Genetic parameters for functional longevity, type traits, somatic cell scores, milk flow and production in the Italian Brown Swiss

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Abstract

The aim of this study was to estimate genetic parameters for a set of new traits and to update values for production and morphological traits to be used in the selection index of Italian Brown Swiss dairy cattle. Longevity, milking speed and somatic cell scores (SCS) were considered for inclusion in the selection index, and (co)variances with all traits of the selection index were estimated. SCS was considered on a lactation basis while milk flow, the amount of milk (kg) released per time unit (minute), was measured with a flowmeter. Cow functional longevity was the total herd life corrected for the production level. A total of 127,416 first lactation records of cows calving from 1985 to 2003 were considered. In order to maximize the number of records available for each combination of traits, 9 data sets were created. Estimates were obtained from multivariate linear sire models with equal design matrix in subsequent separated analysis. REML algorithms and canonical transformation were used to calculate (co)variance estimates among all traits: functional longevity, milking speed, SCS, 5 production traits (milk, fat and protein yield, fat and protein percent), and 19 type traits. Heritabilities estimated were 0.14±0.02 for SCS, 0.33±0.07 for milk flow, and 0.04±0.01 for functional longevity. Genetic correlation values between SCS and milk yield, fat percent and protein percent were 0.18±0.03, -0.19±0.08, and -0.22±0.08, respectively. Functional longevity had a strong positive genetic correlation with udder depth (0.42±0.10) but a negative correlation with rear leg set (-0.56±0.10). Milk flow was positively correlated with most of the production measures: 0.30±0.18 with milk yield, 0.24±0.17 with fat yields, 0.16±0.20 with protein yield. Additionally, milk flow was genetically correlated with some type traits (0.53±0.14 rear udder width, 0.40±0.16 hock quality, 0.32±0.15 rump angle, -0.25±0.19 udder depth). The correlation between SCS and milk flow showed a value of 0.46±0.26, indicating that faster cows are more susceptible to mastitis.

Introduction

The Italian Brown Swiss dairy cattle population is traditionally selected for milk quality with a strong emphasis on production yield and content (Ghirolidi et al., 2005). The inclusion of functional traits in the selection index, such as longevity, milkability, and somatic cell scores (SCS), was proposed to reduce herd replacement, veterinary and management costs.

Longevity is usually measured as the length of herd productive life, i.e. the time span from first calving to culling. This measurement, adjusted for the cow milk production level, is defined as functional longevity (FL) that indicates the ability of the cow to delay involuntary culling (Ducrocq et al., 1988). The economic importance of longevity can be expressed as the profit gained from extending the cow herd life with the consequent reduction of heifer replacement costs and with the increased number of cows producing in later lactations (Van Arendonk, 1991). Nevertheless, few records are available early in life to estimate reliable breeding values for longevity, and therefore information on type traits, associated to length of life data, can be used to increase the accuracy of selection for longevity (Vollena, 1998b).

Mastitis is one of the most frequent and costly diseases in dairy herds. Direct measurement of clinical mastitis incidence is costly and difficult to implement in national recording schemes. The SCS is used for indirect selection for mastitis resistance in almost all dairy selection programs (Heringstad et al., 2000). Heritability of SCS is greater than heritability of mastitis incidence, and there is a close genetic correlation between SCS and mastitis incidence (Mrode and Swanson, 1996; Heringstad et al., 2000; Carlen et al., 2004).

Milking parameters, such as milk flow or milking speed, affect management costs in dairy herds but resulted in a controversial correlation with mastitis incidence. Rupp and Boichard (1999) did not include milkability in the French udder health index due to the lack of associations estimated with clinical mastitis. In contrast, both the moderate heritability and the need for an international comparison of sires suggested it could be included in the breeding objective of the Italian Brown dairy cattle (Santus and Bagnato, 1998).

In order to include new traits, not previously considered, in the selection index of the Italian Brown Swiss population, (co)variances for new traits should be estimated and previous estimates for all traits should be updated. This study aimed to estimate the genetic parameters to be used to update the selection index of the Italian Brown Swiss dairy population. Results and discussion focus mainly on SCS, milk flow and functional longevity and their relation to production, and type traits.

Materials and methods

Data

Data were provided by the Italian National Brown Cattle Breeders Association (ANARB) and included information on the mature equivalent of 305 days milk (MY), fat (FY) and protein yield (PY), and fat (FP) and protein percent (PF). Data for SCS, average milk flow (AMF), FL, and scores for 19 type traits (Table 1) were also available. Records included 127,416 primiparous cows that calved between 1985 and 2003 in 11,670 herds. SCS were considered on a lactation basis as the mean of monthly test day.

Milking parameters in the population were recorded by technicians of the ANARB on a routine basis using a portable milk flowmeter device (Lactocorder®, WMB AG, Switzerland). At least one record per lactation per cow was...
available. The value of AMF was expressed here as the ratio of total production per milking over the total milking time (kg/min).

The FL was calculated as the true productive life in days from first calving to culling. Only cows which have had the opportunity to survive to 72 months of FL were included in the analyses and no censored or left-truncated records were included. Low milk yield is the major reason for voluntary disposal of a cow and, therefore, FL was corrected for individual cow production level within herd-year according to the method suggested by Ducrocq et al. (1988).

Table 1. Traits analyzed: description, abbreviation, units of measurement, score direction and data collection period.

| Abbreviations | Trait description | Units of measurement*/* | Direction of scores° |
|---------------|-------------------|--------------------------|-----------------------|
| Production traits* |                   |                          |                       |
| MY            | ME 305 milk production | kg                     |                       |
| FY            | ME 305 fat production | kg                      |                       |
| FP            | ME 305 milk fat content | %                     |                       |
| PY            | ME 305 protein production | kg                    |                       |
| PP            | ME 305 milk protein content | %                  |                       |
| Functional traits* |                 |                          |                       |
| SCS           | Logarithmic somatic cell score | Score units |                       |
| AMF           | Average milk flow | kg/min                   |                       |
| FL            | Functional longevity | Days (c)                 |                       |
| Type traits o  |                   |                          |                       |
| STA (a)       | Stature           | Tall                     |                       |
| STR (a)       | Strength          | Strong                   |                       |
| BD (a)        | Body depth        | Deep                     |                       |
| ANG (a)       | Angularity        | Open ribbed              |                       |
| BTL (a)       | Back top line     | Straight and strong      |                       |
| RA (a)        | Rump angle        | Extreme slope            |                       |
| RW (b)        | Rump width        | Wide                     |                       |
| LS (a)        | Rear leg set      | Sickled                  |                       |
| HQ (b)        | Hock quality      | No coarseness or puffiness-adequate flexibility |                       |
| PA (a)        | Fasterns          | Short and strong         |                       |
| HD (b)        | Heel depth        | High                     |                       |
| FUA (a)       | Fore udder attachment | Extremely strong and tight |                       |
| RUW (a)       | Rear udder width  | Wide                     |                       |
| RUH (a)       | Rear udder height | High                     |                       |
| UC (a)        | Udder cleft       | Strong definition        |                       |
| UD (a)        | Udder depth       | Shallow                  |                       |
| TP (b)        | Teat placement    | Inside of quarter        |                       |
| TL (a)        | Teat length       | Long                     |                       |
| FIN (a)       | Final score       | Good conformation        |                       |

ME= Mature Equivalent, (a) recorded before and after 1995, (b) recorded after 1995, (c) FL results in the analysis in 10 days.

The survival analysis techniques, based on hazard function to estimate the instantaneous culling risk of a cow (Ducrocq, 2002), have been chosen as the official methodology for FL analyses in the Brown Swiss population in order to consider all available information, censored and uncensored records. Nevertheless, in this specific research, a linear methodology was applied also to the trait FL in order to obtain multivariate estimates which would have otherwise been impossible with the survival methodology. The 21 classifiers of the ANARB scored 19 type traits based on a linear scale from 1 to 50, with the exception of the final score, for which the range of scale is from 60 to 99 (Table 2). Traits of rump width (RW), hock quality (HQ), heel depth (HD), and teat direction (TD) were only introduced in the evaluation system in 1995, and therefore the number of records for these traits was smaller than for the others. Genealogical information was extracted from the National Herd Book.

A total of 9 data sets were created from the initial data. Not all traits were available for all animals and, therefore, a data set was extracted for each pair of group of traits combination and all cows, with information on both traits considered, were kept in order to minimize the standard error of the estimates (Table 3).

Variance component estimation

Multivariate REML analyses were performed on all data sets using the EQREML software (Meyer, 1986) with the same design matrix for all variables. Analyses were performed using the edited data set for each group of traits in order to guarantee the use of the same observations for all variables in all cows. Data were transformed using a canonical scale in order to reduce the multivariate analysis of $n$ traits to $n$ corresponding univariate analyses (Meyer, 1985). The model included fixed effects of herd-year-season of calving, age at first calving (in months) and classifier. Fixed effects were significant for most traits considered according to results of the GLM procedure of SAS software (SAS Institute, 2001). The same model was chosen for all traits in order to have an equal design matrix.

Random factors were sire and residual effect. A maximum of 1,505 sires were included in the analyses (Table 3). Missing data were removed and the effect of herd-year-season was absorbed during the analysis. A minimum of two records per each level of herd-year-season class and 10 daughters in at least 6 herds per sire were required. A sire model was chosen for this analysis.

Solutions were obtained when the average difference between solutions obtained from 2 successive iteration rounds was less than $10^{-6}$. Correlations were not calculated between 8 traits and FL due to the insufficient number of data in common.

Heritability was estimated as: $h^2 = 4s^2 / p^2$, where $h^2$ is the heritability, $s^2$ is the sire variance, and $p^2$ is the phenotypic variance. Genetic correlations were estimated as $r_{1,2} = \sigma_{1,2}^2 / \sqrt{s^2_1 * s^2_2}$, where $r_{1,2}$ is the genetic correlation between trait 1 and trait 2, $s^2_1$ and $s^2_2$ is the genetic covariance between trait 1 and trait 2, and $\sigma_{1,2}$ is the genetic variances respectively of trait 1 and trait 2. Heritability and correlations are reported only for the largest data set available for each trait combination.

Results

Estimates of heritability

Heritability estimates were presented for the largest data set available for each trait (Table 4). Standard errors of heritability ranged from 0.01 to 0.02. Only TL (0.03) and AMF (0.07) presented higher values due to the small number of records available when com-
pared to the other traits.

Heritabilities for yield traits were 0.22 (MY), 0.18 (PY) and 0.19 (FY). Larger values were estimated for contents with 0.36 for FP and 0.41 for PP. Heritability estimates for functional traits were 0.14 for SCS, 0.33 for AMF and 0.06 for FL. Type trait heritability values ranged from 0.15 (RW) to 0.36 (stature (STA)) in traits related to the general structure, from 0.06 (HD) to 0.12 (rear leg set (LS)) in feet and leg traits, and from 0.17 (fore udder attachment (FUA)) to 0.33 (teat length (TL)) for udder traits.

Genetic correlations

Genetic correlations (Table 5) among yield traits (MY, PY and FY) were strongly positive (from 0.79 to 0.90) but MY were negatively associated with percentages (-0.36 with FP and -0.45 with PP).

SCS had a positive correlation of 0.18 (Table 5) with MY, close to 0 with FY and PY, and negative with FP (-0.19) and PP (-0.22) indicating that low production cows are less susceptible to mastitis incidence. The value of 0.46 estimated between SCS and AMF would also suggest that the stress related to high flows over a short time could increase susceptibility to mastitis. The largest correlation value estimated between SCS and type traits (Table 6) was -0.46 with udder depth (UD) indicating that a shallow udder is associated with lower values of SCS.

Milk flow showed a positive genetic correlation with yields ranging between 0.16 (PY) and 0.30 (MY), and zero or negative values with percentages (-0.01 with FP and -0.26 with PP). The high value of the genetic correlation (0.53) estimated between rear udder width (RUW) and AMF would suggest that a bigger udder, with an expected large production, also results in a high milk flow.

A longer life was genetically related to legs preferably straight rather than sickled (-0.56 genetic correlation with LS), in a cow with a high udder (0.42 genetic correlation with UD) and of moderate size (-0.22 genetic correlation with STA). Strong positive genetic correlations (Table 7) were found between body size and strength (0.83 between STA and STR, and 0.84 between BD and STR). Feet and legs, and udder traits presented small to moderate genetic correlations within and between groups with two very strong correlations between pasterns and HD (0.82), and between RUW and RUH (0.72).

Phenotypic correlations

Phenotypic correlations (results not shown) vary according to traits considered. It is well known that the largest positive relationships are to be found among yield traits (MY, PY and FY) which in this study ranged from 0.86 to 0.94. Correlations between productive traits and SCS were small, as were those with FL, while milk flow had positive values with the amount of milk (MY, PY and FY) produced. Moderate to large correlations were found among traits related to body size (STA, strength (STR), body depth (BD), rump angle (RA), and RW) and a large phenotypic correlation was calculated between pasterns and heel (0.50). Small phenotypic correlations were estimated among leg and udder traits, with values larger than 0.15 only between HQ and rear

### Table 2. Descriptive statistics for production, functional and type traits.

| Trait       | Mean   | SD    | Min    | Max    | CV   |
|-------------|--------|-------|--------|--------|------|
| MY, kg      | 5,894.8| 142.18| 2001   | 14.3   | 24.1 |
| FY, kg      | 234.4  | 59.9  | 62.3   | 565.0  | 25.5 |
| PP, %       | 0.4    | 0.4   | 2.4    | 6.8    | 10.6 |
| PY, kg      | 206.6  | 53.1  | 65.5   | 489.0  | 25.8 |
| PP, %       | 0.3    | 0.2   | 2.1    | 4.7    | 6.7  |
| SCS         | 2.0    | 1.5   | 0.1    | 8.2    | 63.8 |
| AMF, kg/min | 2.0    | 0.6   | 0.3    | 5.2    | 29.2 |
| FL, Gg (x10)| 1239.5 | 731.3 | -34.0  | 4417.0 | 55.1 |
| STA         | 30.7   | 8.0   | 1.0    | 50.0   | 26.0 |
| STR         | 26.1   | 7.6   | 1.0    | 50.0   | 26.1 |
| BD          | 28.9   | 6.8   | 1.0    | 50.0   | 23.6 |
| ANG         | 27.0   | 7.2   | 1.0    | 50.0   | 26.9 |
| BTL         | 24.5   | 4.8   | 1.0    | 50.0   | 19.6 |
| RA          | 25.8   | 5.2   | 1.0    | 50.0   | 20.1 |
| RW          | 24.2   | 6.6   | 1.0    | 50.0   | 27.4 |
| LS          | 26.4   | 6.8   | 1.0    | 50.0   | 25.7 |
| HQ          | 24.3   | 7.7   | 1.0    | 50.0   | 31.7 |
| PA          | 25.7   | 8.6   | 1.0    | 50.0   | 33.4 |
| HD          | 24.8   | 8.4   | 1.0    | 50.0   | 33.9 |
| FUA         | 246.8  | 8.3   | 1.0    | 50.0   | 33.8 |
| RUW         | 27.2   | 9.2   | 1.0    | 50.0   | 33.9 |
| RUH         | 25.3   | 6.9   | 1.0    | 50.0   | 27.1 |
| UC          | 26.2   | 7.5   | 1.0    | 50.0   | 28.6 |
| UD          | 29.2   | 7.2   | 1.0    | 50.0   | 24.5 |
| TP          | 24.8   | 5.8   | 1.0    | 50.0   | 23.2 |
| TL          | 26.4   | 6.4   | 1.0    | 50.0   | 24.1 |
| FIN         | 80.7   | 3.1   | 69.0   | 89.0   | 3.7  |

**Notes:** MY= milk yield, FY= fat yield, PP= fat percent, PY= protein yield, PP= protein percent, SCS= somatic cell scores, AMF= milk flow, FL= functional longevity, STA= stature, STR= strength, BD= body depth, ANG= angularity, BTL= back top line, RA= rump angle, RW= rump width, LS= rear leg set, HQ= hock quality, PA=pasterns, HD= heel depth, FUA=fore udder attachment, RUW=rear udder width, RUH= rear udder height, UC= udder cleft, UD= udder depth, TP=teat placement, TL=teat length, FIN= final score.

### Table 3. Description of the 9 data sets used in the analysis with the number of records of each data set and the number of level of fixed and random effects considered.

| Data Set | Traits included | Number of records | Herd-year-season of calving | Age at calving (months) | Classifier | Sires |
|----------|----------------|-------------------|-----------------------------|--------------------------|------------|-------|
| 1        | Production, type | 127,416           | 50,951                      | 16                       | 37         | 1505  |
| 2        | Production, type | 71,524            | 27,873                      | 16                       | 21         | 957   |
| 3        | SCS, production, type | 43,544 | 16,700                      | 16                       | 19         | 885   |
| 4        | SCS, production, type | 39,212 | 14,837                      | 16                       | 22         | 1002  |
| 5        | AMF, production, type | 3544  | 1206                        | 16                       | 9          | 286   |
| 6        | AMF, production, type | 3540  | 1203                        | 16                       | 9          | 286   |
| 7        | AMF, SCS, production | 2481  | 919                         | 16                       | 9          | 221   |
| 8        | Production, FL    | 104,637           | 38,133                      | 16                       | 29         | 1400  |
| 9        | Type traits, FL   | 56,517            | 18,302                      | 16                       | 21         | 893   |

**Notes:** AMF= milk flow, SCS= somatic cell scores, FL= functional longevity.
udder height (RUH).

Discussion

The average milk production and its contents (MY= 5894.8 kg, PP= 3.48% and FP= 3.98%) were consistent with values reported in the official milk recording statistics for the Italian Brown first parity cows born in the period 1996-2003 (AIA, 2007).

Italian Brown Swiss dairy cattle had phenotypic values for SCS (2.03±1.47) similar to the value of 2.87 reported by Welper and Freeman (1992), of the 2.22±2.05 reported by Dal Zotto et al. (2007), and of the 2.98±1.24 reported by Cole and Null (2009) in the same breed. Less variable data were presented for Swedish and Swiss Holstein primiparous cows (Carlén et al., 2004; Kadarmideen, 2004; Neuenschwander et al., 2005). AMF resulted in slightly lower and more variable values than those reported by Ilahi and Kadarmideen (2004) for the same breed (2.76±0.52 kg/min). Phenotypic averages of type traits, especially when considering the general structure (STA, STR, BD, angularity (ANG), back top line, RA, RW and final score) suggested that the Italian Brown Swiss population have a good dairy cow frame. Legs appeared to be correct with well placed hocks, strong pasterns and a correct high foot. The mammary system showed a good conformation, was well attached to the body in all parts, with an udder above the hocks and strong ligaments.

Heritability

Production and functional traits

Heritabilities for production traits are consistent with those found in previous studies on the same breed (Santus et al., 1993). Heritability of 0.14 for SCS was moderate if compared to values in the literature but estimates depended on several factors related to the data set considered: breed, test day or lactation or single measure of milk recording and the model of analysis (lactation or test day model). The mammary system showed a good conformation, was well attached to the body in all parts, with an udder above the hocks and strong ligaments.

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The heritability estimated for AMF was similar to that reported by Santus and Bagnato (1998) in the same breed. The value of 0.33 suggested a large proportion of additive variance, making selection for this trait and its inclusion in selection criteria feasible. A higher value of heritability, 0.44, was estimated by Ilahi and Kadarmideen (2004) with a Gibbs sampling procedure in the same breed, and values of 0.54 and 0.25 were estimated for Simmental and Holstein breeds by the same authors. In the Brown and Simmental breeds, data were collected electronically while a subjective scoring was used for Holstein cows with the breeder identification of slow and fast milking cows. The subjective system is less reliable than the electronic method and it explains the low value of heritability estimated for Holstein cows by Ilahi and Kadarmideen (2004) and the value of 0.17 estimated in the primiparous French Holstein population (Rupp and Boichard, 1999). Nevertheless, low estimates of heritability (from 0.003 to 0.098) were also reported for milk flow recorded electronically in a Swiss Holstein population using a random regression method (Karacaören et al., 2006). Indeed, this large variability in results would suggest that the heritability of

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AMF largely depends on data collection method and model of analysis, and it would also indicate that an objective measurement would be of great advantage to guarantee data accuracy and, consequently, the reliability of each EBV. The heritability estimated for FL confirmed the estimate reported by Cassandro et al. (1999) in the same breed with a data set of 49,520 records from 1983 to 1986. Heritability estimates in literature ranged from 0.09 to 0.14, than with traditional longevity measurements (Vollem, 1998a; Sewalem et al., 2005) and the use of survival models are suggested also for the Italian Brown Swiss.

Type traits

The heritabilities estimated for type traits were generally consistent with those currently used for EBV estimation in the Italian Brown population and to those recently reported by Dal Zotto et al. (2007) for the same breed. The low heritability of HD (0.06) was in agreement with estimates in primiparous Canadian Holstein (Fatehi et al., 2003) and the value of 0.10 for HQ was in line with estimates (Boelling et al., 2001) in Jersey (0.13), Danish Brown (0.13) and Red and White (0.15) breeds.
Friesian (0.19) and Danish Red (0.26). Udder type traits showed heritabilities similar to values reported for primiparous Holstein cows (Misztal et al., 1992; Rupp and Boichard, 1999) but to some extent smaller than heritabilities found in Swiss Holsteins in all lactations (Neuenschwander et al., 2005).

According to the large number of records, standard errors of heritabilities were generally small and ranged from 0.01 to 0.03 with the exception of AMF heritability estimated in a smaller data set.

Genetic correlation

Production and functional trait

According to literature values (for a review see Mrode and Swanson, 1996), the positive genetic correlation between MY and SCS of 0.18 suggested that individuals with large production are probably susceptible to mastitis, with a consequent increase in SCS values. Lower correlations (-0.04) were estimated in the Brown Swiss with a test day model by Samoré et al. (2007). A similar estimate (0.22) to that estimated here was reported in first parity Swedish Holsteins (Carlén et al., 2004), whereas a larger relationship (0.31) was found in Italian Holstein cows (Samoré, 2003). Data considered here are limited to primiparous cows but it should be remembered that genetic correlation values between production traits and SCS generally decrease, with increasing parity and stage of lactation also presenting change of signs (Pösö and Mäntysaari, 1996; Samoré et al., 2008).

According to estimates reported by Santus and Bagnato (1998), AMF was positively correlated with production suggesting that high yielding cows generally show fast milking speed. Both conformation and physiological factors, i.e. the size of teat opening and the amount of milk in the udder, contribute to determine the milk flow, and high producing cows generally exhibit a large rate of milk release due to the increased udder pressure (Schmidt et al., 1988).

Yields were negatively correlated with FL according to Cassandro et al. (1999) suggesting that the stress of high production in the udder would reduce the cow stayability. In literature, the culling risk estimated with survival analyses increased with low milk and protein production while it decreased with low fat percentages (Samoré et al., 2003; Sewallem et al., 2005).

The value of AMF was positively associated with the SCS level (0.46). Rupp and Boichard (1999) reported a similar value but a genetic correlation close to zero for AMF and mastitis incidence, the functional trait indirectly evaluated with the SCS level. The difference in correlation values could probably be related to the complete draining of the udder which occurs in fast milking cows and the cell concentration of the last milk fraction which is generally from 3 to 10 times greater than SCC in the pre-milk (Rupp and Boichard, 1999). However, the biological interpretation of the relationship between AMF and mastitis incidence is still not clear.

Production traits were positively associated with ANG, FUA, RUW and RUH, with genetic correlation values ranging from 0.22 to 0.45. The association estimated here between FUA and yield traits (0.45 with MY, 0.44 with FY, and 0.44 with PY) indicated that more productive cows also have a stronger fore udder attachment; however, contrasting estimates were reported in the literature for Holstein cows with high producing cows associated with loose fore udder attachments (Misztal et al., 1992; DeGroot et al., 2002). These differences can probably be explained by considering the selection strategies for type and production specific to each breed and to the different production levels in Holstein and Brown Swiss cows.

From the genetic correlations estimated here and in the literature (Misztal et al., 1992; DeGroot et al., 2002), negative between UD and MY, and positive between UD and RUW or UD and FUA, it can be concluded that high udders are genetically associated with small volumes and smaller production.

Most of the genetic correlations between SCS and type traits estimated here were low and in agreement with findings in Brown Swiss by Kadarmideen (2004) and by de Haas et al. (2007), with the exception of the correlation between SCS and RUW which was estimated here (0.15) as an opposite sign compared to the -0.27 estimated by de Haas et al. (2007).

The negative association between SCS and UD (-0.46) is well known in literature in several breeds (DeGroot et al., 2002; Kadarmideen, 2004; Samoré and Groen, 2006) and it would suggest that cows with deep udders are also more susceptible to mastitis (Nash et al., 2000). There was almost no genetic correlation between SCS and RUH in Italian Brown Swiss, and similar values near zero were estimated by Samoré and Groen (2006) in Italian Holstein Friesian. A genetic selection to reduce mastitis incidence through SCS and type traits would probably include SCS and some udder traits strongly genetically related to SCS, i.e. UD, RUW, and udder cleft (UC). In spite of the low or nil genetic relationship between SCS and FUA, the trait FUA would also probably be included due to its importance in udder selection and to the genetic correlations with the other udder traits (Samoré and Groen, 2006).

AMF had a strong positive genetic correlation with RUW (0.53) and smaller correlations with FUA (0.19), RUH (0.09), and UC (0.18). This pattern would suggest that a well developed udder well attached to the body would result in fast milking. Moreover, fast milking cows (high AMF) were shown to be genetically associated with legs moderately tending to sickle, with good quality hocks, a sloping rump, long pasterns and a low heel.

The negative genetic correlation between AMF and UD indicated that deep udders would release milk faster than shallow ones, probably related to the larger amount of milk to be released by single milking.

The negative genetic correlations between structural type traits and FL suggested that cows with higher stature, greater strength, deeper body and more angularity also had a short life.

The comparison of estimates with the results in literature is problematic because of the different definition of traits. In particular, a moderate slope from the hips to the pins (RA) was associated with great longevity both in this study and in Sewallem et al. (2005). Extreme and very sloping rumps were related to high culling risk due to caking difficulties and reproductive problems (Sewallem et al., 2005). Different estimates, but in dual purpose cattle breeds, were reported by Vukasinovic et al. (2002) presenting a positive but low association between stature and herd life, and a negative relationship between rump angle and herd life in Swiss Simmental and Red and White cows. According to Vukasinovic et al. (2002), the longevity was genetically associat ed with legs that tend to be straight and with a deep udder.

When considering the correlations among type traits, genetic correlations (from 0.23 to 0.84) among structural traits (STA, STR, BD, ANG, back top line and RW) indicated that a balanced cow structure was also maintained in an increase in size. Angular cows appeared to have correctly set legs and hocks, and showed a well shaped udder, with genetic correlations between angularity and udder and leg traits (LS, HQ, FUA, RUW, RUH and UC) ranging from 0.35 to 0.75. The genetic correlation estimated seemed, therefore, to suggest that the improvement of legs and hocks could also have some positive effects on production traits.

Conclusions

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Genetic parameter estimates have been used to update genetic parameters for breeding value evaluation of the Italian Brown Swiss dairy population. The heritabilities of functional traits such as SCS (0.14) and AMF (0.33) suggested that they may be considered as selection criteria in the Italian Brown population with their inclusion in the selection index. Moreover, the comparison of estimates for milk flow with literature findings indicated that the use of electronic flow meters is recommended because this guarantees an objective data collection and consequently, the availability of reliable data for genetic improvement.

In setting up selection programs, the whole pattern of genetic (co)variances among traits should be considered before choosing traits to be included in the index, in order to select for high yielding and fast producing cows. Particular attention should be given to the unfavorable association between longevity, SCS and production to ensure functionality and high production. Finally, the positive genetic relationships between angularity, hock quality and udder traits would suggest that cows producing high yields of milk and protein would also have correctly set legs and hocks and a well shaped udder.

All the parameters estimated here were used to update parameters in the selection program of the Italian Brown population.

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