



Proposal of an udder health genetic index for the Italian Holstein Friesian based on first lactation data

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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 0.05 (udder balance) to 0.24 (udder depth) for conformation traits and 0.14 for LSCS. Genetic correlations with LSCS were -0.31 for udder depth and 0.28 for rear udder width. Other genetic correlations for conformation traits and LSCS varied from -0.16 to -0.03. A second data set, including 4398 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.

Key Words: Udder health index, Somatic cell count, Milking Speed, Conformation traits, Holstein Friesian.

RIASSUNTO

PROPOSTA DI UN INDICE GENETICO PER LA SALUTE DELLA MAMMELLA
PER LA FRISONA ITALIANA BASATO SUI DATI DI PRIMA LATTAZIONE

L'articolo stima le correlazioni genetiche tra i caratteri morfologici della mammella e il punteggio lineare della conta delle cellule somatiche nel latte (SCS) per formulare un indice genetico per la salute della mammella. I dati utilizzati sono inerenti a 1.268.762 prime lattazioni di Frisone Italiana con dati sia per i caratteri morfologici sia per la conta delle cellule somatiche (SCC). I singoli controlli di SCC sono stati trasformati in SCS e successivamente è stata calcolata la media di lattazione (LSCS) come media geometrica dei singoli controlli

tra 5 e 305 giorni. Sono stati analizzati due diversi archivi di dati. Il primo archivio con 11.203 dati è stato usato per 8 analisi multiple-trait a due caratteri considerando le informazioni relative alle LSCS e a un carattere morfologico alla volta. I modelli utilizzati includono per le LSCS gli effetti fissi di allevamento-anno-stagione e per i caratteri morfologici gli effetti di allevamento-anno-data di controllo e l'interazione dell'età al parto in mesi per la stagione di parto. Le ereditabilità variano da 0,05 (equilibrio della mammella) a 0,24 (profondità della mammella) per i caratteri morfologici e 0,14 per le LSCS. Le correlazioni genetiche con le LSCS sono -0,31 per la profondità della mammella e 0,28 per la larghezza posteriore della mammella. Le altre correlazioni genetiche tra i caratteri morfologici e le LSCS variano da -0,16 a -0,03. Un secondo archivio di dati (4.398 dati) è stato estratto per stimare le correlazioni tra i 5 caratteri da includere in un indice genetico aggregato per la salute della mammella. Utilizzando queste stime, e le stime riportate in letteratura per la resistenza diretta alle mastiti, è stato proposto un indice aggregato per la salute della mammella (UHI) per la Frisone Italiana: $UHI = -15 EBV_{SCS} + 1,5 EBV_{FUA} + 0,15 EBV_{UDD}$, dove EBV sono il valore genetico stimato per gli SCS, attacco anteriore della mammella (FUA), e profondità della mammella (UDD). La selezione per valori più bassi di SCS, mammelle meno profonde e con un attacco anteriore più forte porta a una maggiore resistenza alle mastiti. La velocità di mungitura non è inclusa in questa proposta di indice per la salute della mammella poiché il suo legame con i punteggi lineari delle cellule (SCS) è di tipo non-lineare e la raccolta di questi dati in Italia ha una bassa precisione.

Parole chiave: Correlazioni genetiche, Indice per la salute della mammella, Conta delle cellule somatiche, Caratteri morfologici, Frisone Italiana.

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 0.70 (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 indi-

rect 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 udder composite index aggregates the following traits: fore udder attachment, rear udder high, ligament, udder depth and teat placement. This 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 and methods

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 4398 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.

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.

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 with 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

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

ters 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:

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

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 months) 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

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 305 d (LSCS).

	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)		

Standard error of estimates between brackets.

(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 the accuracy it was therefore considered that information were collected on 100 or 200 daughters per bull.

Results

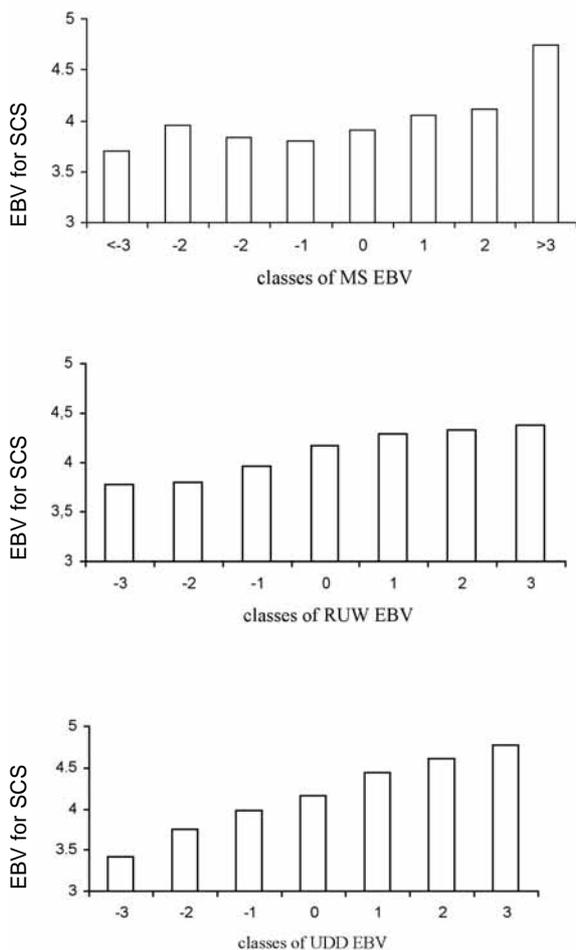
Heritabilities

Estimates of heritabilities for the various traits are in Table 2. The lactation measure of SCS had a heritability of 0.14. Among udder conformation traits, the minimum value of heritability was for udder balance (0.05) and most of the other udder morphological traits had heritabilities around 0.12. The most heritable trait was udder depth (0.24). Standard errors of heritabilities were between 0.02 and 0.03 for all traits.

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 (-0.31), followed by rear udder width (0.28). 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 the two standard errors (0.09 and 0.12). When compared to estimated values, standard errors of other genetic correlations were generally quite large ranging from 0.11 to 0.16. Considering the

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



observed relationships, although not all were significantly different from zero, a strongly attached udder to the fore abdominal wall (-0.16), and with short teats (0.13) was genetically related to smaller values of LSCS. The remaining udder conformation traits had smaller genetic correlations with LSCS, ranging from -0.11 for central ligament to -0.03 for udder balance. Environmental correlations were generally low, ranging from -0.07 (central ligament) to 0.00 (udder balance) with small standard errors (around 0.02).

Udder health index

Genetic and environmental correlation between LSCS, FUA, RUW, UDD, and TLE were esti-

mated 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 (0.76). The strong genetic correlation of LSCS with RUW (0.28) and with UDD (-0.31), already estimated by the two trait model, were confirmed and increased in magnitude (0.47 and -0.35, respectively). In contrast, the genetic correlation of LSCS with FUA estimated with the five-trait model, was smaller (-0.03 versus -0.16) 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.

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 0.07 and Calo's correlation was 0.09. 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 class-

Table 3. Heritabilities (on diagonal), genetic (above the diagonal) and phenotypic (below diagonal) correlations used to calculate the udder health index.

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

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).

es 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.

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 (0.08) and with a geometrical lactation average (0.13). Mrode and Swanson (1996) found smaller values of heritabilities in their review with an average of 0.11 ± 0.04 . More recent studies reported values between 0.11 and 0.23 (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 -0.15 to 0.27), and Boettcher *et al.* (1998) estimated values near zero (-0.03).

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 har-

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 305 d (LSCS), udder depth (UDD), rear udder width (RUW), fore udder attachment (FUA), and teat length (TLE).

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%

For each index it is reported the relative percentage response obtained when compared to the response obtained with 200 daughters direct mastitis (MR) information.

monized 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 (0.09). Stronger genetic correlations have been reported, with values ranging from 0.18 to 0.57 (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 use 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.

Recently breeding values for SCS were improved in Italy based on three lactations data (Canavesi *et al.*, 2004) but, genetic improvement in a dairy cattle population depends largely on bull selection, as both sires of bulls and sires of cows. The proof of a young bull is based on first parity daughters information both for type and SCC. Later on, bull information is increasing with more first parity daughters data for type and SCS and with later parities information only for SCS. This accumulation of data increases the reliability of estimated breeding values for SCS and can change the absolute genetic value of a bull and, by consequence its rank. Somatic cell 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 SCS, 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. Moreover first parity data are not selected for mastitis while later parities only include selected animals that survived the first parity culling. For these reasons, the authors believe that also with the use of SCS data of three lactations, the comparison between selection response obtained using the direct trait of MR or the indirect trait SCS is expected to give approximately the same results as with SCS on first parity only.

A selection response similar to the one achieved when selecting on the direct trait, mas-

titis 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, 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:

$$\text{UHI} = -14.49 \text{EBV}_{\text{SCS}} + 1.29 \text{EBV}_{\text{FUA}} + 0.11 \text{EBV}_{\text{UDD}}$$

which approximates to

$$\text{UHI} = -15 \text{EBV}_{\text{SCS}} + 1.5 \text{EBV}_{\text{FUA}} + 0.15 \text{EBV}_{\text{UDD}}.$$

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.

Genetic correlations were estimated using a sample data set and further samples could maybe lead to slightly different estimates of (co)variances, and therefore few small differences in selection response using more than two indirect traits. But genetic correlations between traits included in the proposed index were in range with values reported in literature and therefore no substantial differences are expected by the authors also with repeating samples extraction.

Conclusions

Using a large data set, genetic correlations between udder conformation traits and SCS were estimated in Italian Holstein Friesian data. The measure of LSCS resulted to have large genetic correlations with udder depth and with rear udder width. An aggregated udder health index to select for a reduce mastitis incidence was proposed for the Italian Holstein. 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.

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