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Short communication: Genetic correlation and heritability of milk coagulation traits within and across lactations in Holstein cows using multiple-lactation random regression animal models

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ABSTRACT

Genetic parameters of milk rennet coagulation time (RCT) and curd firmness (a_{30}) among the first 3 lactations in Holstein cows were estimated. The data set included 39,960 test-day records from 5,216 Estonian Holstein cows (the progeny of 306 sires), which were recorded from April 2005 to May 2010 in 98 herds across the country. A multiple-lactation random regression animal model was used. Individual milk samples from each cow were collected during routine milk recording. These samples were analyzed for milk composition and coagulation traits with intervals of 2 to 3 mo in each lactation (7 to 305 DIM) and from first to third lactation. Mean heritabilities were 0.36, 0.32, and 0.28 for log-transformed RCT [ln(RCT)] and 0.47, 0.40, and 0.62 for a_{30} for parities 1, 2, and 3, respectively. Mean repeatabilities for ln(RCT) were 0.53, 0.55, and 0.56, but 0.59, 0.61, and 0.68 for a_{30} for parities 1, 2 and 3, respectively. Mean genetic correlations between ln(RCT) and a_{30} were −0.19, −0.14, and 0.02 for parities 1, 2, and 3, respectively. Mean genetic correlations were 0.91, 0.79, and 0.99 for ln(RCT), and 0.95, 0.94, and 0.94 for a_{30} between parities 1 and 2, 1 and 3, and 2 and 3, respectively. Due to these high genetic correlations, we concluded that for a proper genetic evaluation of milk coagulation properties it is sufficient to record RCT and a_{30} only in the first lactation.
Key words: milk coagulation property, genetic correlation, random regression, multiple-lactation model

Short Communication

Several studies have confirmed the role of milk coagulation properties (**MCP**) in cheese making (Wedholm et al., 2006; De Marchi et al., 2008; Pretto et al., 2013). Exploitable additive genetic variation exists for MCP traits, and heritability estimates range from 0.25 to 0.28 for rennet coagulation time (**RCT**; min) and from 0.15 to 0.52 for curd firmness ($\mathbf{a_{30}}$; mm) (Ikonen et al., 2004; Cassandro et al., 2008; Vallas et al., 2010; Chessa et al., 2014). High repeatability has been reported for MCP traits using a repeatability animal model, ranging from 0.39 to 0.45 for RCT and from 0.42 to 0.50 for a_{30} (Vallas et al., 2010; Tiezzi et al., 2013).

The effect of including MCP traits in a selection index on genetic gain has been estimated, and routine genetic evaluation of these traits has been proposed (Pretto et al., 2012). If genetic evaluation for MCP is to be developed, genetic correlations for MCP within and between different parities need to be known. This information would decrease the cost of phenotypic recording. Recording of MCP can be carried out by direct and indirect methodologies (De Marchi et al., 2009; Pretto et al., 2011), which can be too expensive for regular recording of all lactations and all national cow populations.

Few studies have modeled MCP using a random regression animal model, with the exceptions of Vallas et al. (2010, 2012). However, the correlations between different parities have not been explored. The objective of our study was to estimate heritability and genetic correlation for milk RCT and a_{30} within and between the first 3 lactations in Holstein cows using a multiple-lactation random regression animal model.

The current work was part of a development project for the Bio-Competence Centre of Healthy Dairy Products in Estonia already described in 2 previous studies (Vallas et al., 2010, 2012). The data set used included 39,960 repeated test-day records from 5,216 Estonian Holstein cows (the progeny of 306 sires) recorded from April 2005 to May 2010 in 98 herds across the country. Individual milk samples from each cow were collected during routine milk recording with intervals of 2 to 3 mo during a lactation (7 to 305 DIM). Samples were taken during the first 3 lactations. The mean number of records per animal were 3.9 (range: 1–7), 3.6 (range: 1–7), and 3.2 (range: 1–6) in parities 1, 2, and 3, respectively. On average, animals had records available for 2.1 parities.

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The samples were combined with preservative and stored at cool temperature until the analysis according to International Committee for Animal Recording procedures (ICAR, 2009). The samples were analyzed for fat and protein percentages using MilkoScan 4000 and MilkoScan FT6000 instruments (Foss, Hillerød, Denmark) and for SCC using Fossomatic 4000 and Fossomatic 5000 cell counters (Foss) at the Milk Analysis Laboratory of the Estonian Animal Recording Centre (Tartu, Estonia). The pH and MCP were determined at the Milk Quality Laboratory of the Estonian University of Life Sciences. To determine the pH level of the milk, a Seven Multi pH meter (Mettler Toledo GmbH, Greifensee, Switzerland) was used. Milk coagulation time and a_{30} were determined using an Optigraph (Ysebaert, Frepillon, France) and the method described by Vallas et al. (2010).

Following the recommendations of the International Committee for Animal Recording (ICAR, 2009), data were excluded if milk yield was outside a range of 3 to 99 kg/d, if the fat content was outside a range of 1.5 to 9%, or if the protein content was outside a range of 1 to 7%. Additionally, a sample was discarded if the pH was lower than 6.5 and the sample age was more than 12 d. Furthermore, noncoagulated milk samples (a_{30} = <3 mm, n = 135) and herds with less than 5 cows were excluded. Statistics describing the final data set are reported in Table 1.

Information about the cows, herds, and pedigrees was obtained from the Estonian Animal Recording Centre and the Animal Breeders' Association of Estonia (Keava, Estonia). Genetic parameters for MCP traits were estimated using a random regression animal model where the traits RCT and a_{30} recorded in lactations 1, 2, and 3 were treated as separate traits. The model was

$$y_{ijklm}(t) = \mu + \sum_{p=1}^{q} b_p \lg_p(t) + F_i + h_j + \sum_{p=0}^{q} a_{kp} \lg_p(t) + \sum_{p=0}^{q} pe_{lp} \lg_p(t) + \varepsilon_{ijklm}(t),$$

where $y_{ijklm}(t)$ is observation of milk coagulation traits (RCT and a_{30}) on tth DIM; μ is model intercept; $\lg_p(t)$ is the covariate in the qth order Legendre polynomial; b_p is a fixed regression coefficient of $\lg_p(t)$; F_i indicates a subclass of other fixed effects including sample age (12 levels), year-season of sampling (21 levels), season of calving (4 levels); h_j is random herd effect; a_{kp} is a random animal k-specific regression coefficient of $\lg_p(t)$; pe_{lp} is a cow l-specific random permanent environmental regression coefficient of $\lg_p(t)$; and $\varepsilon_{ijklm}(t)$ is the random error term. Order q varied from 2 to 3, depending on the trait studied. For normalization of the RCT data, log-transformation was used. Three generations of ancestors were included in the analysis and 20,791 animals were included in the additive genetic relationship matrix. Heritabilities were estimated with univariate models, and genetic correlations were derived from bivariate models. The models were performed using the software package VCE-6 (Groeneveld et al., 2008). Heritability and repeatability estimates for each DIM were calculated as described by Vallas et al. (2010). Further, lactation-specific curves and change of additive genetic variation during lactation were estimated by SAS software version 9.2 (SAS Institute Inc., Cary, NC), based on the regression coefficients and covariance matrices of Legendre polynomials respectively.

Mean phenotypic RCT and a_{30} for parities 1, 2, and 3 had a similar change across DIM (Figure 1). The MCP values in the figure are means within groups of 10

Table 1. Descriptive statistics for DIM, milk yield and composition, and milk coagulation per lactation (mean ± SD)

	Parity[1]		
Trait	I	II	III
DIM	162.40 ± 84.60	156.50 ± 88.60	149.60 ± 89.50
Milk yield, kg/d	25.92 ± 7.16	29.34 ± 10.05	30.74 ± 10.68
Fat, %	4.03 ± 0.72	4.08 ± 0.82	4.11 ± 0.83
Protein, %	3.37 ± 0.32	3.39 ± 0.35	3.35 ± 0.35
SCS,[2] units	2.91 ± 1.91	3.50 ± 2.05	3.80 ± 2.09
pH	6.65 ± 0.06	6.65 ± 0.06	6.65 ± 0.07
RCT,[3] min	10.39 ± 2.35	9.98 ± 1.98	9.36 ± 1.80
ln(RCT)	2.32 ± 0.21	2.28 ± 0.18	2.22 ± 0.17
a_{30},[4] mm	26.72 ± 7.37	26.21 ± 8.01	26.01 ± 8.07

[1]Parity I = 5,200 cows, n – 20,349; parity II = 3,670 cows, n = 13,069; parity III = 2,012 cows, n = 6,542.

[2]SCS = [3 + $\log_2$ (somatic cell count/10^5)].

[3]RCT = milk rennet coagulation time.

[4]a_{30} = curd firmness.