



## Genetic correlations between type and test-day milk yield in small dual-purpose cattle populations: The Aosta Red Pied breed as a case study

Serena Mazza, Nadia Guzzo, Cristina Sartori,<sup>1</sup> and Roberto Mantovani

Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy

### ABSTRACT

This study aimed at estimating the relationships between linear type traits and milk production in the dual-purpose Aosta Red Pied (ARP) cattle breed, by expressing type traits as factor scores with the same biological meaning of the individual traits. Factor analysis was applied to individual type traits for muscularity and udder of 32,275 first-parity ARP cows, obtaining 3 factor scores for individual muscularity (F1), udder side (F2), and udder conformation (F3). Data from 169,008 test-day records of milk, fat, and protein yield (kg), belonging to the first 3 lactations of 16,605 cows, were also analyzed. After obtaining genetic parameters for both morphological factors and milk production traits through a series of AIREML single-trait models, bivariate analyses were performed on a data set accounting for 201,283 records of 35,530 cows, to assess the phenotypic and genetic correlations among all factor scores and milk yield traits. The heritability estimates obtained proved to be moderate for both groups of traits, ranging from 0.132 (fat) to 0.314 (F1). Muscularity factor showed moderate and negative genetic correlations ( $r_a$ ) with udder size ( $-0.376$ ) and udder conformation (0.214) factors. A low and negative  $r_a$  was found between udder factors. Strong and positive  $r_a$  were found among all the 3 milk production traits and F2 ( $r_a \geq 0.597$ ). Negative  $r_a$  with milk traits were obtained for both F1 and F3, ranging from  $-0.417$  to  $-0.221$ . Phenotypic correlations were lower than the genetic ones, and sometimes close to zero. The antagonism between milk production and meat attitude traits suggests that great attention should be paid in assigning proper weight to the traits, comprising functional traits such as udder conformation, included in selection indices for the dual-purpose breed. The  $r_a$  obtained for factor scores are consistent with previous estimates for the corresponding individual type traits, and this con-

firms the possible use of factor analysis to improve type traits relevant to beef attitude.

**Key words:** dual-purpose cattle, genetic parameters, test-day milk, type traits, factor analysis

### INTRODUCTION

Increased milk yield is a primary goal in dairy cattle breeding because of its preeminent importance in determining herd profitability (De Lorenzo and Everett, 1982). In dual-purpose cattle, equilibrium between selection for milk and meat is required, especially in local populations, in which the bond between the history, the products, and the specific environment of the breed is significant (Gandini and Villa, 2003). Selection for meat is based in some breeds on muscularity traits scored during routinely linear type evaluation (e.g., Italian Simmental, Frigo et al., 2013). Emphasis on linear type trait evaluation has been placed over time on dairy breeds, and genetic relationships between type traits and yield have been widely studied (e.g., Thompson et al., 1981; Vanraden et al., 1990; DeGroot et al., 2002). Linear type traits are visual characteristics of an animal expressed as a range of values within 2 biological extremes (Berry et al., 2004). These traits are described with numerical scores following the specific classification system of each breed and they usually approximate to a normal distribution (Norman et al., 1988). An advantage of this system is to quantify a trait using different degrees of expression rather than its desirability (Samoré et al., 1997). Conversely, the high number of traits scored and the high degree of correlation usually observed when they refer to the same body part can produce biased correlation estimates due to collinearity (Sieber et al., 1987). To overcome this problem, factor analysis has been proposed as a useful procedure to remove the redundancy from high correlated traits, deriving a new set of less correlated traits called factors (Vukasinovič et al., 1997). The main derived factors typically include correlated traits and may assume a biological meaning (Ali et al., 1998). Factor analysis has been widely studied as a tool for genetic evaluation

Received March 1, 2016.

Accepted June 17, 2016.

<sup>1</sup>Corresponding author: [cristina.sartori@unipd.it](mailto:cristina.sartori@unipd.it)

of type traits in some Italian cattle, both in specialized beef breeds (Chianina, Marchigiana, and Romagnola; Forabosco et al., 2005), and in local dual-purpose cattle as Rendena and Aosta Red Pied (Mantovani et al., 2005; Mazza et al., 2016). Dwelling on the milk yield, current genetic evaluation largely uses single test day (**TD**) records to enable earlier selection decisions (Bilal and Khan, 2009) and to improve selection accuracy respect to the traditional 305-d lactation yields (Schaeffer et al., 2000). In Italy, a multi trait-random regression TD model (Kirkpatrick et al., 1994) is used for the Italian Holstein (Muir et al., 2007), whereas repeatability TD models (Meyer, 1995) are applied for the Italian Brown (Dal Zotto, 2000), Italian Simmental (Degano et al., 2003), and local dual-purpose Rendena breed (Guzzo et al., 2009). A repeatability TD model, considering consecutive test-day samples from the same lactation as repeated observations (Bilal and Khan, 2009), is particularly adaptable to dual-purpose local breeds showing fewer cows with evaluation and records per cow than specialized cosmopolitan breeds. In addition, dual-purpose local breeds are often characterized by mountain grazing activity during the summer, and the absence of TD in the final part of lactation leads to poor genetic evaluations at extremes when random regression models are used (Misztal, 2008).

For dual-purpose breeds, the understanding of the relationship between milk yields and traits related to meat attitude is of particular interest to allow the proper combination of traits when selection is simultaneous for antagonistic aspects. Selection indexes in dual-purpose cattle typically provide a greater emphasis to milk yield (Aass, 1996), often expressed as fat or protein yield, or combination of both, and also include some beef traits such as the muscularity score measured on cattle or (sometimes and) in vivo or postmortem carcass evaluations performed on young bulls [e.g., in Austrian Simmental (Sölkner et al., 2000) and in Rendena (our unpublished data)]. Some selection indexes for dual-purpose attitude have also recently included functional traits such as longevity or somatic cells (Krupová et al., 2016). Negative genetic correlations have been found between milk yield and postmortem carcass traits (Pirchner, 1986; Liinamo et al., 2001), and between milk and type traits related to muscularity (e.g., de Haas et al., 2007; Frigo et al., 2013). Only few studies have been already focused on the genetic aspects of the dual-purpose attitude, despite the evidence that a stronger selection for one attitude may cause a genetic detriment in the other (e.g., Sölkner et al., 2000). This issue is particularly relevant in local dual-purpose breeds, in which the maintenance of a nonspecialized beef or dairy conformation may help to preserve some

valuable functional characteristics (e.g., health, longevity, fertility, and robustness; Krupová et al., 2016).

The Aosta Red Pied (**ARP**) is a local dual-purpose breed mainly raised in the Aosta Valley region (northwest of Italy), and originated from short headed animals that lived in Central-Western Europe (Feliuss et al., 2011). Those animals, presenting a red and white coat, with white head and light muzzles, were brought from Burgundy to north Italy at the end of the 5th century (Del Bo et al., 2001). The ARP is one of the most diffused breeds of the Western Alps because of its high adaptability to living and producing in the harsh conditions of the Alpine areas. In 2014 the total number of ARP animals registered in the Herd Book, cows and bulls, was 23,721, 12,868, and 228, respectively (FAO, 2015). The ARP cows are usually characterized by strong shoulders, well covered by muscles, and an udder that is sufficiently developed to identify an animal with a prevalent milk aptitude but also good meat characteristics (ANABoRaVa, 2015a). The milk yield of ARP is mainly used to produce the Fontina cheese, labeled PDO (Protected Designation of Origin). In 2014, the average milk yield per lactation was 3,921 kg, with milk fat and protein percentages of 3.48 and 3.25, respectively (ANABoRaVa, personal communication). In 2015 the traditional lactation model used for the genetic evaluation of milk traits in Valdostana breed was replaced by a repeatability TD model developed by AIA (Cappelloni, 2013; ANABoRaVa, 2015b). The beef attitude is selected instead by using the muscularity traits of the linear type evaluation.

Considering the ARP as a case study for other small, local dual-purpose breeds, this study has aimed at estimating genetic parameters between linear type traits expressed as morphological factor scores and TD milk yields evaluated through a repeatability TD model. Traits retained for the factor analysis were those mostly related to the dual-purpose attitude, which are muscularity and udder traits. The attempt of estimating heritability and genetic correlations with TD milk yield traits by using the factorization of some linear type traits scored on primiparous cows is a novelty of this study.

## MATERIALS AND METHODS

### Data Editing

Data were provided by the National Association of Breeders of Valdostana cattle (**ANABoRaVa**) and included conformation and productive information. Linear type traits for the ARP breed have been referred as morphological traits (**MORPH**) in the study.

About these traits, only records with DIM between 10 and 350 d, and with age at calving between 22 and 48 mo, were retained. Furthermore, herd-year-classifier contemporary groups with less than 2 records were discarded. The final data set considered 10 morphological traits belonging to 32,275 first parity cows of the ARP breed evaluated from 1997 to 2012 in 1,086 different herds and by 15 different trained classifiers. Only traits related to muscularity and udder were retained for a factor analysis, as they are the ones mainly related to beef and milk attitude (Mazza et al., 2016). Hence, 4 individual muscularity traits (front muscularity; back, loins, and rump; thigh, buttocks side view; thigh, buttocks rear view) and 6 individual udder traits (fore udder attach; rear udder attach; udder width; udder depth; teat placement rear view; teat length) scored on a linear scale from 1 to 5 points were considered (Table 1). All traits showed a normal distribution assessed preliminarily through Proc UNIVARIATE of SAS (SAS Institute Inc., Cary, NC). Higher phenotypic scores are desirable for muscularity traits and for the first 3 udder traits, whereas udder depth, teat placement rear view, and teat length have optimum intermediate values.

The initial milk yield traits data set included 510,870 TD records of individual milk, fat, and protein daily productions (kg) measured in lactating cows under routinely national milk recording realized between 1994 and 2009. Only the first 3 lactations were considered for the study, and test-day records with missing milk, fat, and protein yields were discarded. Furthermore, information collected between 5 and 250 DIM were retained.

This upper limit was established because the cows in late lactation are typically excluded from the milk recording in the summer season (the breed has a strong seasonality of calving). Only lactations with at least 4 controls and herd-TD within lactation with at least 2 milk recordings were retained. After editing, 169,008 TD belonging to 16,605 cows evaluated in 833 different herds remained for further analysis. The strong reduction of data set after editing is primarily due to the decision to retain only 3 among all the available lactations that ARP cows may have during their career. The pedigree files obtained for genetic analysis included all known ancestors of animals with records up to the 10th generation, and accounted for 58,474 animals for the morphological data set and 41,991 animals for the TD data set to carry out single trait analyses.

Finally, for the bi-trait analyses between milk production and morphological traits, the 2 data files described above were joined into a single data set accounting for 201,283 records belonging to 35,530 cows with records for at least 1 trait. Among them, 13,350 cows had both MORPH (1 record per cow) and TD information (4 or more individual TD data). The pedigree file of the bi-trait data set contained 61,475 animals tracing back subjects up to 10 generations.

### Statistical Analyses and Models

In the first step, a factor analysis was computed using raw morphological data (Kaiser, 1958) belonging to the MORPH data set following the same procedure previously applied on all morphological traits of ARP

**Table 1.** Descriptive statistics of individual morphological and milk yield traits measured in Aosta Red Pied cows used in the study<sup>1</sup>

Trait	Minimum	Maximum	Mean	SD	CV
Morphological trait (score) <sup>2</sup>	1	5			
Front muscularity	Scarce	Developed	2.88	0.86	0.30
Back, loins, and rump	Scarce	Developed	2.95	0.86	0.29
Thigh, buttocks: side view	Hollow	Rounded	3.07	0.87	0.28
Thigh, buttocks: rear view	Hollow	Rounded	3.05	0.90	0.30
Fore udder attachment	Short	Long	3.09	0.97	0.31
Rear udder attachment	Low	High	3.24	0.89	0.27
Udder width	Narrow	Broad	3.23	0.91	0.28
Udder depth	Deep	Shallow	3.20	0.80	0.25
Teat placement rear view	Diverging	Converging	2.81	0.65	0.23
Teat length	Short	Long	2.93	0.76	0.26
Test-day yield <sup>3</sup> (kg/d)					
Milk	0.200	33.80	13.23	4.62	0.35
Fat	0.002	1.547	0.45	0.17	0.38
Protein	0.007	1.338	0.43	0.15	0.35

<sup>1</sup>Descriptors of the biological extremes are reported for the type traits.

<sup>2</sup>Obtained from a data set accounting for 32,275 individual records obtained from primiparous Aosta Red Pied cows.

<sup>3</sup>Obtained from a data set accounting for 169,008 test-days belonging to the first 3 lactations of 16,605 Aosta Red Pied cows.

(Mazza et al., 2016). Briefly, following the description of Macciotta et al. (2012), factor analysis encompasses the linear modeling of  $n$  original observed variables toward a limited set of  $p$  latent variables (called factors), that could be represented as

$$y_i = b_{i1}X_1 + \dots + b_{ip}X_p + e_i,$$

where  $y_i$  is the  $i$ th measure;  $X_1, \dots, X_p$  are a set of common factors underlying the  $i$ th measure;  $b_{i1}, \dots, b_{ip}$  are the factor coefficients or loadings, that are the correlation between the respective common factor and the  $i$ th measure; and  $e_i$  is the  $i$ th unique factor specific for each measure. The Varimax orthogonal rotation method of coefficients (Kaiser, 1958) was chosen to obtain a clearer interpretation of each latent factor extracted, and the factors retained were identified on the basis of their biological meaning and relationship with the original variables, as well as showing an eigenvalue  $\geq 1$  as threshold (Kaiser criterion; Russel, 2002). The individual factor scores obtained for each retained latent factor were then treated as a new variable to be analyzed (Macciotta et al., 2006).

Morphological factor traits were then analyzed in single trait animal model using the AIREML program from the BLUPF90 family (Misztal, 2008), by applying the following model, in accordance with a previous study carried out on the ARP breed (Mazza et al., 2016):

$$y_{ijkl} = \text{HYC}_i + \text{AC}_j + \text{DIM}_k + a_l + e_{ijkl}, \quad [1]$$

where  $y_{ijkl}$  is the morphological factor score for cow  $l$ ;  $\text{HYC}_i$ ,  $\text{AC}_j$ , and  $\text{DIM}_k$  are 3 fixed systematic effects of herd-year-classifier (7,280 different levels), age at calving (5 classes), and DIM (7 classes of 30-d intervals), respectively;  $a_l$  is the random additive effect of cow  $l$ ; and  $e_{ijkl}$  is the random residual term.

In a second step, a repeatability single trait TD model on milk, fat, and protein TD records was run as a linear mixed model through the AIREML program from the BLUPF90 family (Misztal, 2008):

$$y_{ijklmnop} = \text{HTDL}_{ij} + \text{GL}_k + \sum_{n=1}^4 \alpha_{jln} \times z_n(t) + \sum_{n=1}^4 \beta_{jmn} \times z_n(t) + \text{Pe}_o + a_o + e_{ijklmnop}, \quad [2]$$

where  $y_{ijklmnop}$  is the TD record  $p$  (milk, fat, or protein) of the cow  $o$ ;  $\text{HTDL}_{ij}$  is the fixed effect of the herd-test-day  $i$  for lactation  $j$  (46,722 levels);  $\text{GL}_k$  is the fixed effect of gestation length class  $k$  (16 classes of 15-d intervals);  $\alpha_{jln}$  is the fixed regression coefficient

$n$  specific to the age at calving  $l$  and lactation  $j$  (42 classes);  $\beta_{jmn}$  is the fixed regression coefficient  $n$  specific to the month  $m$  of the year in which the cow had the calving, and lactation  $j$  (36 classes);  $\text{Pe}_o$  is the random permanent environmental effect of the cow  $o$ ;  $a_o$  is the random additive genetic effect of the cow  $o$ ;  $z_n(t)$  is a vector of covariates of size  $n$  (with  $n = 4$ ) describing the shape of lactation curve of fixed effects evaluated at DIM  $t$ ; and  $e_{ijklmnop}$  is the random residual term. The fixed regression coefficients were fitted with a 4th order Legendre polynomials (Strabel and Misztal, 1999).

Last, a series of 15 bivariate analyses considering all the possible trait pairs obtained by using both TD records (milk, fat, and protein one by one) and the factor scores achieved at first step through the MORPH data set were set up to estimate (co)variance components for the variance components specified under the univariate models [1] and [2]. The effects in the previous 2 models were used jointly in the bivariate model (Kadarmideen and Wegmann, 2003).

The assumptions on estimated (co)variances for the bi-trait analyses were obtained as  $\mathbf{Pe} \otimes \mathbf{I}$ ,  $\mathbf{G} \otimes \mathbf{A}$  and  $\mathbf{R} \otimes \mathbf{I}$ , with  $\mathbf{Pe}$ ,  $\mathbf{G}$ , and  $\mathbf{R}$  as  $2 \times 2$  matrices respectively including the permanent environmental, additive genetic, and residual (co)variance matrices of the respective trait pair;  $\mathbf{A}$  and  $\mathbf{I}$  are the additive relationships matrix and an identity matrix; and  $\otimes$  is the Kronecker product. The residual covariance was set at zero in bi-trait analyses of MORPH versus TD data because those traits were recorded at different times. A permanent environmental covariance was assumed in bivariate analyses including morphological traits although they were recorded only once in individuals, to make it possible to investigate feasible biological relationships between trait pairs due to the common environment represented by the individual (Careau et al., 2013), and to avoid a possible overestimation of the genetic covariance. The permanent environmental variance for morphological traits has to be summed to the residual variance (Henderson, 1985; Hanford et al., 2002).

Genetic and phenotypic correlations between traits were calculated using the corresponding variances and covariances [phenotypic (co)variances included the sum of all the other respective (co)variances]. The standard error of heritability and correlations were calculated following the "delta method" outlined in Lynch and Walsh (1998) and considering the variances of the estimated (co)variance matrices.

## RESULTS

Descriptive statistics of all analyzed variables are reported in Table 1. The means of the individual mor-

phological traits approximated the value of 3; that is, the most desirable value for udder depth, teat placement rear view, and teat length. The lowest and highest mean values observed for morphological traits were for teat placement rear view and rear udder attachment. In general, milk traits proved more variable than morphological scores, with a mean CV that was almost 30% greater than for the latter traits (Table 1).

A description of each phenotypic factor based on the traits with loading coefficients  $\leq -0.30$  or  $\geq 0.30$  (Mantovani et al., 2005) is shown in Table 2. From loading coefficients of factor analysis, it was evident that factor 1 (**F1**) included the 4 individual muscularity traits (front muscularity; back, loins, and rump; thigh and buttocks: side and rear view); factor 2 (**F2**) represented 3 udder size traits, typically providing information about udder size (fore and rear udder attachments and udder width); and factor 3 (**F3**) included 3 further udder traits related to udder conformation (udder depth, teat placement rear view, and teat length). Teat length was counted in F3 with an opposite sign with respect to its phenotypic variation (i.e., increasing values of F3 corresponded to a decrease in trait phenotypic score). The 3 factors accounted for 63.8% of the total variance of traits, almost half of this by the first factor. Eigenvalues of retained factors were greater than 1, and ranged from 3.082 of F1 to 1.145 of F3. The proportion of variation in the morphological traits explained by the 3 retained factors (i.e., the communality of each trait) was  $\geq 0.70$  for the muscularity traits and for rear udder attachment and udder width,  $\geq 0.50$  for fore udder attachment and udder depth, and  $< 0.50$  for teat length and teat placement rear view, in order. The latter is the trait whose variation is least explained by the 3 factors (communality = 0.398), whereas the thigh, buttocks rear view is the trait showing the greatest proportion of

variance (communality = 0.790) accounted for by the 3 factors.

Heritability estimates ( $h^2$ ) from the univariate analysis (Table 3) for morphological factors described above proved moderate ( $h^2 = 0.314$  for F1,  $h^2 = 0.166$  for F2, and  $h^2 = 0.196$  for F3) and slightly lower estimates were found for yield traits ( $h^2 = 0.198$  for milk,  $h^2 = 0.132$  for fat, and  $h^2 = 0.169$  for protein). Standard errors of heritability ( $SE_h^2$ ) estimates were low, with values between  $SE_h^2 = 0.013$  and  $SE_h^2 = 0.018$  for all analyzed traits. Substantial variance estimates were obtained for milk yield, in particular for the permanent environmental variance, showing a value of 3.554.

Table 4 reported the genetic and the phenotypic correlations estimated within and between morphological factor scores and test-day milk traits, and the respective standard errors. The udder size factor (i.e., F2) showed negative genetic correlations with both muscularity and udder conformation factors. However, a positive but low genetic correlation was found between muscularity (F1) and udder conformation (F3) factors. Phenotypic correlations within the 3 factors were very low and close to zero. All 3 milk yield traits showed positive and high genetic correlations. The phenotypic correlations were slightly lower than the genetic ones apart from milk and protein yield, but greater than the phenotypic correlations within factors. Regarding the genetic correlations between morphological factors and milk-related traits, F1 and F3 showed medium negative associations with all 3 productive traits ( $r_a = -0.38 \pm 0.04$  and  $-0.25 \pm 0.03$ ), whereas F2 gave strong and positive genetic correlations with them ( $r_a = 0.65 \pm 0.04$ ). The phenotypic correlations had the same sign but were lower in magnitude than the genetic ones. For all genetic correlations, the standard errors were lower than 0.07, whereas for the phenotypic correlations they

**Table 2.** Phenotypic factors, loading of individual morphological traits (coefficients  $\leq -0.30$  or  $\geq 0.30$  are reported), communality and eigenvalues obtained after Varimax rotation of 10 morphological traits recorded on 32,275 Aosta Red Pied cows

Morphological trait	Varimax phenotypic factor			Communality
	Factor 1	Factor 2	Factor 3	
Front muscularity	0.854			0.730
Back, loins, and rump	0.878			0.772
Thigh, buttocks: side view	0.881			0.778
Thigh, buttocks: rear view	0.888			0.790
Fore udder attachment		0.716		0.525
Rear udder attachment		0.854		0.730
Udder width		0.850		0.728
Udder depth			0.704	0.513
Teat placement rear view			0.497	0.398
Teat length			-0.620	0.418
Variance explained (%)	30.75	21.50	11.57	
Eigenvalue	3.082	2.155	1.145	

**Table 3.** Estimated variances, heritability ( $h^2$ ), and standard error of heritability ( $SE_h^2$ ) for morphological factor scores and test-day milk yield (single trait analyses)

Trait	Variance <sup>1</sup>			$h^2$	$SE_h^2$
	$\sigma_{pe}^2$	$\sigma_a^2$	$\sigma_e^2$		
Morphological factor score <sup>2</sup>					
Factor 1: Muscularity	—	0.251	0.549	0.314	0.017
Factor 2: Udder size	—	0.130	0.651	0.166	0.014
Factor 3: Udder conformation	—	0.162	0.667	0.196	0.015
Test-day yield <sup>3</sup> (kg/d)					
Milk	3.554	1.311	1.740	0.198	0.018
Fat	0.004	0.002	0.006	0.132	0.013
Protein	0.003	0.001	0.002	0.169	0.016

<sup>1</sup>Where  $\sigma_{pe}^2$  is the permanent environmental variance;  $\sigma_a^2$  is the additive genetic variance; and  $\sigma_e^2$  is the residual variance.

<sup>2</sup>Estimated from a data set accounting for 32,275 individual records obtained from primiparous Aosta Red Pied cows.

<sup>3</sup>Estimated from a data set accounting for 169,008 test-days belonging to 16,605 Aosta Red Pied cows.

were under 0.001. In both cases, lower estimates were found within TD trait correlations.

## DISCUSSION

Several studies have reported high genetic correlations among traits referring to the same body region (Foster, 1985; Vanraden et al., 1990; Mazza et al., 2014). As a result of this and also due to the very high number of linear type traits usually scored, factor analysis has been successfully applied to cattle breeding to remove redundant information and apply a smaller set of derived factors. Factor scores have been reported for type traits in few breeds, such as Swiss Brown (Vukasinović et al., 1997), Rendena (Mazza et al., 2016), Chianina,

Marchigiana, and Romagnola (Forabosco et al., 2005), or referred to large sets of other traits [e.g., milk production traits (Macciotta et al., 2006) and fighting behavior (Pelayo et al., 2015)].

In the present study, a subset of the whole number of morphological traits routinely scored, those related to dairy and beef characteristics, allowed us to describe 3 main factors with a quite clear biological meaning. An advantage of factor analysis is that, consistent with the sign and magnitude of the loading coefficients, particular factors can be easily interpreted physically or biologically (Vukasinović et al., 1997; Macciotta et al., 2006) and they may work as target traits in animal breeding programs. Each of the 3 factors obtained in this study can be easily interpreted as a descriptor of

**Table 4.** Genetic (above the diagonal) and phenotypic (below the diagonal) correlations within morphological factor scores and test-day milk traits, and between factor scores and milk traits (SE of estimates are in parentheses)<sup>1</sup>

Trait	Morphological factor score <sup>2</sup>			Test-day yield		
	F1	F2	F3	Milk	Fat	Protein
Morphological factor score						
F1		−0.376 (0.048)	0.214 (0.049)	−0.417 (0.051)	−0.374 (0.054)	−0.347 (0.055)
F2	−0.088 (0.006)		−0.117 (0.060)	0.682 (0.047)	0.597 (0.053)	0.663 (0.049)
F3	0.059 (0.007)	0.076 (0.006)		−0.284 (0.063)	−0.221 (0.066)	−0.248 (0.065)
Test-day yield (kg/d)						
Milk	−0.141 (0.009)	0.294 (0.007)	−0.067 (0.009)		0.790 (0.023)	0.874 (0.013)
Fat	−0.099 (0.007)	0.224 (0.007)	−0.037 (0.007)	0.761 (0.002)		0.863 (0.017)
Protein	−0.102 (0.008)	0.278 (0.007)	−0.060 (0.008)	0.910 (0.001)	0.763 (0.002)	

<sup>1</sup>Obtained from a data set accounting for 201,283 records belonging to 35,530 animals (13,350 with both morphological factor scores and test-day milk traits).

<sup>2</sup>F1 = factor 1 (i.e., muscularity), F2 = factor 2 (i.e., udder size), and F3 = factor 3 (i.e., udder conformation).

specific morphological features such as muscularity, udder size, and udder conformation. The Varimax rotation (Kaiser, 1958) applied in the analysis allowed us to obtain factors with a low number of large loadings, and therefore each factor represented only a few variables which often have biological relationships.

The heritability estimates of morphological factors obtained in this study were in agreement with a previous analysis carried out on the same breed (Mazza et al., 2016), with the muscularity factor showing the greatest heritability value ( $h^2 = 0.31$ ), followed by the udder conformation factor ( $h^2 = 0.20$ ) and the udder size factor ( $h^2 = 0.17$ ). Slightly higher heritability estimates for factor scores underlying the same biological meaning ( $h^2 = 0.40$ ,  $h^2 = 0.31$ ,  $h^2 = 0.45$ , respectively) were found in the same study for the Rendena breed (Mazza et al., 2016). To compare these results with other studies on heritability of factors is very difficult, as literature reports only a little research focused on the genetics of factors obtained from factor analysis. In their work on Swiss Brown cattle, Vukasinovič et al. (1997) recognized phenotypic factors similar to the ones found in Mazza et al. (2016) and those in the present study (referring to udder, teats, and muscularity), but no estimates of variance components for factor scores were performed by either Vukasinovič et al. (1997) or Forabosco et al. (2005), who reported a factor 1 of muscle development in 3 breeds belonging to the Italian beef cattle. Nevertheless, several studies on dual-purpose breeds showed values of heritability for the individual linear type traits similar to the estimates for factors with the same biological meaning (e.g., Wiggans et al., 2004; Zavadilová et al., 2009; Mazza et al., 2013), and this stimulates a possible use of factor analysis in animal breeding (e.g., to summarize the information of many type traits involved in selection practice). Studies on relationships between type, 305-d milk yield, and milk quality traits have been conducted on some specialized Italian dairy breeds. Generally, traits associated with body size have shown positive correlations with 305-d milk yield in Holstein (Foster et al., 1989; Misztal et al., 1992). Some udder-related traits, such as udder cleft and depth, had negative relationships with milk production, whereas rear udder height and rear udder width presented small positive correlations (Foster et al., 1989; Short and Lawlor, 1992; Sanjabi et al., 2003).

Concerning the heritabilities for milk yield traits, the estimates for the current study are in agreement with those reported in literature obtained with the same or a different kind of model, although the mean productive levels of the ARP cows are typically much lower than those observed in specialized breeds (Mostert et al., 2006), in which a stronger selective pressure for

milk is exerted. The heritability estimates reported in this study for milk, fat, and protein yield were close to values obtained for specialized Holstein as in Swalve (1995), where values of  $h^2 = 0.28$  for milk,  $h^2 = 0.18$  for fat, and  $h^2 = 0.19$  for protein yield have been reported. In the Guernsey breed, Mostert et al. (2006) estimated heritability values of  $h^2 = 0.24$  for milk,  $h^2 = 0.13$  for fat, and  $h^2 = 0.19$  for protein yields. Using a repeatability test-day model similar to the one of this study, the heritability estimates in the local Italian dual-purpose Rendena breed were closer to observations reported for more specialized breeds [i.e.,  $h^2 = 0.21$  for milk,  $h^2 = 0.17$  for fat, and  $h^2 = 0.17$  for protein (Guzzo et al., 2009)]. Slightly lower heritability values ranging from  $h^2 = 0.10$  for fat to  $h^2 = 0.18$  for milk yield were reported for the Jersey breed by Mostert et al. (2006), and also for the Italian Brown Swiss by Dal Zotto et al. (2005), who estimated heritability at  $h^2 = 0.11$ .

Genetic and phenotypic correlations within morphological factors observed in this study reflect the correlations between individual morphological traits included in each factor (Mazza et al., 2015). The negative genetic correlation between muscularity and udder size factors (F1 and F2, respectively) observed ( $r_a = -0.376$ ; F1 vs. F2) is in accordance with findings on genetic correlations between the individual fleshiness traits and the 3 individual udder size traits in the same breed, ranging from  $-0.42$  to  $-0.19$  (Mazza et al., 2015). In addition, analyses carried out on the Italian Rendena dual-purpose breeds characterized by traits to be evaluated and scoring system similar to the ARP, genetic correlations between muscularity traits and udder size traits obtained after factorization had a similar range [i.e., from  $-0.53$  to  $-0.26$  (Mazza et al., 2014)]. Comparable negative correlations between muscularity and udder size traits have also been reported in some specialized dairy and beef cattle, as for example the Ayrshire (from  $r_a = -0.41$  to  $r_a = -0.12$ ; Mrode and Swanson, 1994) and in the Italian Piemontese beef cattle (from  $r_a = -0.19$  to  $r_a = -0.15$ ; Mantovani et al., 2010). These results indicate that a too high selective pressure for meat production and for more accentuated muscle development, leads to smaller and lower udders. Consequently, the strong and positive genetic correlations observed in this study between udder size factor and the 3 milk yield traits mean that wider udders produce more milk, as expected from a biological point of view. The positive genetic correlations among udder size traits, especially rear udder attachment and udder width, and milk yield underlie the development of the dairy form of the breeds specialized for milk production. Indeed, strong genetic correlations were reported for udder size and milk yield traits in Holstein Friesian cattle (Sanjabi et al., 2003; Berry et al., 2004), in the

Guernsey breed (Norman et al., 1988; Cruickshank et al., 2002), in the Brown Swiss (Samoré et al., 2010), and in the Aosta Chestnut breed (Sartori et al., 2015), closely related to the ARP. Samoré et al. (2010), for example, reported for the Italian Brown Swiss genetic correlations from 0.22 to 0.45 of production traits with fore udder attach, rear udder width, and rear udder height, indicating that the more productive cows are characterized by a greater udder size.

Regarding the genetic correlations within the group of the milk yield traits, the strong and positive genetic correlations are in agreement with literature reported for other breeds. For example, Mostert et al. (2006) described genetic correlations between milk, fat, and protein, using a repeatability TD model, ranging from 0.89 to 0.91 in the Ayrshire breed, from 0.85 to 0.92 in the Guernsey breed, from 0.80 to 0.97 in the Holstein, and from 0.78 to 0.90 in the Jersey breed. Slightly lower but positive genetic correlations among milk, fat, and protein were also found in Holstein-Friesian, Brown Swiss, and their crosses by Dechow et al. (2007) who estimated  $r_a$  values ranging between 0.46 and 0.81. In the study of Dechow et al. (2007), the phenotypic correlations among milk yield traits were close to the genetic ones, as found in the present study, where a strong correlation within milk yield traits was also observed at phenotypic level. Conversely, the negative genetic correlations observed between muscularity factor and milk yield traits reflect the correlations between individual muscularity traits and milk found in Aosta Chestnut (Sartori et al., 2015) and in other dual-purpose (e.g., Red and White, de Haas et al., 2007; Simmental, Frigo et al., 2013; and Rendena, Mazza et al., 2014) or dairy breeds (e.g., Brown Swiss, de Haas et al., 2007). These findings provide examples of the antagonism existing between dairy and beef attitudes, explained by Royal et al. (2002) as the result of the gluconeogenesis occurring in milk production, involving the mobilization of energy from tissues and from both fat and protein reserves.

Some morphological traits accounted for in the udder conformation factor (F3) have shown different correlations between them and with udder size traits depending on the study considered. For example, genetic correlation between teat placement rear view and fore udder attach produced a similar value in the ARP ( $r_a = -0.21$ ; Mazza et al., 2015) or in the Brown Swiss breed ( $r_a = -0.29$ ; Samoré et al., 2010), but proved quite different in Holstein-Friesian ( $r_a = 0.01$ ; Berry et al., 2004). Udder conformation traits entered in F3 with different signs of loadings both in the present study and in previous works on ARP and Rendena breeds (Mantovani et al., 2005; Mazza et al., 2016), and the low and negative genetic relationship with F2 obtained in this study summarize the various relation-

ships involving traits related to udder conformation. The genetic relationships of udder conformation with milk yield traits and muscularity factor, respectively negative and positive, suggest that a strong selection for milk production leads to a wider but also slightly enlarged and misshapen udder, whereas a selection for muscularity and meat production observes a shift to a narrower udder. Optimal values for udder conformation are likely to be reached when a balanced selection for both milk and meat attitudes is carried out considering that udder conformation traits, underlying the factor, have intermediate optima. Udder width, the type trait entering F3 with the greater loading, also showed positive genetic correlations with muscularity traits both in ARP (Mazza et al., 2015) and other breeds (e.g., Brown Swiss, Samoré et al., 2010; Rendena, Mazza et al., 2014), and negative correlation with milk yield (e.g., Berry et al., 2004; Samoré et al., 2010).

## CONCLUSIONS

Results of this study indicated the muscularity factor and the milk yield as traits with a medium heritability. Based on the estimated genetic correlation, selection for increasing milk production is expected to decrease muscularity and udder conformation, whereas it expands the udder size. These results could be of interest in planning correct weights for antagonistic traits related to milk and beef attitude in a selection process when the goal is for the dual purpose, as in the ARP breed used in this investigation as a case study. Furthermore, the introduction of functional traits such as udder conformation in selection aims may be substantial in dual-purpose breeds, sometimes forced to stronger selective pressure for milk improvement. Finally, from this study it is possible to observe that, for dual-purpose breeds, factor scores represent feasible options to simultaneously improve type traits relevant to beef attitude.

## ACKNOWLEDGMENTS

The authors are grateful to the National Breeders Association of the Valdostana breed (ANABoRaVa), Aosta, Italy, for providing data and for its financial support to the study.

## REFERENCES

- Aass, L. 1996. Variation in carcass and meat quality traits and their relations to growth in dual purpose cattle. *Livest. Prod. Sci.* 46:1–12.
- Ali, A. K., K. R. Koots, and E. B. Burnside. 1998. Factor analysis of genetic evaluations for type traits of Canadian Holstein sires and cows. *Asian-australas. J. Anim. Sci.* 11:463–469.
- ANABoRaVa (Associazione Nazionale Allevatori Bovini di Razza Valdostana). 2015a. *Disciplinare del libro genealogico della razza bo-*



- vina Valdostana. Accessed Nov. 5, 2015. <http://www.anaborava.it/pdf/disciplinare%20ANABORAVA%20completo.pdf>.
- ANABORaVa (Associazione Nazionale Allevatori Bovini di Razza Valdostana). 2015b. Attività CTC. Accessed Nov. 15, 2015. [http://www.anaborava.it/lg\\_attivitactc.html](http://www.anaborava.it/lg_attivitactc.html).
- Berry, D. P., F. Buckley, P. Dillon, R. D. Evans, and R. F. Veerkamp. 2004. Genetic relationships among linear type traits, milk yield, body weight, fertility and somatic cell count in primiparous dairy cows. *Ir. J. Agric. Food Res.* 43:161–176.
- Bilal, G., and M. S. Khan. 2009. Use of test-day milk yield for genetic evaluation in dairy cattle: A review. *Pakistan Vet. J.* 29:35–41.
- Cappelloni, M. 2013. Sviluppo di metodi per la gestione di razze autoctone italiane. PhD Thesis. University of Padua, Padua, Italy.
- Careau, V., M. E. Wolak, P. A. Carter, and T. Garland. 2013. Limits to behavioural evolution: The quantitative genetics of a complex trait under directional selection. *Evolution* 67:3102–3119.
- Cruickshank, J., K. A. Weigel, M. R. Dentine, and W. Kirkpatrick. 2002. Indirect prediction of herd life in Guernsey dairy cattle. *J. Dairy Sci.* 85:1307–1313.
- Dal Zotto, R. 2000. Comparison of different test day models for genetic evaluation of Italian Brown dairy cattle. *Interbull Bull.* 25:95–98.
- Dal Zotto, R., P. Carnier, L. Gallo, G. Bittante, and M. Cassandro. 2005. Genetic relationship between body condition score, fertility, type and production traits in Brown Swiss dairy cows. *Ital. J. Anim. Sci.* 4:30–32.
- de Haas, Y., L. L. G. Janss, and H. N. Kadarmideen. 2007. Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. *J. Anim. Breed. Genet.* 124:12–19.
- De Lorenzo, M. A., and R. W. Everett. 1982. Relationships between milk and fat production, type, and stayability in Holstein sire evaluation. *J. Dairy Sci.* 65:1277–1285.
- Dechow, C. D., G. W. Rogers, J. B. Cooper, M. I. Phelps, and A. L. Mosholder. 2007. Milk, fat, protein, somatic cell score, and days open among Holstein, Brown Swiss, and their crosses. *J. Dairy Sci.* 90:3542–3549.
- Degano, L., D. Marcomin, D. Vicario, B. Contiero, and P. Carnier. 2003. Applicability of different test day models and effect on time at first evaluation of Italian Simmental bulls. *Ital. J. Anim. Sci.* 2(Suppl. 1):43–45.
- DeGroot, B. J., J. F. Keown, L. D. Van Vleck, and E. L. Marotz. 2002. Genetic parameters and responses of linear type, yield traits, and somatic cell scores to divergent selection for predicted transmitting ability for type in Holsteins. *J. Dairy Sci.* 85:1578–1585.
- Del Bo, L., M. Polli, M. Longeri, G. Ceriotti, C. Looft, A. Barre-Dirie, G. Dolf, and M. Zanotti. 2001. Genetic diversity among some cattle breeds in the Alpine area. *J. Anim. Breed. Genet.* 118:317–325.
- FAO. 2015. Valdostana Pezzata Rossa. Accessed Nov. 5, 2015. [http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=66cf740b766d7420a481dc b00be88a2f,reportsreport8a\\_50001614](http://dad.fao.org/cgi-bin/EfabisWeb.cgi?sid=66cf740b766d7420a481dc b00be88a2f,reportsreport8a_50001614).
- Felius, M., P. A. Koolmees, B. Theunissen, J. A. Lenstra, and European Cattle Genetic Diversity Consortium. 2011. On the breeds of cattle—Historic and current classifications. *Diversity (Basel)* 3:660–692.
- Forabosco, F., E. Rossetti, F. M. Sarti, F. Panella, G. Bittante, R. Mantovani, and F. Filippini. 2005. Morphological factorials for females of the Chianina, Marchigiana and Romagnola breeds. Pages 163–168 in *Proc. 4th World Italian Beef Cattle Congress*, Gubbio, Italy.
- Foster, W. W. 1985. Effects of first lactation linear type scores on first lactation production and herd life of Holstein dairy cattle. MS Thesis. Parks Library, Department of Animal Science, Iowa State Univ., Ames.
- Foster, W. W., A. E. Freeman, P. J. Berger, and A. Kuck. 1989. Association of type traits scored linearly with production and herd life of Holsteins. *J. Dairy Sci.* 72:2651–2664.
- Frigo, E., A. B. Samorè, D. Vicario, A. Bagnato, and O. Pedron. 2013. Heritabilities and genetic correlations of body condition score and muscularity with productive traits and their trend functions in Italian Simmental cattle. *Ital. J. Anim. Sci.* 12:240–246.
- Gandini, G. C., and E. Villa. 2003. Analysis of the cultural value of local livestock breeds: A methodology. *J. Anim. Breed. Genet.* 120:1–11.
- Guzzo, N., C. Sartori, and R. Mantovani. 2009. Test day-milk yields variance component estimation using repeatability or random regression models in the Rendena breed. *Ital. J. Anim. Sci.* 8(Suppl. 3):71–73.
- Hanford, K. J., L. D. Van Vleck, and G. D. Snowder. 2002. Estimates of genetic parameters and genetic change for reproduction, weight, and wool characteristics of Columbia sheep. *J. Anim. Sci.* 80:3086–3098.
- Henderson, C. R. 1985. Equivalent linear models to reduce computations. *J. Dairy Sci.* 68:2267–2277.
- Kadarmideen, H. N., and S. Wegmann. 2003. Genetic relationship among body condition score, type, fertility and production traits in Swiss Holstein cattle. *AAABG* 15:77–81.
- Kaiser, H. F. 1958. The Varimax criterion for analytic rotation in factor analysis. *Psychometrika* 23:187–200.
- Kirkpatrick, M., W. G. Hill, and R. Thompson. 1994. Estimating the covariance structure of traits during growth and ageing, illustrated with lactation in dairy cattle. *Genet. Res.* 64:57–69.
- Krupová, Z., E. Krupa, M. Michalíčková, M. Wolfová, and R. Kasarda. 2016. Economic values for health and feed efficiency traits of dual-purpose cattle in marginal areas. *J. Dairy Sci.* 99:644–656.
- Liinamo, A. E., M. Ojala, and J. Van Arendonk. 2001. Genetic relationship of meat and milk production in Finnish Ayrshire. *Livest. Prod. Sci.* 69:1–8.
- Lynch, M., and B. Walsh. 1998. *Genetics and Analysis of Quantitative Traits*. Vol. 1. Sinauer, Sunderland, MA.
- Macciotta, N. P. P., A. Cecchinato, M. Mele, and G. Bittante. 2012. Use of multivariate factor analysis to define new indicator variables for milk composition and coagulation properties in Brown Swiss cows. *J. Dairy Sci.* 95:7346–7354.
- Macciotta, N. P. P., D. Vicario, and A. Cappio-Borlino. 2006. Use of multivariate analysis to extract latent variables related to level of production and lactation persistency in dairy cattle. *J. Dairy Sci.* 89:3188–3194.
- Mantovani, R., M. Cassandro, B. Contiero, A. Albera, and G. Bittante. 2010. Genetic evaluation of type traits in hypertrophic Piemontese cows. *J. Anim. Sci.* 88:3504–3512.
- Mantovani, R., I. Cerchiaro, and B. Contiero. 2005. Factor analysis for genetic evaluation of linear type traits in dual purpose breeds. *Ital. J. Anim. Sci.* 4:31–33.
- Mazza, S., N. Guzzo, C. Sartori, D. P. Berry, and R. Mantovani. 2014. Genetic parameters for linear type traits in the Rendena dual-purpose breed. *J. Anim. Breed. Genet.* 131:27–35.
- Mazza, S., N. Guzzo, C. Sartori, and R. Mantovani. 2016. Factor analysis for genetic evaluation of linear type traits in dual-purpose autochthonous breeds. *Animal* 10:372–380.
- Mazza, S., C. Sartori, D. P. Berry, and R. Mantovani. 2013. Factors affecting linear type traits of Valdostana cattle. *Agric. Consepec. Sci.* 78:207–211.
- Mazza, S., C. Sartori, and R. Mantovani. 2015. Genetic parameters of type traits in two strains of dual purpose autochthonous Valdostana cattle. *Livest. Sci.* 178:35–42.
- Meyer, K. 1995. Estimates of genetic parameters for mature weight of Australian beef cows and its relationship to early growth and skeletal measures. *Livest. Prod. Sci.* 44:125–137.
- Misztal, I. 2008. Reliable computing in estimation of variance components. *J. Anim. Breed. Genet.* 125:363–370.
- Misztal, I., T. J. Lawlor, T. H. Short, and P. M. Vanraden. 1992. Multiple-trait estimation of variance components of yield and type traits using an animal model. *J. Dairy Sci.* 75:544–551.
- Mostert, B. E., H. E. Theron, F. H. J. Kanfer, and E. van Marle-Köster. 2006. Test-day models for South African dairy cattle for participation in international evaluations. *S. Afr. J. Anim. Sci.* 36:58–70.
- Mrode, R. A., and G. J. T. Swanson. 1994. Genetic and phenotypic relationships between conformation and production traits in Ayrshire heifers. *Anim. Prod.* 58:335–338.

- Muir, B. L., G. Kistemaker, J. Jamrozik, and F. Canavesi. 2007. Genetic parameters for a multiple-lactation random regression test-day model in Italian Holsteins. *J. Dairy Sci.* 90:1564–1574.
- Norman, H. D., R. L. Powell, J. R. Wright, and B. G. Cassel. 1988. Phenotypic and genetic relationship between linear functional type traits and milk yield for five breeds. *J. Dairy Sci.* 71:1880–1896.
- Pelayo, R., M. Solé, M. J. Sánchez, A. Molina, and M. Valera. 2015. Behavioural linear standardized scoring system of the Lidia cattle breed by testing in herd: Estimation of genetic parameters. *J. Anim. Breed. Genet.* <http://onlinelibrary.wiley.com/doi/10.1111/jbg.12198/pdf>.
- Pirchner, F. 1986. Evaluation of industry breeding programs for dairy cattle milk and meat production. Paper 46 in Proc. 3rd World Congress on Genetics Applied to Livestock Production, Lincoln, NE. Digital Commons Network, Bepress, Berkeley, CA.
- Royal, M. D., J. E. Pryce, J. A. Woolliams, and A. P. F. Flint. 2002. The genetic relationship between commencement of luteal activity and calving interval, body condition score, production, and linear type traits in Holstein-Friesian dairy cattle. *J. Dairy Sci.* 85:3071–3080.
- Russel, D. W. 2002. In search of underlying dimensions: The use (and abuse) of factor analysis in personality and social psychology. *Pers. Soc. Psychol. Bull.* 28:1629–1646.
- Samoré, A. B., G. Pagnacco, and F. Miglior. 1997. Genetic parameters and breeding values for linear type traits in the Haflinger horse. *Livest. Prod. Sci.* 52:105–111.
- Samoré, A. B., R. Rizzi, A. Rossoni, and A. Bagnato. 2010. Genetic parameters for functional longevity, type traits, somatic cell scores, milk flow and production in the Italian Brown Swiss. *Ital. J. Anim. Sci.* 9:145–152.
- Sanjabi, M. R., M. G. Govindaiah, and M. M. Moeini. 2003. Relationships among udder type traits and milk yield of Iranian Holstein-Friesian cattle. Page 141 in Proceedings of the British Society of Animal Science. Cambridge University Press, Cambridge, UK.
- Sartori, C., S. Mazza, N. Guzzo, and R. Mantovani. 2015. Evolution of increased competitiveness in cows trades off with reduced milk yield, fertility and more masculine morphology. *Evolution* 69:2235–2245.
- Schaeffer, L. R., J. Jamrozik, G. J. Kistemaker, and J. Van Doormaal. 2000. Experience with a test-day model. *J. Dairy Sci.* 83:1135–1144.
- Short, T. H., and T. J. Lawlor. 1992. Genetic parameters of conformation traits, milk yield, and herd life in Holsteins. *J. Dairy Sci.* 75:1987–1998.
- Sieber, M., A. E. Freeman, and P. N. Hinz. 1987. Factor analysis for evaluating relationship between first lactation type score and production data in Holstein dairy cows. *J. Dairy Sci.* 70:1018–1026.
- Sölkner, J., J. Miesenberger, A. Willam, C. Fürst, and R. Baumung. 2000. Total merit indices in dual purpose cattle. *Arch. Tierz.* 43:597–608.
- Strabel, T., and I. Misztal. 1999. Genetic parameters for first and second lactation milk yields of Polish Black and White cattle with random regression test-day models. *J. Dairy Sci.* 82:2805–2810.
- Swalve, H. H. 1995. The effect of test day models on the estimation of genetic parameters and breeding values for daily yield traits. *J. Dairy Sci.* 78:929–938.
- Thompson, J. R., A. E. Freeman, D. J. Wilson, C. A. Chapin, P. J. Berger, and A. Kuck. 1981. Evaluation of a linear type program in Holstein. *J. Dairy Sci.* 64:1610–1617.
- Vanraden, P. M., E. L. Jonsen, T. J. Lawlor, and D. A. Funk. 1990. Prediction of transmitting abilities for Holstein type traits. *J. Dairy Sci.* 73:191–197.
- Vukasinovič, N., J. Moll, and N. Künzi. 1997. Factor analysis for evaluating relationship between herd life and type traits in Swiss Brown cattle. *Livest. Prod. Sci.* 49:227–234.
- Wiggans, G. R., N. Gengler, and J. R. Wright. 2004. Type trait (co) variance components for five dairy breeds. *J. Dairy Sci.* 87:2324–2330.
- Zavadilová, L., E. Němcová, M. Štípková, and J. Bouška. 2009. Relationships between longevity and conformation traits in Czech Fleckvieh cows. *Czech J. Anim. Sci.* 54:387–394.