, feeding strategies and practice of alpine pasture were then recruited from the herd book database and used to check for possible further differentiation of farms belonging to the different productive groups identified. The main characteristics of the groups of farms are given in Table 1. The first group (farms with medium production level) consisted in 80 herds with an average 305 DIM milk yield of 4,464 kg/year/cow. The 56% of these farms are located in mountain and in hill environments, and they are characterised by traditional farming systems, i.e., tie-stalls (90%) with feeding based on hay and compound feeds (73%). Moreover, 63% of farms practice the alpine pasture during the summer season (Table 1). The second group of farms (i.e., those with higher production level) consisted in 21 herds with an average 305 DIM milk yield of 6,142 kg/year/cow. The farms are largely situated in plain (67%), and farming systems is mainly traditional although with the presence of modern dairy systems based on loose housing of animals (52%) and TMR feeding practice (33%). Finally, only a small proportion of farms in this group (i.e., 20%) practice the alpine pasture during the summer season.

A random sampling of 49 herds, maintaining the same numerical proportion as in the two medium and high productive groups previously identified were then considered for the subsequent analysis. From these farms a total number of 73,916 test-day (TD) records of milk, fat and protein yields of 9,538 lactations, belonging to 4,582 cows and referred to 9,715 animals in pedigree file, was obtained and used to estimate variance components, heritability and genetic correlations between groups. Individual TD data for milk, fat and protein yields were provided by the National Association of Breeders of Rendena cattle and collected from 1999 to 2014. The TD records allowed to enter the final data set belonged to the first 3 lactations of cows, were registered as first TD within the first 45 DIM, and were recorder between 5 to 305 DIM. Lastly, only the herd-TD within lactation with at least 2 TD records and the lactations with a least 4 TD were retained for analysis.

Statistical Analysis

The (co)variance components estimated for yields traits (kg) between productive groups were obtained via bi-trait repeatability test day models in which milk, fat and protein yields in two productive groups were considered as different traits. The final model may be written as follows:

$$y_{ijklmn} = \mu + \text{HTD-LN}_i + \text{GEST}_j + \sum_{r=0}^{4} \varphi_r \text{AP-LN}_k + \sum_{r=0}^{4} \varphi_r \text{MP-LN}_l + \text{Pe}_m + a_n + e_{ijklmn},$$

where y_{ijklmn} is the test-day record o of milk, fat or protein (kg) of the cow n; μ the overall mean; HTD-LN_i is the fixed effect of herd-test-day within lactation number i (12,905 levels); GEST_j is the fixed effect of the days of gestation class j (18 classes: the first class means no gestation; the further classes accounts for 15 d intervals from 1 to 240 d of gestation; and the last class considers ≥ 241 d of gestation); AP-LN_k is the fixed effect of age at parity within lactation k (42 classes in total); MP-LN_l is the fixed effect of the month of parity l (36 classes corresponding to single month of year within lactation n); Pe_m is the random permanent environmental component; a_n is the additive genetic component, and e_{ijklmn} is the random residual term. The shape of the lactation curve was described by 4th order Legendre polynomials for the fixed effects of AP-LN and MP-LN.

The bi-trait analyses considered the following (co)variance assumptions:

$$\mathbf{A}=\begin{vmatrix} \sigma^2_{a1} & \sigma_{a1\,a2} \\ \sigma_{a1\,a2} & \sigma^2_{a2} \end{vmatrix};\ \mathbf{Pe}=\begin{vmatrix} \sigma^2_{pe1} & \sigma_{pe1\,pe2} \\ \sigma_{pe1\,pe2} & \sigma^2_{pe2} \end{vmatrix};\ \mathbf{R}=\begin{vmatrix} \sigma^2_{e1} & \sigma_{e1e2} \\ \sigma_{e1e2} & \sigma^2_{e2} \end{vmatrix};$$

where A is the matrix of additive genetic (co)variances σ^2_{a1}, σ^2_{a2}, σ_{a1a2} for traits 1 and 2, Pe is the matrix of permanent environmental (co)variances σ^2_{pe1}, σ_{pe1pe2}, σ^2_{pe2}, and R the matrix of residual covariances σ^2_{e1}, σ^2_{e2} and σ_{e1e2}.

Data were analysed via a Bayesian approach through the program “gibbs3f90” (Misztal, 2008). The Gibbs sampler performed 950,000 iterations with a starting burn-in that discarded 50,000 samples. The posterior mean of 3,000 samples (i.e., 1 of every 300 samples of the remaining 900,000) was used as a point estimate of (co)variance components and related parameters under investigation. Lower and upper bounds of the 95% highest posterior density intervals (HPD 95%) for additive, permanent environment and residual effects were estimated from the Gibbs samples. The posterior means and corresponding HPD 95% were also computed for all heritability estimates and correlations between yield traits and the two different farm groups. Heritability were obtained as $h^2 = \sigma^2_a/\sigma^2_p$, with the phenotypic variance σ^2_p as the sum of all the other variances. The genetic correlations of yields traits in different environments were obtained as $r_a = \sigma_{a1a2}/(\sigma^2_{a1}\cdot\sigma^2_{a2})^{\wedge 0.5}$. The heterogeneity of variance was assessed from the genetic correlation (r_a) of the same traits (milk, fat and protein yield) measured in different environments as in Costa (1999). A threshold of $r_a = 0.80$ was considerate to establish if heterogeneity of variance occurred or not (Boettcher et al., 2003). A rank correlation analysis was performed considering estimated breeding values (EBVs) derived from a best linear unbiased prediction (BLUP) bivariate analysis on the same yield trait considering different groups (BLUPF90, Misztal et al., 2008). Each BLUP run was performed by accounting for the appropriate estimates of (co)variances previously obtained via Bayesian approach (i.e., posterior mean). EBVs belonging to bulls evaluated in medium productive farm group were correlated with

EBVs of the same bulls obtained in highly productive farm group. Rank correlation analyses were carried out within traits (milk, fat and protein) considering the bulls that had daughters in both groups.

RESULTS

Table 2 shows some descriptive statistics of the sample dataset and all considered yield traits in two productive groups identified in the Rendena breed. The mean daily milk, fat and protein yield was greater in highly productive than in medium productive farms of 27.6%, 27.3%, and 31.4%, respectively. For each trait analysed the coefficient of variation was slightly greater in medium productive that in highly productive farm group, i.e., resulting about 32% and 30% for milk, 35% and 31% for fat, and 31% and 28% for protein, respectively.

The point estimates, mean and standard deviation of marginal posterior densities, for additive genetic, permanent environment and residual variances, and heritability obtained from bi-trait analysis are presented in Table 3. The differences among variance components for milk yield traits estimated by production farm groups were large in these data. The milk yield showed higher point estimate for additive, permanent environment, and residual variances in highly than in medium productive farm groups of 188%, 43% and 20% respectively. Consequently, the heritability was 0.16 in medium and 0.30 in high productive groups. The HDP 95% for variance components and heritability of milk yield indicated asymmetry in the marginal posterior distribution with a more dispersion of additive and permanent environment variances, and heritability in highly productive farm group as respect to medium productive farms. The point estimate of additive genetic variance in fat and protein yields were 0.003 kg^2 in medium and 0.005 kg^2 in highly productive farm groups and similar values were obtained for the permanent variance estimates (i.e., 0.004 kg^2 and 0.008 kg^2 in medium and highly productive groups, respectively). The heritability of fat and protein yields were about 0.15 in medium productive farm group, while in the other group a point estimate of 0.22 for fat and 0.25 for protein yields were observed. Both in fat and protein yields, the two productive farm groups showed asymmetry in the marginal posterior distribution of variance components and heritability, with still a greater dispersion in highly productive farm group.

The point estimate of the genetic correlations for the same trait but between the two productive farm groups were all high and positive considering all yield traits. A point estimate (mean of the posterior distribution) of 0.90 for milk, 0.88 for fat and 0.88 for protein yields were obtained, respectively. The posterior density obtained for the genetic correlations for the same trait between different productive farm groups showed an overlapping distribution both milk (Figure 1; HDP 95% 0.69-1.11), fat (HDP 95% 0.66-1.11), and protein (HDP 95% 0.67-1.10) yields.

The rank correlations between EBVs of bulls that had daughters in both productive farm groups considering milk, fat and protein yields are reported in Table 4. A total of 499 bulls were evaluated in both productive groups (i.e. 452 and 368 bulls in medium and high productive groups, respectively), 64% of which were shared between productive groups. In all cases, the rank correlation of shared bulls for the 3 traits yield resulted rather high, ranging from 0.97 for fat and protein to 0.98 for milk.

DISCUSSION

Grouped farms based on average milk yields was a simple way for investigating possible effects of heterogeneity of variance in genetic evaluation of production traits (Boldman and Freeman, 1990). However, in the present study, this criterion allowed to found a connection between productive level of farms and management practices in the case of Rendena breed. Genetic, permanent environment and residual variances estimated in medium and high productive levels, in this work, resulted lower and higher, respectively, than the variance components obtained in same breed considering all farms (Guzzo et al., 2009). This could be expected considering that the combination of the two different productive groups represent almost the entire herds. Indeed, without grouping the farms for productive levels the following variance components were obtained: genetic variance of 2.780 for milk, 0.004 for fat and 0.002 for protein; permanent environment variance of 5.500 for milk, 0.006 for fat and 0.005 for protein; residual variance of 4.547 for milk, 0.012 for fat and 0.005 for protein yield (data not shown). Using a repeatability test-day model similar to the one used in this study, Dal Zotto (2005) reported genetic variance values for milk yield in Italian Brown Swiss in the middle between those obtained in medium and high productive groups of the present study. Mazza et al. (2016) reported genetic, permanent environment and residual variances in the local Italian dual purpose Aosta Red Pied breed that were even lower than those estimated in the medium productive group in this study. However, the Aosta Red Pied is characterized by a lower average milk production as compared to the Rendena breed, both considering the whole lactation and a test day base (Guzzo et al., 2009; Mazza et al., 2016). Analyses carried out in this work indicated that the genetic, permanent environment and residual variances are not homogeneous for the different productive groups. In agreement with previous studies (De Veer and Van Vleck, 1987; Boldman and Freeman, 1990; Dong and Mao, 1990; Ceron-Munoz, 2004) using lactations milk yield, estimates of the variance components increased with increased productive level.

The heritability (h^2) values estimated for milk, fat and protein yields in two different productive groups of this work were different from the heritability obtained considering all farms of the same breed by Guzzo at al. (2009), where h^2 values of 0.21 for milk and 0.17 for fat and protein yield were reported. The heritability estimates for milk, fat and protein yield obtained in this study were in the range of values reported for the same traits, using a repeatability test-day model, in specialized Holstein and Jersey (Bormann et al., 2002) and in local Italian dual purpose Aosta Red Pied breed (Mazza, 2016), but were greater than estimates reported by Dal Zotto (2000) in Italian Brown Swiss (i.e., 0.14, 0.09 and 0.13 for milk, fat and protein yields, respectively). In the present study, the heritability of yield traits increased with increased production level. Similar results were reported by numerous studies (De Veer and Van Vleck, 1987; Dong and Mao, 1990; Ceron-Munoz, 2004). Boldman and Freeman (1990), e.g., reported heritability values of 0.18, 0.22 and 0.24 for milk yield in low, medium and high productive herds. Conversely, Costa (1999) obtained for milk and fat yields greater heritability in low than in high herd production level (0.30 vs. 0.22 for milk, and 0.23 vs. 0.20 for fat, respectively) considering the herd-year phenotypic standard deviation for mature equivalent milk as reference for grouping herds. Results from De Veer and Van Vleck (1987), and Weigel et al. (1993) suggested that herd size, management practices, and feeding strategies may be factors responsible for change in variance components and heritability values between different herd or environments. Concerning our study, some possible causes explaining the heterogeneity of variance attained may be mainly identified in the management systems of herds included in the two groups. The highly productive farms' group included indeed both tie-stall and loose housing systems almost in the same proportions (Table 1), whereas in the medium productive group 90% of farms were tie-stalls. Furthermore, the high productive group included a greater proportion of farms that did not practice the summer alpine pasture, being most of them located in plain and adopting management and feeding practices aimed at maximizing milk yield. In addition, farms in the high productive group invested more money in modernity and efficiency of their structures and their herd size resulted on average slightly greater (e.g., 51±38 vs. 41±33 cows; data not shown), i.e., increasing the chance of a within herd greater yield variability among animals than in smaller herds.

The estimates of genetic correlations for milk, fat and protein yields between the two productive groups of farms were around 0.88 or more, well above the threshold of 0.80 suggested by Robertson (1959) as critical point to detect variance heterogeneity. However, the value of correlation for milk yield obtained in this work was lower than the value reported by Boldman and Freeman (1990) and Dong and Mao (1990), which were around 0.97 or greater considering different groups on the basis of their productive level. Correlations similar to those here obtained were also reported from studies that have defined the environments on the basis of management systems or feeding strategies. For example, Boettcher (2003) reported genetic correlations equal to 0.93 for milk, 0.88 for fat and 0.94 for protein yields between conventional and grazing management systems, while Cromie et al. (2006) after clustering herd environments according to the input of concentrate have reported genetic correlations of 0.92 for milk, 0.89 for fat and 0.91 for protein yields.

Estimates of genetic correlations for milk, fat and protein yields in the present study were relatively large between productive groups, suggesting similar rankings for milk, fat and protein yield in different environments. The high rank correlation between EBVs of bulls that had daughters in both productive groups for all traits yield confirmed that the bulls evaluated in a group or another were not affected by a re-ranking due to variance heterogeneity. However other authors (Boldman and Freeman, 1990; Aliloo et al., 2014) reported that unadjusted estimates for heterogeneity had greater impact on cows' evaluation than on bulls' evaluation, considering that bulls are generally evaluated in both environments, while cows are evaluated within herd and compared across herds.

CONCLUSIONS

Results of this study revealed differences in variance components and heritability for milk, fat and protein yields between medium and high productive herd in Rendena breed. Variance components and heritability values increased as the production increase, and consequently, the selection would be more efficient using information form farms with higher average production level. Although the differences in variance components between herd environments, the genetic correlations for milk, fat and protein yields in different environments were high, as well as the rank correlation of bulls having daughters in both environments. The detection of a possible heterogeneity in variance is important when population may be grouped in different, well defined environments as in Rendena breed. However the high genetic correlations between traits in different environments and the high rank correlation between EBVs of bulls, this study suggests that a genetic evaluation not accounting for the heterogeneous variance may be applied without producing biased estimates, at least for bulls EBVs. On the other hand, a more careful selection should be considered for cows, i.e., for bull dams in particular.

REFERENCES

Aliloo, H., Miraie-Ashtiani, S. R., Shahrbabak, M. M., Urioste, J. I., & Sadeghi, M. (2014). Accounting for heterogeneity of phenotypic variance in Iranian Holstein test-day milk yield records. Livestock Science, 167, 25-32.

ANARE (2016) Risultati controlli funzionali 2015. La Rendena, 1-2, 25–29.

Biscarini, F., Nicolazzi, E. L., Stella, A., Boettcher, P. J., & Gandini, G. (2015). Challenges and opportunities in genetic improvement of local livestock breeds.

Boettcher, P. J., Fatehi, J., & Schutz, M. M. (2003). Genotype×environment interactions in conventional versus pasture-based dairies in Canada. Journal of Dairy Science, 86(1), 383-389.

Boldman, K. G., & Freeman, A. E. (1990). Adjustment for heterogeneity of variances by herd production level in dairy cow and sire evaluation1. Journal of Dairy Science, 73(2), 503-512.

Bormann, J., Wiggans, G. R., Druet, T., & Gengler, N. (2002). Estimating effects of permanent environment, lactation stage, age, and pregnancy on test-day yield. Journal of dairy science, 85(1), 263-e1.

Brotherstone, S., & Hill, W. G. (1986). Heterogeneity of variance amongst herds for milk production. Animal production, 42(03), 297-303.

Ceron-Munoz, M. F., Tonhati, H., Costa, C. N., Rojas-Sarmiento, D., & Echeverri, D. E. (2004). Factors that cause genotype by environment interaction and use of a multiple-trait herd-cluster model for milk yield of Holstein cattle from Brazil and Colombia. Journal of dairy science, 87(8), 2687-2692.

Costa, C. N. (1999). An investigation into heterogeneity of variance for milk and fat yields of Holstein cows in Brazilian herd environments. Genetics and molecular biology, 22(3), 375-381.

Cromie, A. R., Kelleher, D. L., Gordon, F. J., & Rath, M. (1999). Genotype by environment interaction for milk production traits in Holstein Friesian dairy cattle in Ireland (Doctoral dissertation, Queen's University of Belfast).

Dal Zotto, R. (2000, May). Comparison of different test-day models for genetic evaluation of Italian Brown dairy cattle. In Proceedings of the international workshop on genetic improvement of functional traits in cattle (Vol. 25, pp. 95-98).

Dal Zotto, R., Carnier, P., Gallo, L., Bittante, G., & Cassandro, M. (2005). Genetic relationship between body condition score, fertility, type and production traits in Brown Swiss dairy cows. Italian Journal of Animal Science, 4(sup3), 30-32.

De Veer, J.C., & Van Vleck, L. D. (1987).Genetic parameters for first lactation milk yields at three levels of herd production. Journal of Dairy Science, 70(7), 1434-1441.

Dong, M. C., & Mao, I. L. (1990). Heterogeneity of (co)variance and heritability m different levels of intraherd milk production variance and of herd average. Journal of Dairy Science, 73(3), 843-851.

Falconer, D. S. (1952). The problem of environment and selection. The American Naturalist, 86(830), 293-298.

Fuerst-Waltl, B., Schwarzenbacher, H., & Fuerst, C. (2013). Genetic relationships under different management systems and their consequences for dairy cattle breeding. Agriculturae Conspectus Scientificus (ACS), 78(3), 183-186.

Gandini, G. C., & Villa, E. (2003). Analysis of the cultural value of local livestock breeds: a methodology. Journal of Animal Breeding and Genetics, 120(1), 1-11.

Guzzo, N., Sartori, C., & Mantovani, R. (2009). Test day-milk yields variance component estimation using repeatability or random regression models in the Rendena breed. Italian Journal of Animal Science, 8(sup3), 71-73.

Hill, W. G., Edwards, M. R., Ahmedm, M.-K. A., & Thompson, R. (1983). Heritability of milk yield and composition at different levels and variability of production. Animal Production, 36: 59-68.

Hill, W. G. (1984). On selection among groups with heterogeneous variance. Animal Production, 39(03), 473-477.

Ibanez, M. A., Carabano, M. J., Foulley, J. L., & Alenda, R. (1996). Heterogeneity of herd-period phenotypic variances in the Spanish Holstein-Friesian cattle: Sources of heterogeneity and genetic evaluation. Livestock Production Science, 45(2), 137-147.

Mazza, S., Guzzo, N., Sartori, C., Berry, D. P., & Mantovani, R. (2014). Genetic parameters for linear type traits in the Rendena dual purpose breed. Journal of Animal Breeding and Genetics, 131(1), 27-35.

Mazza, S., Guzzo, N., Sartori, C., & Mantovani, R. (2016). Genetic correlations between type and test-day milk yield in small dual-purpose cattle populations: The Aosta Red Pied breed as a case study. Journal of Dairy Science, 99(10), 8127-8136.

Mantovani, R., Gallo L., Carnier, P., Cassandro, M., & Bittante, G. (1997). The use of a juvenile selection scheme for genetic improvement of small population: the example of Rendena breed. In: 48th Annual Meeting of the European Association of Animal Production, Vienna, Austria, 25–28 August 1997, 5 pp.

Misztal, I. (2008). Reliable computing in estimation of variance components. Journal of animal breeding and genetics, 125(6), 363-370.

Woolliams, J. A. (1994). Effective sizes of livestock populations to prevent a decline in fitness. Theoretical and Applied Genetics, 89(7-8), 1019-1026.

Meuwissen, T. H. E., De Jong, G., & Engel, B. (1996). Joint estimation of breeding values and heterogeneous variances of large data files. Journal of dairy science, 79(2), 310-316.

Ollivier, L., & Foulley, J. L. (2005). Aggregate diversity: new approach combining within- and between-breed genetic diversity. Livestock Production Science, 95(3), 247-254.

Robertson, A., (1959). The sampling variance of genetic correlation coefficient. Biometrics 15: 469-485.

SAS Institute Inc. (2009) SAS/STAT 9.2 User’s Guide, 2nd edn. SAS Institute Inc, Cary, NC.

Vinson, W. E. (1987). Potential bias in genetic evaluations from differences in variation within herds. Journal of Dairy Science, 70(11), 2450-2455.

Weigel, K. A., Gianola, D., Yandell, B. S., & Keown, J. F. (1993). Identification of factors causing heterogeneous within-herd variance components using a structural model for variances. Journal of Dairy Science, 76(5), 1466-1478.

Wiggans, G. R., & VanRaden, P. M. (1991). Method and effect of adjustment for heterogeneous variance. Journal of dairy science, 74(12), 4350-4357.

Table 1. Number of herds, mean, standard deviation, and range for 305 DIM average milk yield within herd-year and characteristics of herd in the farm groups.

Item	Farm groups	
	Medium productive farms	Highly productive farms
Herds, no.	80	21
Milk yield, kg		
Mean ± SD	4,464.2 ± 529.0	6,142.0 ± 447.5
Range	3,508.1 to 5,450.3	5,531.1 to 739.4
Type of housing, %		
Tie-stall	0.90	0.48
Loose housing	0.10	0.52
Feeding system, %		
Traditional	0.73	0.57
Traditional with silage	0.15	0.10
TMR	0.13	0.33
Geographical area, %		
Hill	0.08	0.05
Mountain	0.49	0.29
Plain	0.44	0.67
Alpine pasture, %		
Yes	0.63	0.19
No	0.38	0.81

Table 2. Descriptive statistics for daily milk, fat and protein yields recorded in medium productive and highly productive farm groups of Rendena cattle in the sample dataset used.

Item	Farm group	
	Medium productive farms	Highly productive farms
Herds, no.	39	10
Test Day records, no.	48,608	25,308
Milk yield, kg/d		
Mean ± SD	15.63 ± 4.96	19.95 ± 5.95
Range	1.60 to 39.80	1.90 to 43.70
Fat yield, kg/d		
Mean ± SD	0.55 ± 0.19	0.70 ± 0.22
Range	0.04 to 1.83	0.03 to 1.98
Protein yield, kg/d		
Mean ± SD	0.51 ± 0.16	0.67 ± 0.19
Range	0.05 to 1.42	0.06 to 1.50

Table 3. Estimated marginal posterior densities and HPD 95% for genetic variance (σ^2_a), permanent environmental variance (σ^2_{pe}), residual variance (σ^2_e), and h^2 for milk, fat and protein yields obtained in two different farm groups of Rendena cattle.

Item	Farm group			
	Medium productive farms		Highly productive farms	
	Mean ± SD	HDP 95%	Mean ± SD	HDP 95%
Milk yield, kg				
σ^2_a	1.737 ± 0.247	1.253; 2.221	5.000 ± 0.682	3.669; 6.340
σ^2_{pe}	4.700 ± 0.308	4.099; 5.308	6.740 ± 0.699	5.374; 8.115
σ^2_e	4.134 ± 0.032	4.072; 4.197	4.950 ± 0.053	4.846; 5.054
h^2	0.164 ± 0.022	0.121; 0.207	0.299 ± 0.036	0.230; 0.369
Fat yield, kg				
σ^2_a	0.003 ± 0.000	0.002; 0.004	0.006 ± 0.001	0.004; 0.007
σ^2_{pe}	0.006 ± 0.000	0.005; 0.007	0.008 ± 0.001	0.006; 0.009
σ^2_e	0.011 ± 0.000	0.011; 0.011	0.013 ± 0.000	0.013; 0.013
h^2	0.147 ± 0.018	0.111; 0.183	0.219 ± 0.027	0.165; 0.273
Protein yield, kg				
σ^2_a	0.002 ± 0.000	0.001; 0.002	0.004 ± 0.001	0.003; 0.006
σ^2_{pe}	0.004 ± 0.000	0.004; 0.004	0.007 ± 0.001	0.005; 0.008
σ^2_e	0.005 ± 0.000	0.005; 0.005	0.006 ± 0.000	0.006; 0.006
h^2	0.152 ± 0.021	0.110; 0.194	0.251 ± 0.035	0.182; 0.321

Figure 1. Estimated marginal posterior densities of genetic correlations between medium and highly productive groups of Rendena farms for milk (continuous line), fat (dashed line) and protein (dotted line) yields.

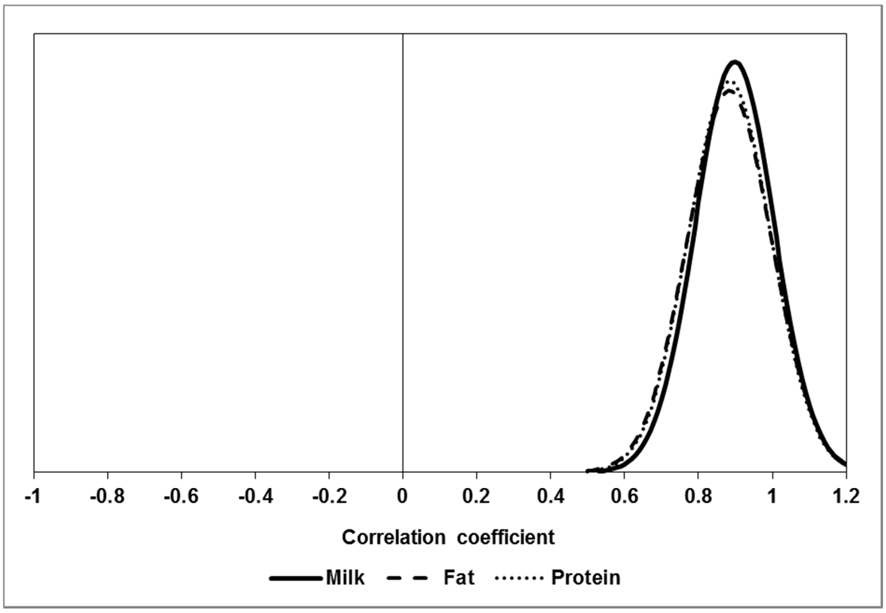


Table 4. Rank correlations obtained from EBV produced by bivariate BLUP analysis of the same trait in medium and highly productive groups of Rendena farms for milk, fat and protein yields. Rand correlations were obtained for bulls with daughters in both groups.

Item	Farm groups	
	Medium productive farms	Highly productive farms
Bulls, no.	452	368
Shared bulls, %	0.64	
Rank correlation, %		
Milk	0.98	
Fat	0.97	
Protein	0.97	

CHAPTER 2

DEVELOPMENT OF A METHOD FOR TEST-DAY MODELS ANALYSIS OF SOMATIC CELL IN RENDENA BREED

Under Submission

ABSTRACT

The objective of this study was to consider different and alternative methods of using somatic cell count (SCC) data recorded during functional controls as udder health indicator in Rendena breed, estimating its genetic parameters and the correlations with the yield traits (milk, fat and protein) under selection. The SCC traits defined for genetic evaluation were: somatic cells score (SCS), the logarithm of the total somatic cell count (LTSCC) and three different thresholds (80,000 cells/ml: SCC80, 150,000: SCC150 and 400,000: SCC400) for SCC related to the incidence of mastitis. A total of 69,796 TD records of milk, fat, protein yields and SCC belonging to 4,325 cows was used to estimate heritability and genetic correlations between SCC and yield traits via bi-trait repeatability test day model using a Bayesian approach. The heritability values estimated for the threshold traits ranged from 0.04 to 0.07, lower than those observed for SCS and LTSCC traits that were equivalent to 0.09 and 0.10, respectively. The highest genetic correlations were estimated between LTSCC and productive traits (0.29 for milk, 0.16 for fat and 0.28 for protein). The others udder health traits considered have showed almost null genetic correlations with the productive traits (from -0.09 between fat yield and SCS, to 0.13 between protein yield and SCC400). These results indicated that the genetic selection for milk, fat and protein production does not increase the content of somatic cells in milk and therefore does not negatively influence the udder health in Rendena breed. However, the complete framework of genetic relationships of SCC with all traits under selection should be considered to evaluate a possible inclusion of SCC in the breeding program.

Key Words: Somatic cell count, udder health, Rendena breed, genetic parameters.

INTRODUCTION

Mastitis is an inflammation of the mammary gland, and it is one of the most frequent and costly diseases in dairy cattle (Nielsen, 2009). Considering the economic consequence of mastitis, selection for mastitis resistance should not be neglect in dairy breeding program, but genetic evaluation of mastitis is difficult because of its low heritability (Urioste et al, 2010; Koeck et al., 2012) and the routine recording of mastitis is not routinely carried out in many countries, including Italy. Usually, the somatic cell count (SCC), that is regularly recorded in functional controls, is considered the most common and suitable indicator of mastitis, in light of its high positive genetic correlation with mastitis and a greater than mastitis heritability (Carlen et al, 2004; Koivula et al., 2005; Vallimont et al., 2009). Recent studies (Macciotta et al., 2012; Bobbo et al., 2014) reported that also other traits such as lactose, pH, lactoferrin and minerals could be used as udder health indicators, opening the space for a deep control of mastitis at herd level using data from functional control.

However, at present the SCC still remain the most diffused method for controlling udder health, and in most countries (Miglior et al., 2005), genetic evaluation of udder health is based on the logarithmic transformation of SCC in somatic cell score (SCS) to achieve normality of distribution (Ali and Shook, 1980). It is well known indeed that SCC data are not normally distributed and some studies have indicated that the logarithmic transformation of SCC produces data with a more normal distribution, increasing heritability, and reducing within-herd heterogeneity (Shook, 2006). Recently, alternative SCC traits have been proposed as new method to highlight mastitis, suggesting possible improvement of genetic evaluations methods for mastitis resistance. The new traits studied should make clearer the dynamic nature of mastitis and to be flexible enough to accommodate for sudden changes in SCC, especially resulting from cases of clinical mastitis. For example, Urioste et al. (2010) have used the measures of days sick during the lactation as a trait to be used for controlling mastitis resistance in dairy cattle; on the other hand, peak patterns have been suggested by de Haas et al. (2008) to better describe the dynamic nature of mastitis cases.

Other traits have been derived directly form SCC by defining a test-day SCC threshold distinguishing healthy or unhealthy cows, or suggesting the occurrence of a subclinical or a clinical mastitis (de Haas et al., 2008; Urioste et al., 2010). Together with SCS and with the other udder health indicators abovementioned, all these traits are aimed to provide reliable indicators of mastitis incidence to be included in breeding programs. Current selection indices in specialized dairy cattle breeds typically include udder health indicators such as SCS to counteract the negative effects of selection for yield on health, longevity and reproduction (e.g., Miglior et al., 2005; Oltenacu and Broom, 2010). Recently, udder health indicators have been also introduced in selection indices of some dual purpose breeds as Austrian Simmental (Fuerst-Waltl et al., 2016), but a number of dual purpose populations has not considered udder health indicators in genetic improvement yet. This is the case of many small autochthonous local breed diffused in Italy like the Rendena, an Italian dual purpose breed native of Trento province in the eastern Italian Alps (Mazza et al., 2014). In this breed the current selection program does not include udder health indicators, although test-day SCC information have been routinely recorded and stored since 1996 (ANARE, 2016). In addition, milk production is increasing in the breed (ANARE, 2016) and considering the positive correlation with the mastitis incidence, there is an increasing interest for mastitis control even in this small breed. Furthermore, milk yield is the most important trait under selection in the dual purpose breeding scheme of the Rendena (65% of incidence in the global selection index), and possible new selection strategies toward udder health is under consideration by the national breeders organization. Therefore, the perspective of new tools in the breeding program of the Rendena cattle is nowadays actual. On the basis of this new possible breeding goal for the Rendena breed, the present study aimed at investigating the feasible inclusion of new udder health traits in the Rendena breeding program. Particularly, the study has considered different and alternative methods of using SCC data from functional controls as udder health indicator in Rendena breed, investigating its genetic parameters and the correlations with other milk production traits at present under selection.

MATERIALS AND METHODS

Data and editing

Production, quality traits (fat and protein content), SCC, and population genealogic data were provided by the National Association of Breeders of Rendena cattle (ANARE). Somatic cells count (SCC) is routinely collected from official milk recording system since 1996 in Rendena cattle. The initial dataset used in the present study consisted of 437,616 monthly test-day (TD) records for milk, fat, protein yields and SCC recorded between 1999 and 2014. For this study, the test-day records with missing milk, fat, protein and SCC yields were discarded and only TD in the first 3 lactations with the first TD record obtained within 45 days in milk (DIM) were allowed to enter the data set. Furthermore, only TD collected between 5 and 305 DIM were retained. Finally, only the lactations with at least 4 TD records and the herd-TD within lactation with at least 2 TD records were retained for analysis. The final edited data set included 187,052 test-day records from 211 herds. A smaller, computationally manageable data set was obtained by sampling randomly 55 herds. A final number of 69,796 TD records for milk, fat, protein yields and SCC of 9,023 lactations, belonging to 4,325 cows was used. The pedigree file obtained for genetic analysis was generated by tracing the pedigrees of 11 generations back. The resulting pedigree file included 9,607 animals.

Definition of somatic cell count traits

Five alternative SCC traits were defined as udder health indicators for further genetic evaluation. The TD SCC converted by logarithm transformation to Somatic Cell Score (SCS) [SCS = 3 + log2(SCC/100,000)] was the first trait considered. As proposed by Urioste et al. (2010) to avoid possible effects of milk dilution, a second trait considering the total amount of SCC was considered. The TD SCC was then multiplied by TD milk yield to obtain the total number of cells and then log-transformed (LTSCC). Finally, knowing that the test-day SCC is an indication of the mammary gland health status the, three different thresholds traits (80,000, 150,000 and 400,000 cells/ml) of somatic cells were defined as possible different levels of mammary infection or inflammation. In this latter case, each test-day SCC was individually classified as a binary trait depending on the threshold considered. Moving from the consideration that a somatic cell count lower than 100,000 cells/ml is typically considered physiological for individual (Hillerton, 1999), a threshold of 80,000 cells/ml was chosen to ensure that cows with a SCC below this threshold did not present infection or inflammation of the mammary gland. A test-day SCC >80,000 cells/ml (SCC80) was registered as 1; otherwise, it was registered as 0. The second threshold trait at 150,000 cells/ml was defined following De Haas et al. (2008), considering this SCC as the limit beyond which the national recording system highlights the animals as likely to exhibit the occurrence of pathological mastitis. A test-day SCC >150,000 cells/ml (SCC150) was registered as 1; otherwise, it was registered as 0. Finally, the presence or absence of TD >400,000 cells/ml (SCC400) was scored as 1 or 0. This threshold was chosen as legal limit of milk merchantability, as it is in many countries including Italy (Jayarao et al, 2004).

Statistical analysis

Bi-traits repeatability test day animal model analyses were run considering the three productive traits (milk, fat and protein) with each of alternative SCC traits in order to estimate the genetic parameters and genetic correlations between traits. The linear model applied was as follows:

$$y_{ijklmn} = \mu + \text{HTD-LN}_i + \text{GEST}_j + \sum_{r=0}^{4} \varphi_r \text{AP-LN}_k + \sum_{r=0}^{4} \varphi_r \text{MP-LN}_l + \text{Pe}_m + a_n + e_{ijklmn},$$

where y_{ijklmn} is the test-day record of milk, fat and protein yield and alternative somatic cell count traits of the cow n; μ the overall mean; HTD-LN_i is the fixed effect of herd-test-day within lactation number i (12,520 levels); GEST_j is the fixed effect of the days of gestation class j (18 classes: the first class means no gestation; the further classes account for 15 d intervals from 1 to 240 d of gestation; and the last class considers ≥ 241 d of gestation); AP-LN_k is the fixed effect of age at parity within lactation k (42 classes in total); MP-LN$_l$ is the fixed effect of the month of parity l (36 classes corresponding to single months of year within lactation n); Pe$_m$ is the random permanent environmental component; a$_n$ is the additive genetic component, and e$_{ijklmn}$ is the random residual term. The shape of the lactation curve was described by 4th order Legendre polynomials for the fixed effects of AP-LN and MP-LN.

The assumptions on estimated (co)variances for the bi-trait analyses were obtained as $\mathbf{G}\otimes\mathbf{A}$, $\mathbf{Pe}\otimes\mathbf{I}$ and $\mathbf{R}\otimes\mathbf{I}$, with **G**, **Pe** and **R** as 2 × 2 matrices respectively including additive genetic, permanent environmental, and residual (co)variance matrices of the respective trait pair; **A** and **I** are the additive relationships matrix and an identity matrix; and ⊗ is the Kronecker product.

Variance components and genetic parameter estimates for SCS and LTSCC were obtained using the program “gibbs3f90”, while for traits expressed as a binary was used “thrgibbs1f90” (Misztal, 2008), both using a Bayesian approach via Gibbs sampling. A single Gibbs chain of 480,000 interactions was run for each bivariate analysis. In all cases, the first 30,000 samples were discarded as burn-in. Samples were stored every 150 iterations to leave 3,000 samples for inferences. The posterior mean of the samples was used as a point estimate of the (co)variance component and the related parameters. The lower and upper bounds of the 95% highest posterior density interval (HPD) were obtained from the estimated marginal densities. The values of variance components, heritability and genetic correlations obtained for the threshold traits were reported in liability scale. The heritability were defined as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2+\sigma_{pe}^2+\sigma_e^2}$$

where σ_a^2, σ_{pe}^2, and σ_e^2 were the additive genetic, permanent environment, and residual variances, respectively.

The additive genetic correlations (r_a) of milk, fat and protein yield and somatic cell traits were obtained as:

$$r_a = \frac{\sigma_{a1,a2}}{\sigma_{a1}\cdot\sigma_{a2}}$$

where $\sigma_{a1,a2}$ was the additive genetic (co)variance between traits 1 and 2, and σ_{a1} and σ_{a2} were the additive genetic standard deviations for traits 1 and 2, respectively.

RESULTS

The basic statistics for yield traits, SCC, SCS and LTSCC are presented in Table 1. Mean of milk, fat and protein yields were 17.09, 0.598 and 0.566 kg/d, and traits showing similar coefficients of variation (CV; 0.34, 0.36 and 0.33, respectively). The mean trait values for SCC, SCS and LTSCC of Rendena cows were 177 (x 1,000) cells/ml, and mean scores of 3 and 7, respectively. A very large standard deviation was in this case observed, in particular for SCC. Compared with the milk, fat and protein production, the SCC and SCS traits showed higher variabilities, with CV of 1.63 and 0.67, respectively. Conversely, the LTSCC trait exhibited a lower CV than values obtained for SCC and SCS. The distribution of test-day records in each threshold trait are reported in Table 2. The test-day records in threshold SCC80 are equally distributed below and above the threshold of 80,000 cells/ml. For SCC150 and SCC400 traits the percentage of test-day records below the thresholds is greater (0.68 and 0.89, respectively) than the records above the thresholds of 150,000 and 400,000 cells/ml. Table 3 presented the mean point estimates of marginal posterior densities, for additive genetic, permanent environment and residual variances obtained from bivariate analysis for the studied traits. The additive genetic variabilities estimated for the SCS and LTSCC were higher than those for the threshold traits (SCC80, SCC150, SCC400), which showed additive genetic variability comparable or higher than those of fat and protein yields.

Posterior heritability values expressed on the liability scale ranged from 0.04 to 0.07 , while heritability values on normal scale were set at 0.09 and 0.10 for SCS and LTSCC traits, respectively. As expected, productive traits showed higher heritability estimates, i.e., 0.22 for milk yield, 0.17 for fat yield and 0.19 for protein yields. The HDP 95% for heritability of all analysed traits indicated asymmetry in the marginal posterior distribution with a more dispersion in heritability for productive traits, SCS and LTSCC. The standard deviation for all the analysed traits was on average very low.

The point estimate of the genetic correlations between productive traits and all considered udder health traits were almost null except with log total somatic cell count (LTSCC). In particular, the point estimate (mean of the posterior distribution) of genetic correlations between milk yield and SCS, LTSCC, SCC80, SCC150 and SCC400 were 0.002, 0.29, -0.06, 0.03 and 0.10, respectively. The posterior density obtained for the genetic correlations (Figure 1) between milk yield and SCS (HDP 95% -0.196; 0.201), SCC80 (HDP 95% -0.255; 0.140), SCC150 (HDP 95% -0.176; 0.240) and SCC400 (HDP 95% -0.155; 0.362) traits were overlapped and all estimates included zero. Conversely, the posterior density for the genetic correlations between milk yield and LTSCC was positive and ranged from 0.104 to 0.479. The fat yield showed the point estimate (mean of the posterior distribution) for genetic correlations of -0.09, 0.156, -0.121, -0.042 and -0.024 with SCS, LTSCC, SCC80, SCC150 and SCC400, respectively. All estimates included zero in the 95% highest posterior density region interval. Finally, the protein yield showed values of the point estimates (mean of the posterior distributions) for genetic correlations of 0.018, 0.282, -0.036, 0.041 and 0.126 with SCS, LTSCC, SCC80, SCC150 and SCC400, respectively. All estimates included zero in the 95% highest posterior density region interval, except with LTSCC (HDP 95% 0.092; 0.473).

DISCUSSION

Rendena is a local breed traditionally selected for dual-purpose (milk and meat), which presents daily production levels on average much lower than those reported by AIA (2016) in specialized Italian Holstein (31.3 kg/d), Italian Brown Swiss breeds (23.6 kg/d) and in dual-purpose Italian Simmental cows (22.0 kg/d).

The udder health indicators in Rendena breed have never been investigated before this study. In Italy, the somatic cell count (SCC) regularly collected during the functional controls is the most commonly used udder health indicator. However, the SCC trait in genetic evaluation is log-transformed because it is not normally distributed. The mean value of SCS observed in Rendena cows in this study was lower than that reported in the same breed by De Marchi et al. (2007), where mean SCS resulted 4.27. Briefly focusing on Italian breeds, Dal Zotto et al. (2007) reported mean SCS of 2.22 in Italian Brown Swiss, whereas Cassandro et al. (2008) in Italian Holstein observed mean SCS comparable to our study (3.08).

The heritability value of SCS observed in this study, 0.09, was in agreement with the heritability reported in others breeds (Reents et al., 1995; Ikonen et al., 1999; Cecchinato et al., 2015). However, a lower heritability value (0.05) was observed in Burlina cattle (Penasa et al., 2010), whereas higher heritability were reported when the trait was evaluate a lactation-basis mean SCS. In these cases, a heritability estimate of 0.14 was observed in Italian Brown Swiss and Swiss Holstein (Samorè et al., 2010 and Kadarmideen, 2004), and of 0.17 in German Holstein (Martin et al., 2013).

Our study on milk somatic cells aiming at introducing an udder health trait in the breeding of Rendena has led to the exploration of possible others trait on the basis of the same phenotype (SCC). A trait little used but reported in literature is the log total somatic cell counts (LTSCC), which was a measure of the amount of SCC present in the daily milk production and then log-transformed, with the purpose to bypass possible effect of dilution. This trait was considered by Heuven et al. (1988), which reported heritability values of 0.06 in first lactation, 0.19 in second lactation and 0.15 in third lactation, all values lower or higher than our result. Alternative traits derived from information present in TD SCC records were studied as indicator traits for mastitis. For example, Green et al. (2004) considered the distribution characteristics of test-day log-transformed SCC (mean, standard deviation, maximum and minimum values) and reported that maximum and standard deviation of log SCC were the best indicators of clinical mastitis, with respect to mean SCC. Others authors (De Haas et al., 2008; Urioste et al., 2010) used the average of test-day SCC calculated over different lactation periods to compare the first versus the second parts of lactation. De Haas et al. (2008) reported greater genetic correlation between clinical mastitis and

SCC in the first part than in the second part of lactation, confirming the results observed in previous studies (Emanuelson et al., 1988; Barkema et al., 1998) showing that the frequency of cases of mastitis is much greater in the first part of the lactation than in the second part Urioste et al. (2010) used the measures of number of days sick during the lactation as a trait to increase mastitis resistance in dairy cattle and found a high correlation between clinical mastitis and number of infectious peaks.

An alternate way is to consider SCC as threshold traits, as in the present study, in which three threshold traits (SCC80, SCC150 and SCC400) have been considered. These traits were treated as dummy variable, and the heritability was reported in a liability scale.

The heritability value estimated for SCC150 trait in this study (0.06) was similar to the heritability reported by De Haas et al. (2008) for "suspicion of IMI" (intramammary infection) trait (0.06), which used the same SCC threshold of the present study. Urioste et al. (2010) using the threshold of TD > 500,000 cells/ml reported heritability value of 0.12 both for SCC traits recorded weekly and monthly, higher than the heritability obtained for threshold trait of SCC400 (0.04) in the present research. On the other hand, Koeck et al. (2012) using the same threshold of Urioste et al. (2010) reported heritability more similar to values obtained in the present study with threshold traits (0.03).

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

To our knowledge no studies have evaluated the genetic relationships between productive traits and SCC threshold traits yet, but many researchers (De Haas et al., 2008; Urioste et al., 2010; Koeck et al., 2012) have found that some of these threshold traits are positively correlated with clinical and subclinical mastitis, suggesting that are probably better predictor of mastitis than classical SCS. The SCC150 trait considered in this study showed close to zero genetic correlations with milk, fat and protein yields. Nevertheless, De Haas et al. (2008), considering this threshold trait "suspicion of IMI", reported high genetic correlation with clinical mastitis (0.68) and very strong correlations with subclinical mastitis (0.96). These results indicate that the trait threshold of SCC150 could be considered in genetic evaluation as indicator of subclinical mastitis. The SCC80 and SCC400 thresholds also, considered in present work, showed almost null genetic correlations with milk, fat and protein yields. The chosen threshold of 80,000 cells/ml was, however, too low to differentiate between healthy and infected cows. However, the SCC400 threshold, which represent the legal limit of milk merchantability, could be confronted with the threshold of TD>500,000 cells/ml (TD>500) considered in the researches of Koeck et al. (2012) and Urioste et al. (2012). In these latter studies, high genetic correlations were obtained between TD>500 and clinical mastitis (0.83) and very strong correlations with subclinical mastitis (0.93), highlighting this threshold trait as one of the best predictors of resistance to mastitis. Results from our study may be considered as a first step into the possible application of a udder health trait in breeding goals of the Italian dual purpose Rendena breed as already carried out in both specialized (Miglior et al., 2005) and in other dual-purpose breeds (Fuerst-Walt et al., 2016). Although somatic cells are not directly selected in Rendena population, yet, a recent study from our group (Sartori et al., unpublished data), have highlighted that the actual breeding goal for dual-purpose in Rendena is favourably improved (via indirect selection) by the progress for beef traits (particularly by ADG), while mammary correctness (e.g. udder depth, suspensory ligament, teat placement side view) is unfavourably linked to udder health, indicating once again that more supported udders with strong suspensor ligament are less susceptible of mastitis.

CONCLUSIONS

The results obtained in this study demonstrated that SCC data could be easily introduced as breeding goal to improve of udder health in the local Rendena breed. The SCS and LTSCC traits have shown the greater genetic variability and heritability as respect to other threshold traits suggested in literature as more reliable predictors of mastitis. In addition, the present selection goal based on milk and beef trait is not heavily conflicting with worsening of somatic cells traits and with udder health in Rendena cattle. Further insights are therefore needed with regard to the threshold traits before possible application in routinely genetic evaluation of the Rendena breed.

REFERENCES

[AIA] Associazione Italiana Allevatori, 2016. Milk recording activity: official statistics. Italian Breeders Association, Rome, Italy.

Ali, A. K. A., & Shook, G. E. (1980). An Optimum Transformation for Somatic Cell Concentration in Milk1. Journal of Dairy Science, 63(3), 487-490.

ANARE (2016) Risultati controlli funzionali 2015. La Rendena, 1-2, 25–29.

Barkema, H. W., Schukken, Y. H., Lam, T. J. G. M., Beiboer, M. L., Wilmink, H., Benedictus, G., & Brand, A. (1998). Incidence of clinical mastitis in dairy herds grouped in three categories by bulk milk somatic cell counts. Journal of dairy science, 81(2), 411-419.

Bobbo, T., Cecchinato, A., Cipolat-Gotet, C., Stocco, G., & Bittante, G. (2014). Effect of breed and dairy system on milk composition and udder health traits in multi-breed dairy herds. Acta Agraria KaposvÃ¡ riensis, 18, 81-88.

Carlén, E., Strandberg, E., & Roth, A. (2004). Genetic parameters for clinical mastitis, somatic cell score, and production in the first three lactations of Swedish Holstein cows. Journal of dairy science, 87(9), 3062-3070.

Cassandro, M., Comin, A., Ojala, M., Dal Zotto, R., De Marchi, M., Gallo, L., & Bittante, G. (2008). Genetic parameters of milk coagulation properties and their relationships with milk yield and quality traits in Italian Holstein cows. Journal of Dairy Science, 91(1), 371-376.

Cecchinato, A., Albera, A., Cipolat-Gotet, C., Ferragina, A., & Bittante, G. (2015). Genetic parameters of cheese yield and curd nutrient recovery or whey loss traits predicted using Fourier-transform infrared spectroscopy of samples collected during milk recording on Holstein, Brown Swiss, and Simmental dairy cows. Journal of dairy science, 98(7), 4914-4927.

Dal Zotto, R., De Marchi, M., Dalvit, C., Cassandro, M., Gallo, L., Carnier, P., & Bittante, G. (2007). Heritabilities and genetic correlations of body condition score and calving interval with yield, somatic cell score, and linear type traits in Brown Swiss cattle. Journal of dairy science, 90(12), 5737-5743.

Dechow, C. D., Rogers, G. W., Cooper, J. B., Phelps, M. I., & Mosholder, A. L. (2007). Milk, fat, protein, somatic cell score, and days open among Holstein, Brown Swiss, and their crosses. Journal of dairy science, 90(7), 3542-3549.

De Haas, Y., W. Ouweltjes, J. ten Napel, J. J. Windig, & G. de Jong. 2008. Alternative somatic cell count traits as mastitis indicators for genetic selection. J. Dairy Sci. 91:2501–2511.

De Marchi, M., Dal Zotto, R., Cassandro, M., & Bittante, G. (2007). Milk coagulation ability of five dairy cattle breeds. Journal of Dairy Science, 90(8), 3986-3992.

Emanuelson, U., Danell, B., & Philipsson, J. (1988). Genetic parameters for clinical mastitis, somatic cell counts, and milk production estimated by multiple-trait restricted maximum likelihood. Journal of Dairy Science, 71(2), 467-476.

Fuerst-Waltl, B., Fuerst, C., Obritzhauser, W., & Egger-Danner, C. (2016). Sustainable breeding objectives and possible selection response: Finding the balance between economics and breeders' preferences. Journal of Dairy Science, 99(12), 9796-9809.

Green, M. J., Green, L. E., Schukken, Y. H., Bradley, A. J., Peeler, E. J., Barkema, H. W., & Medley, G. F. (2004). Somatic cell count distributions during lactation predict clinical mastitis. Journal of dairy science, 87(5), 1256-1264.

Heuven, H. C. M., Bovenhuis, H., & Politiek, R. D. (1988). Inheritance of somatic cell count and its genetic relationship with milk yield in different parities. Livestock Production Science, 18(2), 115-127.

Hillerton, J. E. (1999). Redefining mastitis based on somatic cell count. International Dairy Federation.

Ikonen, T., Ahlfors, K., Kempe, R., Ojala, M., & Ruottinen, O. (1999). Genetic parameters for the milk coagulation properties and prevalence of noncoagulating milk in Finnish dairy cows. Journal of Dairy Science, 82(1), 205-214.

Kadarmideen, H. N. (2004). Genetic correlations among body condition score, somatic cell score, milk production, fertility and conformation traits in dairy cows. Animal science, 79(02), 191-201.

Koeck, A., Miglior, F., Kelton, D. F., & Schenkel, F. S. (2012). Alternative somatic cell count traits to improve mastitis resistance in Canadian Holsteins. Journal of dairy science, 95(1), 432-439.

Koivula, M., Mäntysaari, E. A., Negussie, E., & Serenius, T. (2005). Genetic and phenotypic relationships among milk yield and somatic cell count before and after clinical mastitis. Journal of Dairy Science, 88(2), 827-833.

Jayarao, B. M., Pillai, S. R., Sawant, A. A., Wolfgang, D. R., & Hegde, N. V. (2004). Guidelines for monitoring bulk tank milk somatic cell and bacterial counts. Journal of Dairy Science, 87(10), 3561-3573.

Macciotta, N. P. P., Cecchinato, A., Mele, M., & Bittante, G. (2012). Use of multivariate factor analysis to define new indicator variables for milk composition and coagulation properties in Brown Swiss cows. Journal of dairy science, 95(12), 7346-7354.

Martin, G., Wensch-Dorendorf, M., Schafberg, R., & Swalve, H. H. (2013). A comparison of udder health trait definitions in German Holstein dairy cattle based on mastitis treatment data. Livestock Science, 151(2), 219-227.

Mazza, S., Guzzo, N., Sartori, C., Berry, D. P., & Mantovani, R. (2014). Genetic parameters for linear type traits in the Rendena dual-purpose breed. Journal of Animal Breeding and Genetics, 131(1), 27-35.

Miglior, F., Muir, B. L., & Van Doormaal, B. J. (2005). Selection indices in Holstein cattle of various countries. Journal of dairy science, 88(3), 1255-1263.

Misztal, I. (2008). Reliable computing in estimation of variance components. Journal of animal breeding and genetics, 125(6), 363-370.

Nielsen, C. (2009). Economic impact of mastitis in dairy cows. (Vol. 2009, No. 29).

Oltenacu P.A. & Broom D.M. (2010). The impact of genetic selection for increased milk yield on the welfare of dairy cows. Animal Welfare 19, 39–49.

Penasa, M., Cecchinato, A., Battagin, M., De Marchi, M., Pretto, D., & Cassandro, M. (2010). Bayesian inference of genetic parameters for test-day milk yield, milk quality traits, and somatic cell score in Burlina cows. Journal of applied genetics, 51(4), 489-495.

Reents, R., Jamrozik, J., Schaeffer, L. R., & Dekkers, J. C. M. (1995). Estimation of genetic parameters for test day records of somatic cell score. Journal of Dairy Science, 78(12), 2847-2857.

Samoré, A. B., Rizzi, R., Rossoni, A., & Bagnato, A. (2010). Genetic parameters for functional longevity, type traits, somatic cell scores, milk flow and production in the Italian Brown Swiss. Italian Journal of Animal Science, 9(2), e28.

Shook, G. E. (2006). Major advances in determining appropriate selection goals. J. Dairy Sci. 89:1349–1361.

Urioste, J. I., Franzén, J., & Strandberg, E. (2010). Phenotypic and genetic characterization of novel somatic cell count traits from weekly or monthly observations. Journal of Dairy Science, 93(12), 5930-5941.

Urioste, J. I., Franzén, J., Windig, J. J., & Strandberg, E. (2012). Genetic relationships among mastitis and alternative somatic cell count traits in the first 3 lactations of Swedish Holsteins. Journal of dairy science, 95(6), 3428-3434.

Vallimont, J. E., Dechow, C. D., Sattler, C. G., & Clay, J. S. (2009). Heritability estimates associated with alternative definitions of mastitis and correlations with somatic cell score and yield. Journal of dairy science, 92(7), 3402-3410.

Table 1. Descriptive statistics for productive traits and somatic cell expressed as count (SCC), score (SCS) and score of total SCC in daily milk production (LTSCC).

Item	**Mean**	**SD**	**Min**	**Max**
Milk, kg/d	17.09	5.751	0.600	43.70
Fat, kg/d	0.598	0.217	0.022	1.980
Protein, kg/d	0.566	0.186	0.022	1.500
Somatic Cell Count, SCC (x 1,000 cells/ml)	177	289	1	19,349
Somatic Cell Score, SCS	3	2	-4	11
Log daily total somatic cell count, LTSCC	7	2	-1	15

Table 2. Test-day records distribution in each threshold.

Item	-	+
SCC80	0.50	0.50
SCC150	0.68	0.32
SCC400	0.89	0.11

Table 3. Estimated marginal posterior densities and HPD 95% (in parentheses) for genetic variance (σ^2_a), permanent environmental variance (σ^2_{pe}), residual variance (σ^2_e), and h^2 of productive traits and threshold somatic cell count traits.

Trait	$\boldsymbol{\sigma^2_a}$	$\boldsymbol{\sigma^2_{pe}}$	$\boldsymbol{\sigma^2_e}$	$\mathbf{h^2}$
Milk	$2.865^{(2.286; 3.444)}$	$3.651^{(3.211; 4.091)}$	$6.376^{(6.299; 6.453)}$	$0.222(^{0.181; 0.263)}$
Fat	$0.004^{(0.003; 0.004)}$	$0.004^{(0.004; 0.005)}$	$0.014^{(0.014; 0.014)}$	$0.169^{(0.137; 0.200)}$
Protein	$0.003^{(0.002; 0.003)}$	$0.004^{(0.003; 0.004)}$	$0.007^{(0.007; 0.007)}$	$0.192^{(0.154; 0.231)}$
SCS	$0.242^{(0.154; 0.330)}$	$0.635^{(0.561; 0.708)}$	$1.900^{(1.877; 1.923)}$	$0.087^{(0.056; 0.118)}$
LTSCC	$0.266^{(0.181;0.351)}$	$0.575^{(0.506; 0.645)}$	$1.835^{(1.812; 1.857)}$	$0.099^{(0.069; 0.130)}$
SCC80$^{(*)}$	$0.014^{(0.009; 0.019)}$	$0.038^{(0.034; 0.043)}$	$0.155^{(0.153; 0.157)}$	$0.067^{(0.043; 0.091)}$
SCC150$^{(*)}$	$0.012^{(0.007; 0.016)}$	$0.032^{(0.028; 0.035)}$	$0.141^{(0.140; 0.143)}$	$0.064^{(0.041; 0.088)}$
SCC400$^{(*)}$	$0.004^{(0.002; 0.005)}$	$0.012^{(0.010; 0.013)}$	$0.081^{(0.080; 0.082)}$	$0.036^{(0.018; 0.055)}$

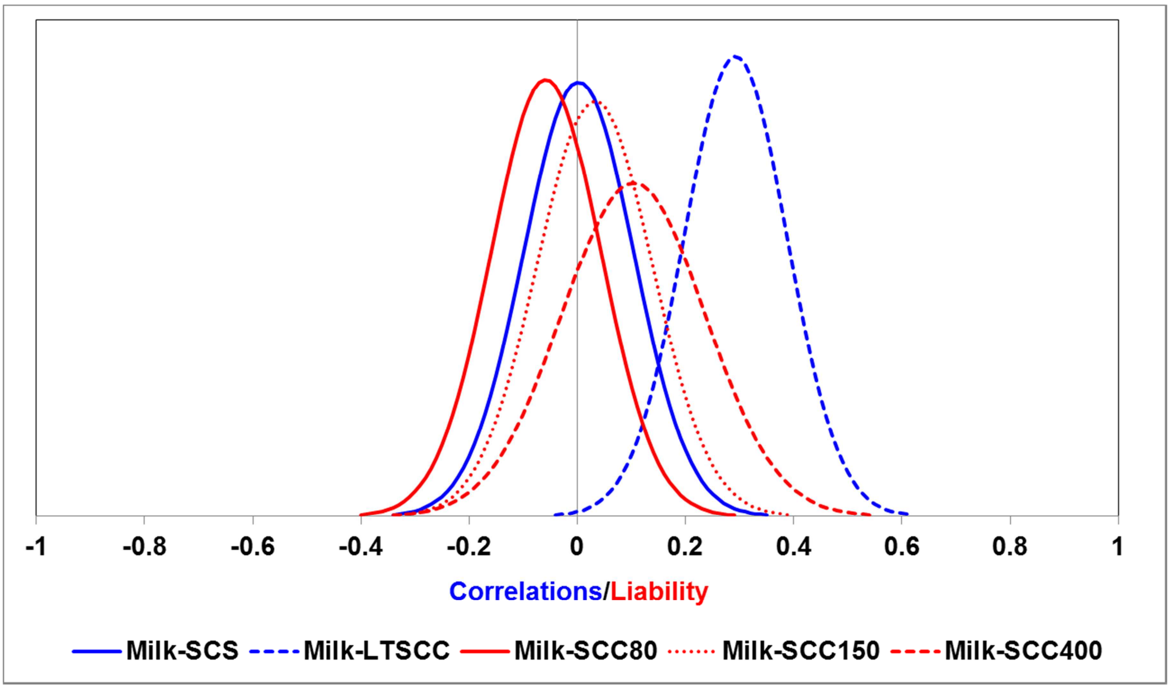
(*) liability scale

Table 4. Estimated marginal posterior densities and HDP 95% (in parentheses) of genetic (r_a) correlations obtained from bivariate animal model analysis between milk, fat and protein yields and alternative somatic cell count traits.

Trait	**Milk**	**Fat**	**Protein**
SCS	$0.002^{(-0.196; 0.201)}$	$-0.090^{(-0.280; 0.101)}$	$0.018^{(-0.187; 0.224)}$
LTSCC	$0.292^{(0.104; 0.479)}$	$0.155^{(-0.028; 0.338)}$	$0.282^{(0.092; 0.473)}$
SCC80$^{(*)}$	$-0.058^{(-0.255; 0.140)}$	$-0.121^{(-0.314; 0.073)}$	$-0.036^{(-0.241; 0.169)}$
SCC150$^{(*)}$	$0.032^{(-0.176; 0.240)}$	$-0.042^{(-0.243; 0.159)}$	$0.041^{(-0.173; 0.256)}$
SCC400$^{(*)}$	$0.103^{(-0.155; 0.362)}$	$-0.024^{(-0.258; 0.211)}$	$0.126^{(-0.138; 0.390)}$

(*) liability scale

Figure 1. Estimated marginal posterior densities of genetic correlations between milk yield and alternative somatic cell count traits of Rendena for SCS (continuous line blue), LTSCC (dashed line blue), SCC80 (continuous line red), SCC150 (dashed line red) and SCC400 (dotted line red)traits.



CHAPTER 3

GENETIC PARAMETERS OF MILK TECHNOLOGICAL TRAITS PREDICTED USING FOURIER-TRANSFORM INFRARED SPECTROSCOPY IN RENDENA BREED

Under Submission

ABSTRACT

The aim of the study was to estimate the heritability and the genetic correlations between milk production, milk composition (fat, protein, lactose) traits and somatic cell score (SCS) with novel traits regarding milk coagulation properties (MCP), curd firming and syneresis traits (CF), total cheese (CY), curd nutrients and energy recoveries (REC) and daily cheese yields (dCY) attainable from milk of the Rendena cattle breed. The new phenotypes were predicted with proper calibration equations from Fourier Transform Infrared spectral analysis of milk. The new milk phenotypes accounted for 4 MCP traits, i.e., rennet coagulation time (RCT, min); time to a curd firmness of 20 mm (k_{20}, min); and curd firmness at 30 and 45 min after rennet addition (a_{30} and a_{45}, respectively; mm), 4 parameters modelling the curd firmness (CF), i.e., the potential asymptotic at infinite time (mm); the CF instant rate constant (%/ min); the syneresis instant rate constant (%/min); and the RCT obtained from modelling individual samples, and 2 traits calculated from individual equations i.e., the maximum CF (CF_{max}, mm); and the time at CF_{max} (t_{max}, min). Additional new traits estimated from FTIR were 3 CY traits: CY fresh curd; CY dry matter; and CY curd moisture expressed as % of weight of processed milk; 4 REC traits calculated as ratio between single nutrient or energy in curd and in processed milk; and 3 dCY traits expressing the amount of cheese, total solids and water obtained from the milk yielded daily by a cow. A total of 9,947 test-day records belonging to 997 cows collected in years 2010-2015 were used in the study. Bi-trait analyses under a repeatability test-day model by means of a Gibbs sampling algorithm were carried out. In general the heritability values obtained for all the predicted traits were comparable and in some case greater than those reported for milk production and composition. Heritability estimates for the traits ranged from 0.11 for fat percentage to 0.39 for time at CF_{max}, whereas SCS showed the lowest heritability (0.01). The improvement of milk production favoured some of the traditional MCP traits, but did not promote cheese yield traits (average genetic correlation of -0.34). However, the relationships between milk production and the nutrients recovery traits were almost null. Conversely, favourable genetic correlations were obtained between milk composition and cheese yields and nutrient recoveries traits (average values of 0.57 and 0.34, respectively). These results suggested that it is possible to efficiently improve the technological properties of milk for cheese production and therefore the economic value of milk in the Rendena breed.

Key Words: genetic parameters, Rendena breed, milk coagulation, cheese cheese yield, whey loss

INTRODUCTION

In recent years the amount of milk used for cheese production has been increased in many countries including Italy, where more than 70% of the available milk is used in the cheese manufacture and 50% of this milk is used to produce PDO (Protected Designation of Origin) products (Cassandro et al., 2008). At the same time, the interest in studying the cheese making technology has been increased in the last two decades worldwide. Milk coagulation properties (MCP) are an important aspect for cheese production and the parameters commonly used to evaluate cheese-making ability of milk are the rennet coagulation time (RCT, min), the time required for curd-firming (k_{20}, min) and curd firmness (a_{30}, mm), which, traditionally, are determinate during a test of 30 min using mechanical lactodynamograph instruments (LDG) as reported by Cipolat-Gotet et al. (2012). Some studies have reported that exploitable additive genetic variation exists for MCP (Ikonen et al., 1999; Cassandro et al., 2008), but LDG methods require a rather long time for analysis and automated measuring devices are insufficient for a routine assessment of MCP in all cows involved in milk recording programs. However, the aspects criticality exhibited by the traditional MCP methods have been overcome by the introduction of alternative methodologies based on of infrared spectroscopy (Laporte et al.,1998; Dal Zotto et al., 2008) as the mid-infrared reflectance spectroscopy (MIRS). This technology is widely used in milk recording programs to predict milk fat and protein contents. Calibration equations to predict MCP of bovine milk by MIR spectroscopy have been developed by Dal Zotto et al. (2008), and following Cecchinato et al. (2009), the predicted MCP using MIRS can be used at population level for genetic purposes. A critical aspect in MCP assessment/prediction is that, in some cases, the RCT is not observed for some samples during the 30-min test interval and therefore samples are classified as non-coagulating, i.e., with missing information on RCT, k_{20}, and a_{30}. A possible solution to this problem has been proposed by extending the lactodynamographic observations and record of curd firmness at 45 and 60 min (a_{45}, a_{60}; Cipolat-Gotet et al., 2012; De Marchi et al., 2013). In this regard, Bittante et al.(2013b), using all available information recorded during of the milk coagulation and curd-firming tests prolonging lactodynamographic observations until 90 min, have developed and proposed a 4 parameters model to describe curd-firming process as a function of time (CF_t). This approach allows to characterize the non-coagulating milk samples, describes more deeply the milk coagulation process and syneresis, and allows to estimate traditional MCPs (RCT, k_{20} and a_{30}) and new parameters of the whole coagulation process, for which a medium heritability has been reported (Cecchinato and Bittante, 2016). In recent years further parameters have been added, in order to answer the requests of the dairy industries. Indeed, the economics and profitability of the cheese-making processes is dependant more from the cheese yield and the proportion of various milk nutrients that are retained in the curd or lost in whey than the MCP (Emmons, 1990). The cheese yield normally is expressed as the percentage ratio between the weights of the curd and of the milk, the first consisting in protein, fat and water retained by the cheese-making process. Both cheese yield and the nutrient recoveries of fat, protein, total solids and energy in the curd, the latter expressed as percentage of the same nutrient in the milk (Cipolat-Gotet et al., 2012), have shown a genetic variability that make them suitable for genetic improvement in dairy cattle (Bittante et al., 2013a).

The Fourier-transform infrared (FTIR) spectroscopy, a type of MIRS, has allowed predicting the above mentioned traits in recent studies. This technology is very rapid and applicable in large-scale contests (Karoui et al., 2010), and already routinely used to predict the fat, protein, and lactose contents of milk. Using the spectra of individual milk samples, a set of calibration equations have recently been developed for predicting these measures (Ferragina et al., 2013) and high correlations between measured and predicted traits have been reported (Bittante et al., 2014), concluding that the predicted traits can be used at population level for selection purposes. Up to now, cheese yield and nutrient recoveries have been predicted in some cosmopolitan breeds (Italian Holstein, Italian Brown Swiss, Italian Simmental; Cecchinato et al., 2015) for whom the spectra of individual milk samples routinely collected have been stored since 2010. However, the proper knowledge of the relationships between cheese making process parameters and milk production and composition may be of importance for breeds in which a certain amount of milk yield is intended to cheese transformation. To date, in cattle, the genetic correlations of milk production and composition with traditional MCP have been estimated in a number of studies (e.g. Ikonen et al., 1999; Cassandro et al., 2008; Cecchinato et al. 2011), whereas genetic correlations involving cheese yield and nutrient recoveries have been found only in the cosmopolitan breeds of the abovementioned study (Cecchinato et al., 2015). No studies have been focused on heritability and genetic correlations for cheese-technology parameters, apart traditional MCP, in local breeds, where cheese production is very important, because of inked to traditional cheese products and the specific environment in which these are obtained. In addition, often in these breeds the whole milk production is addressed to cheese transformation to cover local market requirements of traditional products. In addition, some of these local breeds show milk very suitable for processing into cheese, with better milk coagulation properties than in cosmopolite breeds (De Marchi et al., 2007).

A local breed for which a dataset of individual milk spectra is available is Rendena breed, a dual purpose breed widespread in the Alpine regions of the North East of Italy (Trentino Alto Adige and Veneto) and accounting for about 4,000 cows (ANARE, 2017). The average milk yield, obtained in 2015, was about 5,200 kg per lactation with 3.47% fat and 3.24% protein. Almost all this milk is currently converted in cheese products in both the area of origin (Trento province) and diffusion (Veneto region) of the breed. Focusing on this local breed as case study, this study aimed to estimate the genetic parameters for FTIR predictions of the milk technological traits (MCP, CF, cheese yields, the nutrient recoveries in the curd and the daily cheese yields), and to evaluate their genetic relationships with the milk production and composition. As final layout this study aimed to analyse possible new selection criteria to be implemented, in addition to the present selection for the dual purpose, in the Rendena breed.

MATERIALS AND METHODS

Data and editing

Milk production and composition data were provided by the National Association of Rendena cattle Breeders (ANARE). Milk yield was measured during routinely national milk recording, and a test day milk sample for each individual was collected for predicting fat, protein, lactose and SCC using FTIR spectroscopy (ICAR, 2012). The Breeders Federation of Trento Province provided spectral data obtained from all milk samples collected from farms of the Trento province. A total of 26,743 FTIR spectra test-day records of the Rendena breed realized between 2010 and 2015 in Trento province were preliminary extracted from the database and edited for further analysis. All records contained the test day milk yield, the protein, fat, lactose and SCC content and the whole spectra obtained from FTIR spectroscopy to estimate milk coagulation, curd firming and cheese making ability. Values of SCC were converted by logarithm transformation to SCS [SCS = 3 + log2(SCC/100,000)].

The test-day records with negative milk coagulation, curd firming and cheese-making ability and with missing milk traits were discarded. Only test day records of the first five lactations, collected between 5 to 305 days in milk (DIM) and belonging, for each trait considered in the study, to a range accounting for the mean and ±3 standard deviations within lactation (NL) and 15 d DIM classes, were retained for further analysis. In addition, only the lactations with a least 4 TD records and the herd-TD within lactation with at least 2 TD records were retained in the database. After editing, 9,947 test day records belonged to 1,717 lactations and 997 cows were used. The pedigree file obtained for genetic analysis, extracted from the genealogical database provided by ANARE, included all phenotyped animals and their ancestors up to the 12th generation, including 4,970 animals.

Definition of milk coagulation, curd firming and cheese-making traits FTIR

The milk coagulation and curd firming traits were predicted with proper calibration equations using data recorded in Brown Swiss cows by Cipolat-Gotet et al. (2012). The FTIR predicted traditional single point MCP was defined as: RCT, the time (min) from enzyme addition to gelation of the milk; k_{20}, the time (min) from milk gelation to a curd firmness equivalent to 20 mm; a_{30} (a_{45}), the curd firmness (mm) recorded after 30 (45) min from rennet addition. In addition, the FTIR predicted parameters for modelling the curd-firming and syneresis process over time (CF_t) of each individual milk sample were obtained as described in Bittante et al., 2011; 2013. The predicted parameters were RCT_{eq}, like the traditional RCT (min) but estimated from the prediction equation; CF_P, potential asymptotic curd firmness (mm) at infinite time assuming the absence of syneresis; k_{CF}, curd firming instant rate constant (%/min); and k_{SR}, instant syneresis rate constant (%/min). Two predicted traits derived from CF_t individual equations were CF_{max}, the maximum curd firmness (mm) attained by CF_t individual equations, and t_{max}, i.e., the time (min) at which CF_{max} is achieved. Cheese-making traits were additionally predicted with proper calibration equations developed by Ferragina et al. (2013) based on data recorded on the same Brown Swiss cows by Cipolat-Gotet et al. (2013). The FTIR predicted cheese-making traits included the fresh cheese yield ($\%CY_{CURD}$), the total solid cheese yield ($\%CY_{SOLIDS}$), and the water retained in curd ($\%CY_{WATER}$), all expressed as a percentage of the processed milk; the nutrient recoveries of fat (REC_{FAT}), protein ($REC_{PROTEIN}$), total solids (REC_{SOLIDS}), and energy (REC_{ENERGY}) in the curd as a percentage of the same nutrient contained in the milk were also obtained. The daily fresh cheese yield (dCY_{CURD}), solid cheese yield (dCY_{SOLIDS}), and water cheese yield (dCY_{WATER}) were determined by multiplying the different predicted %CYs (curd, dry matter and water, respectively) by the daily milk yield of individual cows (dMY; kg/d). Predicted traits and their calculation have been fully described in Cipolat-Gotet et al. (2013).

Statistical Analysis

The (co)variance components for milk yield, milk composition and FTIR predicted traits were estimated through bivariate repeatability test day models considering all the possible trait pairs obtained by using both milk yield, milk composition and new FTIR milk predicted phenotypes. The linear mixed model was:

$$y_{ijklmn} = \mu + \text{HTD-LN}_i + \text{GEST}_j + \sum_{r=0}^{4} \varphi_r \text{AP-LN}_k + \sum_{r=0}^{4} \varphi_r \text{MP-LN}_l + \text{Pe}_m + a_n + e_{ijklmn},$$

where y_{ijklmn} is the test-day record of milk yield, milk composition and FTIR predicted traits of the cow n; µ the overall mean; HTD-LN$_i$ is the fixed effect of herd-test-day within lactation number i (2,231 levels, considering up to 5 lactations); GEST$_j$ is the fixed effect of the days of gestation class j (18 classes: the first class means no gestation; the further classes accounts for 15 d intervals from 1 to 240 d of gestation; and the last class considers ≥ 241 d of gestation); AP-LN$_k$ is the fixed effect of age at parity within lactation k (73 classes in total); MP-LN$_l$ is the fixed effect of the month of parity l (60 classes corresponding to single months of year within lactation n); Pe$_m$ is the random permanent environmental component; a_n is the additive genetic component, and e_{ijklmn} is the random residual term. The shape of the lactation curve was described by 4th order Legendre polynomials for the fixed effects of AP-LN and MP-LN.

The bivariate analyses considered the following (co)variance assumptions:

$$\mathbf{G}=\begin{vmatrix} \sigma^2_{a1} & \sigma_{a1\,a2} \\ \sigma_{a1\,a2} & \sigma^2_{a2} \end{vmatrix};\ \mathbf{Pe}=\begin{vmatrix} \sigma^2_{pe1} & \sigma_{pe1\,pe2} \\ \sigma_{pe1\,pe2} & \sigma^2_{pe2} \end{vmatrix};\ \mathbf{R}=\begin{vmatrix} \sigma^2_{e1} & \sigma_{e1e2} \\ \sigma_{e1e2} & \sigma^2_{e2} \end{vmatrix};$$

where **G** is the matrix of additive genetic (co)variances σ^2_{a1}, σ^2_{a2}, σ_{a1a2} for traits 1 and 2, **Pe** is the matrix of permanent environmental (co)variances σ^2_{pe1}, σ_{pe1pe2}, σ^2_{pe2}, and **R** the matrix of residual covariance σ^2_{e1}, σ^2_{e2} and σ_{e1e2}. Matrix **G** multiplied a matrix **A** of additive relationships, whereas **Pe** and **R** multiplied an identity matrix of the same dimensions.

Variance components and genetic parameter estimates were obtained using the program “gibbs3f90”, (Misztal, 2008), which uses a Bayesian approach via Gibbs sampling. A unique Gibbs chain of 480,000 iterations was run for each bivariate analysis. One sample was saved every 150 iterations, and length of the burn-in period was set to 30,000 iterations. The posterior mean of 3,000 samples were used to determine the point estimate of genetic, permanent environment and residual variances, heritabilities, and correlations between milk yield, milk composition and FTIR predicted traits. The lower and upper bounds of the 95% highest posterior density interval (HPD) were obtained from the estimated marginal densities. The heritability (h^2) was defined as:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2+\sigma_{pe}^2+\sigma_e^2};$$

where σ_a^2, σ_{pe}^2, and σ_e^2 were the additive genetic, permanent environment, and residual variances, respectively.

The additive genetic correlations (r_a) of milk yields, quality traits and FTIR predicted traits were obtained as:

$$r_a=\frac{\sigma_{a1,\,a2}}{\sigma_{a1}\,.\,\sigma_{a2}};$$

where $\sigma_{a1,a2}$ was the genetic covariance between traits 1 and 2, and σ_{a1} and σ_{a2} were the genetic standard deviations for traits 1 and 2, respectively.

The phenotypic correlations (r_p) were obtained as:

$$r_p=\frac{\sigma_{p1,\,p2}}{\sigma_{p1}\,.\,\sigma_{p2}};$$

where $\sigma_{p1,p2}$ was the phenotypic covariance between traits 1 and 2, and σ_{p1} and σ_{p2} were the phenotypic standard deviations for traits 1 and 2, respectively.

RESULTS

Descriptive statistics

Descriptive statistics for the investigated traits are presented in Table 1. The Kolmogorov-Smirnov test showed that all traits were normally distributed. Skewness and kurtosis values were within the ranges of ± 2 and ±7, respectively, often indicated to ensure a normal distribution (e.g. Kim, 2013). Milk yield mean was 17.7 kg/d, but characterized by a large coefficients of variation (CV; 32%), and skewness and kurtosis close to zero. The average milk composition and SCS of Rendena breed were 3.48, 3.28, 4.88% and 2.633 for fat, protein, lactose and SCS, respectively. Compared with the milk production, the milk composition showed lower variabilities with CV ranging from 5% for lactose to 17% for fat. The SCS showed a CV of 69%, much higher than those reported for productive and composition milk traits. The fat percentage showed more values around the average with kurtosis of 2.092, while the values of skewness and kurtosis for lactose percentage were -1.116 and 3.316, respectively. All the new phenotypes related to the milk coagulation, curd firming and cheese-making showed a normal distributions. Average values for RCT, k_{20}, a_{30} and a_{45} were 16.39 min, 5.041 min, 31.50 mm, and 30.60 mm, respectively with greater variability (CV between 13 and 33%). Also the parameters modelling the CF (RCT_{eq}, CF_p, k_{CF}, k_{SR}) and maximum curd firmness (CF_{max}, t_{max}) showed high variabilities with values of CV ranging from 13% for CF_{max} to 31% for RCT_{eq}. All the %CY displayed high and equal variabilities (i.e., CV=13%). The average cheese yield ($\%CY_{CURD}$) was 12.8%, half of which was $\%CY_{SOLIDS}$ (6.14%) and half was $\%CY_{WATER}$ (6.98%). The nutrient recovery averaged 47.8% (REC_{SOLIDS}) to 88.9% ($REC_{PROTEIN}$), with low variabilities (CV between 3 and 6%).

Variance components and heritability

The mean point estimates of marginal posterior densities, for additive genetic, permanent environment and residual variances obtained from bivariate analysis for the studied traits are presented in Table 2. Heritability estimate for daily milk production was moderate (0.20), while slightly higher heritabilities were found for milk composition (0.26 both for protein and lactose), with the exception for fat content, which resulted lower (i.e., 0.11). The SCS showed the lowest heritability (0.02) as respect to the others traits, and medium high heritability values were obtained for traditional MCP traits (0.35, 0.30, 0.38 and 0.23 for MCP, K_{20}, a_{30} and a_{45}, respectively), CF model parameters (0.35, 0.23, 0.35 and 0.31 for RCT_{eq}, CF_p, k_{CF} and k_{SR}, respectively) and maximum curd-firmness traits (0.27 and 0.39 for CF_{max} and t_{max}, respectively). Heritability estimates for cheese yield traits resulted moderate (0.24, 0.19 and 0.23 for CY_{CURD}, CY_{SOLIDS} and CY_{WATER}, respectively), but higher than estimates for daily cheese yield traits (dCY; 0.18 on average). Regarding the nutrient recoveries the $REC_{PROTEIN}$ trait shown the higher heritability (i.e., 0.36), while the other recovery traits showed medium-low heritability, i.e., 0.27 for REC_{FAT}, 0.22 for REC_{SOLIDS} and 0.21 for REC_{ENERGY}. The HDP 95% for heritability of all traits studied indicated similar dispersion in the marginal posterior distribution. Only the left HDP 95% of SCS was slightly exceeding zero.

Genetic and phenotypic correlations

Table 3 shows the mean point estimates of marginal posterior densities for additive genetic and phenotypic correlations between milk production, quality traits and all the new phenotypes related to milk coagulation, curd firming and cheese-making traits. The additive genetic correlations were characterized by larger variability estimates than the phenotypic correlations, as reflected by the lower and upper bounds of the 95% highest posterior density. In general, milk yield showed genetic correlations moderate and negative with milk fat, protein and SCS contents. The SCS was negatively associated with milk fat and lactose percentage, while it was positively correlated with protein composition. Very low correlations were found between lactose percentage and milk production and others quality traits (fat and protein contents). Finally, fat and protein percentages tended to be positively correlated. The phenotypic correlations between milk production and quality traits were similar, but generally lower than the corresponding genetic correlations. Milk yield showed strong and positive genetic and phenotypic correlations with daily cheese production traits (dCY_{CURD}, dCY_{SOLIDS}, dCY_{WATER}). The genetic correlations of milk production with the traditional MCP traits, the parameters CF_t and the maximum curd firmness traits resulted highly variable. Milk yield tended to be negatively correlated with RCT, a_{45}, RCT_{eq}, CF_p and with maximum curd firmness traits (CF_{max} and t_{max}) and positively correlated with k_{20}, a_{30} and the constants instant rate the curd-firming (k_{CF}) and the curd syneresis (k_{SR}). Negative correlations were also found for milk production with all the %CY traits (average r_a=-0.34), and with some REC traits (REC_{SOLIDS} and REC_{ENERGY}), while no relationships were found with REC_{FAT} and $REC_{PROTEIN}$. The phenotypic correlations had the same sign, apart from k_{20}, and were lower in magnitude than the genetic correlations, except for RCT, a_{30}, t_{max}, REC_{FAT} and $REC_{PROTEIN}$ traits.

The milk fat percentage was much more correlated with cheese yields and overall nutrient recoveries (REC_{SOLIDS} and REC_{ENERGY}) than with their own recoveries in the curd (REC_{FAT} and $REC_{PROTEIN}$), both genetically and phenotypically. The genetic and phenotypic correlations between fat percentage and traditional MCP traits were variable. The relationship between fat percentage and RCT was low both genetically (r_a=-0.06) and phenotypically (r_p=0.07). The fat content was negatively correlated with k_{20} (r_a=-0.42 and r_p=-0.33; favourably) and positively with a_{30} and a_{45} (r_a=0.21 and 0.50, r_p=0.03 and 0.33 respectively; favourably). The genetic correlation obtained between fat content and pattern RCT_{eq} was negative (-0.12) and higher than the corresponding phenotypic correlation (-0.03). Medium-low and positive genetic correlations were found with CF_p, k_{CF} (model parameters) and CF_{max} (maximum curd firmness) traits, while negative genetic correlations were found with t_{max} trait (-0.12). The phenotypic correlations had the same sign but were lower in magnitude than the genetic ones, except for k_{SR} that showed higher value (-0.21). The milk fat percentage was slightly or null correlated with all daily cheese production traits (dCY). The corresponding phenotypic correlations were much higher. The milk protein percentage showed greater genetic and phenotypic correlation with cheese yield traits (%CY). The genetic and phenotypic correlations between protein content and REC traits were moderate and positive, except that for REC_{FAT} trait, which showed negative genetic correlation (-0.27) and null phenotypic correlation (-0.01). The protein percentage showed moderate and positive genetic correlation with traditional RCT and pattern RCT_{eq} (unfavourably), a45 (favourably), CF_p, CF_{max}, t_{max} traits and negative genetic correlation with a_{30} (unfavourably) and both the constants instant rate for curd-firming (k_{CF}) and curd syneresis (k_{SR}). The phenotypic correlations had the same sign apart for a30 and were lower (as RCT, RCT_{eq}, k_{CF}, k_{SR} and t_{max}) or higher (as k_{20}, a_{30}, a_{45}, CF_p and CF_{max}) in magnitude than the genetic ones. The milk lactose content showed moderate positive genetic and phenotypic correlations with all of the %CY, REC and dCY traits except for REC_{SOLIDS}, which was inconsistent. Moderate genetic correlations were found also between lactose percentage and traditional MCP traits. In particular lactose content was negatively correlated with RCT and k_{20} and positively with a_{30} (0.45). The phenotypic correlations were similar, with slightly higher values than the genetic correlations. Regarding the genetic relationships with CF_t parameters and the maximum curd firmness traits, the lactose content was negatively correlated with RCT_{eq}, k_{SR} and t_{max} and positively correlated with CF_p, CF_{max} and k_{CF}, which showed rather low genetic correlation. The phenotypic correlations concerning these traits were generally lower as respect to the corresponding genetic correlations. The genetic correlations between SCS and traditional MCP, the CF_t model parameters and maximum curd firmness traits were rather high in absolute values. The SCS was positively correlated with RCT and k_{20} (0.82 and 0.75, respectively), with RCT_{eq} of the model CF_t (0.80) and with t_{max} trait (0.77) of the maximum CF, while was negatively correlated with all others traits (a_{30}, a_{45}, CF_p, k_{CF}, k_{SR} and CF_{max}). The corresponding phenotypic correlations were all markedly lower. The SCS showed moderate negative genetic correlations with all of the %CY, REC and dCY traits, except with $REC_{PROTEIN}$ and $\%CY_{WATER}$, which were inconsistent or slightly positive. The phenotypic correlations between SCS and the entire %CY and overall recoveries (REC_{SOLIDS} and REC_{ENERGY}) traits were rather low or almost null. Negative phenotypic correlations were found between SCS and the recoveries of fat and protein and with all dCY traits.

DISCUSSION

The milk of Rendena cows is generally considered very suitable for processing into cheese, with good aptitude for coagulation, (De Marchi et al., 2007; Mantovani et al., 2011). However, milk production and composition of Rendena cows are lower than those reported for cosmopolite Italian Holstein, Italian Brown Swiss and dual purpose Italian Simmental cows (AIA, 2016). The fats and proteins are the main solid components of the milk that affect cheese yield (Verdier-Metz et al., 2001), therefore, the minor fat and protein contents of the milk of Rendena breed, could have affected all of the %CY, %REC, and dCY (kg/d), which were much more low than at those reported for Holstein, Brown Swiss and Simmental cows reared in Trento province, except for $REC_{PROTEIN}$ and REC_{FAT}, which were comparable or higher than corresponding traits reported in the same cosmopolite breeds by Cecchinato et al. (2015).

Heritability

The heritability (h^2) value estimate in the present study for milk yield was alike to that reported in a previous study in the Rendena breed by Guzzo et al., (2009), where h^2 value was of 0.21. On the other hand, heritability around at 0.10 has been reported in Italian Holstein and Brown Swiss breeds by Cecchinato et al., (2011). The h^2 for fat and lactose contents assessed by Cecchinato et al., (2015) in the Brown Swiss population were 0.11 and 0.26, i.e., very close to the values for Rendena here reported, while h^2 for protein content was slightly higher (0.30) than that obtained in this study. Penasa et al. (2010) obtained very high h^2 for fat and protein contents (0.28 and 0.35, respectively) in Burlina cattle, while Cecchinato et al. (2015) reported in Simmental higher h^2 for fat content (0.15), but lower values for protein percentage (0.19) than values estimated for Rendena cattle. The h^2 estimate in this work for SCS was equal to 0.02 very, i.e., lower than values reported by Dal Zotto et al. (2007) for Brown Swiss (0.07) and by Ikonen et al. (1999) for Finnish Ayrshire and Finnish Friesian (0.09).

The estimates of heritability obtained for all the milk technological traits (MCP, CF, cheese yield and cheese nutrient recoveries) were comparable or higher than that of milk yield traits currently included in the breeding goal for the Rendena cattle population (i.e., 0.20, 0.14, 0.20 for milk, fat and protein yields, respectively) and offer an opportunity of being exploited in selection programs aiming at improve cheese-making ability and cheese yields. In particular, the heritability estimated in this study for RCT was higher than that reported in others breeds. For example, Cassandro et al. (2008) reported heritability value of 0.25 in Italian Holstein cows and Tyriseva et al. (2003) in Finnish Ayrshire breed obtained heritability value of 0.28. The heritability of a_{30} obtained in our study was similar at that reported from a sample of Finnish Ayrshire and Holstein-Frisian cows (i.e., 0.40) by Ikonen et al. (1999), but was greater than estimates reported by Cassandro et al. (2008) in Italian Holstein (h^2 = 0.15), Cecchinato et al. (2016) in Brown Swiss (h^2 = 0.18) and Bonfatti et al. (2011) in Italian Simmental cows (h^2 = 0.12). The heritability of the CF_t model parameters and the maximum CF were estimated only in Brown Swiss by Cecchinato et al. (2016), which reported values of heritability ranging from 0.07 for CF_p to 0.25 for t_{max}, lower than values estimated in this study. However, a different repeatability model was applied in this latter study as compared to the present one. The heritability estimates obtained in the present study for the percentage cheese yields were similar than the corresponding estimates of daily milk yield, and higher to that of daily cheese yields. In a previous study of Cecchinato et al. (2015), using FTIR predictions, heritability estimates obtained for cheese yields resulted greater for Italian Holstein and Brown Swiss breeds and lower for Simmental cows as compared to the present study. In agreement with the study of Cecchinato et al. (2015), the heritability estimates for the percentage REC_{FAT} and $REC_{PROTEIN}$ resulted much higher than the corresponding estimates of milk fat and protein contents.

Genetic and phenotypic correlation

The genetic correlations between the milk technological traits (MCP, CF, cheese yields and cheese nutrient recoveries) and the milk production and composition in Rendena breed are useful to understand how these new traits respond to the present selection process based on fat and protein yields, but also to investigate their potential use in selection toward the improvement of milk technological properties for cheese production. The milk yield displayed negative genetic correlation with RCT (favourable) in agreement with the results reported in Holstein and Brown Swiss (-0.33 and -0.15, respectively) by Cecchinato et al. (2011), although almost null genetic correlation was reported by Ikonen et al. (1999) in Finnish Ayrshire and Finnish Friesian (0.02). The relationship between milk yield and a_{30}, in this study, was lower than those observed for Holstein (0.22) by Cassandro et al., (2008) and subsequent confirmed by Cecchinato et al. (2011), which reported also negative correlation for Brown Swiss (-0.18). To our knowledge, no other studies have considered the relationships existing between milk production and composition and the CF_t model parameters. The relationship observed between milk yield and RCT_{eq}, even if weak, confirmed the favourable effect that an increase in milk production produces on the coagulation time. However, the increase of milk production has a negative effect on CF_p, CF_{max} and t_{max} and positive effects on k_{CF} and k_{SR}. As reported in previous studies (Bittante et al., 2013; Cecchinato et al., 2015), the genetic correlations between milk yield and the percentages of the cheese yield traits resulted negative. This effect could be explained by the negative relationship between milk yield and the percentage of fat and protein, which are the main solid components of the curd. However, genetic correlations almost null were obtained in present work between milk production and the recoveries of fat and protein, while negative genetic correlations have been obtained in Holstein and Brown Swiss cattle (Cecchinato et al., 2015). Therefore, these results indicate that a greater selective pressure for milk production could limit differently the percentage cheese yields depending on the breed considered.

The genetic correlations estimated between RCT and milk fat and protein contents in this study were comparable to the corresponding estimates obtained in Finnish Ayrshire (-0.01 and 0.49 for fat and protein, respectively) by Ikonen et al. (1999). The same authors reported similar genetic correlation than those obtained in this study between a_{30} and protein content (i.e., -0.24) and lower genetic correlation between RCT and fat percentage (i.e., 0.09). Cecchinato et al. (2011) obtained almost null relationships in Brown Swiss between the traditional MCP (RCT and a_{30}) and milk protein percentage, and strong positive relationship between a_{30} and protein content in Holstein (0.35) confirming the result obtained in a previous study by Cassandro et al. (2008).

Considering the relationships between fat and protein content with the CF_t model parameters and two predicted traits derivate from CF_t, it is possible to highlight the more favourable effect that the increase of fat content has on modelling CF_t as respect to the percentage of protein. In particular, as observed for traditional RCT, the relationship between RCT_{eq} and fat content was negative (favourable), while it resulted unfavourable with the protein percentage (i.e., positive correlation). Therefore, the increased milk fat and protein content promote the increase of CF_p and CF_{max}, but in the case of protein percentage there is a reduction in the curd-firming rate constant (k_{CF}) and, consequently, an increase in the time (t_{max}) to attain CF_{max}.

Milk proteins are the most important tool for the processes of coagulation and syneresis, but the recovery of fat in the curd is important for the cheese yield. The genetic correlations between the milk fat and protein contents and %CY, in this study, were positive but slightly lower than the corresponding estimates obtained in Holstein, Brown Swiss and Simmental using FTIR predictions (Cecchinato et al., 2015). The solids and energy recoveries were positively related to milk composition but lower, especially, the protein percentage, with the results reported by Cecchinato et al. (2015). The same authors reported that the fat and protein contents of the milk were moderately correlated (in a favourable direction) with the protein recovery in the curd, as in this study, and comparable relationship between fat content and the respective recovery in the curd was observed. The negative genetic correlation obtained between protein content and fat recovery in curd in the present study, are not in agreement with the corresponding estimates reported for Brown Swiss (0.40) by Bittante et al. (2013) using the individual model-cheese production procedure and in Holstein, Brown Swiss and Simmental cows (0.29, 0.22 and 0.01, respectively) by Cecchinato et al. (2015) by the means of the FTIR predictions.

The lactose content, as previously observed for the fat content, showed genetic and phenotypic correlations favourable with the traditional MCP, the CF_t model parameters and the two maximum curd firmness traits. Moreover, positive relationships were observed with %CY, %REC and the dCY (kg/d) in agreement with the results reported by Cecchinato et al. (2015) for all the breeds considered.

The SCS is an important factor that affects the coagulation of milk; indeed, as reported in several studies (Ikonen et al, 2004; Cassandro et al., 2008; Cecchinato et al., 2011), the SCS trait exerts unfavourable phenotypic and genetic effects on both RCT and a_{30}. Moreover, the SCS of milk was negatively related, from a genetic point of view, with all cheese-making traits in agreement with the results obtained by Bittante et al. (2013) using the data of the cheeses model from individual milk samples di Brown Swiss, and confirmed in a successive study by Cecchinato et al.(2015), which used the FTIR predictions in Holstein, Brown Swiss and Simmental cows.

CONCLUSIONS

This preliminary study provided the estimation of genetic parameters in Rendena cattle breed for the milk technological traits (MCP, CF, cheese yields, the nutrient recoveries in the curd and the daily cheese yields), using their FTIR predictions. The heritability obtained from all the predicted traits were comparable and in some case higher than those reported for milk production and composition with an exploitable additive genetic variation to improve genetically the cheese-making ability, the cheese yields and the nutrient recoveries in the curd from the milk of this local cattle breed. The favourable genetic correlations of milk production and composition with %CY and REC highlight that it is possible to frothily improve the technological properties of milk for cheese production in the breed.

REFERENCES

[AIA] Associazione Italiana Allevatori, 2016. Milk recording activity: official statistics. Italian Breeders Association, Rome, Italy.

ANARE (2016) Risultati controlli funzionali 2015. La Rendena, 1-2, 25–29.

Bittante, G. (2011). Modelling rennet coagulation time and curd firmness of milk. Journal of Dairy science, 94(12), 5821-5832.

Bittante, G., Cipolat-Gotet, C., & Cecchinato, A. (2013a). Genetic parameters of different measures of cheese yield and milk nutrient recovery from an individual model cheese-manufacturing process. Journal of Dairy science, 96(12), 7966-7979.

Bittante, G., Contiero, B., & Cecchinato, A. (2013b). Prolonged observation and modelling of milk coagulation, curd firming, and syneresis. International Dairy Journal, 29(2), 115-123.

Bittante, G., Ferragina, A., Cipolat-Gotet, C., & Cecchinato, A. (2014). Comparison between genetic parameters of cheese yield and nutrient recovery or whey loss traits measured from individual model cheese-making methods or predicted from unprocessed bovine milk samples using Fourier-transform infrared spectroscopy. Journal of dairy science, 97(10), 6560-6572.

Bonfatti, V., Cecchinato, A., Gallo, L., Blasco, A., & Carnier, P. (2011). Genetic analysis of detailed milk protein composition and coagulation properties in Simmental cattle. Journal of dairy science, 94(10), 5183-5193.

Cassandro, M., Comin, A., Ojala, M., Dal Zotto, R., De Marchi, M., Gallo, L., & Bittante, G. (2008). Genetic parameters of milk coagulation properties and their relationships with milk yield and quality traits in Italian Holstein cows. Journal of Dairy Science, 91(1), 371-376.

Cecchinato, A., De Marchi, M., Gallo, L., Bittante, G., & Carnier, P. (2009). Mid-infrared spectroscopy predictions as indicator traits in breeding programs for enhanced coagulation properties of milk. Journal of Dairy Science, 92(10), 5304-5313.

Cecchinato, A., Penasa, M., De Marchi, M., Gallo, L., Bittante, G., & Carnier, P. (2011). Genetic parameters of coagulation properties, milk yield, quality, and acidity estimated using coagulating and noncoagulating milk information in Brown Swiss and Holstein-Friesian cows. Journal of dairy science, 94(8), 4205-4213.

Cecchinato, A., Albera, A., Cipolat-Gotet, C., Ferragina, A., & Bittante, G. (2015). Genetic parameters of cheese yield and curd nutrient recovery or whey loss traits predicted using Fourier-transform infrared spectroscopy of samples collected during milk recording on Holstein, Brown Swiss, and Simmental dairy cows. Journal of dairy science, 98(7), 4914-4927.

Cecchinato, A., & Bittante, G. (2016). Genetic and environmental relationships of different measures of individual cheese yield and curd nutrients recovery with coagulation properties of bovine milk. Journal of dairy science, 99(3), 1975-1989.

Cipolat-Gotet, C., Cecchinato, A., De Marchi, M., Penasa, M., & Bittante, G. (2012). Comparison between mechanical and near-infrared methods for assessing coagulation properties of bovine milk. Journal of dairy science, 95(11), 6806-6819.

Cipolat-Gotet, C., Cecchinato, A., De Marchi, M., & Bittante, G. (2013). Factors affecting variation of different measures of cheese yield and milk nutrient recovery from an individual model cheese-manufacturing process. Journal of dairy science, 96(12), 7952-7965.

Dal Zotto, R., De Marchi, M., Dalvit, C., Cassandro, M., Gallo, L., Carnier, P., & Bittante, G. (2007). Heritabilities and genetic correlations of body condition score and calving interval with yield, somatic cell score, and linear type traits in Brown Swiss cattle. Journal of dairy science, 90(12), 5737-5743.

Dal Zotto, R., De Marchi, M., Cecchinato, A., Penasa, M., Cassandro, M., Carnier, P., & Bittante, G. (2008). Reproducibility and repeatability of measures of milk coagulation properties and predictive ability of mid-infrared reflectance spectroscopy. Journal of dairy Science, 91(10), 4103-4112.

De Marchi, M., Dal Zotto, R., Cassandro, M., & Bittante, G. (2007). Milk coagulation ability of five dairy cattle breeds. Journal of Dairy Science, 90(8), 3986-3992.

De Marchi, M., Toffanin, V., Cassandro, M., & Penasa, M. (2013). Prediction of coagulating and noncoagulating milk samples using mid-infrared spectroscopy. Journal of dairy science, 96(7), 4707-4715.

Emmons, D. B., Ernstrom, C. A., Lacroix, C., & Verret, P. (1990). Predictive Formulas for Yield of Cheese from Composition of Milk: A Review1. Journal of dairy science, 73(6), 1365-1394.

Ferragina, A., Cipolat-Gotet, C., Cecchinato, A., & Bittante, G. (2013). The use of Fourier-transform infrared spectroscopy to predict cheese yield and nutrient recovery or whey loss traits from unprocessed bovine milk samples. Journal of dairy science, 96(12), 7980-7990.

Guzzo, N., Sartori, C., & Mantovani, R. (2009). Test day-milk yields variance component estimation using repeatability or random regression models in the Rendena breed. Italian Journal of Animal Science, 8(sup3), 71-73.

Ikonen, T., Ahlfors, K., Kempe, R., Ojala, M., & Ruottinen, O. (1999). Genetic parameters for the milk coagulation properties and prevalence of noncoagulating milk in Finnish dairy cows. Journal of Dairy Science, 82(1), 205-214.

Ikonen, T., Morri, S., Tyrisevä, A. M., Ruottinen, O., & Ojala, M. (2004). Genetic and phenotypic correlations between milk coagulation properties, milk production traits, somatic cell count, casein content, and pH of milk. Journal of dairy science, 87(2), 458-467.

International Committee for Animal Recording (ICAR). 2012. International Agreement of Recordings Practices—Guidelines Approved by the General Assembly held in Cork, Ireland, on June 2012. ICAR. Rome, Italy.

Karoui, R., Downey, G., & Blecker, C. (2010). Mid-infrared spectroscopy coupled with chemometrics: A tool for the analysis of intact food systems and the exploration of their molecular structure−Quality relationships− A review. Chemical reviews, 110(10), 6144-6168.

Kim, H. Y. (2013). Statistical notes for clinical researchers: assessing normal distribution (2) using skewness and kurtosis. Restorative dentistry & endodontics, 38(1), 52-54.

Laporte, M. F., Martel, R., & Paquin, P. (1998). The near-infrared optic probe for monitoring rennet coagulation in cow's milk. International dairy Journal, 8(7), 659-666.

Mantovani, R., De Marchi, M., Cologna, N., Guzzo, N. & Bittante, G. (2011). Breed, housing and feeding systems affect milk coagulation traits and cheese yield and quality. Proceedings of "62rd Annual Meeting of the EAAP", Stavenger 2011 (Abstract). DOI: 10.3920/978-90-8686-731-8.

Misztal, I. (2008). Reliable computing in estimation of variance components. Journal of animal breeding and genetics, 125(6), 363-370.

Penasa, M., Cecchinato, A., Battagin, M., De Marchi, M., Pretto, D., & Cassandro, M. (2010). Bayesian inference of genetic parameters for test-day milk yield, milk quality traits, and somatic cell score in Burlina cows. Journal of applied genetics, 51(4), 489-495.

Verdier-Metz, I., Coulon, J. B., & Pradel, P. (2001). Relationship between milk fat and protein contents and cheese yield. Animal Research, 50(5), 365-371.

Table 1. Descriptive statistics of productive traits, milk composition and milk technological traits of Rendena breed reared in the Trento province.

Item	**Mean**	**SD**	**Skewness**	**Kurtosis**	**Kolmogorov-Smirnov**
Milk Production kg/d	17.67	5.578	0.218	0.096	0.029
Milk composition					
Fat, %	3.483	0.607	0.333	2.092	0.043
Protein, %	3.282	0.329	0.476	0.891	0.035
Lactose, %	4.884	0.219	-1.116	3.316	0.073
SCS, U	2.623	1.817	0.415	-0.213	0.045
Traditional MCP					
RCT, min	16.39	4.788	0.273	0.418	0.024
k_{20}, min	5.041	1.656	0.050	0.163	0.009
a_{30}, mm	31.50	9.069	-0.218	0.184	0.023
a_{45}, mm	30.60	4.008	-0.127	0.508	0.018
CF_t model parameters					
RCT_{eq}, min	17.16	5.208	0.258	0.442	0.024
CF_p, mm	47.08	6.467	-0.164	0.432	0.018
k_{CF}, %/min	14.28	2.738	0.236	0.432	0.020
k_{SR}, %/min	1.455	0.252	0.182	0.426	0.017
Maximum curd firmness					
CF_{max}, mm	35.74	4.722	-0.153	0.193	0.016
t_{max}, min	34.40	9.253	0.113	0.210	0.016
Cheese yields, %					
CY_{CURD}	12.85	1.724	0.362	0.497	0.026
CY_{SOLIDS}	6.137	0.787	0.254	0.902	0.027
CY_{WATER}	6.977	0.904	0.214	0.287	0.016
Curd recoveries, %					
$REC_{PROTEIN}$	77.54	2.185	-0.253	0.532	0.019
REC_{FAT}	88.99	2.317	0.061	0.164	0.010
REC_{SOLIDS}	47.79	2.730	0.269	0.908	0.028
REC_{ENERGY}	63.57	3.300	0.253	0.989	0.029
Daily production of cheese, kg/d					
dCY_{CURD}	2.250	0.726	0.491	0.777	0.033
dCY_{SOLIDS}	1.077	0.353	0.489	0.741	0.033
dCY_{WATER}	1.226	0.403	0.424	0.608	0.029

Table 2. Estimated marginal posterior densities and HPD 95% (in parentheses) for genetic variance (σ^2_a), permanent environmental variance (σ^2_{pe}), residual variance (σ^2_e), and h^2 of production traits, milk composition, traditional milk coagulation proprieties (MCP), curd firming (CF_t) model parameters, maximum curd-firmness traits, cheese yield, nutrient recoveries and daily production of cheese yield in Rendena breed.

Item	$\boldsymbol{\sigma^2_a}$	$\boldsymbol{\sigma^2_{pe}}$	$\boldsymbol{\sigma^2_r}$	$\mathbf{h^2}$
Milk production kg/d	$2.543^{(1.155; 4.256)}$	$4.785^{(3.421; 6.146)}$	$5.208^{(5.034; 5.396)}$	$0.202^{(0.094; 0.327)}$
Milk composition				
Fat, %	$0.029^{(0.011; 0.048)}$	$0.022^{(0.007; 0.036)}$	$0.212^{(0.204; 0.219)}$	$0.111^{(0.050; 0.184)}$
Protien, %	$0.017^{(0.009; 0.025)}$	$0.015^{(0.008; 0.021)}$	$0.031^{(0.030; 0.032)}$	$0.265^{(0.148; 0.392)}$
Lactose, %	$0.008^{(0.004; 0.013)}$	$0.006^{(0.003; 0.009)}$	$0.017^{(0.016; 0.017)}$	$0.261^{(0.140; 0.399)}$
SCS, U	$0.063^{(0.005; 0.194)}$	$0.981^{(0.835; 1.133)}$	$1.372^{(1.326; 1.421)}$	$0.022^{(0.004; 0.088)}$
Traditional MCP				
RCT, min	$5.192^{(3.111; 7.463)}$	$2.737^{(1.173; 4.348)}$	$6.493^{(6.268; 6.722)}$	$0.359^{(0.225; 0.490)}$
k_{20}, min	$0.533^{(0.270; 0.642)}$	$0.290^{(0.111; 0.386)}$	$0.937^{(0.759; 0.814)}$	$0.302^{(0.190; 0.414)}$
a_{30}, mm	$21.20^{(13.58;29.39)}$	$8.619^{(3.087;14.56)}$	$26.44^{(25.50; 27.37)}$	$0.376^{(0.253; 0.496)}$
a_{45}, mm	$1.763^{(0.973;2.673)}$	$1.371^{(0.704; 2.038)}$	$4.606^{(4.448; 4.773)}$	$0.226^{(0.129; 0.333)}$
CF_t model parameters				
RCT_{eq}, min	$6.041^{(3.638; 8.713)}$	$3.122^{(1.301; 5.026)}$	$8.134^{(7.848; 8.419)}$	$0.348^{(0.219; 0.477)}$
CF_p, mm	$5.152^{(3.006; 7.645)}$	$3.590^{(1.814; 5.425)}$	$13.11^{(12.66;13.58)}$	$0.234^{(0.142; 0.336)}$
k_{CF}, %/min	$1.433^{(0.928; 1.960)}$	$0.521^{(0.163; 0.913)}$	$2.150^{(2.077; 2.227)}$	$0.348^{(0.234; 0.457)}$
k_{SR}, %/min	$0.010^{(0.006; 0.014)}$	$0.004^{(0.001; 0.007)}$	$0.019^{(0.018; 0.019)}$	$0.308^{(0.205; 0.407)}$
Maximum curd firmness				
CF_{max}, mm	$3.126^{(1.900; 4.528)}$	$1.846^{(0.870; 2.868)}$	$6.605^{(6.373; 6.836)}$	$0.268^{(0.169; 0.374)}$
t_{max}, min	$22.35^{(14.09; 31.29)}$	$9.551^{(3.538;15.942)}$	$24.88^{(24.02; 5.755)}$	$0.392^{(0.259; 0.521)}$
Cheese yields, %				
CY_{CURD}	$0.388^{(0.231; 0.564)}$	$0.248^{(0.121; 0.375)}$	$0.999^{(0.964; 1.034)}$	$0.235^{(0.145; 0.332)}$
CY_{SOLIDS}	$0.078^{(0.044; 0.118)}$	$0.051^{(0.023; 0.080)}$	$0.282^{(0.044; 0.118)}$	$0.188^{(0.109; 0.277)}$
CY_{WATER}	$0.096^{(0.058; 0.139)}$	$0.061^{(0.030; 0.093)}$	$0.264^{(0.255; 0.273)}$	$0.225^{(0.141; 0.320)}$
Curd recoveries, %				
$REC_{PROTEIN}$	$1.167^{(0.781; 1.579)}$	$0.398^{(0.134;0.686)}$	$1.492^{(1.440; 1.545)}$	$0.380^{(0.265; 0.488)}$
REC_{FAT}	$0.673^{(0.419; 0.956)}$	$0.338^{(0.141; 0.548)}$	$1.445^{(1.396; 1.497)}$	$0.273^{(0.176; 0.373)}$
REC_{SOLIDS}	$1.061^{(0.624; 1.552)}$	$0.585^{(0.250; 0.940)}$	$3.128^{(3.022; 3.240)}$	$0.220^{(0.135; 0.313)}$
REC_{ENERGY}	$1.383^{(0.835; 1.991)}$	$0.590^{(0.182; 1.026)}$	$4.694^{(4.535; 4.860)}$	$0.206^{(0.128; 0.288)}$
Daily production of cheese, kg/d				
dCY_{CURD}	$0.042^{(0.018; 0.071)}$	$0.077^{(0.054; 0.100)}$	$0.113^{(0.109; 0.117)}$	$0.179^{(0.081; 0.297)}$
dCY_{SOLIDS}	$0.010^{(0.004; 0.016)}$	$0.018^{(0.013; 0.024)}$	$0.029^{(0.028; 0.030)}$	$0.171^{(0.077; 0.284)}$
dCY_{WATER}	$0.012^{(0.004; 0.020)}$	$0.023^{(0.016; 0.030)}$	$0.032^{(0.031; 0.034)}$	$0.176^{(0.079; 0.294)}$

Table 3. Estimated marginal posterior densities and HDP 95% (in parentheses) for genetic (r_a) and phenotypic (r_p) correlations obtained in Rendena breed from bivariate animal model analysis between milk production, quality and traditional milk coagulation proprieties (MCP), curd firming (CF_t) model parameters, maximum curd-firmness traits, cheese yield, nutrient recoveries and daily production cheese yield.

Item	r_a					r_p				
	Milk, kg/d	**Fat, %**	**Protein, %**	**Lactose, %**	**SCS, U**	**Milk, kg/d**	**Fat, %**	**Protein, %**	**Lactose, %**	**SCS, U**
Milk composition										
Fat, %	-0.245$^{(-0.672; 0.226)}$					-0.033$^{(-0.075; 0.010)}$				
Protien, %	-0.411$^{(-0.719; -0.031)}$	0.243$^{(-0.190; 0.577)}$				-0.323$^{(-0.369; -0.277)}$	0.208$^{(0.171; 0.246)}$			
Lactose, %	0.131$^{(-0.308; 0.507)}$	0.121$^{(-0.339; 0.519)}$	0.064$^{(-0.315; 0.467)}$			0.178$^{(0.129; 0.227)}$	-0.029$^{(-0.068; 0.010)}$	-0.075$^{(-0.123; -0.028)}$		
SCS, U	-0.564$^{(-0.986; 0.399)}$	-0.455$^{(-0.962; 0.460)}$	0.515$^{(-0.653; 0.991)}$	-0.529$^{(-0.980; 0.440)}$		-0.168$^{(-0.214; -0.121)}$	0.066$^{(0.027; 0.104)}$	0.216$^{(0.167; 0.265)}$	-0.394$^{(-0.447; -0.342)}$	
Traditional MCP										
RCT, min	-0.192$^{(-0.543; 0.195)}$	-0.055$^{(-0.478; 0.348)}$	0.429$^{(0.103; 0.699)}$	-0.167$^{(-0.496; 0.232)}$	0.818$^{(0.230; 0.998)}$	-0.207$^{(-0.259; -0.154)}$	0.066$^{(0.023; 0.109)}$	0.226$^{(0.178; 0.275)}$	-0.325$^{(-0.372; -0.277)}$	0.325$^{(0.274; 0.375)}$
k_{20}, min	0.091$^{(-0.304; 0.493)}$	-0.422$^{(-0.721; -0.032)}$	-0.037$^{(-0.364; 0.329)}$	-0.286$^{(-0.582; 0.070)}$	0.752$^{(0.005; 0.998)}$	-0.010$^{(-0.061; 0.042)}$	-0.327$^{(-0.362; -0.293)}$	-0.296$^{(-0.343; -0.249)}$	-0.346$^{(-0.389; -0.303)}$	0.196$^{(0.149; 0.242)}$
a_{30}, mm	0.074$^{(-0.302; 0.412)}$	0.210$^{(-0.170; 0.570)}$	-0.210$^{(-0.517; 0.113)}$	0.209$^{(-0.145; 0.508)}$	-0.810$^{(-0.997; -0.251)}$	0.112$^{(0.058; 0.166)}$	0.032$^{(-0.010; 0.073)}$	0.045$^{(-0.008; 0.098)}$	0.365$^{(0.317; 0.414)}$	-0.295$^{(-0.348; -0.242)}$
a_{45}, mm	-0.185$^{(-0.598; 0.241)}$	0.504$^{(0.143; 0.768)}$	0.549$^{(0.266; 0.757)}$	0.333$^{(-0.040; 0.639)}$	-0.352$^{(-0.987; 0.804)}$	-0.094$^{(-0.143; -0.046)}$	0.327$^{(0.295; 0.358)}$	0.587$^{(0.557; 0.618)}$	0.390$^{(0.351; 0.429)}$	-0.072$^{(-0.116; -0.027)}$
CF_t model parameters										
RCT_{eq}, min	-0.056$^{(-0.434; 0.349)}$	-0.116$^{(-0.513; 0.306)}$	0.288$^{(-0.060; 0.611)}$	-0.221$^{(-0.533; 0.181)}$	0.799$^{(0.144; 0.998)}$	-0.046$^{(-0.062; -0.031)}$	-0.027$^{(-0.069; 0.014)}$	0.080$^{(0.029; 0.131)}$	-0.385$^{(-0.429; -0.340)}$	0.328$^{(0.278; 0.379)}$
CF_p, mm	-0.129$^{(-0.515; 0.271)}$	0.419$^{(0.046; 0.714)}$	0.495$^{(0.209; 0.708)}$	0.327$^{(-0.042; 0.669)}$	-0.527$^{(-0.989; 0.562)}$	-0.108$^{(-0.156; -0.060)}$	0.222$^{(0.189; 0.255)}$	0.570$^{(0.539; 0.602)}$	0.278$^{(0.236; 0.320)}$	-0.071$^{(-0.115; -0.027)}$
k_{CF}, %/min	0.143$^{(-0.221; 0.480)}$	0.139$^{(-0.251; 0.522)}$	-0.338$^{(-0.626; -0.017)}$	0.071$^{(-0.300; 0.403)}$	-0.742$^{(-0.995; -0.080)}$	0.114$^{(0.062; 0.166)}$	0.120$^{(0.081; 0.159)}$	-0.065$^{(-0.115; -0.015)}$	0.087$^{(0.038; 0.136)}$	-0.183$^{(-0.233; -0.133)}$
k_{SR}, %/min	0.229$^{(-0.136; 0.563)}$	-0.018$^{(-0.389; 0.401)}$	-0.492$^{(-0.745; -0.192)}$	-0.110$^{(-0.458; 0.237)}$	-0.701$^{(-0.994; 0.003)}$	0.099$^{(0.049; 0.149)}$	-0.205$^{(-0.242; -0.168)}$	-0.191$^{(-0.237; -0.145)}$	-0.062$^{(-0.110; -0.015)}$	-0.132$^{(-0.179; -0.085)}$
Maximum curd firmness										
CF_{max}, mm	-0.125$^{(-0.507; 0.267)}$	0.371$^{(0.003; 0.676)}$	0.429$^{(0.135; 0.658)}$	0.415$^{(0.085; 0.701)}$	-0.555$^{(-0.990; 0.512)}$	-0.078$^{(-0.128; -0.029)}$	0.168$^{(0.132; 0.203)}$	0.538$^{(0.503; 0.573)}$	0.405$^{(0.365; 0.445)}$	-0.145$^{(-0.191; -0.099)}$
t_{max}, min	-0.139$^{(-0.486; 0.230)}$	-0.116$^{(-0.501; 0.271)}$	0.428$^{(0.112; 0.697)}$	-0.135$^{(-0.457; 0.246)}$	0.771$^{(0.098; 0.997)}$	-0.192$^{(-0.247; -0.138)}$	-0.032$^{(-0.075; 0.011)}$	0.230$^{(0.180; 0.279)}$	-0.252$^{(-0.301; -0.202)}$	0.296$^{(0.242; 0.350)}$
Cheese yields, %										
CY_{CURD}	-0.344$^{(-0.701; 0.043)}$	0.710$^{(0.490; 0.862)}$	0.740$^{(0.559; 0.875)}$	0.218$^{(-0.166; 0.564)}$	-0.093$^{(-0.982; 0.919)}$	-0.150$^{(-0.197; -0.102)}$	0.688$^{(0.669; 0.707)}$	0.656$^{(0.631; 0.680)}$	0.112$^{(0.068; 0.156)}$	0.039$^{(-0.006; 0.084)}$
CY_{SOLIDS}	-0.312$^{(-0.692; 0.110)}$	0.861$^{(0.736; 0.942)}$	0.591$^{(0.329; 0.789)}$	0.291$^{(-0.108; 0.642)}$	-0.321$^{(-0.987; 0.851)}$	-0.102$^{(-0.148; -0.056)}$	0.868$^{(0.859; 0.877)}$	0.499$^{(0.469; 0.530)}$	0.079$^{(0.037; 0.122)}$	0.059$^{(0.016; 0.101)}$
CY_{WATER}	-0.364$^{(-0.729; 0.021)}$	0.451$^{(0.108; 0.716)}$	0.808$^{(0.638; 0.933)}$	0.417$^{(0.074; 0.713)}$	0.117$^{(-0.938; 0.968)}$	-0.124$^{(-0.171; -0.077)}$	0.290$^{(0.259; 0.321)}$	0.656$^{(0.632; 0.681)}$	0.300$^{(0.260; 0.340)}$	-0.061$^{(-0.106; -0.017)}$
Curd recoveries, %										
$REC_{PROTEIN}$	0.006$^{(-0.362; 0.354)}$	0.291$^{(-0.065; 0.601)}$	0.379$^{(0.073; 0.659)}$	0.474$^{(0.169; 0.722)}$	-0.057$^{(-0.962; 0.919)}$	0.115$^{(0.060; 0.169)}$	0.323$^{(0.286; 0.361)}$	0.127$^{(0.077; 0.176)}$	0.408$^{(0.364; 0.452)}$	-0.318$^{(-0.383; -0.253)}$
REC_{FAT}	0.071$^{(-0.321; 0.420)}$	0.210$^{(-0.160; 0.558)}$	-0.266$^{(-0.572; 0.067)}$	0.304$^{(-0.050; 0.579)}$	-0.663$^{(-0.996; 0.250)}$	0.105$^{(0.056; 0.154)}$	-0.035$^{(-0.072; 0.002)}$	-0.012$^{(-0.060; 0.035)}$	0.400$^{(0.361; 0.440)}$	-0.168$^{(-0.214; -0.122)}$
REC_{SOLIDS}	-0.217$^{(-0.595; 0.191)}$	0.808$^{(0.631; 0.927)}$	0.477$^{(0.182; 0.693)}$	0.081$^{(-0.320; 0.456)}$	-0.317$^{(-0.988; 0.822)}$	-0.111$^{(-0.158; -0.063)}$	0.800$^{(0.786; 0.814)}$	0.502$^{(0.470; 0.535)}$	-0.038$^{(-0.082; 0.006)}$	0.095$^{(0.050; 0.139)}$
REC_{ENERGY}	-0.169$^{(-0.575; 0.229)}$	0.793$^{(0.637; 0.907)}$	0.244$^{(-0.106; 0.535)}$	0.271$^{(-0.118; 0.591)}$	-0.537$^{(-0.990; 0.639)}$	-0.006$^{(-0.053; 0.041)}$	0.843$^{(0.830; 0.856)}$	0.279$^{(0.238; 0.320)}$	0.105$^{(0.063; 0.148)}$	-0.007$^{(-0.050; 0.036)}$
Cheese production, kg/d										
dCY_{CURD}	0.869$^{(0.721; 0.950)}$	0.135$^{(-0.362; 0.579)}$	-0.035$^{(-0.442; 0.394)}$	0.205$^{(-0.272; 0.602)}$	-0.565$^{(-0.994; 0.625)}$	0.880$^{(0.869; 0.891)}$	0.310$^{(0.271; 0.349)}$	-0.005$^{(-0.054; 0.044)}$	0.217$^{(0.169; 0.266)}$	-0.141$^{(-0.186; -0.097)}$
dCY_{SOLIDS}	0.894$^{(0.769; 0.967)}$	0.182$^{(-0.298; 0.607)}$	-0.142$^{(-0.538; 0.294)}$	0.208$^{(-0.271; 0.600)}$	-0.642$^{(-0.996; 0.400)}$	0.874$^{(0.864; 0.885)}$	0.412$^{(0.375; 0.450)}$	-0.067$^{(-0.115; -0.019)}$	0.195$^{(0.147; 0.243)}$	-0.126$^{(-0.170; -0.083)}$
dCY_{WATER}	0.876$^{(0.738; 0.950)}$	-0.046$^{(-0.549; 0.449)}$	-0.026$^{(-0.438; 0.416)}$	0.336$^{(-0.117; 0.720)}$	-0.425$^{(-0.990; 0.828)}$	0.895$^{(0.885; 0.904)}$	0.103$^{(0.063; 0.144)}$	-0.020$^{(-0.070; 0.029)}$	0.292$^{(0.245; 0.340)}$	-0.181$^{(-0.226; -0.137)}$

CHAPTER 4

ANALYSIS OF GENETIC CORRELATIONS BETWEEN BEEF TRAITS IN YOUNG BULLS AND IN PRIMIPAROUS COWS BELONGING TO THE DUAL PURPOSE RENDENA BREED

Under Submission

ABSTRACT

This study aimed at estimating genetic relationships between muscularity type traits obtained in primiparous cows (front muscularity; back, loins, and rump; thigh, buttocks side and rear views) with the same types scored on candidate young bulls at the end of the performance test for beef aptitude, and with the performance test traits (average daily gain, ADG; EUROP fleshiness evaluation; dressing percentage), in local dual-purpose Rendena breed. Muscularity linear type traits recorded on 11,992 first parity cows and the muscularity types scored on 957 candidate young bulls at the end of the performance test were analysed. After obtaining genetic parameters for both muscularity traits of cows and young bulls, and beef performance test traits of young bulls through a series of single-trait REML models, bivariate analyses were performed on a data set accounting for 12,949 records belonging to the same number of animals (females and males) to estimate the genetic correlations among beef traits recorded in the different sexes. The heritability estimates obtained were moderate for both groups of traits and ranged from 0.25 for front muscularity in primiparous cows, to 0.36 for both back, loins and rump and dressing percentage recorded in young bulls. Medium to high genetic correlations were found between performance test and muscularity type traits collected in young bulls (from 0.47 between thigh, buttocks side view and ADG to 0.97 between thigh, buttocks side view and in vivo EUROP score). The genetic relationships between muscularity linear type traits of primiparous cows and performance traits of young bulls were variable (from 0.07 between front (chest and shoulder) and ADG to 0.822 between thigh, buttocks rear view and dressing percentage). Generally, the traits measured during performance test in young bulls and muscularity traits evaluated on primiparous cows were favourably correlated, indicating a common way for the selection route.

Key Words: genetic parameters, Rendena breed, beef traits, muscularity linear type traits

INTRODUCTION

In the present days most part of the European dual purpose cattle breeds are traditional local populations diffused in marginal areas (Gandini and Villa, 2003). Selection in these populations requires a good balance between milk and beef traits, because of the very strict bound that local breeds maintain with milk and beef products obtained in their specific environment (Gandini and Villa, 2003). Selection for beef in cattle is often based primarily on growth and *in vivo* conformation recorded at test stations on young candidate bulls (Andersen et al., 1981; Albera et al., 2001; Sbarra et al, 2013), but also on muscularity traits scored during routinely linear type evaluation (Mantovani et al., 2010; Frigo et al., 2013), or, more recently, on quantitative and qualitative traits data recorded at abattoirs (Reverter et al., 2000; Bonfatti et al., 2013; Sbarra et al., 2013). However, in dual purpose cattle breeds, slaughter data have been introduced for selection purposes only recently and particularly in populations as the French Normande and Montbeliarde (Croué et al., 2016; Croué and Ducrocq, 2017) that are characterized by a wider population size than the remaining European dual purpose breeds. Selection for beef traits in Italian dual purpose cattle breeds is organized through the performance test for young bulls' evaluation (Sbarra et al., 2009), but it is also based on the evaluation of linear type traits on primiparous cows (Frigo et al., 2013; Mazza et al., 2014, 2015, 2016), that are in many cases both included in a global index used for selection (Sölkner et al., 2000; Fuerst-Waltl et al., 2016; Mazza et al., 2016). Among the type traits included in the global index of dual purpose cattle breeds, muscularity and/or mammary traits are the most commonly used (Sölkner et al., 2000; Fuerst-Waltl et al., 2016; Mazza et al., 2016).

The Rendena breed is autochthonous of the Italian Alps and particularly of the homonymous alpine valley located in north-east of Italy, in the province of Trento, enclosed between the Adamello (west) and the Brenta (east) mountain groups. The Rendena has ancient origins and it has survived to the massive introduction of cosmopolitan breeds in the northern part of Italy during the XX century (Forabosco & Mantovani, 2011). At present the Rendena population is mainly raised in the mountainous area of origin and in the flatlands of the Veneto region (provinces of Padua and

Vicenza) in the area called “Destra Brenta”, which lays on the right bank of the river Brenta. This is a highly fertile area of alluvial origin in which a lot of land is under grass, and the remaining is mostly dedicated to the production of maize used for silage. The Destra Brenta is one the most important dairy area of the Veneto region. The coat of the Rendena cattle is usually dark brown accounting for a white ring around the black muzzle. Animals are of small to medium body size and are characterized by a good grazing ability expressed on mountain pastures in both the area of origin and in the Veneto region (Mantovani et al., 1997). The present Rendena population accounts for about 4,000 registered cows selected for the dual purpose attitude through the use of a global index accounting for a protein-and fat- corrected milk yield index, a performance test index, measured on candidate young bulls and based on average daily gain plus *in vivo* estimate of dressing percentage and EUROP score, and muscularity and mammary traits obtained from linear type classification of primiparous cows (Mazza et al., 2014). In recent years accurate analyses of the genetic relationship between milk and meat traits have been carried out in many breeds aiming at identifying the proper combination of traits when antagonistic aspects concur in selection (Liinamo et al., 2001; de Haas et al., 2007; Frigo et al., 2013; Mazza et al., 2016). However, to our knowledge, no previous study has been carried out to evaluate the genetic structure of beef traits obtained in different sexes and at different time during life. The aim of this study was to estimate genetic relationships of muscularity type traits obtained in primiparous cows with the performance test traits and the same types scored on candidate young bulls at the end of the test. The Rendena cattle breed was chosen as case study for other small, local dual-purpose breeds.

MATERIALS AND METHODS

Data were provided by the National Association of Rendena cattle Breeders (ANARE) and included linear type and performance test traits recorded respectively in primiparous cows and in candidate young bulls at the age of about one year (i.e., before the progeny testing for milk yield). Linear type traits recorded between the years 1994 and 2014 on 14,231 first parity Rendena cows were initially considered. The linear type classification system consists of in composite traits and 20 linear description traits (Mazza et al., 2014). The composite traits summarize body size, fleshiness, body shape and udder. The individual type traits describe specific body regions of animal (Mazza et al., 2014). For this study, only 4 individual muscularity traits (front muscularity; back, loins, and rump; thigh, buttocks side view; thigh, buttocks rear view) scored on a linear scale from 1 to 5 points were taken into account (Table 1). To enter the dataset for further analysis, only cows with an age at first calving between 22 and 48 months and with days in milk (DIM) between 10 and 305 days were considered. In addition, data from herd-year-classifier contemporary groups with less than two records were discarded. After editing, the linear type data set considered in records on 11,992 first parity Rendena cows.

For the purpose of the study, type traits were merged with beef traits recorded in 957 Rendena young bulls at performance test station between the years 1997 to 2014. The young bulls were measured for average daily gain (ADG; obtained by linear regression of weight on age recorded 11 times during the stay of young bulls at the test station), estimated *in vivo* dressing percentage, estimated *in vivo* fleshiness score (EUROP scale), and linear type evaluation carried out at the end of test, i.e., at about 11 months of age. For the aim of the research only 4 linear type traits related to muscularity (front muscularity; back, loins, and rump; thigh, buttocks side view; thigh, buttocks rear view) were taken into account (Table 1). Muscularity traits were evaluated in both males and females by visual appraisal by a classifier of the National Association of Rendena cattle Breeders (ANARE). The *in vivo* EUROP score considering the grades E, U, R, O and P, from the best to worst conformation, was transformed in a linear scale from 80 (for P) to 120 (for E) and furtherly subdivided into + or – subclasses (Croué et al, 2016) to which were added or subtracted 3.33 points as respect to the full class, i.e., for a R+ the score was 103.33, while and for the U- 106.66. The whole numeric values, ranging from 76.66 (less muscular) to 123.33 (more muscular), were considered as continuous. Both evaluations of *in vivo* EUROP and dressing percentage for young bulls were carried out by three experts of the slaughter industry and values were averaged by each bull before the analysis. Finally, the two datasets described above were joined into a single data set accounting for 12,949 records belonging to the same number of animals (females and males), for carrying out bivariate animal model analyses. The pedigree file obtained traced back subjects up to 10 generations and contained a total of 19,265 animals.

Genetic analyses and models

(Co)variance components were estimated between each pair of the target traits by running bivariate animal model analyses in the AIREMLF90 program from the BLUPF90 family (Misztal, 2008). For data on young bulls, a series of bi-trait analyses were carried to obtain (co)variance components between type (front muscularity: FM; back, loins, and rump: BLR; thigh, buttocks side view: TBS; and thigh, buttocks rear view: TBR), and performance test traits (ADG, EUROP, and dressing percentage). Otherwise, all the possible trait pairs obtained by combining muscularity linear type traits recorded on primiparous cows with muscularity type traits and performance test traits recorded on young bulls were set up to estimate (co)variance components.

In matrix notation, the models used were as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e};$$

where $\mathbf{y}$ is the vector of a given observer phenotype, $\mathbf{X}$, and $\mathbf{Z}$ are the incidence matrices of fixed effects and genetic effects, respectively, the vectors $\mathbf{u}$ and $\mathbf{e}$ represent the additive genetic and residual effects, respectively, and the vector $\boldsymbol{\beta}$ includes the fixed effects. For type traits recorded on primiparous cows, the fixed effects accounted in the model were, as described in Mazza et al. (2014): the herd year classifier (1,729 levels), the age at calving (9 classes: <24 months, from 25 to 38 using 2-months intervals, and ≥39 months for the last class), and the days in milk (8 classes from 10 to 30 days after calving and from 31 to 210 days after calving using 30-days intervals, or for later evaluation >210 days). For performance test traits the fixed effects considered were the contemporary group effect (84 levels), the parity order of the mother effect (4 classes: 1st parity;

2nd parity; 3rd to 7th parity; over the 8th parity), and, for the estimated dressing percentage and EUROP scores only, the age at the end performance test used as linear covariate.

The assumptions on estimated (co)variances for the bi-trait analyses were obtained as $\mathbf{G}\otimes\mathbf{A}$ and $\mathbf{R}\otimes\mathbf{I}$, with **G**, and **R** as 2 × 2 matrices respectively including the additive genetic, and residual (co)variance matrices of the respective trait pair; **A** and **I** are the additive relationships matrix and an identity matrix; and ⊗ is the Kronecker product. The residual (co)variance was set at zero in bivariate analyses of traits coming from different datasets because those traits were measured at different times.

The heritability (h^2) was defined as:

$$h^2=\frac{\sigma_a^2}{\sigma_a^2+\sigma_e^2};$$

where σ_a^2 and σ_e^2 were the mean additive genetic and mean residual variances estimated in different series of bivariate analyses, respectively.

The additive genetic correlations (r_a) between muscularity type traits measured in both females and males and performance test traits were obtained as:

$$r_a=\frac{\sigma_{a1,\,a2}}{\sigma_{a1}\cdot\sigma_{a2}};$$

where $\sigma_{a1,a2}$ was the genetic covariance between traits 1 and 2, and σ_{a1} and σ_{a2} were the genetic standard deviations for traits 1 and 2, respectively.

The standard error of heritability and correlations were calculated following the “delta method” outlined in Lynch and Walsh (1998) and considering the variances of the estimated (co)variance matrices.

RESULTS

Descriptive statistics of all considered beef traits are reported in Table 1. Mean values for all the individual muscularity type traits in primiparous cows and young bulls were close to 3, although slightly lower in females than in males (2.77 vs. 3.04; 2.93 vs. 3.15; 3.00 vs. 3.24; and 2.83 vs. 2.98

for FM, BLR, TBS and TBR, respectively). An ADG of 1,011 g/d was observed in young bulls under performance test, with *in vivo* EUROP score and dressing percentage (DP) at the end of test, that resulted on average of 98.9 points (R-/R) and 53.7%, respectively. The DP showed the lowest CV (0.012) followed by EUROP score (0.036), muscularity type traits in females (0.28 ± 0.02) and muscularity type traits in young bulls (0.27 ± 0.01).

The estimated (co)variance components and heritability were reported in Table 2. The additive genetic variances evaluated for linear muscularity type traits in primiparous cows were on average lower than the genetic variances observed in the same traits in young bulls (e.g., 0.14 and 0.26 on average, respectively). As a consequence, the heritability values estimated were generally lower in the females as compared to the males, ranging from 0.25 to 0.31 for the primiparous cows, and from 0.28 to 0.41 for young bulls (Table 2). Among muscularity traits, tight and buttocks heritability resulted greater than other traits in females (on average 0.305), while in males they resulted lower than other traits (0.315 on average) considering that back, loins and rump muscularity reached the substantial value of 0.41 (Table 2).

Heritability values for ADG, EUROP, and DP were moderate, i.e., 0.35, 0.34, and 0.36, respectively. In general, standard errors (SE) of heritability were lower in primiparous cows than in young bulls.

Genetic correlations (r_a) between muscularity linear type traits and ADG in young bulls showed moderate genetic correlations, i.e., around 0.52 on average (Table 3). On the other hand, high genetic correlations were found between muscularity type traits and EUROP (from 0.81 with front muscularity to 0.99 with thigh, buttocks side view) and between muscularity and DP (from 0.81 with front muscularity to 0.98 for thigh, buttocks side view). The SE for r_a between muscularity and ADG resulted greater than SE obtained for r_a between muscularity and EUROP and between muscularity and DP (Table 3).

Table 4 reports the genetic correlations between muscularity type traits recorded on primiparous cows and the corresponding type traits evaluated on young bulls. In general, the lowest genetic correlation was found between FM observed in primiparous cows and muscularity traits recorded in young bulls (e.g., 0.53 on average; Table 4), whereas the highest genetic correlation was found between the TBR in females and TBS in males (0.81; Table 4). In general, the single muscularity type traits observed in young bulls showed rather high genetic correlations with the corresponding muscularity type traits in primiparous (i.e., 0.57 for FM, 0.76 for BLR and TBS, and 0.74 for TBR; Table 4). The average SE resulted 0.11 for all genetic correlations between muscularity type traits obtained in the two compared animal categories.

Genetic correlations between muscularity type traits in primiparous and performance test traits recorded in young bulls are reported in Table 5. The lowest genetic correlation (0.07) was found between ADG and FM in females. However, low genetic correlation values were also estimated between ADG and all others muscularity type traits in primiparous cows (e.g., 0.24 on average). On the other hand, EUROP and DP showed moderate r_a with FM in primiparous cows (0.44 and 0.47, respectively), but higher r_a with the remaining traits, i.e., 0.71 and 0.75 with BLR, respectively, 0.78 and 0.80 with TBS, and 0.81 and 0.82 with TBR. Again, SE reached the considerable of 0.11.

DISCUSSION

All muscularity traits scored both in primiparous cows and young bulls have shown to be close to the mean expected values, i.e., mid-point of the score scale, reflecting the tendency toward a normal distribution of these traits as expected at population level. The mean values obtained for primiparous cows in this study are almost the same previously reported by Mazza et al. (2014) for the Rendena breed, but they are also close to values reported by Mazza et al (2015, 2016) for the Aosta Red Pied, another dual purpose Italian local breed, although characterized by a more rounded TBR trait than the Rendena. However, the same muscularity traits have been reported to be more developed in the Aosta Black Pied and Aosta Cestnut (Mazza et al., 2015; Sartori et al., 2015) as compared to the Rendena breed. Therefore, data obtained suggest a general lower muscularity in Rendena primiparous than in Valdostana cattle, but this could be due to the greater milk yield and selection pressure toward this trait in Rendena than in Valdostana autochthonous breeds (Mazza et al., 2014; Mazza et al., 2016). Surprisingly, the mean muscularity scores reported by Forabosco et al. (2004) for Chianina cows were only slightly greater than values reported for the Rendena breed, but this could be attributable to the different age at scoring that is more precocious in Chianina than in Rendena females (Forabosco et al., 2005). Males of the Rendena have shown an average greater score than female considering the same body region; this could be attributable to both the expected sexual differentiation due to sexes, to the younger age at which young bulls are evaluated as compared to cows, and to the feeding plan used for performance tested males as compared to cows, also. Indeed, performance testing is always characterized by *ad libitum* feeding regimen to allow young bulls to fully express their growth potential (Andersen et al., 1981; Sbarra et al, 2013), while cows have a different feeding regimen up to the first parity. The mean ADG in the whole testing period, the mean EUROP score and estimated dressing percentage (evaluated at the end of test), have resulted in a low-moderate growth and conformation for the Rendena young bulls, much lower than values reported for other Italian (Mantovani et al., 1999; Albera et al., 2001) or Irish beef cattle (Crowley et al., 2010), but also lower than growth reported for other dual purpose tested young bulls (i.e., Norvegian dual purpose cattle; Aass, 1996; Czech Pied bulls; Bouška et al., 2003; Simmental in South Africa; Archer and Bergh, 2000). Even in this case the feeding regimen adopted in different test stations around the world is probably the most important source of variation affecting the observed growth rate.

Heritability values obtained in this study resulted only slightly greater (+0.02 on average) than those previously reported for the Rendena primiparous cows by Mazza et al. (2014), but lower than a muscularity factor obtained combining the four muscularity traits in Rendena breeds by Mazza et al. (2016). In this latter study the same muscularity factor obtained for the Aosta Red Pied produced estimates of heritability comparable to those obtained in the present study, confirming the similarities between these two autochthonous Italian breeds. Similar estimates of heritability for muscular trait development (i.e., 0.27) were also obtained by Crowley et al. (2011) using population data for Irish beef cattle breeds, while Frigo et al. (2013) have reported a value of 0.38 for the muscularity of primiparous Italian Simmental cows. Lower values than in the present study were reported by Forabosco et al. (2005) for Chianina cattle, with a mean heritability of 0.20 for 8 different regions scored for muscularity. In general, not accounting for differences across studies and breeds, the heritability of single muscularity traits obtained from population data has always been reported of medium value (Forabosco, 2005; Crowley et al., 2011; Mazza et al., 2014), while factorial or composite traits have shown medium-high heritability (Frigo et al., 2013; Mazza et al., 2016), indicating a more efficient use of the latter as possible traits for selection.

The heritability of the 4 muscularity traits obtained on young bulls aged 11 months resulted on average greater than values reported for females (+0.07), due to the lower age at which the evaluation was carried out that produced also an increase in the genetic variability of traits. Apart from the differences in age, also the more homogeneous conditions due to the test station should have contributed to the greater genetic variance and heritability estimates for males than for females. Indeed, the use of control stations for testing accurately beef traits in an early phase of life has been suggested as the preferable methods since the ’80 also due to the greater heritability attainable (Andersen et al., 1981). However, for similar muscularity traits evaluated on young bulls, Bouquet et al. (2010), have reported much higher heritability in beef Blonde d'Aquitaine and Limousin breeds (i.e., 0.65 and 0.51, respectively). On the other hand, Bonfatti et al. (2013), have reported closer results to our study, with heritability values ranging from 0.22 to 0.44 in Piedmontese tested beef bulls, depending on the body region scored (i.e., lower for front and greater for back). Performance test evaluation of muscularity (scale 1-10) in Norvegian dual purpose cattle has shown even lower heritability, i.e., 0.24 (Aass et al.; 1996), while Sbarra et al. (2009), have reported a wide range of heritability for muscularity visually assessed on performance tested Chianina, Marchigiana and Romagnola beef bulls (0.55 for Chianina; 0.30 for Marchigiana; and 0.19 for Romagnola; respectively). Therefore, literature is rich of many different heritability values for bulls muscularity depending on the breed considered.

The heritability estimates for ADG resulted medium-high and were in range reported for other performance tested bulls of different breeds such as the Norvegian dual purpose cattle (0.30; Aass, 1996), the Czeck Fleckvieh (0.28; Přibyl et al., 2007) and a mixture of breeds including beef (Charolias, Limousin, Aberdeen Angus and Hereford) and Simmental bulls tested in Ireland (0.30; Crowley et al., 2010). For Chianina, Marchigiana and Romagnola tested bulls, Sbarra et al. (2009) estimated a mean heritability of 0.30. However, greater valued for ADG on test stations have been highlighted for Piedmontese (Bonfatti et al., 2013).

The *in vivo* EUROP score and dressing percentage are not easily comparable with literature, being the most part of studies carried out on data from abattoir. In this situation, heritability reported for EUROP score have resulted highly variable, i.e., from 0.24 reported for Piedmontese cattle by Bonfatti et al. (2013), to 0.47 for Limousine, and to 0.62 for Blonde d'Aquitaine (Bouquet et al., 2010). Analysing slaughter data from crosses of 8 paternal breeds, Hickey et al. (2007), highlighted heritability estimates for EUROP ranging from 0.04 for Friesian to 0.36 for limousine. Similarly, heritability of *post mortem* dressing percentage has been reported in literature to be variable considering different breeds and situations. In studies conducted on French beef breeds heritability of dressing percentage has been reported higher than values of 0.28-0.39 reviewed by Rios-Utrera and Van Vleck, (2004), reaching the value of 0.43 for Charolais crosses (Fouilloux et al.; 1999), or 0.47 in Blonde d'Aquitaine and 0.54 in Limousine (Bouquet et al., 2010). On the other hand, lower values have been indicated in earlier studies conducted on Norvegian dual purpose cattle bulls by Aass (1996). In general, results obtained in the present study for *in vivo* EUROP (but also for dressing percentage) reflect the mean heritability observed for the muscularity type scores and for ADG. However, if the similar heritability observed for muscularity type traits and EUROP is expected, being the morphology score and EUROP grade both methods for the visual assessment on animals of the same characteristics, less expected are the similarities with ADG estimates. A medium genetic correlation was indeed estimated for ADG and all 4 muscularity traits in Rendena young bulls, indicating that only a partial group of genes are commonly expressed in these traits. On the other hand, greater genetic correlations, i.e., a more communality in terms of gene expression for different traits, were observed for the 4 muscularity traits when analysed in combination with *in vivo* EUROP and dressing percentage, supporting again, at least for the first trait, the trait similarity with the muscularity type evaluation. Opposite values of correlation between ADG on test and muscularity score have been reported by Albera et al. (2001) on Piedmontese bulls (-0.24), while Filloux et al. (2000) have reported almost null correlations on Charolais (0.06) or low positive genetic correlation on Limousin performance tested bulls. However, Filloux et al. (2000) have also reported a greater genetic correlation between live muscularity assessed on performance tested bulls and the *post mortem* dressing percentage obtained from the progeny of the same Charolais and Limousine bulls (0.28 and 0.59, respectively). Conformation score and ADG have resulted in a very unfavourable genetic correlation (-0.62) in Norvegian dual purpose tested bulls (Aass; 1996), although, again, a positive genetic correlation was reported between *in vivo* visual appraisal of conformation and dressing percentage measured only on unselected bulls (0.52). Results from our study highlight that, in spite of the high genetic correlations between *in vivo* estimates and muscularity traits, performance test traits are still preferable indicators of beef attitude, particularly the dressing percentage appraisal, which is not fully correlated with the muscularity traits.

The genetic correlation between muscularity traits obtained on Rendena primiparous and on young bulls was favourably correlated, although the estimates obtained were, on average, 0.65. This value reflects possible interference on primiparous evaluation due to the milk production, i.e. a thinnest aspect of cows, as respect the young bull evaluation. Comparing the results of this study with other literature reports is very difficult, due to absence of similar studies. The only possible comparison is with live and post mortem conformation data on French beef breeds, for which correlations coefficients ranging between 0.61-0.79 have been reported (Fouxillou et al., 2000; Bouquet et al., 2010). However, very different conditions have occurred in this comparison considering that in both cases data obtained were the results of performance testing of young bulls and fattening of their progeny in commercial conditions.

Muscularity type traits scored on primiparous cows have resulted in medium-low correlation with ADG, and medium-high with *in vivo* estimates of EUROP and dressing percentage, indicating again, at least for animal beef conformation, a common component of the gene-pools involved in the expression of the traits, particularly for the hind quarter. This in spite of different farming and feeding practices between primiparous cows and young tested bulls. No previous studies have reported information about the genetic relationships between these traits.

CONCLUSIONS

This study indicated that traits measured during performance testing of Rendena young bulls are heritable and favourably correlated. Lower heritability exists for muscularity traits evaluated on primiparous cows, but even these traits are favourably correlated to muscularity type traits scored on performance tested bulls, or with growth and *in vivo* commercial evaluation of bulls, indicating a common way for the selection route. Further analysis in term of genetic trend for traits included in the global selection index could be useful to fully understand the relationship among the traits here analysed, allowing additional knowledge on the appropriate weight to give beef traits under selection for the autochthonous Rendena breed. Results of this study may also provide useful suggestions for genetic relationships among possible traits of interest in genetic improvement of other dual purpose breeds.

REFERENCES

Albera, A., Mantovani, R., Bittante, G., Groen, A. F., & Carnier, P. (2001). Genetic parameters for daily live-weight gain, live fleshiness and bone thinness in station-tested Piemontese young bulls. Animal Science, 72(03), 449-456.

Andersen, B. B., De Baerdemaeker, A., Bittante, G., Bonaiti, B., Colleau, J. J., Fimland, E., Jansen, J., Lewis, W. H. E., Politiek, R. D., Seeland, G., Teehan, T. J. & Werkmeister, F. (1981). Performance testing of bulls in AI: Report of a working group of the commission on cattle production. Livestock Production Science, 8(2), 101-119.

Archer, J. A., & Bergh, L. (2000). Duration of performance tests for growth rate, feed intake and feed efficiency in four biological types of beef cattle. Livestock Production Science, 65(1), 47-55.

Aass, L. (1996). Variation in carcass and meat quality traits and their relations to growth in dual purpose cattle. Livestock Production Science, 46(1), 1-12.

Bonfatti, V., Albera, A., & Carnier, P. (2013). Genetic associations between daily BW gain and live fleshiness of station-tested young bulls and carcass and meat quality traits of commercial intact males in Piemontese cattle. Journal of animal science, 91(5), 2057-2066.

Bouška, J., Štípková, M., Frelich, J., Zedníková, J., & Bartoň, L. (2003). Genetic parameters of the traits recorded in the performance test of dual-purpose bulls. Czech J. Anim. Sci, 48(10), 413-418.

Bouquet, A., Fouilloux, M. N., Renand, G., & Phocas, F. (2010). Genetic parameters for growth, muscularity, feed efficiency and carcass traits of young beef bulls. Livestock Science, 129(1), 38-48.

Croué, I., & Ducrocq, V. (2017). Genomic and single-step evaluations of carcass traits of young bulls in dual-purpose cattle. Journal of Animal Breeding and Genetics. DOI 10.1111/jbg.12261.

Croué, I., Fouilloux, M. N., Saintilan, R., & Ducrocq, V. (2016). Carcass traits of young bulls in dual-purpose cattle: genetic parameters and genetic correlations with veal calf, type and production traits. Animal, 7, 1-9.

Crowley, J. J., McGee, M., Kenny, D. A., Crews, D. H., Evans, R. D., & Berry, D. P. (2010). Phenotypic and genetic parameters for different measures of feed efficiency in different breeds of Irish performance-tested beef bulls. Journal of Animal Science, 88(3), 885-894.

Crowley, J. J., Evans, R. D., Mc Hugh, N., Pabiou, T., Kenny, D. A., McGee, M., Crews, D. H. Jr., & Berry, D. P. (2011). Genetic associations between feed efficiency measured in a performance test station and performance of growing cattle in commercial beef herds. Journal of animal science, 89(11), 3382-3393.

de Haas, Y., Janss, L. L. G., & Kadarmideen, H. N. (2007). Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. Journal of Animal Breeding and Genetics, 124(1), 12-19.

Forabosco, F., Bozzi, R., Boettcher, P., Filippini, F., Bijma, P., & Van Arendonk, J. A. M. (2005). Relationship between profitability and type traits and derivation of economic values for reproduction and survival traits in Chianina beef cows. Journal of animal science, 83(9), 2043-2051.

Forabosco, F., & Mantovani, R. (2011). European and indigenous cattle breeds in Italy. *Schiel & Denver Publishing Limited*, Houston, TX.

Forabosco, F., Rossetti, E., Sarti, F. M., Panella, F., Bittante, G., Mantovani, R., & Filippini, F. (2005, April). Morphological factorials for females of the Chianina, Marchigiana and Romagnola breeds. In Proceedings of the 4th World Italian Beef Cattle Congress. Gubbio (Italy), 29th April to 1st May.

Fouilloux, M. N., Renand, G., Gaillard, J., & Ménissier, F. (1999). Genetic parameters of beef traits of Limousin and Charolais progeny-tested AI sires. Genetics Selection Evolution, 31(5), 465.

Frigo, E., Samorè, A. B., Vicario, D., Bagnato, A., & Pedron, O. (2013). Heritabilities and genetic correlations of body condition score and muscularity with productive traits and their trend functions in Italian Simmental cattle. Italian Journal of Animal Science, 12(2), e40.

Fuerst-Waltl, B., Fuerst, C., Obritzhauser, W., & Egger-Danner, C. (2016). Sustainable breeding objectives and possible selection response: Finding the balance between economics and breeders' preferences. Journal of Dairy Science, 99(12), 9796-9809.

Gandini, G. C., & Villa, E. (2003). Analysis of the cultural value of local livestock breeds: a methodology. Journal of Animal Breeding and Genetics, 120(1), 1-11.

Hickey, J. M., Keane, M. G., Kenny, D. A., Cromie, A. R., & Veerkamp, R. F. (2007). Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. Journal of Animal Science, 85(2), 314-321.

Liinamo, A. E., Ojala, M., & van Arendonk, J. (2001). Genetic relationship of meat and milk production in Finnish Ayrshire. Livestock Production Science, 69(1), 1-8.

Lynch, M., & Walsh, B. (1998). *Genetics and analysis of quantitative traits* (Vol. 1, p. 4). Sunderland, MA: Sinauer.

Mantovani, R., Cassandro, M., Contiero, B., Albera, A., & Bittante, G. (2010). Genetic evaluation of type traits in hypertrophic Piemontese cows. Journal of animal science, 88(11), 3504-3512.

Mantovani, R., Contiero, B., Gallo, L., Carnier, P., Cassandro, M., & Bittante, G. (1999). The effect of herd of origin on selection of Chianina, Marchigiana and Romagnola performance tested young bulls. Zootecnica e Nutrizione Animale, 25(3), 109-121.

Mantovani R., Gallo L., Carnier P., Cassandro M., & Bittante G. (1997). The use of a juvenile selection scheme for genetic improvement of small population: the example of Rendena breed. In: 48th Annual Meeting of the European Association of Animal Production, Vienna, Austria, 25–28 August 1997, 5 pp.

Mazza, S., Guzzo, N., Sartori, C., Berry, D. P., & Mantovani, R. (2014). Genetic parameters for linear type traits in the Rendena dual purpose breed. Journal of Animal Breeding and Genetics, 131(1), 27-35.

Mazza, S., Sartori, C., & Mantovani, R. (2015). Genetic parameters of type traits in two strains of dual purpose autochthonous Valdostana cattle. Livestock Science, 178, 35-42.

Mazza, S., Guzzo, N., Sartori, C., & Mantovani, R. (2016). Factor analysis for genetic evaluation of linear type traits in dual-purpose autochthonous breeds. animal, 10(03), 372-380.

Misztal, I. (2008). Reliable computing in estimation of variance components. Journal of animal breeding and genetics, 125(6), 363-370.

Přibyl, J., Krejčová, H., Přibylová, J., Misztal, I., Bohmanová, J., & Štípková, M. (2007). Trajectory of body weight of performance tested dual-purpose bulls. Czech J. Anim. Sci, 52, 315-324.

Reverter, A., Johnston, D. J., Graser, H. U., Wolcott, M. L., & Upton, W. H. (2000). Genetic analyses of live-animal ultrasound and abattoir carcass traits in Australian Angus and Hereford cattle. Journal of Animal Science, 78(7), 1786-1795.

Rios Utrera, A., & Van Vleck, L. D. (2004). Heritability estimates for carcass traits of cattle: a review. Genetics & Molecular Research 3, 380–394.

Sartori, C., Mazza, S., Guzzo, N., & Mantovani, R. (2015). Evolution of increased competitiveness in cows trades off with reduced milk yield, fertility and more masculine morphology. Evolution, 69(8), 2235-2245.

Sbarra, F., Dal Zotto, R., & Mantovani, R. (2009). A survey on cattle performance testing centres in Italy. Italian Journal of Animal Science, 8(sup2), 153-155.

Sbarra, F., Mantovani, R., & Bittante, G. (2009). Heritability of performance test traits in Chianina, Marchigiana and Romagnola breeds. Italian Journal of Animal Science, 8(sup3), 107-109.

Sbarra, F., Mantovani, R., Quaglia, A., & Bittante, G. (2013). Genetics of slaughter precocity, carcass weight, and carcass weight gain in Chianina, Marchigiana, and Romagnola young bulls under protected geographical indication. Journal of animal science, 91(6), 2596-2604.

Solkner, J., Miesenberger, J., Willam, A., Fürst, C., & Baumung, R. (2000). Total merit indices in dual purpose cattle. Archiv fur Tierzucht, 43(6), 597-608.

Table 1. Descriptive statistics of individual linear muscularity type traits and performance test traits measured in Rendena primiparous and young bulls, respectively.

Traits	Minimum	Maximum	Mean	Standard Deviation
Muscularity type traits in primiparous cows (score)	1	5		
Front (chest and shoulder)	Scarce	Developed	2.77	0.82
Back, loins and rump	Scarce	Developed	2.93	0.78
Thigh, buttocks side view	Hollow	Rounded	3.00	0.77
Thigh, buttocks rear view	Hollow	Rounded	2.83	0.80
Muscularity type traits in young bulls (score)	1	5		
Front (chest and shoulder)	Scarce	Developed	3.04	0.82
Back, loins and rump	Scarce	Developed	3.15	0.85
Thigh, buttocks side view	Hollow	Rounded	3.24	0.86
Thigh, buttocks rear view	Hollow	Rounded	2.98	0.84
Performance test traits in young bulls				
ADG[1], g/d	516	1326	1011	106
In vivo EUROP[2], score	80.0	108.9	98.9	3.55
In vivo dressing percentage, %	50.0	55.7	53.7	0.66

[1] ADG = average daily gain;

[2] Grades E, U, R, O and P, were subdivided into +, = or – subclasses and transformed in a linear scale that attributed 100 to R class and ±3.33 points to each subclass below or above the R, obtaining a continuous scale from 76.66 to 123.33.

Table 2. Estimated genetic variance (σ_a^2), residual variance (σ_e^2), heritability (h^2), ad SE of h^2 (within brackets) of muscularity linear type traits scored in primiparous cows and in young bulls, and performance test traits in young bulls of the Rendena breed.

Traits	**σ_a^2**	**σ_e^2**	**h^2**
Muscularity type traits in primarous cows			
Front (chest and shoulder)	0.13	0.38	0.25 (0.02)
Back, loins and rump	0.13	0.36	0.26 (0.02)
Thigh, buttocks side view	0.15	0.34	0.31 (0.02)
Thigh, buttocks rear view	0.15	0.36	0.30 (0.02)
Muscularity type traits in young bulls			
Front (chest and shoulder)	0.25	0.45	0.36 (0.09)
Back, loins and rump	0.31	0.45	0.41 (0.08)
Thigh, buttocks side view	0.27	0.51	0.35 (0.08)
Thigh, buttocks rear view	0.20	0.51	0.28 (0.08)
Performance test traits in young bulls			
ADG[1], g/d	3035.3	5622.7	0.35 (0.08)
In vivo EUROP[2], score	4.20	8.26	0.34 (0.09)
In vivo dressing percentage, %	0.14	0.24	0.36 (0.09)

[1] ADG = average daily gain;

[2] Grades E, U, R, O and P, were subdivided into +, = or – subclasses and transformed in a linear scale that attributed 100 to R class and ±3.33 points to each subclass below or above the R, obtaining a continuous scale from 76.66 to 123.33.

Table 3. Genetic correlations between muscularity linear type traits and performance test traits obtained in Rendena young bulls.

Muscularity traits in young bulls	**Performance test traits in young bulls**		
	ADG[1]	***In vivo*****EUROP**[2]	***In vivo* dressing percentage**
Front (chest and shoulder)	0.501 (0.144)	0.811 (0.075)	0.812 (0.074)
Back, loins and rump	0.524 (0.136)	0.904 (0.051)	0.874 (0.060)
Thigh, buttocks side view	0.478 (0.150)	0.989 (0.029)	0.983 (0.037)
Thigh, buttocks rear view	0.575 (0.138)	0.954 (0.043)	0.926 (0.056)

[1] ADG = average daily gain;

[2] Grades E, U, R, O and P, were subdivided into +, = or – subclasses and transformed in a linear scale that attributed 100 to R class and ±3.33 points to each subclass below or above the R, obtaining a continuous scale from 76.66 to 123.33.

Table 4. Genetic correlations (r_a) and SE of r_a (within brackets) between muscularity linear type traits in primiparous cows, and the corresponding linear type traits evaluate in young bulls of the Rendena breed.

Muscularity traits in primiparous cows	**Muscularity type traits in young bulls**			
	FM	**BLR**	**TBS**	**TBR**
Front (chest and shoulder; FM)	0.574 (0.124)	0.608 (0.109)	0.516 (0.123)	0.402 (0.139)
Back, loins and rump (BLR)	0.678 (0.107)	0.757 (0.093)	0.667 (0.119)	0.563 (0.135)
Thigh, buttocks side view (TBS)	0.566 (0.110)	0.737 (0.085)	0.756 (0.096)	0.659 (0.122)
Thigh, buttocks rear view (TBR)	0.627 (0.107)	0.783 (0.083)	0.811 (0.097)	0.741 (0.118)

Table 5. Genetic correlations between muscularity linear type traits in primiparous cows and performance test traits recorded in young bulls of the Rendena breed.

Muscularity traits in primiparous cows	**Performance test traits in young bulls**		
	ADG[1]	***In vivo* EUROP**[2]	***In vivo* dressing percentage**
Front (chest and shoulder; FM)	0.071 (0.131)	0.434 (0.126)	0.480 (0.122)
Back, loins and rump	0.258 (0.131)	0.711 (0.109)	0.748 (0.107)
Thigh, buttocks side view	0.263 (0.125)	0.776 (0.096)	0.798 (0.102)
Thigh, buttocks rear view	0.209 (0.128)	0.811 (0.096)	0.822 (0.104)

[1] ADG = average daily gain;

[2] Grades E, U, R, O and P, were subdivided into +, = or – subclasses and transformed in a linear scale that attributed 100 to R class and ±3.33 points to each subclass below or above the R, obtaining a continuous scale from 76.66 to 123.33.

GENERAL CONCLUSIONS

This thesis have treated various topics concerning the evaluation of productive traits (milk and meat) already included in the selection index, and possible new traits to consider for the genetic improvement of local dual purpose Rendena breed.

In the first of the four chapters of the thesis, farms of Rendena cattle were grouped on basis of average milk yields for investigating possible effects of heterogeneity of variance in genetic evaluation of production traits. The study allowed to find a connection between productive level of farms and management practices. The genetic analyses conducted for milk, fat and protein yields have revealed that variance components and heritability in medium and high productive groups were heterogeneous. However, the estimates of the genetic correlations of all yield traits between the two productive groups of farms were above the threshold suggested in literature for considering the groups as homogeneous in variance, and the EBV of bulls that had daughters in both productive groups were not affected by a re-ranking due to variance heterogeneity. The study has suggested that a genetic evaluation not accounting for the heterogeneous variance may be applied without producing biased estimates for bulls EBVs, but it could allow for a more careful selection on cows.

The introduction of udder health traits in the selection index could be a useful integration of yield traits in genetic evaluation of the aptitude at the milk production. Therefore, in the second contribution the content of milk somatic cells from functional controls was considered and investigated using different and alternative phenotypes obtained from the somatic cell count. Two-logarithm-based and normally distributed traits, namely the somatic cell score (SCS) and the product of somatic cells and test day milk yield (LTSCC), and three threshold traits linked to the occurrence of pathological mastitis. Results obtained showed an higher genetic variability and heritability of SCS and LTSCC traits as compared to threshold traits. The genetic improvement of milk, fat and protein yields seems to have no negative effects in terms of increase in somatic cells, as suggested by the almost close to zero genetic correlations between somatic cells traits, excluding LTSCC, and milk yield traits. Nevertheless, further insights are needed before considering somatic cells in selection index of Rendena breed.

The economic value of milk could be further improvement through the introduction of novel phenotypes regarding milk technological traits using their FTIR predictions. In the third chapter the genetic parameters of the technological traits and their relationships with milk production and composition were estimated. The results confirm that the milk of Rendena cows is suitable for processing into cheese, with good aptitude for coagulation. All the milk technological traits showed heritability comparable or higher than milk production and composition. The improvement of milk production did not affect the nutrients recovery traits. Moreover, favourable genetic correlations of milk composition with the percentages of cheese yield and nutrient recoveries suggest that it is possible to frothily improve the technological properties of milk for cheese production in the breed. This is an aspect of great importance for the genetic improvement in Rendena, considering that almost all the milk production of the breed is converted into cheese.

Together with the genetic improvement of milk ability, the Rendena shows also a good beef ability, which is measured in young bulls in performance test and in primiparous cows by describing muscularity linear type traits. Moving from the point that linear type evaluation is also performed in young bulls at the end of the performance testing period, the last chapter considered the possibility to include male muscularity linear type traits instead of the female ones in selection practice. This was due by evaluating genetic parameters for muscularity traits collected both in males and females at different times during life, and their relationships with beef traits recorded at performance test. Heritability estimates were moderate and similar for all beef traits. Generally, the traits measured during performance test in young bulls and muscularity traits evaluated on primiparous cows were favourably correlated, indicating a common way for the selection route.

The results of all the chapters shed light on the possibility to consider additional traits, either functional as the somatic cells, or productive, as the milk technological properties, or the male type traits for muscularity, within the routinely genetic improvement of Rendena dual purpose breed. Also the possibility to account for the heterogeneity in variance for milk production may lead to some improvement in selection practice. Nevertheless, further analysis in term of genetic trend for traits included in the global selection index could be useful to properly understand all the relationships among the traits under selection, allowing additional knowledge on appropriate choices in terms of traits to consider and economic weights to be assigned.