Genetic aspects of somatic cell count in the Italian Holstein Friesian population

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Abstract

The objective of this thesis was to evaluate genetic aspects of somatic cell count (SCC) in Italian Holstein Friesian population in order to define how to include this trait in selection criteria. Several values of heritabilities were estimated (.06 to -.21) for three parities using different data sets and model of analysis. A model for breeding value estimations of first parity cows was defined and further improvements of the model were discussed. Genetic correlations with production were highly variable in value and sign depending on parity and model of analysis (-.14 to .24). Variation existed between and within lactation and it was concluded that it is important to account for this variation in selection. When a unique value is necessary, a correlations around zero, indicating a null genetic relationship between production and SCC, should be used. Using an hazard model, it was estimated that an increase in phenotypic level of SCC in Italian Holstein population resulted in higher rate of culling. The approximate genetic correlation between SCC and functional longevity was .31 associating unfavourable values of SCC to poorer longevity. Favourable genetic correlations resulted between udder conformation traits and SCC. A higher udder, strongly attached to the fore abdominal wall, and with short teats was genetically related to smaller values of SCC. Finally an udder health index, including SCC, udder depth, and fore udder attachment was proposed and the inclusion of SCC in the overall selection index was discussed.

Preface

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Contents

Chapter 1

General Introduction

Somatic cells occur normally in milk and consist of many types of cells; including neutrophils, macrophages, lymphocytes, eosinophils, and various epithelial cells from the mammary gland. Cells in milk from a healthy udder are mainly represented by mammary gland epithelium and drain canal cells. Only 8% are leukocytes and less than 1% are macrophages (Walawski, 1999). The concentration of somatic cells in milk is defined as somatic cell count (SCC) and it is the measure of thousands of cells per millilitre of milk. Milk obtained from a normal healthy udder usually contains less than 10^5 somatic cells per ml (Kherli and Shuster, 1994).

SCC and mastitis

The occurrence of an udder infection stimulates the defence of the organism, and the migration of a large number of leukocytes and neutrophils from the blood stream into the infected quarters. As a consequence, the concentration of somatic cells in milk increases, with a large increase in the number of leukocytes, and a small increase in epithelial cells (Sordillo et al., 1996). Leukocytes in milk from an infected quarter represent 50% of SCC. Mastitis is classified as sub-clinical when the infection is latent with no visible changes occurring in the appearance both of milk and udder, but milk production decreases, bacteria are present in milk, SCC increase, and the milk composition is altered (Harmon, 1994). Generally mechanisms of defence of the udder are effective in eradicating the majority of infections (Kherli and Shuster, 1994). If defence is not sufficient in the battle with the bacteria, bacteria multiply in numbers and release a large amount of toxins that have a negative effect on the mammary gland (Kherli and Shuster, 1994). With the appearance of symptoms such as fever, swelling, tenderness of the udder and change in milk properties, mastitis is considered to be clinical.

The distribution of SCC in individual cows milk samples is positively skewed (the mean is greater than the median) and there is a strong heterogeneity of variance among groups or herds (Ali and Shook, 1980). Conventional statistical methods usually assume normally distributed data and homogeneity of variance. The value of SCC is therefore log-transformed to somatic cell score (SCS), by adding a constant of 9 or 10 thousand of cells/ml before applying the logarithmic transformation, in order to obtain a normal

distribution. The formula widely used is: SCS = $\log_2$ (SCC/100)+3 (Ali and Shook, 1980). The measure of SCS has been accepted by the National Co-operative Dairy Improvement Program of the USA as a standard recording scale for SCC. Other researchers have used $\log_e$ logarithmic transformation (Kennedy et al., 1982; Monardes et al., 1983; Heuven et al., 1988) or a $\log_{10}$ logarithmic transformation (Emanuelson et al., 1988; Weller et al., 1992; Mrode et al., 1995). Heuven et al. (1988) reported similar heritability from $\log_2$ and $\log_e$ transformation of SCC. National data for SCC, sent for international breeding value estimation (EBV), are $\log_2$ transformed in eight countries, $\log_{10}$ in two countries, and $\log_e$ transformed only in Great Britain (Mark et al., 2002).

SCC as indirect measure of mastitis in genetic selection

Mastitis is one of the most costly diseases in dairy cattle and is responsible for 50% of the total costs for health care (Shook and Schutz, 1994). A high proportion of culling (from 6 to 17% of culling) can be attributed to mastitis, following milk yield and reproduction (Shook and Shutz, 1994). Moreover there is an increasing public concern in Europe for cow welfare and for product quality. Due to these reasons, the interest for udder health traits in dairy cattle selection is increasing (INTERBULL, 1999). SSC is a good measure to indirectly select for mastitis resistance , especially when a direct measure of clinical mastitis incidence is not available (Colleau and Le Bihan-Duval, 1995; Shook and Schutz, 1994; Emanuelson et al., 1988; Heringstad et al., 2000). The measure of SCC has the following properties:

- it is routinely recorded in most milk recording systems,
- information are available on a population base (INTERBULL, 1996),
- the heritability of SCC is higher than the heritability of the direct trait (clinical mastitis incidence) (for a review: Mrode and Swanson, 1996),
- it reflects the incidence of both clinical and subclinical infections.

The use of SCC for selection purposes have been widely discussed, and it is believed that selection for decreased in SCC would reduce susceptibility to mastitis (Philipsson et al., 1995). Milk presenting an elevation of SCC is a clear indication of the occurrence of infection in the udder. However, somatic cells are present in milk from healthy cows and the increase in SCC is a normal cellular defence of the organism against the attack of pathogens.

Selection for very low SCC could weaken cows resistance to mastitis (Coffey et al., 1986b; Schukken et al., 1994; Suriyasathaporn et al., 2000) and therefore there is concern if the objective of selection would be the lowest level of SCC. Genetic correlations between SCC and clinical mastitis incidence, estimated in literature, vary from moderate to high with an average around .70 (for a review: Mrode and Swanson, 1996), supporting the use of SCC as indirect indicator of mastitis incidence for selection purposes. Philipsson et al. (1995) estimated a linear relationship between the two traits concluding that selection for lower SCC is desirable and that a lower level of SCC reflects a reduced incidence of infection, rather than a reduced ability to react to it. Vecht et al. (1985) and Coffey et al. (1986a) reported that cows with low SCC are at slightly less risk of mastitis later during the current lactation, or in later lactations than cows with initially high SCC. Similarly, Rupp and Boichard (2000) estimated, using a hazard model, that there is no increase in susceptibility to clinical mastitis for cows with very low level of SCC at the beginning of first lactation. Cows with low SCC are at low risk of first mastitis both in herds with high or low mastitis frequency. Furthermore, cows with the lowest mean SCC in the first lactation, had the lowest risk for clinical mastitis in second lactation, suggesting that breeding goals should favour cows with the lowest observed SCC (Rupp et al., 2000).

From these studies it can be concluded that selection for low level of SCC is expected to reduce mastitis incidence and there is no indication that it would affect the ability of the organism to react to udder infection.

Breeding value estimation for somatic cells

Genetic evaluations for SCC are calculated in several countries (INTERBULL, 1996) and international genetic evaluations have been recently implemented on a routine basis by INTERBULL (Mark et al., 2002). Test day SCC transformed into SCS are used in the model of analysis as single tests or aggregated into lactation measures. Differences in methods exists between countries. For example, Germany was using a repeatability test-day model for SCS (Reents et al., 1995) but recently it moved to a test-day random regression model for both SCS and production traits (Liu et al., 2001). Italy (Samoré et al., 2001) uses a test-day repeatability model, while Canada analyses SCS in a multiple trait random regression

model (Schaeffer et al., 2000). Estonia and Switzerland calculate EBV for SCS using a test-day model, and all other countries use models based on lactation averages (Mark et al., 2002). Some evaluations consider only first parity and others also evaluate data from later lactations, either with multiple trait models, as different traits depending on parity, or in single trait models with repeated records. Frequently the data include test days from 5 to 305 days, but other intervals of days in milk are also used, such as 10 to 180 or 5 to 105 (Mark et al., 2002).

Finally EBV for SCC are sometimes combined with other EBV, such as conformation traits and milking speed, in order to obtain an aggregated index for udder health (Boettcher et al., 1998). Such an index is expected to result in more efficient selection than using the single trait of SCC, or even the single trait of direct mastitis incidence (De Jong and Lansbergen. 1996).

Aim and outline of this thesis

The aim of this thesis is to analyse the genetic aspects of SCC in Italian Holstein Friesian in order to study the use of SCC data in genetic selection for a better udder health. Chapter 2 deals with the estimation of heritabilities, genetic and residual variances in first parity SCC, using a test-day repeatability model in three different areas of Northern Italy. Moreover, in the same chapter, the variance due to sire by herd interaction effect is estimated and parameters from the three areas are compared. The resulting small proportion of variance, explained by sire by herd effect, suggests that this interaction effect between areas will have a negligible effect on the genetic evaluation for SCC and it is therefore ignored in the national genetic evaluation. A test-day repeatability model, using first parity data for SCC was introduced as the official model for genetic evaluation of bulls in the Italian Holstein population (Chapter 3). This genetic evaluation aims to identify bulls that regularly have daughters more liable to mastitis by using SCC as indicator of mastitis incidence. The model proposed is used for routine genetic evaluation for SCC in Italian Holstein, since November 2001. In Chapter 4, the impact of SCS is included in survival analysis to evaluate the effect of SCS on culling rates and to estimate the relationship between SCS and longevity. The strong association between the two traits supports the use

of SCS to indirectly select for improved udder health and therefore increased longevity. The relationship between SCS and production is estimated in Chapter 5 using different models: lactation models, test-day random regression model and correlations between EBV. This analysis outlined an apparent complexity of the genetic factors controlling SCS that suggest, in genetic selection, it is important to account for different levels and signs of genetic correlations between SCS and production yields in different parities and, when possible, also within parity. Moreover, the trend in genetic correlations resulting in later parities would partly explain the positive genetic trend in SCS resulting in Italian Holstein population, obtained without applying any direct selection on SCS. Selection for yield traits based on more parities records may have contributed to the decline in SCS due to the favourable correlations with this trait in later parities. A random regression test-day model is under study in Italy for genetic evaluation of production yields and SCS. According to the new model, estimates of specific genetic (co)variances are necessary (Chapter 6). Chapter 7 deals with correlations between SCS, conformation traits, and milking speed. Different possibilities for aggregated breeding values for a better udder health are considered. Selection for lower SCS, and for less deep and strongly attached front udders, would result in higher mastitis resistance. In the General Discussion, issues concerning estimation of breeding values for SCS and selection for improved udder health in Italian Holstein Friesian cows are summarised and discussed. The General Discussion also includes a practical point of view of EBV for SCS and of future application of the findings of this thesis for selection in Italian Holstein Friesian.

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Chapter 2

Impact of area and sire by herd interaction on heritability estimates for somatic cell count in Italian Holstein Friesian cows

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Abstract

The aim of the paper was to estimate variance components for somatic cell scores for Italian Holsteins using data from three different areas of the country. A total of 2,202,804 first parity test day records, collected from 1990 to 1997 in three areas of Italy (Mantova, Milano and Parmigiano cheese area), were available for study. Areas differ in herd size, feeding system and especially in milk use. A minimum standard of quality is also required by some specific cheese production, as for example from the Parmigiano Reggiano cheese chain. These reasons, all together, affect the attention given to the quality level of milk production in herds, and therefore also the sanitary levels.

A pedigree file was extracted from the national database of Holstein Friesian breed. For computational reasons, eight samples of the data were extracted per area. Variance components were estimated by sample using two different test-day repeatability models. The first model included fixed effects of herd-test date, days in milk (30 days interval) and calving month, and random effects of permanent environment, additive genetic and residual error. Estimated heritabilities in the first model ranged from .06 to .09 and repeatabilities from .36 to .45. Only small differences were detected among areas. In the second model a random sire by herd interaction effect was added. Including the sire by herd effect resulted in heritability estimates ranging between .05 and .08 and repeatabilities from .35 to .45. The analysis revealed that only a small fraction of the total variance (.35 to 1.5%) could be explained by sire by herd interaction effect. Based on this research, it appears that parameter estimates for SCS do not differ by region, and inclusion of a sire by herd interaction effect is unnecessary.

Keywords: Somatic cell count, Sire by herd interaction, Holstein Friesian.

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Introduction

Somatic cell count can be used as an indirect measure to identify both clinical and sub-clinical mastitis incidences. Moderate to high genetic correlation between these two traits suggested the use of somatic cells as tool for indirect selection on increased mastitis resistance (Lund et al., 1994; Pösö and Mäntyssari, 1996; Rupp and Boichard, 1999; Weller et al., 1992). Somatic cell counts are relatively easy and inexpensive to collect in combination with routinely milk recording. A logarithmic transformation of somatic cell counts, resulting in somatic cell scores (SCS, Ali and Shook, 1980), gives an approximately normally distributed trait with a higher heritability than mastitis incidence (Emanuelson et al., 1988; Lund et al., 1994; Pösö and Mäntyssari, 1996; Rupp and Boichard, 1999; Weller et al., 1992).

For SCS a large number of estimates of heritabilities and variance components are reported in literature (see review by Mrode and Swanson, 1996). Recent heritabilities estimates ranged between .05 to .19 (Boettcher et al., 1998; Mrode et al., 1998; Rogers et al., 1998; Rupp and Boichard, 1999). Most of these estimates were based on the average SCS during the lactation, calculated from monthly records or from pre-corrected monthly records. Fewer estimates were computed using a test-day model (Carnier et al., 1997; Mrode et al., 1998; Pösö et al., 1997; Reents et al., 1995; Reents and Dopp, 1997).

For genetic evaluation of milk production traits, a test-day model has several advantages over the lactation model (Ptak and Schaeffer, 1993). First, in a test-day model the effect of herd-test date can be included accounting for short-term and systematic environmental effects on traits. Moreover, every test-day record, without a restriction on the number of test-days per lactation, can be included. Reents et al. (1995) estimated heritabilities for first and second parity somatic cell count using a test-day repeatability model. In that study, test-

day records within lactation were considered as repeated measures of the same trait and records in different parities were analyzed as different traits.

In Italy, routine recording of somatic cell counts of individual cows started in 1989. These data are mainly used by farmers for management purposes but there is an increasing interest in using somatic cell score as a trait to select for reduced mastitis incidence. Current breeding schemes mainly focus on production traits and are expected to lead to an increase in mastitis incidence, due to the unfavorable genetic correlations between mastitis incidence and production traits (Emanuelson et al., 1988; Mrode et al., 1998). An early study on Italian Holstein Friesian cows (Carnier et al., 1997) reported different heritabilities for SCS for different stages of lactation but large genetic correlations (on average .87) among tests, suggesting that a repeatability model might be a reasonable solution for estimating breeding values for SCS.

In Italy, large differences between areas occur depending on production environments, herd size, milk price, final destination of milk, i.e. fresh milk or cheese production, and production level. One of the most unique areas is the area of Parmigiano Reggiano Cheese. The milk for this final product should be produced according to special criteria and it should result in a standard of production. One of the main differences with other areas is therefore the size of herds and the specific feeding system that follows very strict regulations. These differences associated to the geographical location are assumed to have an effect on health care of animals, especially for mastitis and SCC concentration in milk. Moreover differences exists between herds within areas and it is also assumed that progeny test of bulls can lead to different results depending on daughters herds. For these reasons it is hypothesized an effect of genotype by herd interaction. Literature estimates of sire by herd variance for SCC using a lactation model are usually low and range from .2% to 2% of the total variance (Banos and Shook, 1990; Da et al., 1992; Mrode et al., 1995; Mrode et al., 1998) depending on breed and model of analysis. No information on sire by herd interaction is available from an analysis based on test-day model for SCC.

Objective of this study was to estimate heritabilities, genetic and residual variances for somatic cell scores in first parity Italian Holstein Friesian cows using a test-day repeatability model for data from three different geographical areas. Estimates of variance due to sire by herd interaction effects were obtained and differences in parameters between areas were examined.

Material and Methods

Data

Monthly test-day records of somatic cell count (SCC, thousands of cells per ml) of Italian Holstein Friesian cows were provided by the Provincial Milk Recording Agencies (APA) and were collected from 1989 to 1997 in Northern Italy (Mantova, Milano, and Parmigiano area). Data included 982,003 first parity test-day records for Mantova, 1,052,271 for Milano, and 168,530 for Parmigiano cheese area. Records were removed when date of calving was not available or when test days occurred before 5 or after 305 d in lac tation. Classes of herd-test date (HTD) were created and HTD classes with only one observation were removed. No restrictions were imposed on the number of test-day records per lactation.

Ten days in milk (DIM) classes were defined. The first class included test days between 6 and 30 DIM and all other classes were 30 d long. Individual somatic cell count (SCC) records for each test day were transformed to somatic cell score (SCS) as (Ali and Shook, 1980):

$$SCS = \log_2 (SCC/100)+3.$$

Variance Component Estimation

Variance components were estimated by area applying two different statistical models. The first model was:

$$SCS_{ijklm} = HTD_i + DIM_j + CM_k + pe_l + a_l + e_{ijklm}$$

where:

- SCS_{ijklm} is test-day observation m on cow l,
- HTD_i is the fixed effect of herd-test date i in which SCS was recorded,
- DIM_j is the fixed effect of stage of lactation period j,
- CM_k is the fixed effect of calving month k,

- pe_l is a random effect accounting for permanent environmental effect (including non-additive genetic effects) associated with all test-day records of cow l,
- a_l is the random additive genetic effect of cow l and,
- e_{ijklm} is the random residual error term.

To quantify the herd-by-sire interaction effect, the model was extended by including h*s random effect, were h is the herd and s is the sire of the animal respectively. Levels with only 1 record were deleted. Other effects, i.e. age at calving, were tested but found not significant and therefore not included in the final analysis.

Due to computing limitations, estimation of variance component using all data was unfeasible. Three samples of data from Mantova (MN1, MN2, MN3) and Milano (MI1, MI2, MI3) and two samples of data from the Parmigiano area (PA1, PA2) were obtained. Samples were created by drawing from the whole data sets all test-day records pertaining to randomly sampled herds. Sampling was repeated as many times as needed to get a minimum number of nearly 80,000 test-day records in each data set. To account for additive genetic relationships, a pedigree file tracing back three generations (parents, grandparents, and great-grandparents) was extracted from the National Herd Book file for each sample. Two phantom groups were defined, one for male and one for female unknown parents. Depending on the sample, the number of cows ranged from 10,083 to 14,016. For the Parmigiano area, the two samples of data were obtained by splitting the original data set.

Variance components for each sample were estimated using the ASREML software which uses an Average Information Matrix algorithm (Gilmour et al., 1995).

Likelihoods of models, with and without the sire by herd interaction, were compared using the test statistic (TS) = -2 times the difference between their logarithmic likelihood. Log likelihoods were obtained from ASREML software. Under the null hypothesis, TS is asymptotically distributed as χ^2 distribution with p degrees of freedom where p is the difference in the number of estimated variance parameters (Wilks, 1938).

Results and Discussion

Descriptive Statistics

Characteristics of each data sample are in Table 1. The number of test-day records in a sample ranged from 78,625 to 84,475. The average number of test-day records per cow was 7. The smallest number of test-day records per cow as well as per herd test date occurred in the Parmigiano area whereas the largest number was found in the area of Milano.

In addition, average herd size was larger in the area of Milano. The average herd size and number of samples per cow were in agreement with official national statistics (Anafi, 1997).

A wide range is observed in number of sire by herd classes between areas (Table 1). Milano had a smaller number of sire by herd levels due to the larger herd size and the use of a smaller number of sires per herd. On average, SCS was highest in Milano area while Parmigiano area had the lowest level of SCS (Table 1). This difference might be related to the differences in production level and in management. Inconsistent results are reported in literature for genetic and phenotypic correlations between SCC and production (Hortet et al., 1999; Mrode et al., 1998; Pösö and Mäntyssari, 1996; Rupp and Boichard, 1999). The higher production level per cow of Milano and Mantova might be causing a higher risk of udder infection with a general increase in SCC. Moreover, the more precise management of smaller farms aiming to a high milk quality could explain the lower level of SCC in the area of Parmigiano cheese.

Estimates of Variance Components

The average estimate was .07 (.06 to .09) for heritability and .42 (.36 to .45) for repeatability (Table 2). Recent literature estimates with test-day models are between .02 to .10, with differences depending on data set used and model applied (Carnier et al., 1997; Detilleux et al., 1997; Mrode et al., 1998; Pösö et al., 1997). In first parity cows, values of .08 and .09, which are in agreement with our findings, have been reported (Detilleux et al., 1997; Pösö et al., 1997; Reents and Dopp, 1997).

Table 1. Information per data sample: number of records, number of cows, number of animals in the pedigree file, number of herd-test date levels (htd), number of records by cow and herd-test date, number of sire by herd effects, and average and standard deviation (in brackets) of unadjusted SCS.

Area sample	Records	Cows	Pedigree file	HTD	Records/cow	Records/HTD	Sire by herd	SCS
Mantova	81,818	11,448	28,002	5,919	7.14	13.82	5,011	2.86 (1.79)
Mantova	82,588	11,539	27,943	5,197	7.16	15.89	4,348	2.87 (1.75)
Mantova	80,631	11,355	26,021	5,493	7.10	14.67	4,686	2.80 (1.77)
Parmigiano area	83,006	14,016	40,489	5,810	5.92	14.29	5,993	2.95 (1.67)
Parmigiano area	84,475	13,484	41,116	6,675	6.26	12.66	6,611	3.05 (1.72)
Milano	82,998	10,426	23,049	2,525	7.96	32.87	2,758	3.17 (1.69)
Milano	78,625	10,083	22,873	3,374	7.80	23.30	3,013	3.11 (1.66)
Milano	79,166	10,136	22,762	2,425	7.81	32.65	2,408	3.05 (1.63)

Usually genetic parameters estimated with test-day model are smaller than estimates with lactation model (Charfeddine et al., 1997; Mrode and Swanson, 1996; Mrode et al., 1998; Pösö et al., 1997), although about 7 test days per cow were considered in the analysis. Test-day models have other advantages as a more complete inclusion of all information and record in progress leading to a higher reliability of breeding values estimation (Pösö et al., 1997). When considering somatic cells, the lactation model averages the SCC along the lactation smoothing the differences between tests. Somatic cells are used as indirect indicator of mastitis and the deviation from a normal pattern is important to detect the infection event. The increase in lactation average can depend from a single test day with high somatic cells but the biological interpretation of the pattern of SCC along the lactation as a genetic trait would be more precise (Schukken et al., 1997).

Table 2. Estimates (standard errors in brackets) of additive genetic variance (σ^2_A), permanent environmental variance (σ^2_{PE}), residual variance (σ^2_e), heritability (h^2) and repeatability (r) in the different samples using the first model.

Area sample	σ^2_A	σ^2_{PE}	σ^2_e	h^2	r
Mantova	0.177	1.100	1.663	0.060 (0.010)	0.434 (0.002)
Mantova	0.228	1.032	1.557	0.081 (0.011)	0.447 (0.014)
Mantova	0.225	1.002	1.588	0.080 (0.011)	0.436 (0.014)
Parmigiano area	0.182	0.917	1.334	0.075 (0.011)	0.452 (0.015)
Parmigiano area	0.211	0.919	1.436	0.082 (0.012)	0.440 (0.015)
Milano	0.230	0.817	1.592	0.087 (0.010)	0.397 (0.013)
Milano	0.142	0.753	1.594	0.057 (0.009)	0.360 (0.012)
Milano	0.174	0.774	1.547	0.070 (0.010)	0.380 (0.010)

In the data considered, the age at calving did not have a significant effect in the pre-analysis using a General Linear Model procedure and therefore it was not included in the model of analysis. The lack of significance was maybe due to the fact that only first parity cows were considered. When somatic cells of later parities are also considered, the effect of age at calving should be tested again. An optimum selection program would aim to select for no clinical events of mastitis at the lowest acceptable level of SCC (Schukken et al., 1997). Moreover also other correlated traits as udder type traits, clinical events, and milking

speed should be included in an aggregated index for udder health taking into account for the genetic relationships between traits (De Jong et al., 1996; Boettcher et al., 1998).

Area Differences

The average heritabilities estimated in the different areas were similar (Table 2) and smaller than difference between samples within the same area. Some difference was found for average repeatability estimates, with .44, .38 and .45 for Mantova, Milano and the area of Parmigiano, respectively. However, differences between samples within an area were larger than differences across areas. Sampling data sets means that also the group of daughters contributing to breeding values of bulls in each sample will be different.

In Italian data (Carnier et al., 1997) heritabilities found ranged from .02 to .14, with an average of .08. SCS in 10 lactation stages, were considered as different traits. The wide range in these estimates make a direct comparison with results in our study difficult, although the average values were in agreement with results of this research.

Although small differences were found in the genetic parameters estimated in different areas, the importance of SCS as a parameter for milk quality, however, differs between areas. Milk quality is of greater importance in the area of Parmigiano Reggiano cheese, due to the product destination and the farm size.

Sire by Herd Interaction

The proportion of total variance explained by sire by herd effect ranged from .004 to .015 (Table 3). The inclusion of the sire by herd effect in the model only slightly decreased the estimates of additive and permanent variance. The results of likelihood ratio test confirmed that the likelihood of a model including a sire by herd effect did not significantly differ from the likelihood of a model ignoring such an effect.

Table 3. Estimates (standard errors in brackets) of additive genetic variance (σ^2_A), permanent environmental variance (σ^2_{PE}), herd by sire interaction variance ($\sigma^2_{h\,x\,s}$), residual variance (σ^2_e), proportion of total variance due to herd by sire interaction (c^2), heritability (h^2) and repeatability (r) in the different samples using the model including sire by herd interaction random effect.

Area sample	σ^2_A	σ^2_{PE}	$\sigma^2_{h\,x\,s}$	σ^2_e	c^2	h^2	r
Mantova	0.169	1.089	0.022	1.662	.008	0.057 (0.011)	0.427 (0.014)
Mantova	0.222	1.029	0.010	1.557	.004	0.079 (0.011)	0.444 (0.015)
Mantova	0.204	0.985	0.042	1.588	.015	0.072(0.011)	0.422 (0.014)
Parmigiano area	0.175	0.911	0.014	1.335	.006	0.072 (0.011)	0.446 (0.010)
Parmigiano area	0.207	0.911	0.014	1.436	.006	0.081 (0.012)	0.435 (0.010)
Milano	0.208	0.807	0.036	1.592	.014	0.079 (0.011)	0.384 (0.010)
Milano	0.131	0.740	0.027	1.594	.011	0.053 (0.004)	0.350 (0.010)
Milano	0.168	0.771	0.010	1.547	.004	0.067 (0.010)	0.376 (0.010)

No results for sire by herd interaction effects on SCS have been reported in literature for a test-day model. Similar or slightly larger proportions have been reported for sire by herd effect on lactation average models (Banos and Shook, 1990; Da et al., 1992; Mrode et al., 1995; Mrode et al., 1998). Based on estimates from our study the sire by herd interaction effect can be ignored in the genetic evaluation within regions.

Conclusions

Estimates of heritability for SCS were in agreement with literature estimates. Differences in estimates of heritability and genetic variance were found between the different samples but differences between areas were small. This suggests that the use of same values for heritability and repeatability in the national evaluation of somatic cell count data is justified.

Estimation of genetic parameters and the analysis of effects to be included in the model are the first step towards the implementation of a genetic evaluation for somatic cell scores in Italian Holstein Friesian population. The accuracy of evaluation can be increased through the inclusion of information collected in later parities. In that case parameters in later lactation and phenotypic and genetic correlation between parities should be estimated.

The small proportion of variance explained by sire by herd effect found in this research, which is in agreement with literature estimates, suggests that this interaction effect between areas will have a negligible effect on the genetic evaluation for SCC and it can be ignored in the national genetic evaluation.

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Chapter 3

Breeding value prediction for SCC in Italian Holstein Friesian using a test day repeatability model

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Abstract

Somatic cell count (SCC) can be used as an indirect measure to identify mastitis. 5,697,833 test days of 796,866 primiparous cows from 9 provinces of Italy have been analysed. Breeding values for SCC, transformed in somatic cell score (SCS), were estimated in the Italian Holstein Friesian dairy cows population using a test-day repeatability animal model. Heritability of .8 and within lactation repeatability of .44, previously estimated on Italian data, were used in the model. Fixed effects considered were herd-test date, days in milk and interaction between month at calving and age at calving. At least two generations of ancestors were extracted from the pedigree and included in the analysis. Breeding values were expressed in standard deviation units and referred to a genetic base.

Keywords: SCS, Breeding values, Test-day repeatability model

Acknowledgements

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Introduction

Somatic cell count (SCC) can be used as an indirect measure to identify both clinical and sub-clinical mastitis. Data are monthly recorded in Italy since 1989. There is an increasing interest, at national and international level, in using SCC to reduce the mastitis incidence that is increasing due to selection on production. A previous study on Italian Holstein Friesian cows (Carnier et al., 1997) reports different heritabilities for SCS at different stages of lactation. Large genetic correlations (on average 0.87) among tests suggest that a repeatability test-day model might be a reasonable solution to estimate breeding values for SCS.

The aim of the present research is to estimate breeding values for somatic cells in order to identify bulls that regularly have daughters more liable to mastitis.

Material and Methods

Monthly test days of SCC of primiparous from 9 provinces of Italy were available (Table 1). Data sets were aggregated and SCC smaller than 5,000 and greater than 6,400,000 cells/ml milk were deleted. A double restriction concerning the parity and the age at calving (between 18 and 36 month) was imposed. Ten lactation stages (DIM) were created dividing the lactation in 30 days intervals from 5 to 305 days of lactation. The effect of herd-test date (HTD) was included; minimum number of test days per HTD was two. SCC were transformed to somatic cell score (SCS) computed as (Ali and Shook, 1980): SCS = $\log_2(SCC/100) + 3$. No limitations were imposed to the minimum number of test-day records per lactation. The pedigree was extracted from the National Herd Book keeping at least two generations of ancestors and included 1,259,231 animals. Phantom groups were assigned to unknown parents depending on year of birth and origin.

The complete data set was analysed using the following model:

$$SCS_{ijklm} = HTD_i + DIM_j + CM\text{-}AC_k + PE_l + a_l + e_{ijklm}$$

where: SCS_{ijklm} is test-day observation m of cow l, HTD_i is a fixed effect of herd-test date i in which the observation on SCS trait was taken, DIM_j is the fixed effect of lactation stage j, $CM\text{-}AC_k$ is the fixed effect of the k level of the interaction between calving month and the age at calving, PE_l is the permanent environmental random effect to account for common environmental effects associated with all test-day records of cow l, A_l is the random animal effect and e_{ijklm} is the random error term.

Breeding values were predicted using a test-day repeatability animal model iterating on data. Heritability was set to .08 and repeatability to .44 as previously estimated in the population (Samoré, 2000, unpublished). Reliability was estimated following the method published by Meyer (1989).

Results and Discussion

On average seven test days (TD) per cow were available. Data sets had different size depending on number of cows in the area and number of year of SCC recording. After the editing, 5,697,833 test days were available.

Table 1. Data set used for breeding value estimation (TD = test days).

Provinces	**TD in data set**	**Primiparous TD**	**Cows**	**TD/cow**
Cuneo	1,316,007	390,413	56,735	6.9
Brescia	4,205,902	1,236,541	176,822	7.0
Vicenza	1,213,478	328,566	44,366	7.4
Oristano	521,734	143,686	20,728	6.9
Piacenza	745,372	203,070	31,785	6.4
Cremona	5,929,924	1,490,266	203,935	7.3
Reggio Emilia	2,847,964	666,232	92,099	7.2
Modena	1,017,274	273,990	45,438	6.0
Mantova	3,261,623	965,069	124,958	7.7
Total or average	21,059,278	5,697,833	796,866	7.0

Breeding values were defined relative to a genetic base (average estimated breeding value (EBV) of cows born in 1995 is zero) and expressed in deviation standard units. With the data of this analysis the base have a value of 0 and the standard deviation correspond to .25 SCS. EBVs will be probably published that higher values will correspond to a higher resistance to mastitis, therefore with a change of sign. On the other side, lower values will correspond to an unfavourable effect. According with this transformation EBV of bulls vary from –5.0 to +4.7. Reliability of bulls varies from 30 to 93%. Although this is a subsample of the total population, the data set used allows the prediction of EBVs for all bulls officially proven for production in Italy with at least 10 daughters in five herds (approximated reliability of proof is 67%). Indeed some of them have in this data set only 20% of daughters when compared to the production EBVs files. Therefore the collection of a more complete data set will be desirable for an estimation of high reliable EBVs. Trends, both genetic and phenotypic (Figure 1), resulted to be favourable. A decrease in phenotypic average of SCS is observed starting from 1993 according to the milk price quality regulation and regional policies. From 1994 selection index of Italian Holstein Friesian included also the mammary composite index (ICM). The genetic correlations between type traits of ICM and SCS are probably responsible of the positive genetic trend for SCS. EBVs will be used to identify genetic difference among bulls in order to identify sires that regularly have daughters more liable to mastitis.

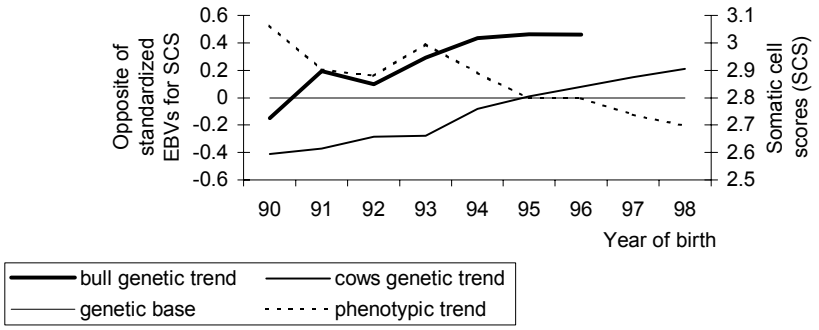

Figure 1. Genetic and phenotypic trends.

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Chapter 4

Relationship between SCC and functional longevity assessed using survival analysis in Italian Holstein Friesian cows

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Abstract

The relationship between somatic cell scores (SCS) and longevity was assessed for Italian Holstein Friesian dairy cows using survival analysis. The data of somatic cell count (SCC) test day information of 512,979 cows were provided by 9 provinces from Northern Italy. Pedigree information was extracted from the national herd book. Two survival models were run: a model similar to the one used for genetic evaluation on length of productive life, and a second one adding the phenotypic level of 10 classes of test-day SCS of the cow. A cow with a test-day in the highest class of phenotypic level for SCS had more than 3 times greater risk of being culled when compared to risk for the class with the lowest SCS level. The genetic correlation between the risk of being culled and SCS was estimated to be 0.31, based on the correlation between sire EBV. The rank of bulls resulting from the genetic evaluation on survival did not change significantly with the inclusion of SCS in the model (rank correlation of 0.98). It is concluded that the phenotypic level of SCS plays an important role in culling decision of farmers of Italian Holstein Friesian dairy cows and SCS is genetically associated to the functional longevity of cows.

Keywords: Somatic cell count, Longevity, Survival analysis, Culling.

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Introduction

Udder health traits and longevity are both considered important for inclusion in a total merit index (INTERBULL, 1999). Breeding values for longevity have been estimated for the Italian Holstein Friesian using survival analysis starting from November 2000 (Schneider et al., 2000), following other countries like France (Ducrocq, 1999), Switzerland (Vukasinovic et al., 1999) and the Netherlands (Vollema et al., 2000). Selection to reduce the mastitis liability can be performed using the direct trait, disease incidence, and using indirect indicators. Somatic cell count (SCC) is considered to be a good indirect parameter to start selection for mastitis resistance (Colleau and Le Bihan-Duval, 1995) and is often used for this purpose, especially in breeding programs in countries where the direct measures of mastitis incidence are not available (De Jong and Lansbergen, 1996; Heringstad et al., 2000). In Italy, sire EBV (estimated breeding values) for SCC have been routinely estimated since November 2001 (Samoré et al., 2001).

Udder health and longevity are related traits. Mastitis incidence, a direct trait for udder health, is considered to have an important effect on culling decisions (Beaudeau et al., 1994; Gröhn et al., 1998; Neerhof et al., 2000) especially for mastitis occurring before the peak of lactation (Beaudeau et al., 1994). Beaudeau et al. (1995) estimated, for primiparous cows with clinical mastitis occurring within 45d after calving, a rate of culling 1.3 times greater than for a healthy cow. Neerhof et al. (2000) found similar results. Correlation coefficients between 0.22 and 0.33 were found between breeding values for longevity and mastitis resistance (Nielsen and Aamand, 1995). The effect of the indirect measure of udder health, the SCC monthly level, on culling has been firstly assessed by Beaudeau et al. (1995) on a data set of about 3,500 cows considering three levels of SCC. Higher rate of culling was associated to higher concentration of SCC. A negative genetic correlation of –0.32 between SCC and herd life was estimated from UK Holstein data (Mrode et al., 2000) indicating that higher SCC was associated with a reduced longevity.

The aim of the study was to evaluate the effect of phenotypic measure of test-day SCC on culling decisions from farmers in a population data through routine milk recording. The genetic relationship between longevity and SCC in Italian Holstein Friesian dairy cows was also assessed.

Material and Methods

Data

Productive life was calculated from national milk recording Italian Holstein Friesian database as the number of days between first calving and the last known milk recording test-day. The last test-day was assumed to be the culling date because culling dates and reasons were not systematically recorded. For the purpose of the survival analysis, records were considered uncensored (complete information) if the last test-day reported was at least 6 months before the end of the study period following the approach used by Vukasinovic et al. (1997). The period of 6 months was chosen for the Italian situation calculating the interval between two milk recordings, the time necessary to transmit data, and the possibility that a cow is in the dry period. All other cows were assumed to be alive at the end of the study period and were considered as censored. For cows changing herds during their productive lives, only records of survival in the initial herd were included. Records from such animals or from herds with an annual decrease in size larger than 50% were treated as censored.

Data for SCC were collected and provided by nine provincial milk recording associations in Northern Italy and included records from 1994 onwards. Not all provinces provided data from that year and the amount of data per province was also different depending mainly on the number of cows with milk recordings in the area (Samoré et al., 2001). Herds were required to have at least 15 cows and age at first calving was required to be less then 42 months. Test-day information included in the analysis had to be collected at least 5 days after calving and SCC records had to have at least 5,000 cells per ml. Individual SCC were transformed into somatic cell score (SCS) as: $SCS=\log_2 (SCC/100)+3$ (Ali and Shook, 1980). The level of SCS was considered both as an indirect measure of health status of udder and as a milk quality parameter, and it was included in the analysis as a time dependent variable changing at each test-day along the lactation. All test-days for all lactations were therefore considered in the analysis, and the level of SCS was kept constant from the previous test-day to the following one, regardless of the time interval between test-days. The absolute level of SCS was partitioned into 10 classes. All test-day records used in the analysis were required to have information on SCC in order to estimate the culling rate associated to the phenotypic level of this trait.

After editing, the data set included 3,062,749 test-days, of 512,221 cows with an average of 7.2 test-days per lactation. Pedigree information were extracted from the national herd book of Italian Holstein Friesian and relationships between bulls were traced through sire and maternal grandsire including 4,511 bulls.

Models

The hazard function of a cow was modelled as in Ducrocq et al. (1988). A proportional hazard model was used: the hazard function was described as the product of a baseline hazard function, depending only on time, and of an exponential function of risk factors, described by (possibly time dependent) fixed and random effects. The following Weibull model was used to estimate the bulls EBV for longevity:

$$\lambda(t)=\lambda_o(t)\ \exp\{\ l_i(\tau) + m_j(\zeta) + p_k(\zeta) + f_l(\zeta) + a_m + z_n(t') + l_o(t') + h_q(t') + s_r\ \}$$

where,

- $\lambda(t)$ is the hazard of a cow, t days after calving,
- $\lambda_o(t) = (\lambda\rho\ (\lambda t)^{\rho-1})$ is the Weibull baseline hazard function, with scale parameter λ, and shape parameter ρ.
- $l_i(\tau)$ is the time dependent effect of stage of lactation by lactation number i (lactation 1, 2, 3, 4, 5 and 6 + and 5 stages of lactation). It was considered as a piecewise constant function, which changed whenever an animal entered in a new parity×stage of lactation class. Changes in stage of lactation were defined to occur at calving and at 90, 180, 279, and 365 days after calving.
- $m_j(\zeta)$ is the time dependent class for maximum daily milk yield expressed as deviations within herd-years. This effect was considered to be piecewise constant changing level at the beginning of a new lactation. Nine classes, with equal frequencies of observations, were defined for first lactation and nine for later lactations. Cows without yield data were assigned to the average herd-year peak production class of their respective lactations.
- $p_k(\zeta)$ and $f_l(\zeta)$ are the time dependent classes of standardised deviations of protein content (percentage) k (305-day) and fat content (percentage) l (305-day) within herd-year, which were assumed to be time dependent covariates piecewise constant and changing in value at the beginning of a new lactation. Five classes were considered, < -

1.5 SD, between –1.5 and –0.5 SD, between –0.5 and +0.5 SD, between +0.5 and +1.5 SD and > +1.5 SD.

- a_m is the time independent effect of age at first calving (m=20 to 42 months of age).
- z_n (t') is the time dependent effect of annual change in herd size n. Four classes were defined: decrease of 15 to 50%, stable size (-15 to +15%), increase of 15 to 50%, and increase >50%. This variable was assumed to be a time dependent covariate, piecewise constant, with changes on April 1st of each year, which is the beginning of the new agricultural year in Italy with the definition of milk quota of production per herd. Records from herd decreasing in size more than 50% were considered as censored.
- l_o(t') time dependent effect of year-season l, assumed to be piecewise constant with changes at January 1st, April 1st, July 1st and October 1st. Including year-season in the model simultaneously with h_p(t') is a way to recognise that the mean of the log-gamma distribution of the herd-year-season effect may vary with time because of the existence of a trend over time, of abnormal culling periods, or of random variations (Ducrocq, 1999).
- h_p(t') is the random time dependent effect of herd-year-season p, assumed to be piecewise constant with changes at January 1st, April 1st, July 1st and October 1st. Herd-year-season effects were assumed to follow a log-gamma distribution, and were algebraically integrated out from the joint posterior density during the Bayesian analysis.
- s_r is the random time independent effect of sire of the cow. Sire effects were assumed to follow a multivariate normal distribution with variance-covariance matrix A σ^2_s.

A second model was also analysed on the same data set adding to the previous model the time dependent effect of c_p(t'') of SCS level. This effect was considered to be piecewise constant changing level at the beginning of a new lactation and, within lactation, at each test-day. Ten classes of 1 SCS interval were created according to table 3. A higher level of phenotypic SCS was considered to be associated to mastitis and to poorer milk quality, resulting in increase of culling and lower milk revenue. The biological meaning of this effect on culling was considered to be common to all herds and therefore SCS was included in the model as the absolute observed value rather than as the deviation from contemporary group.

Method

Survival analysis was performed using the Survival Kit (Ducrocq and Sölkner, 1998). Two separate analyses were performed on the same data set according to the two models previously described. All the effects included in the model were tested with a likelihood ratio test comparing the full model, including only all fixed effects, with a reduced model excluding the effect of interest. The shape parameter ρ and the intercept describing the Weibull distribution and the sire variance were estimated from each analysis. Heritabilities, on the original scale, were estimated as (Yazdi et al., 2002): $h^2 = (4 * \sigma_s^2) / (\sigma_s^2 + \sigma_{hys}^2 + 1) = (4 * \sigma_s^2) / [(\sigma_s^2 + \text{trigamma}(\gamma) + 1)]$, where σ_s^2 is the estimated sire variance, σ_{hys}^2 is the herd-year-season variance, and γ is the estimated gamma parameter for herd*year*season effect.

Estimates for class effects were expressed as rate ratios (RR). The RR can be interpreted as the ratio of rate of culling of two individuals differing only by one level of one effect. For each effect, the RR of the class with the largest frequency of uncensored failures was set to 1. The RR of the other classes was expressed relative to this one. The average milk production classes in first and later parities were set as reference classes for this factor.

Relationship between longevity and somatic cells

The correlation coefficient (r_{gij}) between longevity EBV (i) obtained from the two Weibull models and SCS EBV of sires (j), previously estimated (Samoré et al., 2001), were calculated and corrected to approximate genetic correlations using the approach proposed by Calo et al. (1973) to account for estimated reliabilities: $r_{gij} = r_{ij} / \sqrt{(b_i * b_j)}$, where r_{ij} is the Pearson correlation between i and j bulls EBV for longevity and SCS and b_i and b_j are reliabilities of EBV for longevity and for SCS. Bulls were required to have at least 10 daughters in 5 herds for SCS and 10 uncensored daughters for longevity EBV. Reliabilities for SCS were estimated following the method published by Meyer (1989) and reliabilities for longevity as $b_i = n / (n + 1/\sigma_s^2)$, were n is the number of uncensored daughters of the sire and σ_s^2 is the sire variance (Yazdi et al., 2002).

Results

Data and models

Right censored records in this study were 57% of the total number of records considered. Shape parameters ρ had similar values for the longevity model (2.17) and for the model including SCS level (2.15). Sire variances were 0.028 for the model without SCS, and 0.025 for the model including this effect, corresponding to heritabilities of 0.07 and 0.06, respectively. Values of 2.26 and 2.23 were found for the parameter γ, which is a measure of the variance associated with the random effect of the herd-year-season.

Effects in the model

All effects included in the model were significant (P<0.001) when tested with a likelihood ratio test (Table 1).

Table 1. Results of the likelihood ratio tests for the model including SCS level. Effects considered are: stage of lactation by lactation number (stage), within herd-year standardised deviations of peak of lactation for first and later parities (milk), and standardised deviations of protein content (protein %) and fat content (fat %), change in herd size (herd size), age at first calving, fixed effect of year-season and SCS test-days phenotypic level. All the effects resulted to be significant (P < .0001).

Effect	Degree of freedom	–2 Change in log Likelihood
Stage	29	56,832
Milk	17	29,654
Protein %	4	25,047
Fat %	4	6,598
Age at first calving	22	1,102
Herd size	3	2,705
Year-season	23	102,700
SCS phenotypic level	9	19,964

The effect of the interaction between parity and stage of lactation was illustrated as estimated hazard rate of a "reference cow", assuming a calving interval of 400 days. The effect of lactation stage is time dependent and it was expressed as hazard (Fig. 1): $\lambda(t) = \rho \lambda^{\rho-1} * \exp\{ l_i(\tau)\}$, to account for the intercept (grand mean), which is independent on time,

and the estimates for each stage associated with the time scale (Ducrocq 1994; Ducrocq 1999). The rate of culling increased, as expected, approaching the end of each lactation and in later parities.

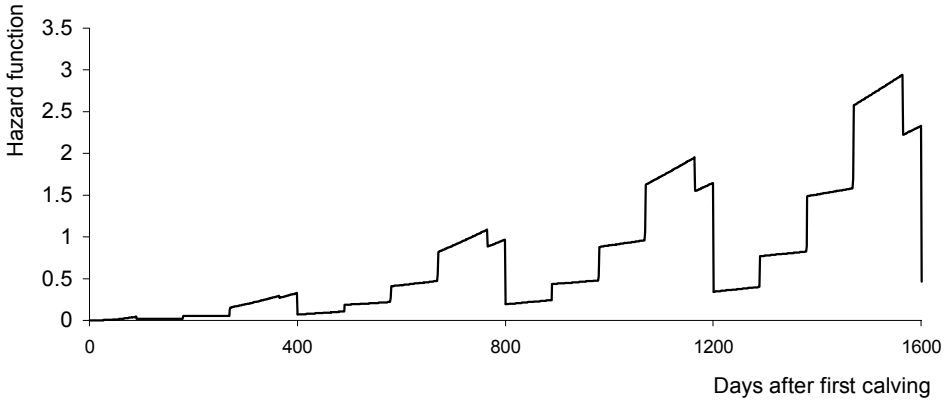

Figure 1. Estimated hazard function of an average cow with 400 days calving interval

Greater milk production at peak of lactation was associated to a smaller RR both in first and later lactations (Fig. 2). Rate of culling ranged from 0.63 to 2.47 in first lactation and from 0.45 to 1.56 in pluriparous cows. The average production class, number 5, was set as reference class with rate equal to 1. An increase in culling rate level, compared to the general trend of the other classes, was due to the inclusion in that class of missing values. Culling rate was larger in first than in later parities.

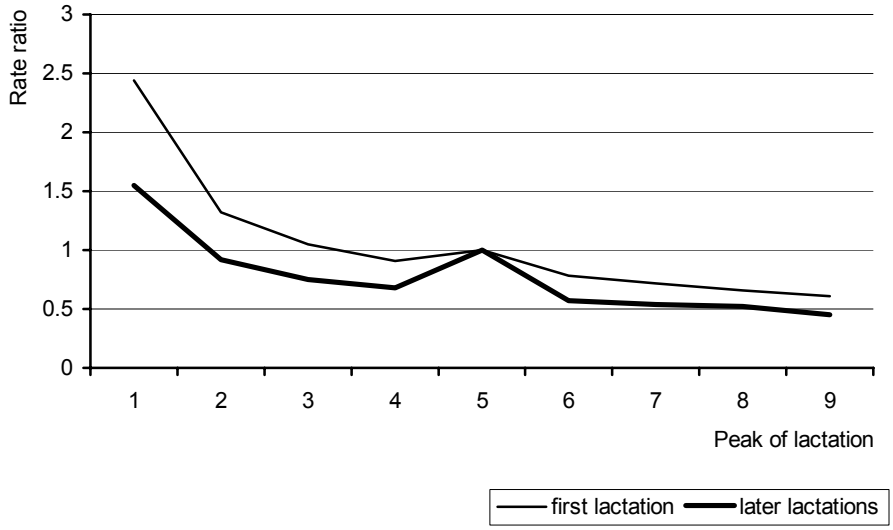

Figure 2. Rate ratio for 9 class percentiles of peak of lactation fixed effect in first and later lactations in the basic model, not including SCS phenotypic level.

In the model including SCS phenotypic level, the culling rate resulted in similar range both for first (0.61 to 2.44) and later parities (0.45 to 1.55). The lowest level of protein percentage deviation resulted in more than three times higher rate of culling than the average class (Table 2). The maximum decrease of rate, associated to the increase in protein contents, was only half of the reference level. Fat content presented an opposite trend but with a smaller range between the maximum and the minimum level classes (Table 2).

Models including SCS phenotypic level resulted in comparable RRs both for protein and for fat percentages (Table 2) and no changes in rate were detected also for the other fixed effects considered.

Table 2. Rate ratio for classes of within herd-year SDs of 305-day deviation of protein percentage, and fat percentage estimated using two different models excluding (longevity model) and including (SCS model) the effect of SCS phenotypic level. Classes of production: 1 = less than -1.5 SD, 2 = –1.5 to –0.5 SD, 3 =–0.5 to +0.5 SD, 4= +0.5 to +1.5 SD, 5 = more than 1.5 SD.

Classes	Protein %		Fat %	
	Longevity model	SCS model	Longevity model	SCS model
1	3.23	3.41	0.86	0.86
2	1.17	1.22	0.78	0.78
3	1.00	1.00	1.00	1.00
4	0.65	0.65	1.07	1.09
5	0.60	0.59	1.64	1.69

The effect of age at first calving resulted in an increase in culling rate with age from 0.73 (20 months of age) to 1.39 (42 months of age) with the RR set to 1.0 for calving at 30 months of age. The annual change in herd size was associated with a higher rate of culling of 23% in shrinking herd (15 to 50 % decrease in herd size) than in stable herds (reference class). Herds annually increasing from 15 to 50% and more than 50% in size showed a decrease in rate of culling when compared to stable herds (-8% and –12% respectively).

Over the six years from which the data were taken, the rate of culling associated to the fixed effect of year season (Fig. 3) generally slightly increased from the beginning of 1994. A sharp increase of culling was detected at the end of 1996. Starting from 1996, in Italy the payment of fees for extra production, out of European quota system, was directly requested to farmers. To avoid extra annual production, and the payment of fees, breeders reduced the number of producing animals before the end of the year. The same pattern, although with a smaller effect, resulted at the end of each year when farm quotas were defined.

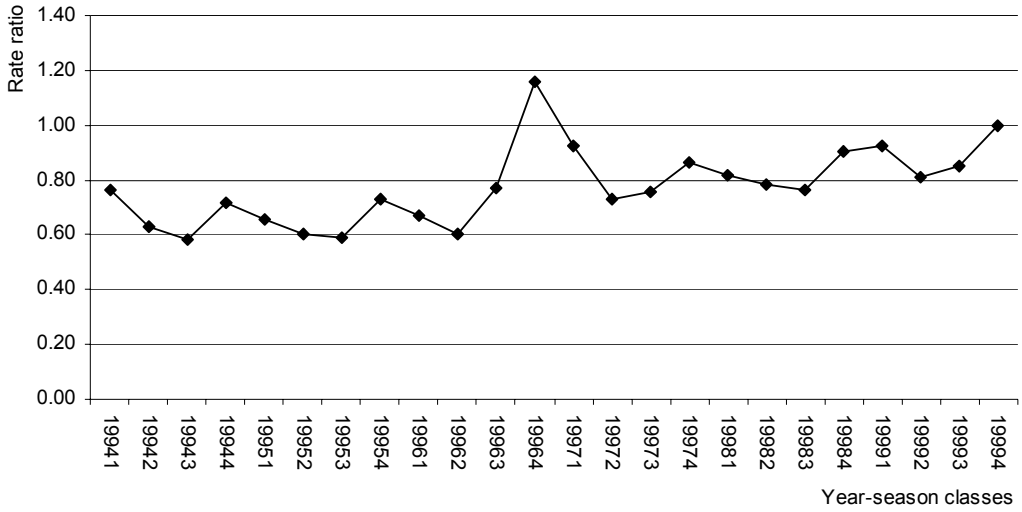

Figure 3. Rate ratio for year-season fixed effect (years from 1994 to 1999 and seasons change: 1= January 1st, 2= April 1st, 3= July 1st and 4= October 1st).

Somatic cell count phenotypic and genetic level

The effect of phenotypic level of SCS was proportionally associated to a culling rate increasing, from 0.51 to 2.89 for the lowest and highest classes, respectively (Table 3). Culling rate was expressed relative to the SCS class with the largest number of uncensored failures, the sixth class (4.5 to 5.5 points of SCS), with a culling rate of 1 (Table 3). The RR differed by 0.4 between the lowest to the fifth classes, and by 1.9 between the sixth to the highest classes. These results indicated that increasing SCS was associated with increased culling, especially at the upper end of the range of SCS although it should be considered that the precision of ratio decreased with the increase in SCS level due to the smaller number of uncensored failures (from 14,029 to 2,113 uncensored failures).

Table 3. Ten classes of SCS at interval of 1 SCS (SCS range), number of uncensored failure (# failure), and relative rate ratio (RR).

Classes	SCS range	# Failure	RR
1	≤0.5	14,029	0.51
2	0.6-1.5	25,169	0.58
3	1.6-2.5	39,395	0.64
4	2.6-3.5	45,415	0.74
5	3.6-4.5	36,691	0.87
6	4.6-5.5	25,171	1.00
7	5.6-6.5	16,077	1.20
8	6.6-7.5	10,163	1.48
9	7.6-8.5	5,832	1.96
10	>8.5	2,113	2.89

Genetic relationship between somatic cell count and longevity

The survival analyses and the estimation of EBV for SCS (Samoré et al., 2001) were based on the same data set. The restrictions imposed on minimum number of herds and daughters and the availability of EBV for longevity reduced the number of bulls to 2,142. The correlation between sire EBV for SCS and the sire EBV for culling rate obtained with the longevity model was 0.31, indicating that higher values of SCS were associated to a higher rate of culling. The inclusion of phenotypic SCS in survival analysis did not change significantly the rank of bulls for culling rate. The rank correlation between longevity estimates, with or without accounting for SCS phenotypic level of daughters, was 0.98.

Discussion

Data and models

The comparable values of shape parameters here estimated for the two models, longevity and SCS model, indicated a similar baseline hazard function increasing over time. Values of 2.15 and 2.17 were slightly higher than the previous estimate of 2 on Italian Holstein data, with a model that included milk yield in terms of average lactational production (Schneider and Miglior, 1999). Ducrocq (1999) used a value of 2 for the genetic evaluation of French dairy bulls for longevity, but other studies reported lower values such as 0.97 for the Danish Holstein (Neerhof et al., 2000) and 1.49 for the Dutch (Vollema et al., 2000) Holstein populations.

Sire variances estimated in this study were greater than previous estimates on the same population (Schneider and Miglior, 1999; Schneider et al., 2000). The main difference between the model used in this analysis and previous ones was the measure used to account for within herd production level. The definition for production (peak of lactation or 305d lactation or average production) included in the analysis to estimate functional longevity, has a large effect on genetic variance parameter estimation.

Heritability resulted to be 0.07 and 0.06, depending on the model. Literature estimates from survival analyses of heritabilities on the observed scale have often been higher, such as 0.22 (Ducrocq and Sölkner, 1998; Neerhof et al., 2000), or 0.15 (Dürr et al., 1999), or, 0.11 and 0.098 (Vollema et al. 2000).

Lower values of γ indicate larger variability among herd-years. Values of 2.26 and 2.23 estimated in this study were smaller than 2.6 (Schneider et al., 2000) and larger than 1.96 (Schneider and Miglior, 1999) previously obtained in the same population. Vollema et al. (2000) reported values for γ of 4.19 for Black and White and 1.57 for Red and White dairy cows, and Vukasinovic et al. (1999) used a value of 4. The size of γ, found in this study, indicates that large variability among herd-years exists in Italian Holstein.

Effects in the model

The survival analysis was based on test day milk recording information collected not before than 5 d after calving. Therefore culling events at calving could not be accounted for.

Level of production was accounted for by using information on peak of lactation. This measure is expected to be a better indicator because less affected by diseases, e.g. mastitis after the peak, than the average lactation production level (Schneider and Miglior, 1999) or a 305d production (Schneider et al., 2000). Moreover peak is considered to be a better indicator of voluntary culling because the culling decision is usually taken after the period of maximum of production. Production after the peak is lower and success of pregnancy, health status and reproductive problems are known. Using the average yields or 305d production to account for voluntary culling does not properly consider that cows that will be culled at the end of lactation are often not inseminated and, therefore have a smaller deviation from their contemporaries than would have been expected if they had been pregnant (Roxström and Strandberg, 2002). Cows with missing information on peak yield were assigned to the average class of deviation from contemporaries. This led to a culling rate higher than expected for this class, especially if compared to the previous and the following levels of production (Fig. 2). Lactation with missing values for production could have been deleted, but then some information on SCS level, the aim of the study, would have been excluded from the analysis. Another possibility would have been to set up a dummy class. Treating missing values separately, as missing values most often corresponded to culled cows, led to very high rates of culling estimated for dummies classes for production level. The rate of culling associated to milk contents reflected national selection objectives putting a larger importance to protein than to fat content. Production measures were always significant in survival analyses reported in literature and lactation yields in the current lactation resulted to have the highest impact when compared with the value of the previous lactation (Vollema et al., 2000). The inclusion of SCS in the model did not affect the estimates of culling rate for production levels.

The fixed effect of year-season was included in the model simultaneously with $h_q(t')$ in a way to specify that the mean of the random herd-year-season could vary with time (Ducrocq, 1999) and therefore in order to take into account the culling trend of abnormal culling period and the random deviation of year-season from this base level. The inclusion of this effect was already found to result in a better fit to the model for Italian data (Schneider et al., 2000).

Somatic cell count phenotypic and genetic level

Cows with test-days in the highest classes of SCS had almost 3 times higher rate of culling than the average level. Lower rate was reported by Beaudeau et al. (1995) with a range of 1.7 from highest to lowest class for SCC. Differences in the size of rate associated to SCC, or SCS level, could be attributed to populations analysed, data sets size, or number of classes considered. In both cases a higher rate of culling was found for higher SCS. Given that SCS were considered as an indicator of both clinical and sub-clinical mastitis incidence, results can be compared with studies analysing the rate of culling directly associated to mastitis incidence. Beaudeau et al. (1995) found that udder health disorders were always highly related to an increase of culling rate, with results depending on lactation period of mastitis occurrence. Neerhof et al. (2000) found a rate of culling 1.69 greater than healthy contemporary mates.

Genetic relationship between somatic cell count and longevity

Antagonistic genetic correlations between SCS and longevity have been reported in literature, ranging from 0.16 to 0.36 (Nielsen and Aamand, 1995; Mrode et al, 2000; Roxström and Strandberg, 2002). Analyses of the direct trait, mastitis incidence, resulted in similar antagonistic relationships with longevity, with values ranging from 0.22 to 0.53 (Nielsen and Aamand, 1995; Neerhof et al., 2000; Roxström and Strandberg, 2002). Roxström and Strandberg (2002) defined the trait mastitis-determined length of production life and found correlations of 0.75 and 0.88 with SCC and mastitis, respectively. The association with longevity was unfavourable and the relationship between the two traits was strong, indicating that SCC affected the mastitis-determined longevity with a correlation similar to the one estimated for the direct mastitis.

In this research, the genetic correlation between SCS and longevity was estimated from the correlation between sire EBV for the two traits. This procedure yields an approximation of the genetic correlation. Direct estimation through a multiple trait analysis was not possible because models used to obtain EBV for longevity and SCS were highly different. An alternative method would be to use a multiple trait model procedure similar to the one currently used by INTERBULL for international sire evaluations (MACE) as proposed by Druet et al. (1999) and by Larroque and Ducrocq (1999). This procedure would allow the use of different models, for each trait, and would provide a reliable estimate of genetic correlations. However, like the method used in this study, this procedure would not account

for female pedigree information and it has some additional weakness, as pointed out by these authors, that may be potentially important for traits with low heritabilities.

Conclusions

An increase in phenotypic level of SCS was associated to an increase in rate of culling. A small increase in SCS level was associated to a great increase in culling rate for high SCS level, but a small increase in culling was estimated for the lowest five classes of SCS. Considering the full scale of SCS, the rate increased more than 3 times for cows with highest level of SCS when compared with lowest level of SCS.

Factors related to SCS are not expected to be included in a survival model to estimate breeding values for longevity because a cow with better survival is also less sensitive to factors causing the increase in SCS. The inclusion of SCS level in the model, as analysed in this study, was necessary to estimate the relative culling rate due to this factor and to estimate the longevity without the effect of SCS. The latter estimate is interesting when breeding values for both traits, SCS and longevity, would be aggregated in a selection index.

Effects considered in the model in the current study, especially the milk production accounted for as peak yield and not as 305d production, should also be considered for the model to routinely estimate longevity EBV. Similar changes would require a new estimation of variance parameters on national level, leading probably to higher sire variance and lower herd-year-season variance.

The genetic correlation between longevity and SCS, estimated through correlations between EBV, was 0.31 indicating that bulls with unfavourable genetic value for SCS are also associated to poorer longevity.

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Chapter 5

Genetic parameters for SCS and protein yield in Italian Holstein Friesian using various data sets and models

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Submitted

Abstract

Genetic parameters for SCC in Italian Holstein Friesian were estimated with particular emphasis on the sign and level of genetic correlation with protein yields. Three models of analysis were applied. First approximate genetic correlations were estimated from correlation between EBV, corrected for the accuracy level. Genetic relationship between SCS and protein yields resulted to be favourable. A random sample of three lactations, including 26,531 records with information on 305d protein yields and on lactation average of SCS, was used to estimate lactation genetic and environmental (co)variance components in three lactations. Two three-traits analyses and 9 bi-trait analyses were applied, including fixed effects for herd-year-season and age by season of calving and the random effect of animal. Genetic correlations between protein and SCS in first lactation were antagonistic (0.31) indicating that an increase in lactation protein yield was associated with increased SCS. In later lactations, genetic correlations between SCS and protein yield were decreased, with values near zero in second (0.01) and third (0.09) parity. As third model of analysis, a RR TD model was applied on 82,368 TD records on milk (kg), fat (kg), protein (kg) and SCS from the first three lactations, from 5,675 cows. The model included the fixed effect of herd-test date, season by age of calving, and random effects for animal and permanent environmental. Shape of lactation curve was modelled using Wilmink's function on days in milk (DIM). Residual covariances differed across 4 stages in each lactation. In total the model estimated 666 genetic, 666 permanent environmental and 120 residual (co)variances. When averaging genetic correlations between the same DIM of different traits (protein yields and SCS) and parities, genetic correlations ranged from -.14 to .60. Genetic correlations between the same trait in different parities were quite large and positive (.45 to .60 for protein and .26 to .40 for SCS). Genetic correlations between SCS and protein were null or negative, and therefore favourable, with values ranging from .00 to -.14. For first parity, the average genetic correlation between SCS and protein was -.02, and the magnitude of this correlation increased to more favourable levels in second and third parity (-.14). Correlations between SCS and protein across different lactations were near zero. Finally genetic correlations were also evaluated for specific stages of lactation. At the beginning of first parity, genetic correlations were positive, and therefore unfavourable, but changed in sign at mid-lactation (165 DIM). A similar pattern was also observed for second lactation,

but with an earlier change in sign occurring at 45 DIM. In third parity estimates were negative, and therefore favourable, for all DIM.

Although variability among results is great, it was summarized that correlations between SCS and protein yields tend to be zero to slightly positive (unfavourable) in first lactation and from zero to negative (favourable) in later lactations. It was concluded that due to the apparent complexity of the genetic factors controlling SCS, in theory one may need to account for different levels and signs of genetic correlations between SCS and production yields in different parities and, if possible, also within parities.

Keywords: Somatic cell scores; Protein yields; Genetic correlations.

Introduction

The interest for udder health traits in dairy cattle is increasing (INTERBULL, 1999) and SCC are considered to be a good indirect measure to select for mastitis resistance, especially when direct measure of clinical mastitis incidence is not available (Emanuelson et al., 1988; Colleau and Le Bihan-Duval, 1995; Heringstad et al., 2000). The trait SCC has the properties of being highly genetically correlated with clinical mastitis (CM) and more highly heritable than direct measures of CM (for a review: Mrode and Swanson, 1996). In addition, SCC is indicative of both CM and subclinical mastitis. Finally, SCC data are routinely recorded in most milk recording systems, making available large amounts of information for estimation of breeding values. Selection for milk yield will result in a higher incidence of mastitis (Emanuelson et al., 1988) unless SCC or specific traits would be included in the selection index (Veerkamp et al., 1995).

Unfavourable positive genetic correlations between milk production and SCC have been reported by several studies based on first parity records with values ranging between 0.06 to 0.82 (Mrode and Swanson, 1996; Mrode et al., 1998; Rupp and Boichard, 1999). A different result was obtained by Mrode and Swanson (1996) for later parities, however, as they observed low to moderate negative (favourable) genetic correlation between the traits in second lactation and in a variety of values in third and later parities. The different direction of genetic correlations was concluded to have resulted from culling in the first parity based on mastitis incidence and on milk production. Changes in the pattern of genetic relationships between production and SCC in first and later parities were also reported by Pösö and Mäntysaari (1996) and Haile-Mariam et al., (2001). Coffey et al. (1986) found a favourable relationship between production and SCC, with approximate genetic correlations of –0.14 with milk yield and –0.09 with fat yield, using sire evaluations for SCC and production yields.

Genetic evaluation for SCS started in Italy in November 2001, using a test-day repeatability model on first parity records (Samoré et al., 2001a). Genetic parameters for test-day repeatability models have been estimated in a previous research in different areas of Italy (Samoré et al., 2001b).

The national Holstein Association of Italy is currently researching the application of a random regression (RR) test-day (TD) model for genetic evaluation of production traits and SCC. The approach is analogous to the one adopted in Canada for breeding value estimation (Schaeffer et al., 2000) Although Italian and Canadian Holstein populations have similar size and comparable selection objectives and recording systems, the estimation of specific (co)variance components specific to the Italian population is necessary because genetic correlations between countries are smaller than 1 (Schaeffer, 1994). With the RR TD model, positive, and therefore unfavourable, genetic correlations between SCS, the log transformation of SCC, and production were reported for first lactation in Canada, but favourable correlations resulted for later lactations (Jamrozik et al., 1998).

The general goal of this study was to estimate genetic parameters for SCC in the Italian Holstein population, with particular emphasis on the sign and level of genetic correlation with production traits. Of additional interest was the examination of the pattern of genetic correlations in different parities and stages of lactation. The specific objective of this paper was to estimate genetic parameters for SCC and protein yield in order to define the relationship existing between production and SCC. The following methods were used: 1) estimation of correlation between sire EBV for SCS and for protein yields; 2) estimation of (co)variances between lactation average SCS and 305day protein yield, and 3) estimation of (co)variances between records of SCS and protein yields using a RR multiple trait test-day model.

Material and Methods

Data

Monthly test-day records of somatic cell count (SCC, thousands of cells per ml) of Italian Holstein Friesian cows were provided by Provincial Milk Recording Agencies (APA) and were collected from 1989 to 2001 in Italy. Records were removed when date of calving was not available or when the test date occurred before 5 or after 305 d in lactation. No restrictions were imposed on the number of test-day records per lactation. Individual

somatic cell count (SCC) records for each test day were transformed to somatic cell score (SCS) as:

$SCS = \log_2 (SCC/100)+3$ (Ali and Shook, 1980).

Pedigree files tracing back three generations (parents, grandparents, and great-grandparents) were extracted from the National Herd Book file for each data set analysed. Two phantom groups were defined, one for male and one for female unknown parents.

EBV correlations

Sire EBV from the Italian official evaluation were used to obtain approximate genetic correlations between SCS and production traits. The EBV for SCS were obtained by using a test-day repeatability model to evaluate first parity records, as described by Samoré et al. (2001a). A lactation model was used for production EBV (Canavesi et al., 1994), based on data from the first three lactations (Canavesi et al., 1999). The official EBV release of November 2001 for both traits was used in the analysis. Included in this study were EBV for 4,229 bulls that had at least 20 daughters in 10 herds for production and at least 10 daughters in 5 herds for SCS. In addition, bulls (i.e. their daughters) had a minimum of 29 TD for SCS. An estimation of the relationship between the SCS and production was initially calculated using the simple correlation coefficient (r_{gij}) between EBV (i) for protein yield and EBV (j) for SCS. This value was converted to an approximate genetic correlation by using the approach proposed by Calo et al. (1973) to account for differences in the estimated reliabilities of the EBV across sires:

$$r_{gij} = r_{ij} / \sqrt{(b_i * b_j)},$$

where r_{ij} is the Pearson correlation between i and j bulls EBV for protein yield and SCS and b_i and b_j are reliabilities of EBV for protein yield and for SCS. Reliabilities for SCS and for protein had been estimated using the method published by Meyer (1989).

Lactation (co)variances

A data set of 5,292,362 lactations was available with information both on SCS and protein yield. The SCS were recorded as geometrical lactation mean (LSCS) and protein

was simple 305 day yield (Santus et al., 1996). Lactations were restricted to first, second and third lactation. Due to computing limitations, estimation of variance components using all data was unfeasible and a sample was created by drawing from the whole data set all lactation records pertaining to randomly sampled herds. Sampling was repeated as many times as needed to get a number of 26,531 lactations from 13,746 cows. The sampled data included 52% first parity records, 31% from second parity and 17% from third parities (Table 1). First parity was required for all cows.

Table 1. Sample numbers, geometrical SCS lactation mean (LSCS)±SD, and protein yields lactation mean (P_{305})± SD for parity.

Parity	Lactations	LSCS	P_{305}
First	13,746	3.09±1.23	269±47
Second	8,357	3.46±1.31	296±55
Third	4,428	3.78±1.39	300±57

The effect of age at calving in months (from 20 to 38 months) and four seasons of calving of three months each (1=from January to March, 2=from April to June, 3=July to September, 4=October to December) were defined. Herd-year-seasons (HYS) were used to establish contemporary groups. The pedigree included at least three generations of ancestors and was extracted from the national herd book. A total of 6 traits, protein yield and LSCS in the three parities, were analysed using the following model:

$$y_{ijlk} = HYS_i + AS_l + a_{ijl} + e_{ijlk},$$

where y_{ijlk} is the record k on one of the two traits in one of the three lactations in the i HYS class and l age-season (AS) class, HYS_i is the i level of the fixed effect of herd-year-season of calving, AS_l is the fixed effect of class of age by season of calving, a_l is the random additive effect of cow l and e_{ijlm} is the residual effect associated to the observation. Eleven analyses were performed: 2 three-trait analyses, in which the three traits were the three different lactations for protein and SCS, respectively; and 9 bi-variate analyses, in which the two traits were SCS in a given lactation and protein in another (or possibly the

same) lactation. Genetic parameters and (co)variance components for LSCS and protein yield were estimated using the ASREML software (Gilmour et al., 1995).

Test day (co)variances

Information on 10,955,039 TD records on milk (kg), fat (kg), protein (kg), and SCS (on log2 scale) from the first three lactations of Italian Holstein Friesian cattle were available. A sample of data was created by random selection of herds with at least 1,000 records. Year of calving was required to be between 1990 and 1998. All traits, milk, fat, protein yields and SCS, had to be recorded on each TD. For each lactation, two classes of age by four seasons of calving were created. Thresholds to delineate the two classes of age for each parity were 28 months for first, 41 months for second, and 55 months for third lactation; and seasons were defined as: January to March, April to June, July to September, and October to December. The sample included 82,368 test day records from 5,675 cows. Data were distributed such that 52% of TD were in first lactation, 31% in second and 17% in third. The corresponding numbers of levels of herd-test-day (HTD) were 2,544 for first, 2,197 for second, and 1,725 for third lactation.

The model of TD analysis was an animal model with multiple trait (MT) RR. Traits were considered across lactations. The model for trait i in lactation j was:

$$y_{ijtlmno} = HTD_{ijl} + \Sigma b_{ijnp} z_{tp} + \Sigma a_{ijmp} z_{tp} + \Sigma p_{ijmp} z_{tp} + e_{ijtlmno},$$

where $y_{ijklmno}$ was the record o on cow m made on day t within herd-test day effect l, for a cow in the subclass n for season-age of calving, HTD_{ijl} was fixed HTD effect, b_{ijnp} were fixed regression coefficients specific to subclass n, a_{ijmp} were random regression coefficients specific to cow m, p_{ijmp} were random permanent environmental coefficients specific for cow m, $e_{ijtlmno}$ was the residual effect for each observation, and z_{tp} were covariates assumed to be the same for both fixed and random regressions. Shapes of lactation curves were modelled using Wilmink's function (1987) as:

$$W(t) = w_0 + w_1 t + w_2 \exp(-0.05t).$$

Vectors a_m and p_m included 36 elements (4 traits, 3 lactations, 3 covariates) with random regression coefficients for animal m. Covariance matrices were G for genetic and P for permanent environmental. Residual effects on different days in milk (DIM) were considered uncorrelated within and between cows. Residual covariances differed across 4 stages in each lactation: 5 to 45 DIM, 46 to 115 DIM, 116 to 265 DIM, and 266 to 305 DIM.

In total the model estimated 666 genetic, 666 permanent environmental, and 120 residual (co)variances. A Bayesian approach, as described in Jamrozik et al. (1998), was used to obtain the means of the posterior distributions for all parameters of the model. For the Italian data set two chains of 55,000 samples were generated. The first 5,000 samples were discarded as the burn-in period. Values obtained were averaged across the chains.

Results

EBV correlations

Correlation between Italian bulls breeding values for SCS (first lactation) and for protein yield (three lactations) resulted in a correlation of 0.20. The sign of SCS EBV is reverted in Italy (Samoré et al., 2001a), with higher values corresponding to the favourable effect of smaller SCS, so this correlation was favourable. Accounting for the level of reliability of both traits, this result corresponded to an approximate genetic correlation of 0.24. This value means that higher protein production would be genetically associated with decreased values for SCS.

Lactation (co)variances

Heritabilities estimated based on lactational records (Table 2) increased from first parity to later lactations, both for LSCS (0.18 to 0.21) and for protein yields (0.31 to 0.35). Strong genetic correlations between different parities of the same traits were found, with values >0.90 between adjacent lactations and smaller values, but still >0.80, between first and third lactations.

Genetic correlations between protein and LSCS in first lactation were antagonistic (0.31) indicating that an increase in lactational protein yields was associated with increased LSCS. Similar values were obtained for correlations between first parity LSCS and the other

parities of protein yield (0.20 and 0.26, respectively). In later lactations, correlations between SCS and protein were decreased, with values near zero in second (0.01) and third (0.09) parity. Residual correlations between SCS and protein yields were null or negative and, therefore, had opposites sign from genetic correlations. Residual correlations between LSCS and protein of different parities were not significantly different from zero.

Table 2. Heritabilities (on diagonal), genetic (above the diagonal) and environmental (below) correlation coefficients (x100) for 305 d protein yield (P_{305}), and geometrical SCS lactation mean (LSCS), in first (1), second (2), and third (3) lactation. Standard errors in parenthesis.

	LSCS1	**LSCS2**	**LSCS3**	**P_{305}1**	**P_{305}2**	**P_{305}3**
LSCS1	.18 (.02)	.93 (.04)	.87 (.07)	.31 (.06)	.06 (.08)	.15 (.11)
LSCS2	.25 (.02)	.21 (.03)	.92 (.05)	.20 (.08)	.01 (.09)	.10 .(12)
LSCS3	.18 (.02)	.36 (.03)	.21 (.04)	.26 (.11)	.10 (.13)	.09 (.16)
P_{305}1	-.16 (.02)	.00 (.02)	.05 (.03)	.30 (.02)	.90 (.03)	.82 (.04)
P_{305}2	-.07 (.02)	-.18 (.03)	-.02 (.03)	.43 (.02)	.31 (.03)	.92 (.03)
P_{305}3	-.02 (.03)	-.10 (.12)	-.21 (.04)	.32 (.03)	.59 (.03)	.35 (.04)

Test day (co)variances

An analysis with the RR TD model yields estimates for a large number of (co)variances, which can be used to estimate heritabilities and correlations, both genetic and environmental, for different combinations of DIM, parities and traits. According to the paper objective, estimates were analysed with emphasis on protein yields and SCS. Average values of daily heritabilities from 5 to 305 DIM ranged from .30 to .38 for protein and from .15 to .25 for SCS (Table 3). Estimates generally increased with parity for both traits.

Correlations were estimated between all combinations of traits, parities and DIM. When averaging correlations between the same DIM of different traits (SCS and protein kg) and parities, genetic correlations ranged from -.14 to .60 and environmental correlations from -.19 to .41 (Table 3). Genetic correlations between the same trait in different parities were quite large and positive (.45 to .60 for protein and .26 to .40 for SCS). Genetic correlations between SCS and protein were null or negative, and therefore favourable, with values ranging from .00 to –.14. The greatest genetic correlations (in magnitude) were observed

between SCS and protein within the same parity, and all of these estimates were negative (favourable). For first parity, the average genetic correlation between SCS and protein was -.02, and the magnitude of this correlation increased to more favourable levels in second and third parity (-.14). Favourable average genetic correlations indicated that greater protein yields were associated to lower values of SCS. Correlations between SCS and protein across different lactations were near zero.

Table 3. Average values, from 5 to 305 days from calving, of heritabilities (on diagonal), genetic (above the diagonal) and permanent environmental (below) correlation coefficients (x100) for SCS (S), and protein (P), in first (1), second (2), and third (3) lactation. Correlations are with the corresponding parameter for the same day from calving.

	S1	**S2**	**S3**	**P1**	**P2**	**P3**
S1	.15	.29	.26	-.02	-.09	-.08
S2	.28	.19	.40	.00	-.14	-.12
S3	.20	.41	.25	.01	-.05	-.14
P1	-.11	-.04	-.03	.30	.52	.45
P2	.00	-.19	-.09	.33	.35	.60
P3	.01	-.10	-.24	.18	.33	.38

Correlations between SCS and protein were also evaluated for specific stages of lactation (Table 4). At the beginning of first parity, genetic correlations were positive, and therefore unfavourable, but changed in sign at mid-lactation (165 DIM in Table 4). A similar pattern was also observed for second lactation, but with an earlier change in sign occurring at 45 DIM. In third parity estimates were negative, and therefore favourable, for all DIM. This result suggests that the null average genetic correlations in first parity (Table 3) was the result of averaging positive and negative correlations, at the beginning or at the end of the lactation, respectively. The negative genetic correlation for third parity was constant for all DIM.

Average correlations for permanent environmental effects were positive between different parities of the same trait and negative between two traits (Table 3). Similar correlations were also found for specific DIM (Table 4).

Table 4. Genetic and permanent environmental correlations coefficients (x100) between TD protein and SCS, in Italian Holstein, on selected days in milk (DIM) in the three lactations.

Correlation	Lactation	DIM									
		15	45	75	105	135	165	195	225	255	285
Genetic	First	.08	.05	.04	.03	.02	-.01	-.03	-.07	-.10	-.14
	Second	.06	-.03	-.06	-.07	-.09	-.12	-.16	-.21	-.26	-.32
	Third	-.10	-.09	-.08	-.08	-.09	-.12	-.15	-.19	-.22	-.25
Permanent environmental	First	-.06	-.10	-.11	-.11	-.11	-.11	-.12	-.12	-.13	-.14
	Second	-.02	-.15	-.17	-.17	-.18	-.19	-.21	-.23	-.26	-.29
	Third	-.16	-.21	-.21	-.21	-.22	-.23	-.25	-.27	-.28	-.30

Discussion

Heritabilities

Estimates of heritabilities for SCS based on lactational means (.18 to .22) and daily values, according to the RR TD model (.15 to .25), were greater than were previous estimates obtained using a TD repeatability model (Samoré et al., 2001b). Although both studies used data from Italian Holstein Friesian cows data sampling strategies differed between studies. In the first study (Samoré et al., 2001b) only first parity data were sampled from specific geographical areas of Italy, while data used in the current research included three lactations and records were extracted on a national scale. But the main difference is between models: lactation model, TD repeatability model and a RR TD model. Similar differences were also found for Canadian Holstein between RR TD model heritabilities (Samoré et al., 2002) and heritabilities estimated with a TD repeatability model (Reents et al., 1995).

The strong genetic correlations between SCS in different parities affected the value of first parity heritability estimated using a MT lactation model (.18) or using a RR MT TDM (.15).

A large variety of heritability values are applied for SCS breeding values estimation in the world. Two main groups of heritabilities can be summarized in values used with lactation models (.08 to .15) and with TD models (.12 to .31) (Mark et al., 2002).

For protein yields, heritabilities estimated with different models in the present research were consistent. Values ranged from .30 to .35 using a lactation model and from .30 to .38 for three parities. A value of .31 in first parity Italian Holstein cows was estimated by Bagnato et al. (1996) and similar values are currently used in breeding value estimation for protein for most of other Holstein populations (INTERBULL, 2000).

Genetic correlations

Approximate genetic correlations, estimated as correlation between breeding values, resulted in a small positive relationship between protein yield and SCS suggesting a favourable genetic association between high production and smaller level of SCS. The favourable correlation found can partly be explained by the joint selection of sires, directly for yields and indirectly for SCC, through selection for correlated udder type traits. Breeding values for SCS were based on first parity TD records, while genetic indexes for protein were calculated using three parities yields. This difference can partly explain the different sign of value estimated when compared with most of the estimates from the literature (Mrode and Swanson, 1996). Generally unfavourable relationships between SCS and protein in first parity, have been reported, with values typically ranging from around .09 (Mrode et al., 1998) to .74 (Monardes et al., 1984). The same antagonistic genetic relationship with milk yield was also reported in more recent studies on first lactation data for Finnish Ayrshire (Pösö and Mäntysaari, 1996), Holsteins (Mrode et al., 1998; Rupp and Boichard, 1999), and Jersey (Roman and Wilcox, 2000) dairy cows. A favourable relationship between milk yields and SCC was found by Coffey et al. (1986) using the approach of correlation between breeding values of 57 bulls with at least 10 daughters.

Estimates of genetic correlations between SCS and yield in second and third parity (Mrode and Swanson, 1996) have been inconsistent in their sign. Similar to this study, some researchers have also reported a change in sign to negative (favourable) relationship between SCS and protein (Monardes et al., 1984; Monardes and Hayes, 1985; Schutz et al., 1990) in later lactations.

The daily correlations obtained using a RR TD model indicated decreasing genetic correlations between SCS and protein across a given lactation. In first parity, positive correlations at the beginning of first lactation changed to zero or negative values. In second and third parities, correlations changed from zero to negative values, or from negative to

more negative values. The pattern of genetic correlations resulted in average genetic correlations over DIM, from 5 to 305 days, near zero in first parity and negative in later parities. Using the lactation model, genetic correlations resulted in different values and sign, with a strong positive (unfavourable) genetic correlations in first parity and smaller positive correlations (near zero) in later parities. Haile-Mariam et al. (2001) analysed the trend of genetic correlations between SCC and protein yields over lactations and within lactation for different DIM. The large positive (unfavourable) genetic correlation at the beginning of first lactation decreased to negative or zero correlation with an increase in DIM. The same pattern was also found for second and third lactation but with a rapid change to zero and then to negative genetic correlations.

Although variability among results is great, one can summarize that correlations between SCS and protein yields tend to be zero to slightly positive (unfavourable) in first lactation and from zero to negative (favourable) in later lactations. This pattern of genetic correlations would also help explain the favourable genetic trend recently reported for Italian Holstein Friesian for SCS (Samoré et al., 2001a), which occurred despite a general emphasis on increased protein yield and no formal selection for decreased SCS. The selection for increased yields might have indirectly resulted in a correlated decrease in genetic level of SCS, since EBV for yields were based on multiple lactations. A similar analysis of SCS genetic trend was also reported for Australian dairy cattle (Haile-Miriam et al., 2002). In Italy the joint selection for udder type traits (Biffani et al., 2002), including traits favourably correlated to SCS (Mrode and Swanson, 1996), probably also contributed to avoid any increase in SCS genetic level.

Value of SCC is often used as indirect measure of mastitis incidence but values of correlations found between yields and clinical mastitis incidence resulted in stronger antagonistic relationship than values estimated between production and SCC (Pösö and Mäntysaari, 1996; Rupp and Boichard, 1999). Similar positive estimates for genetic correlations between yields and mastitis incidence were also reported for different data sets and parities (Emanuelson, 1988; Emanuelson et al., 1988; Lyons et al., 1991; Heringstad et al., 1999).

Biological interpretation

The change in values of genetic correlation between SCS and protein yields with increasing lactation number was explained by Haile-Mariam et al. (2001) as the result of the

balance of two mechanisms. Cow with high milk yields may be more susceptible to infection resulting in a positive (unfavourable) genetic correlation at the beginning of first parity. But mastitis events also cause damage to the texture of the udder and lead to smaller production in later parities resulting in a negative correlation.

Two more reasons were also reported in literature for the change in sign of genetic correlations between SCC and production yields. First, the change in sign of correlation was explained as the result of infection caused by different pathogens. At the beginning of first lactation mastitis is mainly caused by environmental pathogens, while major pathogens plays an important role in the second part of lactation. The mechanisms of defence against infection by contagious and environmental pathogens may be different (Detilleux et al., 1997), especially in the increase in SCC, and may therefore lead to different correlations between SCC and production. Second, the cows that survive to produce in later parities result from selection on high production yields and on sensibility to mastitis. These interpretations can explain the change in sign of correlations from first to second lactation but more difficult is the interpretation of the further negative trend from second to later lactations.

Conclusions

Estimates of genetic correlations between protein yields and SCS were calculated based on a number of different models of analysis. Correlations were generally near zero or slightly positive in first lactation, especially in early lactation, while estimates based on later parities were near zero or negative. A trend in genetic correlation was also observed within lactation. The change in sign of genetic correlations over lactations, and within lactation, would contribute to explain the favourable genetic trend in SCS resulting in Italian Holstein Friesian cows obtained also before applying any direct selection for SCS. Selection for yields traits based on more parities records may have contributed to the decline in SCS genetic level due to favourable genetic correlations with this trait in later parities.

Although genetic correlation between yields and SCC is not highly unfavourable, more strongly antagonistic correlations have been reported between yields and clinical mastitis (Pösö and Mäntysaari, 1996; Rupp and Boichard, 1999). It may thus be important to include

SCC with a negative weight in a selection index to indirectly slow the increase in mastitis incidence that would be caused by selection on yields. Moreover the definition of a proper selection index requires the estimation of genetic correlations between traits. Because of the apparent complexity of the genetic factors controlling SCS, in theory one may need to account for different levels and signs of genetic correlations between SCS and production yields in different parities and, if possible, also within parity.

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Chapter 6

Genetic parameters for production traits and somatic cell scores estimated with a multiple trait random regression model in Italian Holsteins

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Abstract

Genetic parameters for production traits and somatic cell scores (SCS) were estimated for Italian Holstein Friesian using a test day multiple trait random regression model. Average heritabilities for production traits resulted to be in a range from 0.30 to 0.38, increasing with lactation number. The SCS heritabilities were 0.15, 0.19, and 0.25, for the three lactations. Genetic correlations between production traits were high (till 0.89) and negative or null correlation coefficients were found between SCS and production traits. Variances were compared to Canadian estimates, obtained with the same model. Trends, over days in milk, were similar for the two countries, for all lactations and traits, but with different levels.

Keywords: Genetic parameters, Random regression model, Holstein Friesian.

Introduction

In Italy a random regression (RR) test day (TD) model, analogous to the one adopted in Canada for breeding value estimation (Schaeffer et al., 2000), is under study for genetic evaluation of Holstein dairy cows. Italian and Canadian Holstein populations have similar size,and comparable selection objectives and recording systems. Nevertheless, in Italy, specific covariance parameters need to be estimated to be used in a RR TD model that will substitute the lactation model actually in use. The objectives of this study were: 1) the estimation of (co)variance parameters for production traits and somatic cell scores in Italian Holstein to be used in a national RR TD model; and 2) the comparison of TD RR (co)variance estimates from Italian and Canadian Holstein populations.

Material and Methods

Data

Italian data consisted of TD records on milk (kg), fat(kg), protein(kg) and SCS (on log2 scale) from the first three lactation of Holstein Friesian cattle. A sample of data was created by random selection of herds with at least 1000 records. Year of calving was required to be between 1990 and 1998. All four traits had to be recorded on each TD. For each lactation, two classes of age by four seasons of calving were created. Thresholds for two classes of age for each parity are 28 months for first, 41 months for second, and 55 months for third lactation, and seasons were defined as: January to March, April to June, July to September, October to December. The sample included 82,368 test day records from 5,675 cows. Data were distributed 51% of TD in first, 32% in second and 17% in third lactation. The corresponding levels of herd-test-day (HTD) were 2,544 for first, 2,197 for second, and 1,725 for third lactation. Data used for the Canadian analysis are described in Jamrozik et al. (1998).

Model

The model of TD analysis was an animal model with multiple trait (MT) RR. Traits were considered across lactations. The model for trait i in lactation j was:

$$y_{ijtlmno} = HTD_{ijl} + \Sigma b_{ijnp} z_{tp} + \Sigma a_{ijmp} z_{tp} + \Sigma p_{ijmp} z_{tp} + e_{ijtlmno},$$

where $y_{ijklmno}$ was the record o on cow m made on day t within herd-test day effect l, for a cow in the subclass n for season-age of calving, HTD_{ijl} was fixed HTD effect, b_{ijnp} were fixed regression coefficients specific to subclass n, a_{ijmp} were random regression coefficients specific to cow m, p_{ijmp} were random permanent environmental coefficients specific for cow m, $e_{ijtlmno}$ was the residual effect for each observation, and z_{tp} were covariates assumed to be the same for both fixed and random regressions.

Shapes of lactation curves were modelled using Wilmink's function (1987) as:

$$W(t) = w_0 + w_1 t + w_2 \exp(-0.05t).$$

Vectors a_m and p_m included 36 elements (4 traits, 3 lactations, 3 covariates) with random regression coefficients for animal m. Covariance matrices were G for genetic and P for permanent environmental. Residual effects on different days in milk (DIM) were considered uncorrelated within and between cows. Residual covariances differed across 4 stages in each lactation: 5 to 45 DIM, 46 to 115 DIM, 116 to 265 DIM, and 266 to 305 DIM.

In total the model estimated 666 genetic, 666 permanent environmental, and 120 residual (co)variances. A Bayesian approach, as described in Jamrozik et al. (1998), was used to obtain the means of the posterior distributions for all parameters of the model. For the Italian data set two chains of 55,000 samples were generated. The first 5,000 samples were discarded as the burn-in period. Values obtained were averaged across the chains.

Canadian data had been previously analysed using the same model.

Results and Discussion

Italian Parameters

Covariance estimates were used to calculate average daily heritabilities, genetic and permanent environmental correlations. These values are shown in Table 1

Table 1. Average values, from 5 to 305 days from calving, of additive genetic variance (on diagonal), genetic (above the diagonal) and permanent environmental (below) correlation coefficients (x100) for milk (M), fat (F), protein (P), and SCS (S), in first (1), second (2), and third (3) lactation. Correlations are with the corresponding parameter for the same day from calving.

	M1	**F1**	**P1**	**S1**	**M2**	**F2**	**P2**	**S2**	**M3**	**F3**	**P3**	**S3**
M1	7.88	56	89	-2	59	29	50	4	51	27	43	4
F1	75	0.01	36	-4	24	44	28	-2	17	37	21	-1
P1	94	45	0.01	-2	48	32	52	0	42	30	45	1
S1	-18	-11	-11	0.50	0	-4	0	29	1	-4	1	26
M2	37	17	28	-9	13.24	56	80	-16	65	44	60	-5
F2	28	29	26	-11	78	0.02	46	-14	25	51	31	-6
P2	37	20	33	-9	93	51	0.01	-14	54	46	60	-5
S2	-7	-6	-4	28	-29	-19	-19	0.67	-9	-14	-10	40
M3	25	12	17	-10	43	23	31	-12	17.24	53	75	-14
F3	15	22	14	-9	33	34	27	-14	68	0.03	43	-12
P3	20	14	18	-8	41	26	33	-12	81	50	0.02	-14
S3	-5	-5	-3	20	-14	-10	-9	41	-23	-16	-24	0.96

Heritabilities increased for all traits from first to third lactation (Table 2). Lowest values were for SCS, from 0.15 to 0.25, but estimates for this trait were higher than results obtained with a TD fixed regression analysis in Italian data (Samoré et al., 2001). Production traits had heritabilities (0.30-0.38) comparable to 0.30 used in national evaluation with a lactation model. Genetic correlations between production traits were high, especially between milk and protein. Differing from most of the literature (Mrode and Swanson, 1995), also in first parity, SCS had favourable or null genetic correlations with production traits. From these results, genetic selection for production should not be expected to cause unfavourable increase in SCS level in Italian Holstein.

Comparison of Italian and Canadian Variances

Additive genetic variances in Italy and Canada showed a similar trend over DIM, but at different levels (Figure 1). Generally, for all traits and lactations, variances initially decreased at the beginning of lactation (5-45 DIM), remained constant in the central period, and tended to increase at the end (after 255 DIM).

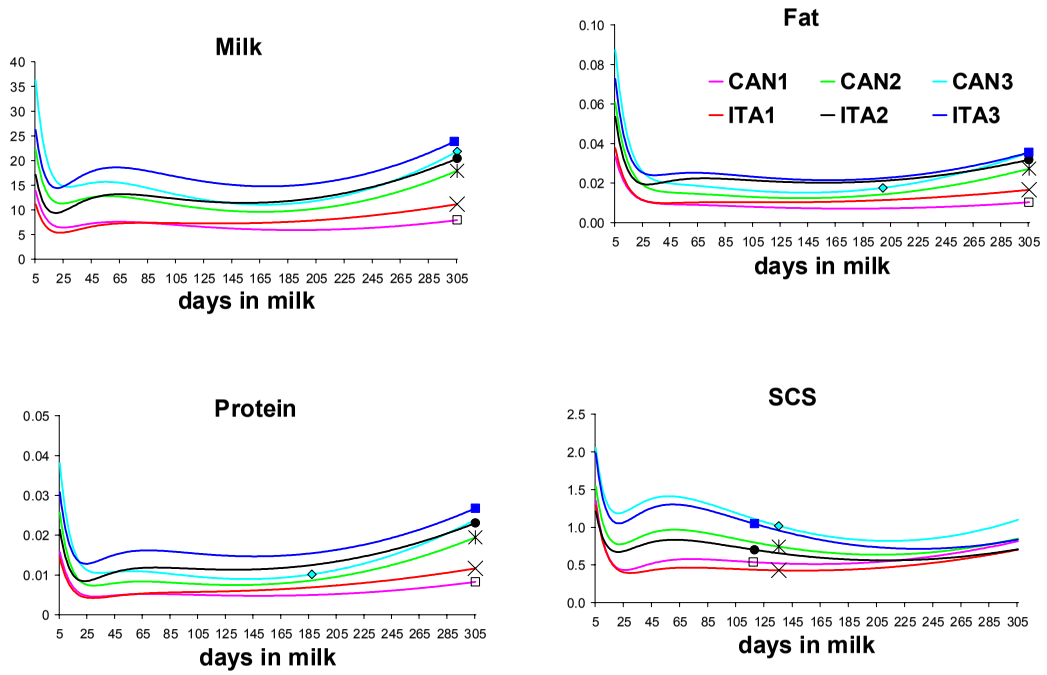
Similar shapes of the curves between the two populations were also observed for permanent environmental variances (no figure). Residual variances resulted in higher values in Italy than in Canada. Average heritabilities, from 5 to 305 DIM, tended to be higher in Canada than in Italy (Table 2), with the exception of fat and protein in second lactation. Greatest differences between the two populations were observed for SCS. Similar results had been previously observed based on estimates from lactation models (INTERBULL, 2000) for production traits.

Table 2. Average values, from 5 to 305 days from calving, of heritabilities (x100) for milk (M), fat (F), protein (P), and SCS (S), in first (1), second (2), and third (3) lactation in Canadian and Italian Holstein.

	M1	**F1**	**P1**	**S1**	**M2**	**F2**	**P2**	**S2**	**M3**	**F3**	**P3**	**S3**
Canada	38	33	34	25	36	28	34	27	41	35	38	35
Italy	33	30	30	15	34	34	35	19	37	32	38	25

Conclusions

Estimates of (co)variances obtained in this study for the Italian Holstein will be used as parameters for multiple trait random regression model that will be soon adopted for genetic evaluations of production traits and SCS in Italy. Estimates of (co)variances for Italy and Canada followed the same trend across lactations, but at different levels. This result seems to suggest that the two populations are genetically comparable but the differences in (co)variance parameters should be accounted for in international comparisons.



Symbols: ITA1=X, ITA2=●, ITA3 =■, CAN1=□, CAN2=✷, CAN3=◆.

Figure 1. Trend of additive variances for milk, fat, protein, and SCS, in first (1), second (2), and third (3) lactations, in Canadian (CAN) and Italian (ITA) Holsteins.

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Chapter 7

Genetic and environmental correlations for SCS, conformation traits, and milking speed in first lactation Italian Holstein cows and proposal of an Italian udder health index

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Submitted

Abstract

Genetic correlations between udder conformation traits and SCS were estimated in Italian Holstein Friesian data. A total of 1,268,762 first parity Italian Holstein cows had information both on conformation traits and SCC. Test day SCC were transformed to SCS and they were geometrically averaged from 5 to 305 days to obtain a lactation measure (LSCS). Two data sets were analysed. The first data set included 11,203 records and was used in 8 two-trait analyses, considering information on LSCS, and one conformation trait at a time. Models used included the fixed effect of herd-year-season for LSCS, and for conformation traits the fixed effect of herd-year-date of scoring and the interaction of age at calving in months by season of calving. Heritabilities ranged from .05 (udder balance) to .24 (udder depth) for conformation traits and .14 for LSCS. Genetic correlations with LSCS were -.31 for udder depth and .28 for rear udder width. Other genetic correlations for conformation traits and LSCS varied from -.16 to -.03. A second data set, including 4,398 records was extracted to estimate genetic correlations between 5 traits that are being considered for inclusion in an udder health index. Using these estimates, and literature estimates for direct mastitis resistance, an udder health index (UHI) for the Italian Holstein was proposed : UHI = -15 EBV_{SCS} + 1.5 EBV_{FUA} + 0.15 EBV_{UDD}, where EBV are the estimated breeding values for SCS, fore udder attachment (FUA), and udder depth (UDD). Selection for lower value of SCS, shallow udder with stronger fore attachment should result in increased mastitis resistance. The inclusion of milking speed in the udder health index was not proposed because of its non-linear relationship with SCS and the low reliability of data collection in Italy for this trait.

Keywords: Genetic correlations, Udder health index, Somatic cell count, Conformation traits, Holstein Friesian.

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Introduction

Selection for improved udder health is of primary importance in dairy cattle populations (INTERBULL, 1999). Breeding organisations in Scandinavian countries select for udder health using mastitis incidence (Heringstad et al., 2000). Indirect traits can be used for selection for mastitis resistance with the predominant indirect trait being somatic cell count (SCC), which is considered to be a good alternative for mastitis data (Colleau and Le Bihan-Duval, 1995). The value of SCC is currently used in some countries where the direct measures of mastitis incidence is not available (De Jong and Lansbergen, 1996; Heringstad et al., 2000). The value of SCC is routinely recorded in most milk recording systems and the information is available on a population at moderate costs (Shook and Schutz, 1994; Zhang et al., 1994). The genetic relationship between SCC and clinical mastitis is favourable with moderate to high estimates, averaging .70 (Mrode and Swanson, 1996; Rupp and Boichard, 1999). The heritability of SCC is much higher than that of clinical mastitis (as reviewed by Mrode and Swanson, 1996).

An udder health index including not only SCC but also udder conformation traits and milking speed with SCC or mastitis data is expected to give a higher selection response when compared to indirect selection on SCC only (De Jong and Lansbergen, 1996). Rogers et al. (1991) suggested the inclusion of udder morphological traits and SCC in an index to reduce mastitis. In The Netherlands, an udder health index combines information on somatic cell scores (SCS), udder depth, fore udder attachment, teat length and milking speed (De Jong and Lansbergen, 1996). Boettcher et al. (1998) for Canada proposed an udder health index including milking speed, three SCS measures, one for each parity, and udder conformation traits (udder depth and front teat length). Rupp and Boichard (1999) suggested that SCC, udder depth, udder balance, fore udder attachment, and clinical mastitis should be considered for inclusion in an udder health index in France. Milking speed was not included in the proposed French index due to the lack of association with clinical mastitis. Using also the direct measure of mastitis incidence, Denmark have set up an udder health index including the following traits: four traits for incidence of mastitis, depending on days in milk of mastitis occurrence, geometric mean of SCS in the first period of first parity, and linear score for dairy form, udder depth and fore udder support (Nielsen et al., 2000).

In Italy, a composite index for udder conformation has been in use since 1993 (INTERBULL, 1996) aiming to improve udder health, milkability, and functional longevity.

The index does not include SCS. Extension of the composite conformation index to an udder health index, requires estimation of correlations among udder conformation traits, SCS and milking speed.

The objective of this study was to estimate genetic and environmental correlations between SCS, conformation traits, and milking speed, in Italian Holstein Friesian first parity cows. This study aims to identify traits to be included in an aggregate udder health index for Italian Holstein cows.

Material

Conformation and SCC data

A total of 1,268,762 first parity Italian Holstein cows had information both on conformation traits and SCC. Cows were required to have information on all udder conformation traits and SCC, with the exception of teat placement, collected in Italy since 1998. Conformation data were collected all over Italy by national classifiers and SCC by provincial recording agencies from 1989 to 2001. Udder conformation was scored for 8 traits with a scale ranging from 1 to 50 (Table 1). Test-day records of SCC were transformed to somatic cell score (SCS) as SCS = $\log_2$ (SCC/100)+3 (Ali and Shook, 1980). The geometrical lactation average (LSCS) was estimated based on tests from day 5 to day 305 after calving. The average of LSCS was 2.48 and phenotypic averages of conformation traits were between 23 and 28 (Table 1).

Due to computational limitations, estimation of variance component using all data was infeasible and therefore editing and sampling procedures were applied. A minimum of 100 records per herd was required, reducing the number of herds to 26% of the total number, but maintaining the distribution over the country. Two data sets were extracted by drawing from the whole data set all records pertaining to randomly sampled herds. The first data set was used for two-trait analyses and included 11,203 records, while a smaller data set was extracted for a five trait model analysis. Only 4,398 records were included in the second dataset because of the larger complexity of calculation. Relationships were traced back in a pedigree file to three generations (parents, grandparents, and great-grandparents) extracting information, for each sample, from the National Herd Book file. Pedigree included 39,105

animals for the first data set, and 17,617 for the second one. Two phantom groups were defined, one for male and one for female unknown parents, for each of the two pedigrees.

Table 1. Description of traits, phenotypic averages and standard deviations (SD).

Trait	Description of trait	Average	SD
Fore udder attachment	1=loose to 50=strong	24.26	6.08
Rear udder height	1=low to 50=high attachment	25.18	5.95
Rear udder width	1=narrow to 50=wide attachment	27.34	6.47
Ligament	1=weak to 50=strong cleft	27.93	5.96
Udder depth	1=below to 50=above hock udder	28.03	6.98
Teat placement	1=wide to 50=close teats	24.78	5.82
Teat length	1=short to 50=long teats	23.82	5.93
Udder balance	1=low rear to 50=high rear	24.73	6.80
LSCS	geometrical lactation mean of SCS test-days	2.48	1.50

Milking speed data

In Italy, farmers are asked to identify cows that are slower in milking compared to the herd average. This information is collected during milk recording and it is used for milking speed genetic evaluation of bulls. No information on fast milking cows, milking speed scores, neither precision timing measures are recorded.

Methods

LSCS and milking speed

Due to the low accuracy of the employed system of data recording, it is not possible to accurately estimate genetic correlation between milking speed and SCS from phenotypic information directly. An approximate estimation of the existing relationship between milking speed and SCS was calculated as correlation coefficient (r_{gij}) between milking speed breeding value estimations (EBV(i)) and SCS EBV (j) of sires (Samoré et al., 2001a). Breeding values for milking speed (INTERBULL, 1996) are estimated using an animal model and published only for bulls. The correlation coefficient was used to approximate genetic

correlation width the approach proposed by Calo et al. (1973) to account for estimated reliabilities: $r_{gij} = r_{ij} / \sqrt{(b_i * b_j)}$, where r_{ij} is the Pearson correlation between bulls EBV for milking speed and SCS and b_i and b_j are the reliabilities of the EBV for milking speed and for SCS. The official release of EBV for both traits of November 2001 was used for the analysis. For breeding values, larger values of EBV were associated to lower SCS points, while milking speed EBV was expressed as number of slow daughters recorded. Bulls were required to have at least 10 daughters in 5 herds both for SCS and 50 daughters in 20 herds for milking speed, resulting in 2,540 bulls with EBV for both traits.

Covariances estimates for SCS and conformation traits

Genetic and environmental correlations between LSCS and conformation traits were estimated using the ASREML software, which uses an Average Information Matrix algorithm (Gilmour et al., 1995). A total of 8 two trait animal model analyses were performed, considering information on LSCS, and one conformation trait at a time. The model for LSCS was different from the model used for conformation traits. The model used for conformation traits was:

$$Y_{ijkl} = HYD_i + ASj + a_k + e_{ijkl}$$

where: Y_{ijkl} is the score for a linear conformation trait of the k^{th} animal; HYD_i is the fixed effect of i^{th} interaction herd-year date of scoring; AS_j is the fixed effect of j^{th} interaction of age at calving in month by season of calving; a_k is the random additive genetic effect for the k^{th} animal; and e_{ijkl} is the random residual error term. Age at calving was in months (from 20 to 38) and four seasons of three months of calving each (1=from January to March, 2=from April to June, 3=July to September,4=October to December) were defined.

The model used for LSCS was:

$$Y_{ikl} = HYS_i + a_k + e_{ikl}$$

where: Y_{ijkl} is the LSCS of the k^{th} animal; HYS_i is the fixed effect of i^{th} interaction herd-year-season of calving; a_{ij} is the random additive genetic effect for the k^{th} animal; and e_{ikl} is the random residual error term.

In order to evaluate an aggregated udder health index, covariance components between LSCS, fore udder attachment, rear udder width, udder depth, and teat length were also estimated using a multiple trait model. Models used in the five trait analysis, for LSCS and for conformation traits, were the same as previously described for the two trait models.

Moreover, the linearity of relationships between SCS and conformation traits was evaluated by associating the official bulls breeding values for SCS (Samoré et al., 2001a) and for conformation traits (INTERBULL, 1996).

Udder health index

Different hypotheses of udder health indexes were compared, considering the resulting genetic response and the correlation between the aggregated genotype and the index. The udder health index (UHI) was calculated as:

$$UHI = b_1 * X_{HS(LSCS)} + b_2 * X_{HS(FUA)} + b_3 * X_{HS(RUW)} + b_4 * X_{HS(UD)} + b_5 * X_{HS(TLE)}$$

where X_{HS} were the average of daughters performance (half sibs) information for each trait and b was the relative weighting factor for each of the following traits: LSCS, udder depth (UD), rear udder width (RUW), fore udder attachment (FUA), and teat lengths (TLE). Values of b where estimated as $P^{-1}G$ with P being the phenotypic covariance matrix of traits in the selection index and G being the matrix with genetic (co)variances between traits in the index and the aggregate genotype. The aggregate genotype or objective of selection was defined as: H = MR; where MR is the mastitis resistance. Covariances between traits used in the index were estimated for Italian Holstein in the previous step, with the exception of MR. Mastitis events were not available to be included in the covariance component estimation and therefore literature values were used for this trait (De Jong and Lansbergen, 1996). The genetic superiority (R) or response, defined as the predicted average breeding value of selected individuals, was estimated as: $R = i * r_{IH} * \sigma_H$, where r_{IH} was the correlation between index and the aggregated genotype, σ_H was the standard deviation of the aggregated genotype and i was the selection intensity which was set equal to 1. In practice, the formula of the udder health index will combine EBV with a certain accuracy. To approximate that accuracy it was therefore considered that information were collected on 100 or 200 daughters per bull.

Results

Heritabilities

Estimates of heritabilities for the various traits are in Table 2. The lactation measure of SCS had a heritability of .14. Among udder conformation traits, the minimum value of heritability was for udder balance (.05) and most of the other udder morphological traits had heritabilities around .12. The most heritable trait was udder depth (.24). Standard errors of heritabilities were between .02 and .03 for all traits.

Table 2. Heritabilities (h^2) of type traits, environmental (r_e) and genetic (r_g) correlations between conformation traits and lactation geometrical mean of SCS from 5 to 305d (LSCS). Standard error of estimates between brackets.

	h^2	r_e	r_g
Fore udder attachment	0.15 (0.02)	-0.05 (0.02)	-0.16 (0.11)
Rear udder height	0.17 (0.02)	-0.06 (0.02)	-0.01 (0.11)
Rear udder width	0.12 (0.02)	-0.03 (0.02)	0.28 (0.12)
Ligament	0.13 (0.02)	-0.07 (0.02)	-0.11 (0.12)
Udder depth	0.24 (0.03)	-0.06 (0.02)	-0.31 (0.09)
Teat placement	0.12 (0.02)	-0.02 (0.02)	-0.07 (0.12)
Teat length	0.15 (0.02)	-0.04 (0.02)	0.13 (0.11)
Udder balance	0.05 (0.02)	0.00 (0.02)	-0.03 (0.16)
LSCS	0.14 (0.02)		

Genetic and environmental correlations with SCS

Correlations of udder conformation traits with LSCS were generally favourable. Udder depth was the trait with the highest correlation, in term of absolute value (–.31), followed by rear udder width (.28) Smaller values of LSCS were genetically associated with higher udders (highest distance from the lowest part of the udder floor to the hock), and with narrow rear udders. Relationships between LSCS and udder depth or rear udder width were significant with values greater than two standard errors (.09 and .12). When compared to estimated values, standard errors of other genetic correlations were generally quite large ranging from .11 to .16. Considering the observed relationships, although not all were

significantly different from zero, a strongly attached udder to the fore abdominal wall (-.16), and with short teats (.13) was genetically related to smaller values of LSCS. The remaining udder conformation traits had smaller genetic correlations with LSCS, ranging from –.11 for central ligament to –.03 for udder balance. Environmental correlations were generally low, ranging from –.07 (central ligament) to .00 (udder balance) with small standard errors (around .02).

Udder health index

Genetic and environmental correlation between LSCS, FUA, RUW, UDD, and TLE were estimated using a five trait model (Table 3) and were used to calculate different possible udder health indexes. The highest genetic correlation was found for UDD and FUA (.76). The strong genetic correlation of LSCS with RUW (.28) and with UDD (-.31), already estimated by the two trait model, were confirmed and increased in magnitude (.47 and -.35, respectively). In contrast, the genetic correlation of LSCS with FUA estimated with the five-trait model, was smaller (-.03 versus –.16) than values obtained from bi-trait models, and the correlation with TLE increased from .13 to .22, although changes were expected given the high standard error of estimates in the two trait models.

Table 3. Heritabilities (on diagonal), genetic (above the diagonal) and phenotypic (below diagonal) correlations used to calculate the udder health index. Traits included are the mastitis resistance (MR), considered as the reverted measure of mastitis incidence, the geometrical lactation average of somatic cell score (LSCS), udder depth (UDD), rear udder width (RUW), fore udder attachment (FUA), and teat length (TLE). Values for LSCS, FUA, RUW, UDD and TLE were estimated using a five trait model. Estimates for mastitis resistance were obtained from literature (De Jong and Lansbergen, 1996).

Trait	MR	LSCS	FUA	RUW	UDD	TLE
MR	0.03	-0.72	0.36	0.03	0.46	-0.12
LSCS	-0.40	0.09	-0.03	0.47	-0.35	0.22
FUA	0.10	-0.05	0.17	0.24	0.76	-0.30
RUW	0.10	-0.02	0.20	0.11	-0.29	0.00
UDD	0.10	-0.06	0.39	-0.11	0.23	-0.21
TLE	0.10	-0.01	0.03	0.12	-0.07	0.21

Table 4. Different index hypothesis including 200 daughters information for each of the following traits: mastitis resistance (MR), somatic cell score geometrical mean from 5 to 305d (LSCS), udder depth (UDD), rear udder width (RUW), fore udder attachment (FUA), and teat length (TLE). For each index it is reported the relative percentage response obtained when compared to the response obtained with 200 daughters direct mastitis (MR) information.

Traits in the udder health index	**Response relative to MR response**
MR (200 daughters)	100%
MR (100 daughters)	85%
LSCS	84%
UDD	57%
FUA	44%
TLE	15%
RUW	4%
LSCS+FUA	94%
LSCS+RUW	93%
LSCS+UDD	90%
LSCS+TLE	84%
LSCS+RUW+UDD	101%
LSCS+FUA+RUW	99%
LSCS+FUA+TLE	95%
LSCS+FUA+UDD	94%
LSCS+RUW+TLE	93%
LSCS+UDD+TLE	91%
LSCS+RUW+UDD+TLE	102%
LSCS+FUA+RUW+UDD	101%
LSCS+FUA+RUW+TLE	99%
LSCS+FUA+UDD+TLE	95%
FUA+RUW+UDD+TLE	61%
LSCS+FUA+RUW+UDD+TLE	102%

Using parameters obtained from the five trait model, several combinations of selection index for mastitis resistance were tested (Table 4). Response obtained with each index was related to the response (100%) that could be obtained with direct selection on mastitis resistance, when data would be available on 200 daughters. Using only one trait, the most efficient indirect measure was LSCS, where the response represented the 84% of those obtained with MR. Conformation traits were less efficient in indirectly selecting for MR. The best single conformation trait was UDD giving 57% of response. Including two traits simultaneously in the index increased the success in response to a maximum of 94% with LSCS and UDD or to 93% with LSCS and RUW. Increasing the number of traits, the relative response raised to a maximum of 101% by including LSCS, RUW and UDD. The maximum response obtained with four traits, was when including LSCS, RUW, UDD, and TLE (102%) or LSCS, FUA, RUW, and UDD (101%). Including additional traits did not give any further additional gain.

Milking speed and non-linear relationship

The Spearman correlation between bulls breeding values for milking speed and for SCS was .07 and Calo's correlation was .09. This suggested the evidence of a small, but unfavourable, genetic correlation associating high level of SCS with an larger number of slow milking cows. However, a non-linear relationship between bulls breeding values for SCS and milking speed was detected when associating the average values for SCS with classes of milking speed EBV (Figure 1). Most of bulls had average values of SCS EBV and only the extreme bulls with the highest values for milking speed EBV resulted in a small level of SCS, i.e. bulls with large numbers of slow milking cows were genetically associated to low levels of SCS. In contrast, extreme bulls with the smallest values for EBV for milking speed resulted in small genetic level for SCS, and therefore in unfavourable results. All the other classes of milking speed EBV corresponded to bulls with average values for SCS EBV.

A similar non-linear relationship between EBV was found for SCS and rear udder width trait (Figure 1), while udder depth EBV had a quasi-linear association with SCS EBV.

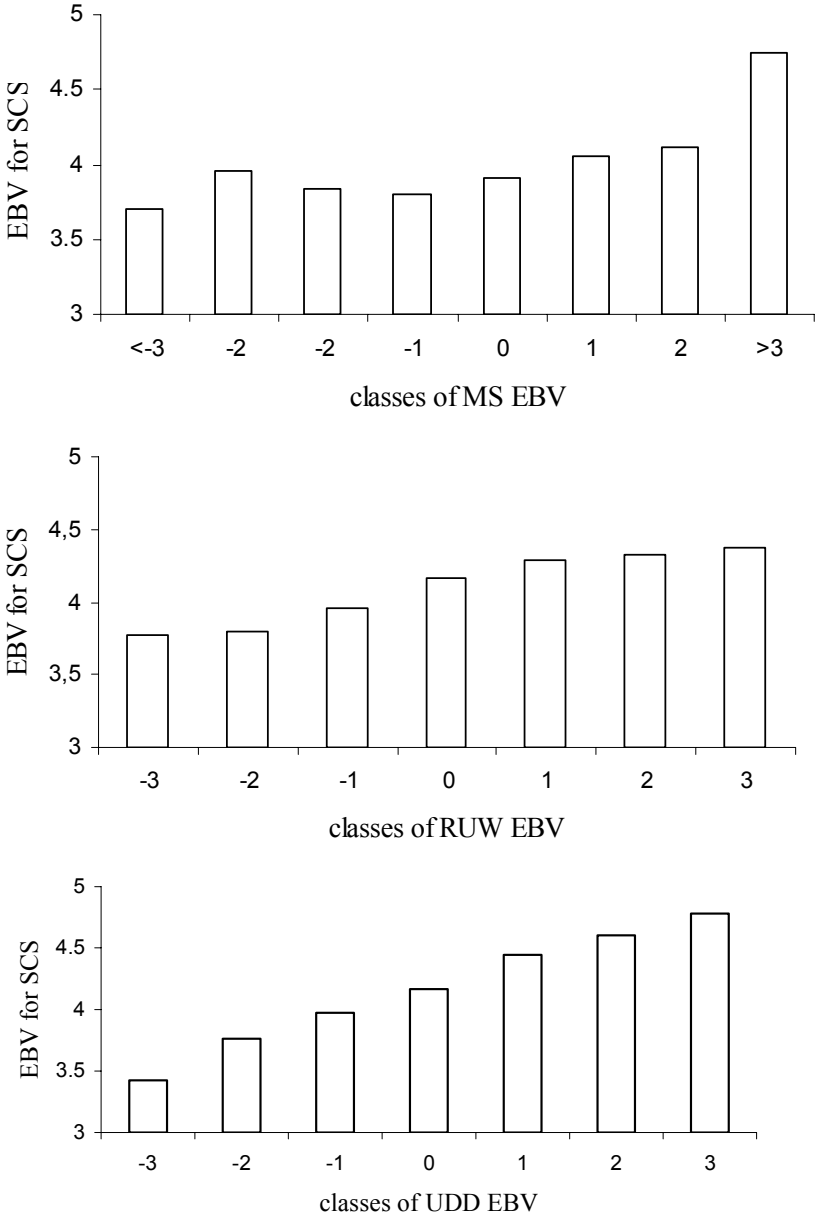

Figure 1. Relationship between milking speed, rear udder width (RUW), udder depth (UDD) and somatic cell scores (SCS) bulls breeding values.

Discussion

Values of heritabilities estimated for conformation traits were similar to previous ones in the same population (Cassandro et al., 1997) and to values currently used for EBV calculation (INTERBULL, 1996), but were generally smaller than estimates from the French Holstein population (Rupp and Boichard, 1999). Heritability of LSCS was greater than previous estimates of test-day SCS estimated with a repeatability TDM (Samoré et al., 2001b). A similar difference was reported for the Finnish Ayrshire by Pösö et al. (1997) between heritability estimates for SCS with a TDM (.08) and with a geometrical lactation average (.13). Mrode and Swanson (1996) found smaller values of heritabilities in their review with an average of .11±.04. More recent studies reported values between .11 and .23 (Pösö and Mäntysaari, 1996; Luttinen and Juga, 1997; Nielsen et al., 1997; Pryce et al., 1997; Boettcher et al., 1998; Mrode et al., 1998; Rupp and Boichard, 1999).

The favourable genetic correlations between udder traits and SCS estimated in Italian Holstein, are in agreement with other similar studies. A shallow, tightly attached udder with short and closed teats is genetically associated with lower values of SCS. Similar correlations with udder traits have been reported (Seykora and McDaniel, 1986; Rogers et al., 1991; Boettcher et al., 1998; Rupp and Boichard, 1999) for UDD, FUA, and ligament, while RUW and udder balance resulted in different genetic correlations coefficients. In this analysis, RUW has a positive correlation with SCS. Moreover, the relationship between SCS and RUW bull EBV is non-linear. Rogers et al. (1991) reported various genetic correlations between RUW and SCS (from -.15 to .27), and Boettcher et al. (1998) estimated values near zero (-.03).

In contrast with the results of Rupp and Boichard (1999), the genetic correlation between SCS and udder balance in this study was almost null. Udder balance trait is not internationally harmonized by ICAR (2002) and this can explain the difference in genetic correlations resulting in various countries, probably due to different trait definitions. According to literature results (Seykora and McDaniell, 1986; Rogers et al., 1991; Rupp and Boichard, 1999), teat distances and teat lengths resulted in favourable associations with SCS.

Milking speed

Fast milking was slightly associated with higher SCS level (.09). Stronger genetic correlations have been reported, with values ranging from .18 to .57 (Seykora and McDaniell, 1986; Lund et al., 1994; Luttinen and Juga, 1997; Boettcher et al., 1998, Rupp and Boichard, 1999). However the association of SCS and milking speed was non-linear for the Italian Holstein. This suggested that an association between fast milking cows and high level of SCS existed, but that the patterns of this relationship, for slow and fast milking cows, were different. The inclusion of milking speed in an udder health selection should therefore account for this non-linear relationship. One possibility could be the setting of a threshold value where fast milking cows above the defined threshold are slightly penalised.. The collection of more informative data, with more classes of milking speed, might be useful to better evaluate the genetic relationship between SCS and milking speed. However previous literature results (Lawstuen et al., 1988; Lund et al., 1994; Luttinen and Juga, 1997; Rupp and Boichard, 1999) reported favourable genetic correlations between milking speed and the direct trait of mastitis incidence. Rupp and Boichard (1999) suggested that probably the association with SCS could depend to some extent by a more complete draining of the udder and not by the easier flow of milk out of the udder, which could be assumed to be associated with easier entry of pathogens, and therefore increased risk of mastitis.

Proposal for an udder health index

In Italian Holsteins, a bull needs at least 10 daughter scores in 5 herds to be considered progeny tested for type traits and SCS but the number of daughters per bull varied from this minimum number to over 40,000 daughters for old proven bulls. In Italy, it is common for sires of bulls to have more than 200 daughters. Considering this situation, an average number of 200 daughters per bull was assumed in the analysis. The same number of daughters per bull was also assumed to have mastitis resistance observations, and all cows would be scored both for udder morphology and for udder disease incidence. Although no current system for collection of mastitis exists in Italy, it is likely that a future system would be at a reduced scale at first and thus providing a lower number of daughter observations than would be available for other traits. The selection response, obtained with an index based on 100 daughters with mastitis incidence data, would be reduced to 85% of the response achieved with 200 daughters.

The value of SCS was the most important trait to be used for indirect selection for mastitis, confirming the previous result by De Jong and Lansbergen (1996). Information on SCS are already collected in most countries (INTERBULL, 1996) and the us of SCS is considered suitable for mastitis resistance selection when considering its genetic properties (Mrode and Swanson, 1996). When the number of daughter observations for SCS is higher than the number of observations for daughter clinical resistance, i.e. 200 daughters with SCS and only 100 daughters with observations for clinical mastitis, the selection responses were comparable.

A selection response similar to the one achieved when selecting on the direct trait, mastitis resistance, was obtained when RUW and UDD were added to the proposed Italian udder health index which contains SCS, UDD, and FUA. The conformation trait of UDD was highly genetically correlated with SCS, and also with mastitis (Rupp and Boichard, 1999). This relationship would explain the increase in selection response obtained with its inclusion in the index. In contrast, the increase in udder health selection response with the inclusion of RUW was probably due to the high genetic correlation with SCS and with UDD. However, the genetic relationship between RUW and udder health traits, both SCS and clinical mastitis, has had significantly different estimates from previous studies and also for different parities (Rogers et al., 1991; Schutz et al., 1993; Rogers et al., 1998; Nash et al., 2000). Moreover, the association between SCS and RUW EBV suggested a non-linear relationship in the Italian Holstein Friesian population. Furthermore, previous studies have not supported its inclusion in an udder health index, and selection for RUW would also produce smaller udders, with narrow attachments and higher udders. Due to the genetic correlations between udder conformation traits and production (Bagnato et al., 1995), improved RUW would be antagonistic with production and breeders would not support this choice. All these factors suggest the exclusion of RUW from an udder health index, although this would slightly reduce the genetic response in mastitis resistance. The proposed index for Italian Holstein would therefore include SCS, UDD and FUA. Another possibility would be to use TLE, and not FUA, but the effect of TLE on selection response seems mainly due to the slightly higher heritability than FUA, and to the genetic correlations with other traits. A bi-trait index, only including SCS and TLE, would result in a lower selection response than that obtained with SCS and one of the other conformation trait used. Therefore FUA is preferred to TLE for the inclusion in the udder health index. The inclusion of more than three traits in the index would not further increase genetic response.

The udder health selection index (UHI) proposed would be:

$$UHI = -14.49\ EBV_{SCS} + 1.29\ EBV_{FUA} + 0.11\ EBV_{UDD,}$$

which approximates to

$$UHI = -15\ EBV_{SCS} + 1.5\ EBV_{FUA} + 0.15\ EBV_{UDD,}.$$

Strong front attached udders are genetically highly correlated to udder depth (Table 3) and it is also believed that a strongly attached front udder would result in better udder depth in later lactations, although a scientific proof of this argument is not possible at the moment because conformation traits data are collected only on primiparous cows.

Milking speed was not proposed for inclusion in an udder health index for Italian Holstein but it should be considered when better strategies of data collection would be set up. Furthermore, if the non-linear relationship between SCS and milking speed can be confirmed, milking speed should not be included as linear trait in the udder health index but as a threshold trait only, penalising animals with high milking speed.

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Chapter 8

General Discussion

Mastitis is of major concern in dairy cattle selection policy. Udder infections are the most costly diseases (National Mastitis Council, 1996) and there is an increasing concern about milk quality products and animal welfare. High level of SCC, considered as indirect measure of mastitis incidence, cause an economic loss, as reduced milk production, increased veterinary and management costs, and reduced price for the lower milk quality (National Mastitis Council, 1996). It is of primary interest to breeders to select for improved udder health in order not to loose their image of producing product of high quality and to guarantee the cow welfare. Moreover high levels of SCC also directly affect breeders interests through the increase in culling rate and the consequent reduced longevity (Chapter 4).

The value of SCC resulted to be a good indirect measure to select for mastitis resistance, especially when direct measure of clinical mastitis incidence is not available (Emanuelson et al., 1988; Colleau and Le Bihan-Duval, 1995; Heringstad et al., 2000). The advantage of SCC is that it is routinely recorded in most milk recording systems with moderate costs (Shook and Schutz, 1994; Zhang et al., 1994).

The estimation of breeding value for SCC is the first step to consider mastitis in a genetic selection program (Chapter 3). The aggregation of conformation traits and milking speed measures with SCC is a further step to more efficiently select for udder health (Chapter 7). Moreover, selection response depends on the choice of sires and dams of the next generation that is generally based on a selection index aggregating all economic important traits. The final step to select for mastitis resistance in a breeding program would be therefore the inclusion of the udder health index into the general selection index.

Udder selection in Italian Holstein Friesian

Udder selection in Italy was firstly based on the udder composite index aiming to improve udder conformation and indirectly to select for functional longevity and udder health (Rozzi, 1989). Data on SCC have been collected at a provincial level in Italy since 1989 for management purposes. With the beginning of this thesis, a large practical work was made in order to collect historical provincial data bases for somatic cell count into a national base and to set a regular flow of new data. The first genetic evaluation for SCC was released in November 2001 as the result of this data collection and of research presented in Chapter 2 and 3. The genetic evaluation for SCC was immediately included in the new general

selection index (PFT). Genetic correlations used at this stage were mainly extracted from literature but new estimates specific for the Italian Holstein population were estimated in Chapter 4, 5 and 7. Breeding value estimations for SCC were also applied in several practical applications offered to breeders. The aggregation of SCC into an udder health index, together with some conformation measures, was proposed in Chapter 7 and its inclusion into the selection index is discussed in this chapter.

The interest in udder health is increasing in Italy and some future applications are discussed in this chapter. Moreover a test-day random regression model is under study for genetic evaluation of somatic cells and production traits requiring new estimations of (co)variance components (Chapter 6). A further line of interesting researches would be open with the collection of direct data on mastitis incidence and with the evaluations of its genetic relationship with all traits of economic interest because, although SCC are generally used as an indirect indicator of udder health, it should be remembered that evidence has been reported that the pattern of SCC can change with the pathogen causing mastitis (de Haas et al., 2002), and that genetic correlations with SCC and with mastitis are not always comparable, i.e. genetic correlation with production yields (Chapter 5). It is therefore of importance to consider that SCC analysis would be enhanced and completed using direct data on mastitis incidence, when available, and that these data would also be useful to monitor cow immunity and udder health.

Breeding value estimations for SCC

Heritability estimates

Values of SCC heritabilities for Italian Holstein Frisian were estimated in this thesis using different models and data sets. Values obtained ranged from .06 to .25 depending on area considered and on model of analysis used (Table 1). Heritability obtained with a test-day repeatability model resulted in lower values (Chapter 2) than using a lactation model (Chapters 6 and 7) or a random regression test-day model (Chapter 6). Factors affecting differences in estimates in the models can be summarised based on the amount of residual variance estimated and the precision of environmental factors definition. Model of analysis based on test days considers single measures and leads therefore to higher estimates of residual variances and, by consequence to smaller heritability values. When measures are

averaged along the lactation the residual variance estimated is smaller, and the heritability larger relative to in single test-day analysis. Moreover, the test day data are affected by factors such as breed, geographical area, herd management, weather conditions, lactation number, age at calving, month of calving, days in milk, pregnancy status, medical treatments and milking times per day. In lactation models, test days are averaged assuming that factors affecting each test day are the same. While models based on test days data can account for short-term and systematic environmental effects specific of each test day, especially with the inclusion of herd-test date effect (Ptak and Schaeffer, 1993). And a further extension of test-day models was the random regression test-day model, accounting for random regression coefficients specific for each animals (Shaeffer and Dekkers, 1994). The amount of environmental and residual variance estimated is therefore different for each model, influencing, by consequence, the value of heritability resulting. Higher heritabilities were found with lactation average measures than with test-day measures (Heuven et al., 1988) and lower values were found in Finnish Ayrshire (Pösö et al., 1997) for heritabilities estimated with a test-day model (.08) than estimates with a geometrical lactation average (.13). In contrast, when accounting for random regression coefficients, higher heritabilities resulted for Canadian Holstein estimated with a random regression test-day model (Samoré et al., 2002) if compared to a test-day repeatability model (Reents et al., 1995).

Table 1. Values of SCC heritabilities for Italian Holstein Frisian estimated in this thesis from lactation average values or test day and using different model.

Measure	**Lactation**			**Model**[a]	**Chapter**
	1st	**2nd**	**3rd**		
Lactation average	.14			MT SCC-type	7
	.18	.21	.21	MT 3 lactations SCC	6
Test day	.06-.09			TD Repeatability	2
	.15	.19	.25	TD RR	6

[a]MT = multiple trait model, TD = test-day model, RR = random regression model.

Estimated trends of heritabilities over lactation number in literature are inconsistent. Some found an increase in values in second and third lactation (Coffey et al., 1985), while others found a decrease in later parities (Monardes et al., 1984; Banos and Shook, 1990). In

Italian Holsteins, heritability seems to slightly increase with lactation number, both when using a lactation average (Chapter 7) and when using a random regression test-day model (Chapter 6).

The definition of heritability value to be used in selection depends on the model of analysis used for breeding values estimation. The final aim of selection is the correct estimation of breeding values, as the best measure of genetic values of animals, and the accuracy of the model chosen is the most important parameter to consider, more important than the absolute value of heritability. In Italian Holstein Friesian, SCC breeding values are now estimated using a test-day repeatability model and the heritability used is .08, a value between .06 and .09 (Chapter 2). If the model of analysis will be changed, e.g. to a random regression test day, the heritability should be updated according to the new model. According to this statement, the main difference now existing between heritabilities, used in different countries for SCC, depends in fact from the models of analysis used (Mark et al., 2002).

Breeding value estimation for SCC in Italian Holstein

Estimation of breeding values for SCC was first officially published for Italian Holsteins in November 2001 according to the test-day repeatability model on first parity cows described in Chapter 3. The model does not include the sire by herd effect because the estimated proportion of variance explained by this effect was small (Chapter 2). This result was in agreement with literature estimates and suggested that this interaction effect will have a negligible effect on breeding value estimations for SCC and that it can be ignored in a national genetic evaluation.

Genetic evaluations for all traits, including SCC, are calculated and published every three months. The number of test days available increased over time (Table 2) and corresponded to about 7.1 test day per cow. In order to safeguard reliability of breeding values estimation, data are published only for bulls having at least 10 daughters in 5 herds corresponding to an approximated reliability of proofs of 67%. Genetic evaluation aims to identify bulls that regularly have daughters more prone to mastitis. Breeding values were defined relative to a genetic base and expressed on a standardised scale. In the November 2002 genetic evaluation release, each unit of the scale corresponded to .39 SCS. All values were set to positive numbers and the sign of indexes was changed in order that higher values corresponded to increased resistance to mastitis and lower values corresponded to an

unfavourable effect. The first breeding value release showed a range from 0 to 12, but starting from February 2002, the scale was compressed in order to reduce variability of estimated breeding values of bulls and to a range comparable to other functional traits in Italy. After these transformations, bulls breeding values varied in November 2002 from 0 to +8 (Table 2).

Table 2. Data describing breeding value estimations for SCC in Italian Holstein Friesian: number of first parity test day (# TD), number of cows with data, number of bulls estimated breeding values (EBV) published and range of EBV.

Evaluation	# TD	cows with TD	bulls EBV[a]	EBV[b]
November 2001	10,584,724	1,491,920	4,547	0-12 (6)[c]
February 2002	11,070,288	1,565,202	4,785	0-8 (4)
May 2002	11,576,911	1,639,732	4,934	0-8 (4)
August 2002	12,133,892	1,708,372	5,074	0-8 (4)
November 2002	12,533,666	1,757,465	5,192	0-8 (4)

[a] bulls officially published with at least 10 daughters in 5 herds.

[b] low EBV= unfavourable; high EBV= favourable; average within parenthesis.

[c] standardisation factors changed in February 2002

Models used for SCC genetic evaluations largely differ between countries (Mark et al., 2002) between sire models (e.g Sweden) and animal models (e.g. Finland), between single trait (e.g. Germany) and multiple trait analyses (e.g. Denmark), and from lactation average based (e.g. France), to test-day repeatability (e.g. Estonia), and to random regression test-day models (e.g. Canada). When compared to models used for production genetic evaluation, differences for SCC seem to be larger, indicating that there is not a general agreement on the best model to be used for SCC breeding value estimation. The model now used in Italy for Holstein Friesians is a test-day repeatability model based on first parity data (Chapter 3). A multiple trait random regression test-day model for SCC and production is under study (Chapter 6), and it will be probably adopted for breeding value estimation starting from the end of 2003. This model would have the advantage of accounting for random regression coefficients specific for each animal, and of jointly evaluating four traits (milk, fat and protein yields and SCC) accounting for all genetic correlations, and their trends between and within lactations (Chapter 5).

Practical application of SCC breeding values

After the first release in November 2001, results of SCC breeding values were used to produce several genetic and management services for breeders. First SCC breeding values were included into the new selection index (PFT) including fat and protein, as contents and yields, general type, udder composite index, functional longevity, feet and legs, and SCC (Biffani et al., 2002). The introduction of this new selection index, substituting the previous index (ILQM) (Rozzi, 1989), aimed to improve both milk quality and cow functionality. With the inclusion of SCC breeding values in the PFT, SCC genetic evaluations also contribute now to the choice of bulls in the sire-advising programme, a service for selection of artificial insemination bulls and individual mating of heifers and cows provided by ANAFI to breeders (Samoré et al., 1999). A list of bulls, which maximises the objective, given the pre-chosen limits, is suggested to the farmer. At this stage SCC breeding value is considered through the accounting of PFT index. Then, in a second stage, the program proposes the distribution of semen for individual matings of heifers and cows. At present, individual SCC genetic evaluation are not accounted for because of the low reliability of cow indexes, but further improvements are under study to evaluate how to account for SCC. Another service is provided by ANAFI to breeders, aiming to analyse genetic and environmental levels and trends at farm level and to compare them to regional and national situations. At present the analysis concentrates on production, reproduction and morphological traits. Analyses have started to include SCC figures in that service.

The udder health index

Genetic correlations between SCC and udder conformation traits

Udder conformation traits were favourably genetically correlated with lactation averages of SCC (Chapter 7). A higher udder, strongly attached to the fore abdominal wall, and with short teats was genetically related to smaller values of SCC according to previous literature results (Seykora and McDaniel, 1986; Rogers et al., 1991; Boettcher et al., 1998; Rupp and Boichard, 1999). A strong positive genetic correlation, associating narrow rear udder width with small values of SCC was found in Chapter 7, while literature reported a wide range of genetic correlations (Rogers et al., 1991), or almost null correlations (Boettcher et al., 1998) between rear udder width and SCC. The controversial results can probably be explained by

the non-linear relationship between breeding values for rear udder width and for SCC. A flat trend was detected for low levels of rear udder width genetic values, a positive trend for medium breeding values, and a flat trend again for high breeding value classes (Chapter 7). This could have lead to the apparent positive genetic correlation in Italian Holstein Friesian. Udder traits are generally selected to increased the ease of handling with milking of cows and to indirectly contribute to milk production selection. From that point of view, increased rear udder width is thus selected for because larger udders are associated with increased production. Despite the moderately high correlation with SCC, rear udder width was not considered for inclusion in an Italian udder health index. The other udder conformation traits had only small genetic relationships with SCC (Chapter 7).

Genetic correlation between SCC and milking speed

Genetic correlation between SCC and milking speed was estimated in this thesis as approximate correlation based on breeding value estimations for the two traits (Chapter 7). The poor data available in Italian Holstein Friesian did not allow better analyses because they are based on farmer indications of cows requiring more milking time when compared to the herd average. From that analysis, fast milking was slightly associated to higher SCC level (.09). Literature reports in contrast stronger genetic correlations ranging from .18 to .57 (Seykora and McDaniell, 1986; Lund et al., 1994; Luttinen and Juga, 1997; Boettcher et al., 1998, Rupp and Boichard, 1999). But, similarly to rear udder width, a non-linear relationship was detected between SCC and milking speed. Based on data now available, the only possible suggestion for inclusion in udder health index is the setting of a threshold value slightly penalising fast milking cows. The eventual availability of more complete data, perhaps accounting for the exact milking speed using a chronometer, is expected in order to allow a better estimation of the genetic relationship between milking speed and SCC in Italian Holstein Friesian population.

A proposal for an udder health index

According to the suggestion of Rogers et al. (1991), an udder health index including SCC, fore udder attachment (FUA), and udder depth (UDD) was proposed for Italian Holsteins cows to select for mastitis resistance with the following formula: UHI = -15 EBV_{SCC} + 1.5 EBV_{FUA} + 0.15 EBV_{UDD}, where EBV are the estimated breeding values.

Similar indexes were reported in literature (De Jong and Lansbergen, 1996; Boettcher et al., 1998; Rupp and Boichard, 1999). The composite index is expected to give higher selection response for mastitis resistance when compared to selection using single indirect measures for mastitis incidence (De Jong and Lansbergen, 1996). Selection for increased udder health in Italian Holstein should be therefore for lower values of SCC, higher (less deep) and tightly attached fore udder. This would result in 94% of the genetic response obtained with the direct trait of mastitis resistance (Chapter 7).

Milking speed is not considered in the udder health index. Data collected only record the number of slow milking cows based on farmer observation. Moreover the non-linear genetic relationship detected between SCC and milking speed (Chapter 7) suggests the importance of more accurate analyses of genetic relationships between milking speed and the direct trait of mastitis incidence, with the implementation of a more precise data recording. Moreover, if the non-linear relationship estimated would be confirmed also for mastitis resistance, the best way to consider milking speed in an aggregated selection would be by setting a threshold value penalising fast milking cows.

Udder health in a breeding program

Genetic and phenotypic trends for SCC in Italy

Genetic and phenotypic trends in Italian Holstein Friesian population are reported in Figure 1. Data used concerned more than 1,700,000 cows from all areas of Italy and were used in the November 2002 release of breeding values. Direct genetic selection for SCC only started in Italy in November 2001, with the first release of genetic evaluations. Nevertheless, the genetic trend was favourable, i.e. a decreasing trend from 1990 to 2000, as the results of two different indirect genetic selections on SCC. First, the strong weight given to the udder composite index (ICM) in the Holstein Friesian selection index (ILQM) (Rozzi, 1989) probably resulted in a favourable indirect effect in SCC genetic level due to the favourable genetic correlations between SCC and udder linear traits (Chapter 7). Second, selection for yields traits in Italy was based on multiple parity records and this may have contributed to the decline in the genetic level of SCC due to the favourable genetic correlations between SCC and production in later parities (Chapter 6). In contrast, the phenotypic trend was almost stable, and that happened although the milk price quality

regulation and regional policies introduced in Italy around 1990 should have increased breeders attention to environmental factors causing mastitis. The same trend, analysed in Chapter 3, resulted to be slightly favourable. That first analysis was limited to part of SCC data, mainly collected in few regions of Italy where probably breeders and regional selection policy attention to udder health problems has been more effective. Moreover, strong differences in milk price definitions, also with regards to milk quality, exist in Italy depending on areas and milk destination.

A favourable genetic trend, as reported in Figure 1, would suggest that the calculation of breeding values for SCC may be not necessary for Italian Holstein Friesian. But, it should be remembered that, although the genetic trend for SCC is favourable, and the genetic correlations between yields and SCC is not highly unfavourable, more strongly antagonistic correlations have been reported between yield and clinical mastitis (Pösö and Mäntysaari, 1996; Rupp and Boichard, 1999) than between yield and SCC. Direct genetic correlations between mastitis incidence and production are not available for Italian situation, but other results suggest that the genetic selection for SCC with breeding value estimations for this trait, and its inclusion with a negative weight in a selection index, can therefore contribute to counteract the increase in mastitis incidence that would be caused by selection on yields.

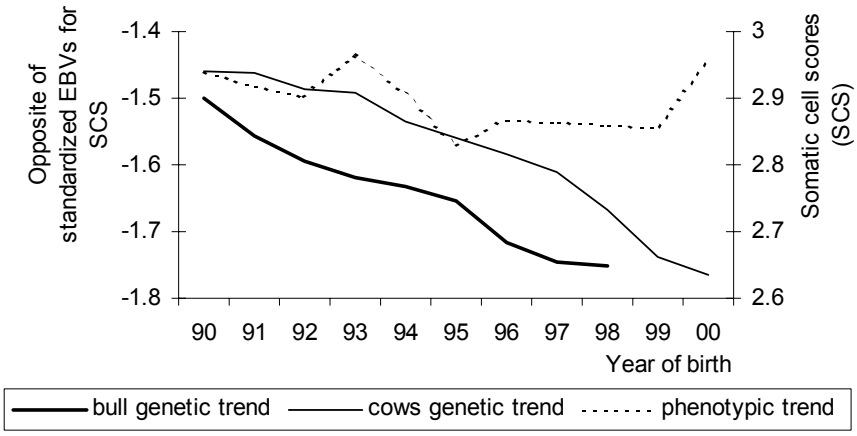

Figure 1. Genetic and phenotypic trend of SCS in Italian Holstein Friesian – November 2002.

Genetic correlations between SCC and production traits

Literature reports different values for genetic correlations between production traits and SCC (for a review Mrode and Swanson, 1996). But, apart from Coffey et al. (1986), who reported negative and favourable genetic correlations, most studies resulted in unfavourable genetic correlations (i.e. high milk associated with high level of SCC). Several different values of genetic correlations were estimated in this thesis (Table 3). Chapter 6 reports the estimates of genetic correlation between SCC and protein obtained using various models of analysis. Favourable correlations were found when approximating genetic correlations from estimated breeding values correlations, and antagonistic relationships were calculated using 305 days information. Estimates obtained using a random regression test-day model resulted in values near zero or slightly unfavourable in first lactation, especially in early lactation, and near zero or favourable in later lactation. Moreover a trend in genetic correlation over days in milk, within lactation, was observed, with sometimes a change in sign. Results from milk and fat yield were very similar to those for protein (Table 3). This apparent complexity of the genetic factors controlling SCC, would require accounting for dynamics of genetic correlations between SCC and production yields in different parities and within parity. The application of a random regression test-day model for breeding value estimation offers the opportunity to incorporate the covariance trends between and within lactation. Comparable trends of genetic correlations over days in milk within lactation were recently reported by Haile-Mariam et al. (2002) supporting the conclusion that the genetic relationship between production and SCC changes during lactation and with lactation number.

Table 3. Values of genetic correlations between SCC and production traits for Italian Holstein Frisian estimated in this thesis.

Model	Lactation			Trait	Chapter
	1st	2nd	3rd		
Calo's corr between EBV[a]	.22[b]			Milk kg	6
	.24[b]			Fat kg	
	.24[b]			Protein kg	
Lactation model (305d)	.31	.01	.09	Protein kg	6
RR TD model MT (TD)	-.02	-.16	-.14	Milk kg	5
	-.04	-.14	-.12	Fat kg	5
	-.02	-.14	-.14	Protein kg	5

[a] EBV=estimated breeding values

[b] The sign of SCC EBV is reverted and therefore a positive correlation indicates a favourable association.

Genetic improvement in a dairy cattle population depends largely on bull selection, as both sires of bulls and sires of cows. In the Italian Holstein Friesian population, young bulls are considered to be proven when they have information on lactations of at least 20 daughters in 20 different herds for production and 10 daughters in 5 herds for SCC. This means that the first proof of a bull is based on first parity information both for production and SCC. Later on, bull information is increasing with more first parity lactations and with later parities lactations. This accumulation of data increases the reliability of estimated breeding values and can change the absolute genetic value of a bull and, by consequence its rank. In Italy, bulls can be used as sire of bulls if they have a genetic value in the top 1% of the whole list of bulls, and in the top 5% for sire of cows. Information on later lactations will therefore also contribute to the estimation of genetic values, and to the rank position. Nevertheless, the availability of these data, in a significant relative percentage when compared to first parity yields, would happen later when a bull is already used as sire in the population and, generally, only slightly influences its first parity proof. This means that most of bull selection choices are based on first parity data and that, by consequence, the identification of correct genetic correlation between SCC and production should mainly be based on first parity data. First parity data are also not selected for mastitis while later parities only includes selected animals that survived the first parity culling.

Moreover, according to results reported in Chapter 5, there is a trend in genetic correlations also within first lactation. Genetic correlations between SCC and production are generally unfavourable at the beginning of lactation and change to favourable at 165 days in milk. Averaging estimates for all days in milk, genetic correlation in first parity resulted to be –.02, and therefore in a value near zero. According to these results, and to the analysis of bull selection dynamics, probably the best value to be used in defining the selection index for Italian Holstein Friesian population should be a null genetic correlation between production and SCC. This value would thus be different from most of the genetic correlations reported in previous studies, which tend to be unfavourable (Mrode and Swanson, 1996).

Genetic correlations between SCC and functional longevity

Using an hazard model, an increase in phenotypic level of SCC in Italian Holstein cows resulted in an increased rate of culling as the result of two joint effects (Chapter 4). First, the increase in SCC phenotypic level is usually a signal of clinical or sub-clinical udder infection. Second, milk pricing policies penalises high SCC and therefore breeders cull cows with elevated SCC. The approximate genetic correlation between SCC and functional longevity was estimated to be .31 (Chapter 4) associating unfavourable values of SCC with poorer longevity. This supports the antagonistic relationships between SCC and longevity reported in literature (Nielsen and Pedersen, 1995; Mrode et al., 2000; Roxtröm and Strandberg, 2002). From these results it can be concluded that selection for longevity is also connected to an indirect selection on SCC level, if this trait is not included in the hazard model. Functional longevity includes all information connected to the length of life of a cow not accounting for production level. It should therefore also consider the culling due to SCC level, as an indirect measure of mastitis or as milk quality parameter. Based on this statement, now the inclusion of SCC phenotypic level in the hazard model for longevity is not expected. At the moment of the inclusion of both SCC and functional longevity in a selection index precaution would be necessary in order not to give extra emphasis to SCC level, and, indirectly, to mastitis incidence.

As previously pointed out, functional longevity should be a measure of possibility of life of a cow not considering voluntary culling connected with production level. The way of accounting for production level is therefore of primary importance in a longevity model definition. Now, in Italy, the hazard model for longevity breeding values includes

information on 305 days production level (Schneider et al., 2000) and a previous analysis considered the average lactation production (Schneider and Miglior, 1999). Chapter 4 considered milk production using the peak of lactation assuming that this measure is a better indicator of voluntary culling because the culling decision is usually taken after the period of maximum of production and production after the peak depends also on pregnancy and health status. The other measure of production level does not account for the fact that cows culled at the end of lactation are often not inseminated and, therefore, have a smaller deviation from their contemporaries than would have been expected if they had been pregnant (Roxström and Strandberg, 2002). Based on that assumption, a re-consideration of the way how to account for production level in the hazard model for Italian Holstein Friesian population is suggested for the future in order to improve genetic evaluations of functional longevity.

Udder health and the general selection index

The selection index (PFT) now used in Italy for Italian Holstein includes direct breeding values for the following traits, with their relative emphasis (Biffani et al., 2002): fat kg (12%), protein kg (42%), fat % (2%), protein % (3%), type (4%), and SCC (10%). Moreover three sub-indexes are included: udder composite index, ICM (13%), functional feet and legs (6%), and functional longevity (8%). The composite udder index receives a large importance in the selection index and includes the following linear traits: udder depth (26%), ligament (21%), fore udder attachment (19%), rear udder height (17%), and teat placement (17%). Moreover the combined index for longevity also accounts for udder traits, as the result of a MACE procedure (Schaeffer et al., 1994), considering direct survival estimates of longevity and indirect information on udder traits (ICM) and functional feet and legs (IAP). A strong emphasis is therefore given to udder traits in the selection index (PFT). The favourable genetic correlations of SCC with these traits (Chapter 7), and with the udder composite index (42%), would suggest that selection is already partially for an improved udder health. The udder composite index (ICM) includes more traits (5) than the proposed udder health index. Its aim is the selection both for improved workability and increased functional longevity, while the final aim of an udder health index is to improve mastitis resistance aggregating indirect measures (SCC and morphology traits). To include udder health information in the selection index, the single breeding value for SCC should be replaced with the proposed composite index for udder health. The new index should be

based on the desired economic weight, accounting for the genetic and phenotypic correlations between all traits in the index. Including the udder health index, the weight attributed to udder type traits should therefore be reconsidered in order to avoid double counting.

Selection for improved udder health is of primary importance in dairy cattle populations (INTERBULL, 1999) and it is now included in selection index in most countries (VanRaden, 2002). The strongest emphasis to udder health is given in Scandinavian countries with the joint use of direct mastitis incidence and SCC in Denmark, Finland and Sweden (Heringstad et al., 2000; Pedersen et al., 2002), while Norway only uses information on clinical mastitis (Heringstad et al., 2000; Swendsen and A.-Ranberg, 2000). Other countries in the world select for udder health using indirect measures such as SCC, udder conformation and longevity. Generally it is possible to distinguish between two main selection policies: European and American. In Europe, most countries attribute a relative weight to udder health, in the selection index, larger than 10%, when considering SCC and udder conformation. In France 13% is attributed to SCC (Institut de l'Elevage, 2002), in Italy 10% is given to SCC and 13% to udder conformation composite index (Biffani et al., 2002), and in Netherlands udder health receives 11% of weight in the selection index (De Jong and Harbers, 2001). Germany recently reduced the relative weight attributed to SCC in the selection index from 14 to 5% (Rensing et al., 2002), but increased the emphasis given to longevity that indirectly partly account for culling due to mastitis. In contrast, in American countries, SCC only receives a relative weight of 5% in the selection index. In the United States 5% is attributed to SCC, 11% to productive life, and 10% to udder composite (Holstein Association USA, 2002). In Canada 5% is attributed to udder health, and 38% to durability including a large number of aspects as herd life, mammary system, feet and legs and capacity information (Van Doormal, 2001).

General conclusions

The value of SCC can be efficiently used to indirectly select for mastitis resistance in a population without direct recording of mastitis incidence. In Italy, SCC data were collected from 1989 and were available for estimation of breeding values. A test-day repeatability model on first parity SCC data (as described in Chapter 3) is used for breeding value estimation since November 2001 in order to identify bulls that regularly have daughters susceptible to mastitis. Data were analysed as single test days considering a correlation of one between subsequent observations and a constant variance for all observations (Chapter 3). To allow individual variation along the lactation, the implementation of a multiple trait random regression test-day model for Italian Holstein cows is under study, both for production and for SCC traits (Chapter 5 and 6).

Large differences existed between values of heritabilities estimated depending on model of analysis used. Genetic relationship between SCC and production resulted in different values depending on parities and model of analysis. Because of the apparent complexity of the genetic factors controlling SCC, in theory one may need to account for different levels and signs of genetic correlations between SCC and production yields in different parities and, if possible, also within parity. Considering the dynamic of selection and the pattern of genetic correlation, the best value to consider for genetic correlation between production and SCC in Italy is a value near zero, and not an unfavourable relationship as previously suggested in literature. The genetic relationship between udder conformation traits and SCC generally resulted in favourable direction suggesting the opportunity of aggregating morphological traits breeding values, with SCC breeding values, into a composite udder health index (Chapter 7). A selection for lower values of SCC, for less deeply and strongly attached front udders should result in higher mastitis resistance. The inclusion of milking speed in the index now is not anticipated because of the low reliability of data collection (Chapter 7).

The interest in SCC breeding values increased over time leading to its inclusion in the new selection index (PFT) of Italian Holsteins in November 2001 (Biffani et al., 2002). The new selection index aims to improve the population for production quality and functional traits. When compared to the previous index (ILQM), greater emphasis was given to cow functionality through the inclusion of SCC, longevity, feet and legs, in addition to udder morphological traits. Genetic correlations with SCC used in its definition were based on literature values because not yet estimated for Italian Holstein cows. Parameters for the

Italian Holstein population have been estimated in this thesis and can be considered for improvement of selection policy. The proposed udder health index could be included in the selection index. It would replace breeding values for SCC in the index and weights attributed to udder conformation traits would be re-evaluated in order to avoid double counting.

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Summary

Somatic cells can be used as a good indirect measure to select for mastitis resistance, especially when direct measure of mastitis incidence is not recorded. Final aim of this thesis was to evaluate how to include somatic cell counts (SCC) in Italian Holstein Friesian selection criteria through the evaluation of its genetic aspects. Heritability was estimated using different models and data sets and the association of SCC with other traits in selection objectives was evaluated through the estimation of genetic correlations with production, udder conformation, functional longevity, and milking speed. Breeding value estimation for SCC was performed using a test day repeatability model and SCC was included in the selection index. Finally an udder health index aggregating SCC and some udder conformation traits was proposed.

Genetic parameters

Table 1 summarizes values of heritabilities estimated and reported in this thesis in different chapters. Values largely differed (from .06 to .21) depending on model of analysis, data set considered and parity. Second and third parities resulted in larger heritabilities (.19 to .25) than first parity. The smallest values of heritability were estimated with a test-day repeatability model (.06-.09) in first parity data. The appropriate value of heritability to be used in breeding value estimation depends on the model of analysis considered.

Table 1. Values of SCC heritabilities for Italian Holstein Frisian estimated from lactation average values or test day records and using different model.

Measure	**Lactation**			**Model[a]**	**Chapter**
	1st	**2nd**	**3rd**		
Lactation average	.14			MT SCC-type	7
	.18	.21	.21	MT 3 lactations SCC	6
Test day	.06-.09			TD Repeatability	2
	.15	.19	.25	TD RR	6

[a]MT = multiple trait model, TD = test-day model, RR = random regression model.

The genetic association between SCC and production was deeply analysed in Chapters 5 and 6 (Table 2). Genetic correlations differed in sign and values depending on parities and model of analysis used. An apparent complexity of the genetic factors controlling SCC was detected suggesting that the dynamics of genetic correlations between SCC and production in different parities and within parity should be accounted for. Moreover it was concluded that, when a unique value of correlation for all parities and days in milk within parities must be used, the genetic association between SCC and production may be considered near zero in Italian Holstein, and not an unfavourable relationship as previously suggested in literature.

Table 2. Values of genetic correlations between SCC and production traits for Italian Holstein Frisian estimated in this thesis.

Model	**Lactation**			**Trait**	**Chapter**
	1st	**2nd**	**3rd**		
Calo's corr between EBV[a]	.22[b]			Milk kg	6
	.24[b]			Fat kg	
	.24[b]			Protein kg	
Lactation model (305d)	.31	.01	.09	Protein kg	6
RR TD model MT (TD)	-.02	-.16	-.14	Milk kg	5
	-.04	-.14	-.12	Fat kg	5
	-.02	-.14	-.14	Protein kg	5

[a] EBV=estimated breeding values

[b] The sign of SCC EBV is reverted and therefore a positive correlation indicates a favourable association.

Udder conformation traits were favourably genetically correlated with lactation averages of SCC (Chapter 7): a higher udder, strongly attached to the fore abdominal wall, and with short teats was genetically related to smaller values of SCC. A strong positive genetic correlation, associating narrow rear udder width with small values of SCC was found (Chapter 7) with a controversial result from literature estimates. A non-linear relationship was detected between breeding values for rear udder width and SCC. This may explain the apparent positive correlation found here.

Poor data for milking speed were available because information recorded were based on farmer indications. Therefore the genetic correlation between SCC and milking speed was estimated (Chapter 7) as approximate correlation based on breeding value estimations for the two traits. The correlation between milking speed and SCC had a value of .09, slightly associating fast milking cows with higher SCC. But, similarly to rear udder width, a non-linear relationship was detected between SCC and milking speed.

Using an hazard model (Chapter 4), an increase in phenotypic level of SCC in Italian Holstein cows resulted in an increased rate of culling. An approximate genetic correlation between SCC and functional longevity of .31 was estimated associating unfavourable values of SCC to poorer longevity.

Breeding value estimation

A test day repeatability model for breeding value estimations of first parity SCC was set up (Chapter 3). Model included fixed effects of herd-test date, age of calving by month of calving, and days in milk. Genetic parameters for this model were those estimated in this thesis and exposed in Chapter 2. Genetic evaluation aims to identify bulls that regularly have daughters more prone to mastitis. Several routine evaluations have already been performed using this model.

A test day random regression model, allowing individual variation along the lactation, both for production and for SCC traits, for three lactations, is under evaluations and it will probably be officially adopted from 2004. Genetic parameters to be used with this model were estimated in Chapter 5 and 6 and were compared with Canadian results obtained with the same model of analysis.

Genetic correlations with SCC used in the definition of the overall selection index of Italian Holstein Friesian were based on literature. Parameters for the Italian Holstein population have been estimated in this thesis and can be now considered for improvement of selection policy. Furthermore an udder health index, including SCC and some udder conformation traits, was proposed in Chapter 7, and its inclusion in the selection index, substituting the SCC value, was discussed in Chapter 8. The udder health index would include SCC, udder depth, and fore udder attachment. The inclusion of milking speed in the index now is not considered because of the low reliability of data collection (Chapter 7).

Riassunto

Il livello di concentrazione di cellule somatiche nel latte è strettamente legato alla salute della mammella e può essere considerato un buon indicatore dell'incidenza delle mastiti sia cliniche sia sub-cliniche. Obiettivo di questa tesi è stata la stima dei parametri genetici delle cellule somatiche nella Frisona Italiana al fine di inserire tale carattere tra i criteri di selezione. In una prima fase sono state stimate l'ereditabilità e le correlazioni genetiche con tutti i caratteri oggetto di selezione. Quindi, con i parametri genetici stimati, è stato possibile definire un modello di valutazione genetica e considerare l'inclusione delle cellule nell'indice di selezione nazionale. Infine è stato proposto un indice genetico per la salute della mammella che aggreghi le cellule somatiche ad alcuni caratteri morfologici lineari.

Stima dei parametri genetici

Nella tabella 1 sono riassunti i valori di ereditabilità stimati nella tesi e riportati nei diversi capitoli. I valori ottenuti sono molto variabili (da 0,06 a 0,21) a seconda del modello di analisi, dell'archivio di dati e dell'ordine di parto considerati.

Tabella 1. Valori di ereditabilità delle cellule somatiche nella Frisona Italiana stimati in questa tesi utilizzando diversi modelli di analisi.

Misura	**Lattazione**			**Modello di analisi**[a]	**Capitolo**
	1st	**2nd**	**3rd**		
Media di lattazione	.14			MT SCC-type	7
	.18	.21	.21	MT 3 lactations SCC	6
Singoli controlli	.06-.09			TD Repeatability	2
	.15	.19	.25	TD RR	6

[a]MT = modello di tipo multiple trait, TD = modello basato sui singoli controlli, RR = modello di tipo random regression model.

Le cellule somatiche in bovine in seconda e terza lattazione, generalmente, hanno una ereditabilità maggiore (0,19 e 0,25) rispetto alla prima lattazione e i valori più bassi di ereditabilità sono stati stimati per la prima lattazione con il modello cosiddetto test-day repeatability (da 0,06 a 0,29), cioè quel modello che utilizza i singoli controlli e che considera una correlazione pari a 1 tra osservazioni successive e una varianza costante per

tutte le osservazioni. Molti sono i valori di ereditabilità ottenuti ma il valore corretto da utilizzare dipende dal modello di analisi adottato.

Il grado di associazione genetica tra cellule somatiche e produzione è stato oggetto di approfondite analisi nei capitoli 5 e 6 (Tabella 2). Le correlazioni genetiche ottenute variano profondamente per segno ed entità a seconda dell'ordine di parto a cui sono riferite e del modello di analisi considerato. In particolare le correlazioni variano sia tra lattazioni successive sia all'interno della stessa lattazione. In base a questo risultato sarebbe quindi importante tenere conto dell'andamento delle correlazioni genetiche tra cellule somatiche e produzione in tutte le fasi della selezione. Nel caso in cui sia necessario disporre di un solo valore di associazione genetica tra produzione e cellule per la Frisona Italiana, considerando le dinamiche selettive della razza per la scelta dei riproduttori, la correlazione genetica da utilizzare dovrebbe essere vicina allo zero e non una correlazione sfavorevole come suggerito in letteratura.

Tabella 2. Valori di correlazione genetica tra cellule somatiche e caratteri produttivi nella Frisona Italiana, stimati in questa tesi.

Modello di analisi	**Lattazione**			**Carattere**	**Capitolo**
	1st	**2nd**	**3rd**		
Correlazioni di Calo tra IG[a]	.22[b]			Latte kg	6
	.24[b]			Grasso kg	
	.24[b]			Proteina kg	
Modello a lattazione (305gg)	.31	.01	.09	Proteina kg	6
Modello RR TD MT	-.02	-.16	-.14	Latte kg	5
	-.04	-.14	-.12	Grasso kg	5
	-.02	-.14	-.14	Proteina kg	5

[a] IG=indici genetici

[b] Il segno degli indici genetici delle cellule somatiche è invertito e quindi una correlazione positiva indica una favorevole associazione.

I caratteri morfologici lineari della mammella, ora selezionati nella Frisona Italiana, risultano avere correlazioni favorevoli con le cellule somatiche (Capitolo 7). Una mammella più profonda, saldamente attaccata alla parte anteriore della parete addominale e con capezzoli corti é associata geneticamente a minori cellule somatiche. La larghezza posteriore della mammella risulta avere, nella Frisona Italiana, una forte correlazione genetica con minori livelli di cellule somatiche. I risultati riportati in letteratura per questo

carattere sono tuttavia variabili. Inoltre il legame tra gli indici genetici dei tori per la larghezza posteriore della mammella e gli indici per le cellule somatiche risulta di tipo non-lineare. Ciò spiegherebbe l'apparente correlazione positiva ottenuta.

I dati per la velocità di mungitura vengono raccolti per la Frisona Italiana solo in base alle indicazioni degli allevatori che segnalano le vacche lente in mungitura rispetto alla media di stalla. Con i dati a disposizione è stato quindi possibile stimare le correlazioni genetiche tra cellule somatiche e velocità di mungitura solo come correlazione tra gli indici genetici (Capitolo 7) ottenendo un valore pari a 0,09. In base a questo risultato le vacche più veloci in mungitura sarebbero associate a maggiori livelli di cellule somatiche. Tuttavia, come già rivelato per la larghezza posteriore della mammella, anche in questo caso è stata individuata una relazione con le cellule somatiche di tipo non-lineare che toglierebbe significato alla correlazione genetica.

Il legame tra cellule somatiche e longevità funzionale nella Frisona Italiana è stato stimato nel Capitolo 4 con un modello di tipo hazard model. Valori fenotipici maggiori per le cellule somatiche risulterebbero associati ad un maggiore tasso di rimonta e la correlazione genetica tra cellule somatiche e longevità funzionale risulterebbe pari a 0,31, cioè una peggiore longevità sarebbe associata a maggiori livelli di cellule somatiche.

Indici genetici

Utilizzando i valori di ereditabilità e ripetibilità stimati nel capitolo 2, è stato definito un modello di valutazione genetica per le cellule somatiche di tipo test-day repeatability model. I dati utilizzati sono i singoli controlli delle primipare e nel modello di analisi i controlli successivi vengono considerati come misure ripetute dello stesso carattere. I fattori fissi considerati sono l'allevamento-giorno di controllo, l'età al parto, il mese di parto e i giorni di lattazione. Gli indici genetici per le cellule hanno l'obiettivo di individuare i tori che regolarmente hanno figlie più sensibili alle infezioni mammarie.

Questo modello è attualmente in uso per le valutazioni genetiche ufficiali delle cellule somatiche anche se è già allo studio una valutazione genetica basata sui singoli controlli di tipo random regression model. La nuova valutazione genetica considererebbe

congiuntamente sia la concentrazione di cellule somatiche sia i caratteri produttivi: latte, grasso e proteina. Questo modello sarà probabilmente adottato nel 2004 e, a differenza di quello ora ufficiale, considererà l'esistenza di variazioni individuali lungo la lattazione e comprenderà le tre lattazioni. Nei capitoli 5 e 6 sono stati stimati i parametri genetici da utilizzare con il modello test-day random regression model e i risultati sono stati confrontati con quelli ottenuti per la popolazione canadese con lo stesso modello di analisi.

Le correlazioni genetiche con le cellule somatiche utilizzate nella definizione del nuovo indice di selezione nazionale sono state ricavate dalla letteratura. Ora potranno essere utilizzati i parametri di correlazione genetica stimati in questa tesi. Aggregando le cellule somatiche, la profondità della mammella e l'attacco anteriore della mammella, è stato inoltre proposto un indice di selezione per la salute della mammella (Capitolo 7). Questo indice potrebbe essere incluso nell'indice di selezione (Capitolo 8) al posto del singolo valore relativo alle cellule somatiche. La velocità di mungitura non è stata considerata tra i caratteri da includere nell'indice per la salute della mammella a causa della sua associazione non-lineare con le cellule somatiche (Capitolo 7).

Samenvatting

Somatische cellen kunnen gebruikt worden als een goede, indirekte parameter om te selecteren voor mastitis resistentie, vooral in die gevallen waar mastitis niet direkt geregistreerd wordt. Het uiteindelijke doel van dit proefschrift was karakterisering van de genetische aspecten van het somatische cel getal (SCC) om te beoordelen of SCC gebruikt kan worden bij selectie van Italian Holstein Friesian. Erfelijkheidsgraden zijn geschat met behulp van verschillende modellen en datasets en het verband tussen SCC en andere selectiekenmerken is onderzocht. Genetische correlaties met produktie, uier-kenmerken, functionele levensduur en melksnelheid zijn geschat. Fokwaardeschatting voor SCC is uitgevoerd met behulp van een 'test-day repeatability' model en SCC was opgenomen in de selectie-index. Tenslotte is een uiergezondheidsindex die SCC en andere uierkenmerken samenvoegt voorgesteld.

Genetische parameters

Tabel 1 geeft erfelijkheidsgraden weer die in de verschillende hoofdstukken van dit proefschrift geschat zijn. Afhankelijk van het gebruikte model, dataset en pariteit, liepen de waarden sterk uiteen (van .06 tot .21). Tweede en derde pariteit gaven hogere erfelijkheidsgraden (.19 tot .25) dan eerste pariteit, zowel met een lactatie model als met een 'test-day random regression' model. De laagste erfelijkheidsgraad is geschat met een 'test-day repeatability' model (.06-.09) in de eerste pariteit. De correcte erfelijkheidsgraad die gebruikt moet worden bij de fokwaardeschatting hangt af van het model van analyse.

Tabel 1. Erfelijkheidsgraden voor SCC voor Italian Holstein Friesian geschat in dit proefschrift uit lactatie-gemiddelden of test dag, gebruik makend van verschillende modellen.

Meting	**Lactatie**			**Model**[a]	**Hoofdstuk**
	1st	**2nd**	**3rd**		
Lactatie gemiddelde	.14			MT SCC-type	7
	.18	.21	.21	MT 3 lactaties SCC	6
Test dag	.06-.09			TD Repeatability	2
	.15	.19	.25	TD RR	6

[a]MT = multiple trait model, TD = test-day model, RR = random regression model.

Het genetische verband tussen SCC en produktie is uitvoerig geanalyseerd in Hoofdstuk 5 en 6 (Tabel 2). Genetische correlaties verschilden in teken (positief of negatief) en waarde, afhankelijk van pariteit en type model. De ogenschijnlijke complexiteit van de genetische faktoren die SCC beïnvloeden duidt er op dat rekening gehouden moet worden met verschillen in genetische correlaties tussen SCC en produktie-kenmerken, zowel tussen als binnen pariteiten. Bovendien werd geconcludeerd dat bij gebruik van een unieke correlatie-waarde voor elke pariteit en dagen-in-melk binnen pariteit, het genetische verband tussen SCC en produktie essentieel als nul kan worden beschouwd voor Italian Holstein. Deze waarde verschilde van ongunstige verbanden die eerder in literatuur gerapporteerd zijn.

Tabel 2. Genetische correlaties tussen SCC en produktie-kenmerken voor Italian Holstein Friesian, zoals geschat in dit proefschrift.

Model	**Lactatie**			**Kenmerk**	**Hoofdstuk**
	1st	**2nd**	**3rd**		
Calo's corr tussen EBV[a]	.22[b]			Melk kg	6
	.24[b]			Vet kg	
	.24[b]			Eiwit kg	
Lactatie model (305d)	.31	.01	.09	Eiwit kg	6
RR TD model MT (TD)	-.02	-.16	-.14	Melk kg	5
	-.04	-.14	-.12	Vet kg	5
	-.02	-.14	-.14	Eiwit kg	5

[a] EBV=fokwaarden

[b] Het teken (+/-) van SCC EBV is omgekeerd en daarom betekent een positieve correlatie een gunstig verband.

Uierkenmerken vertoonden een gunstige genetische correlatie met lactatie gemiddelden van SCC (Hoofdstuk 7). Een hoger uier, stevig aan de buikwand vastgehecht met korte spenen, was genetisch gerelateerd aan lagere SCC-waarden. In tegenstelling tot schattingen uit de literatuur, was er een sterke positieve genetische correlatie tussen achteruierbreedte en SCC (nauwe achteruierbreedte-lage SCC) (Hoofdstuk 7). Deze positieve genetische correlatie wordt waarschijnlijk verklaard door het niet-lineaire verband tussen fokwaarde voor achteruierbreedte en SCC.

Voor melksnelheid waren kwalitatief slechte gegevens beschikbaar, omdat de geregistreerde data gebaseerd waren op koeien die meer melktijd nodig hadden dan het populatiegemiddelde. Om die reden is de genetische correlatie tussen SCC en melk-snelheid in Hoofdstuk 7 geschat als een ruwe correlatie die gebaseerd was op fokwaardeschattingen voor de twee kenmerken. Dit resulteerde in een waarde van 0.09, wat er lichtelijk op duidt dat koeien met een hoge melksnelheid ook hoge SCC-waarden hebben. Echter, vergelijkbaar met achteruierbreedte, was er sprake van een niet-lineair verband tussen SCC en melksnelheid.

Bij gebruik van een 'hazard' model (Hoofdstuk 4) leidde een toename in het waargenomen SCC in Italian Holstein koeien tot een toegenomen afvoerpercentage. In ditzelfde hoofdstuk werd een genetische correlatie van .31 gevonden tussen SCC en functionele levensduur. Dit duidt er op dat ongunstige SCC waarden gerelateerd zijn aan een kortere levensduur.

Fokwaardeschatting

In Hoofdstuk 3 is een 'test day repeatability' model voor fokwaardeschatting van eerste pariteits-SCC ontwikkeld. Het model bevatte de volgende 'fixed' effekten: 'herd-test date', leeftijd bij afkalven en dagen in melk. Genetische parameters voor dit model zijn geschat in Hoofdstuk 2. Het doel van genetische evaluatie is om stieren te identificeren die regelmatig dochters krijgen die vatbaar zijn voor mastitis. Verscheidene routine evaluaties zijn reeds uitgevoerd, gebruikmakend van dit model.

Momenteel wordt een 'test day random regression' model geëvalueerd dat individuele variatie tijdens de lactatie voor produktie- en SCC kenmerken voor drie lactaties kan modelleren. Dit model kan waarschijnlijk in 2004 officieel in gebruik genomen worden. De genetische parameters die op dit model kunnen worden toegepast zijn geschat in Hoofdstuk 5 en 6 en zijn vergeleken met Canadese resulaten die verkregen waren met hetzelfde model.

Vanaf november 2001, tegelijk met het eerste officiële verschijnen van de fokwaardeschatting, was SCC opgenomen in de nieuwe algemene selectie index (PFT) met als doel de populatie te verbeteren op produktie- en functionele kenmerken. De genetische correlaties van SCC met andere kenmerken waren gebaseerd op literatuurwaarden, omdat nog geen schattingen voor Italian Holstein koeien beschikbaar waren.

Parameters voor de Italian Holstein populatie zijn geschat in dit proefschrift en kunnen overwogen worden ter verbetering van de selectie. Verder is in Hoofdstuk 7 een uier-gezondheids-index voorgesteld, inclusief SCC en bepaalde uierkenmerken. Het gebruik van deze index in de selectie-index ter vervanging van de SSC-waarde is bediscussieerd in Hoofdstuk 8. De uier index zou SCC, uierdiepte en voor-uier aanhechting bevatten. Melksnelheid zal waarschijnlijk niet in de index worden opgenomen, vanwege de lage betrouwbaarheid van de verzamelde data (Hoofdstuk 7).

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Curriculum Vitae

Antonia Bianca Samoré was born October 27th, 1968 in Milan, Italy. Antonia attended a scientific secondary education and completed with distinction the Degree in Animal Science at Milan University in 1991. Her Degree thesis was on breeding values estimations for Italian Haflinger Horse. After her Degree, she worked at Milan University developing preservation programmes for endangered Italian cattle breeds. In February 1992 she moved to Florence to work as geneticist for the Italian Breeders Association of Haflinger Horse (ANACRHA) developing genetic improvement strategies. Since 1991, she is responsible for Italian Haflinger Horse breeding values estimations and genetic selection. While working, she continued her education with a two years post-university specialisation course in "Genetic Selection of Domestic Animals and Zootechnical Production" that she attended with a fellowship and finished with distinction in 1994. In 1995 she worked as geneticist for the Research Office of the Italian Breeders Association (AIA, Rome) with the responsibility for the genetic improvement of Italian horse breeds. At the end of 1995 she obtained a fellowship to work and study abroad. She joined the Animal Breeding and Genetics Group at Wageningen University and she studied here for 13 months under the supervision of Prof. Johan van Arendonk. In January 1997 she obtained the MSc-Degree in Animal Breeding with distinction. When she left Wageningen she was employed by the Italian Holstein Friesian dairy cattle Breeders Association (ANAFI) in Cremona to work for the Research and Development Office. She combined her PhD project with activities at ANAFI. The project was a joint activity of ANAFI and Wageningen University where she spent some months each years.

Antonia is now working for the Research and Development Office of ANAFI, and still also responsible for Italian Haflinger Horse selection and breeding value estimation.