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Short communication: Genetic relationships of milk coagulation properties with body condition score and linear type traits in Holstein-Friesian cows[1]

M. Cassandro,* M. Battagin,† M. Penasa,*[2] and M. De Marchi*
*Department of Agronomy, Food, Natural Resources, Animals and Environment, University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy
†Associazione Nazionale Allevatori Frisona Italiana, 26100 Cremona, Italy

ABSTRACT

Milk coagulation properties (MCP) are gaining popularity among dairy cattle producers and the improvement of traits associated with MCP is expected to result in a benefit for the dairy industry, especially in countries with a long tradition in cheese production. The objectives of this study were to estimate genetic correlations of MCP with body condition score (BCS) and type traits using data from first-parity Italian Holstein-Friesian cattle. The data analyzed consisted of 18,460 MCP records from 4,036 cows with information on both BCS and conformation traits. The cows were daughters of 246 sires and the pedigree file included a total of 37,559 animals. Genetic relationships of MCP with BCS and type traits were estimated using bivariate animal models. The model for MCP included fixed effects of stage of lactation, and random effects of herd-test-date, cow permanent environment, additive genetic animal, and residual. Fixed factors considered in the model for BCS and type traits were herd-date of evaluation and interaction between age at scoring and stage of lactation of the cow, and random terms were additive genetic animal, cow permanent environment, and residual. Genetic relationships between MCP and BCS, and MCP and type traits were generally low and significant only in a few cases, suggesting that MCP can be selected for without detrimental effects on BCS and linear type traits.

Key words: milk coagulation ability, type trait, body condition score, genetic correlation

Short Communication

Milk coagulation properties (**MCP**) have been proposed as technological traits to improve the efficiency of the cheese-making process and cheese yield (Riddell-Lawrence and Hicks, 1989; Pretto et al., 2013) and are especially popular in countries with a long tradition in cheese making. In Italy, more than 70% of the overall milk production is used to manufacture cheese and thus MCP are of great importance. The assessment of MCP at a population level depends on the availability of fast and cheap technologies such as mid-infrared spectroscopy (**MIRS**), which has been successfully used for the prediction of MCP (De Marchi et al., 2013, 2014; Penasa et al., 2014). Several studies have estimated the additive genetic variance and heritability of coagulation properties, especially rennet coagulation time (**RCT**, min) and curd firmness ($\mathbf{a_{30}}$, mm; e.g., Ikonen et al., 2004; Penasa et al., 2010), suggesting that selection for enhancing these characteristics is feasible.

An important functional and managerial trait in dairy cow is BCS, which is useful to appraise the body fat reserves and energy status of cattle. Changes in BCS reflect both the body composition and energy balance of the animal, which are critical for metabolic stability, health, and fertility. Impaired reproductive performance has a large economic impact on efficiency of dairy production, and this problem has been exacerbated by selection for milk yield (Pryce et al., 1998). The improvement of milk production has led to a worsening of the average body condition of the cow, partly as a consequence of antagonistic genetic correlations between milk yield and BCS (Pryce et al., 2001; Kadarmideen and Wegmann, 2003).

The Italian Holstein Friesian Cattle Breeders Association (**ANAFI**) has been collecting linear type traits and BCS on first-lactation cows since 1984 and 2007, respectively (Battagin et al., 2012, 2013). Conformation traits are scored using a 1- to 50-point scale system, and BCS is based on a 1 (thin) to 5 (fat) scale with 0.25-point increments (Edmonson et al., 1989). Whereas genetic evaluation for conformation has a long history in Italian Holstein-Friesian cattle, evaluation for

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[2]Corresponding author: mauro.penasa@unipd.it

BCS has been introduced only recently. No estimates of genetic relationships of MCP with BCS and linear type traits are currently available in the literature and thus the objective of this study was to assess genetic correlations between MCP and BCS and conformation using data of first-lactation Holstein-Friesian cows.

Since 2011, the laboratory of the Breeders Association of Veneto region (Padova, Italy) has added the analysis of MCP to its portfolio. Individual milk samples are routinely collected in dairy herds of Veneto region and analyzed for traditional quality traits and MCP using MIRS models installed on Milko-Scan FT6000 (Foss Electric A/S, Hillerød, Denmark). Coefficients of determination in cross-validation were 0.76 and 0.70 for RCT and a_{30}, respectively [full details on fitting statistics of MIRS equations used to predict MCP can be retrieved from De Marchi et al. (2012, 2013)]. First-lactation records from September 2011 to January 2013 were obtained from the aforementioned laboratory and edited following Tiezzi et al. (2013). Briefly, Holstein-Friesian cows between 5 and 365 DIM, with at least 2 test-day records and belonging to herd-test-date (**HTD**) classes with a minimum of 3 contemporary animals were considered. Sires were required to have at least 5 daughters in 3 herds. Records with RCT outside the range 5 to 30 min were removed from the dataset because this is the range on which the calibration model was built. Moreover, records on RCT and a_{30} were discarded if they deviated more than 3.5 SD from the respective mean, or if the corresponding record for milk yield, fat content, or protein content were beyond the mean ± 3.5 SD. Body condition score and linear type traits were recorded by ANAFI once in first-parity cows between 20 and 38 mo of age, and a description is presented in Table 1. At least 2 contemporary animals in a given herd-date of evaluation were required. After editing, 18,460 records of RCT and a_{30} from 4,036 cows progeny of 246 bulls and with information on BCS and linear type traits were available for genetic analysis. The pedigree file (37,559 animals) was supplied by ANAFI, and included individuals with phenotypic records and all their ancestors up to 8 generations back.

Genetic relationships of MCP with BCS and type traits were obtained under 40 sequential bivariate analyses in which a milk coagulation characteristic (RCT or a_{30}) was analyzed simultaneously with BCS or a type trait. The model for MCP included fixed systematic effects of stage of lactation (10 classes of DIM, the first being a class from 5 to 30 d, followed by 8 classes of 30 d each, and the last being a class from 270 to 365 d), and the model for BCS and type traits included fixed systematic effects of herd-date of evaluation (435 levels) and the interaction between age at scoring and stage of lactation of the cow (116 levels). Age at scoring was grouped in 12 classes, the first being a class from 20 to 22 mo, classes that were in the middle of this distribution were 1 mo each, and the last being a class from 33 to 38 mo. The general form of the linear animal model was as follows:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_1h} + \mathbf{Z_2p} + \mathbf{Z_3a} + \mathbf{e},$$

where $\mathbf{y}$ is the vector of observations for RCT, a_{30}, BCS, or type trait; $\mathbf{b}$ is the vector of fixed effects as previously described; $\mathbf{h}$ is the vector of random effects of HTD (only for MCP); $\mathbf{p}$ is the vector of cow permanent environmental effects; $\mathbf{a}$ is the vector of random effects of additive genetic animal; and $\mathbf{e}$ is the vector of random residuals. $\mathbf{X}$, $\mathbf{Z_1}$, $\mathbf{Z_2}$, and $\mathbf{Z_3}$ are incidence matrices of appropriate order relating the corresponding effects to the dependent variable. For the random effects, the following (co)variance structure was assumed:

$$\mathrm{Var}\begin{bmatrix}\mathbf{a}_1\\ \mathbf{a}_2\\ \mathbf{h}_1\\ \mathbf{p}_1\\ \mathbf{p}_2\\ \mathbf{e}_1\\ \mathbf{e}_2\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma^2_{a1} & \mathbf{A}\sigma_{a1a2} & 0 & 0 & 0 & 0 & 0\\ & \mathbf{A}\sigma^2_{a2} & 0 & 0 & 0 & 0 & 0\\ & & \mathbf{I}\sigma^2_{h1} & 0 & 0 & 0 & 0\\ & & & \mathbf{I}\sigma^2_{p1} & \mathbf{I}\sigma_{p1p2} & 0 & 0\\ & \textit{symm.} & & & \mathbf{I}\sigma^2_{p2} & 0 & 0\\ & & & & & \mathbf{I}\sigma^2_{e1} & 0\\ & & & & & & \mathbf{I}\sigma^2_{e2}\end{bmatrix},$$

where σ^2_{a1} and σ^2_{a2} are the additive genetic variances of traits 1 (RCT or a_{30}) and 2 (BCS or type trait), respectively; σ^2_{h1} is the HTD variance of trait 1; σ^2_{p1} is the cow permanent environmental variance of trait 1; σ^2_{e1} and σ^2_{e2} are the residual variances of traits 1 and 2, respectively; σ_{a1a2} is the additive genetic covariance between traits 1 and 2; $\mathbf{I}$ is an identity matrix of appropriate order; and $\mathbf{A}$ is the numerator of Wright's relationship matrix among animals. Due to the data structure (repeated measures for RCT and a_{30}, and single measures for type traits and BCS) and to avoid possible biases in the estimation of genetic covariances, the residual covariance between MCP and type traits or BCS was estimated by including a permanent variance for traits measured once (σ^2_{p2}) and a permanent environmental covariance (σ_{p1p2}) between repeated and singly measured traits. Following Hanford et al. (2002), the estimated σ_{p1p2} corresponds to the residual covariance between traits, and for singly measured characteristics, whereas the actual residual variance is given by ($\sigma^2_{e2} + \sigma^2_{p2}$). Morrissey et al. (2012) and Careau et al. (2013) reported that the aforementioned approach does not entail that it is possible to assess a permanent en-