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 [$\ln(\text{RCT})$] and 0.47, 0.40, and 0.62 for a_{30} for parities 1, 2, and 3, respectively. Mean repeatabilities for $\ln(\text{RCT})$ 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 $\ln(\text{RCT})$ 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 $\ln(\text{RCT})$, 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 (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 t th DIM; μ is model intercept; $\lg_p(t)$ is the covariate in the q th 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 $\pm$ SD)

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

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

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

³RCT = milk rennet coagulation time.

⁴ a_{30} = curd firmness.

Figure 1. Mean phenotypic milk rennet coagulation time (RCT) and curd firmness (a_{30}) for parities 1, 2, and 3 in Holstein cows across DIM.

DIM, from 5 to 305 DIM. The mean RCT value showed a tendency to increase in the first part of lactation, especially in the first 2 parities, and stabilized thereafter across the whole lactation. The mean a_{30} value increased throughout the lactation, although it started at a slightly higher level in the first 3 mo of the first parity.

To estimate the change of heritability, repeatability, and genetic correlations within or across lactations for RCT and a_{30} , multiple-lactation random regression animal models were used. On average, about 32% of the variation in RCT and 50% of that of the a_{30} during the first 3 lactations was additive genetic (Figure 2). The mean (minimum and maximum) heritabilities were 0.36 (0.28, 0.41), 0.32 (0.27, 0.36), and 0.28 (0.16, 0.33) for $\ln(\text{RCT})$ and 0.47 (0.29, 0.52), 0.40 (0.21, 0.47), and 0.62 (0.54, 0.68) for a_{30} for parities 1, 2, and 3, respectively (Figure 2). The mean (minimum and maximum) repeatabilities for $\ln(\text{RCT})$ were 0.53 (0.41, 0.57), 0.55 (0.48, 0.70), and 0.56 (0.37, 0.76) for parities 1, 2, and 3, respectively; for a_{30} the mean values were 0.59 (0.49, 0.70), 0.61 (0.57, 0.70), and 0.68 (0.66, 0.74) for parities 1, 2, and 3, respectively. The average heritability was quite different between lactations, especially for a_{30} , with a very high value in the third lactation (0.62). However, the magnitude of the repeatabilities was quite the same over lactations and the differences in heritabilities may be caused just by the differences in data and pedigree structure at different lactations (less than 40% of cows with the first lactation data had data also from the third lactation). Meanwhile this difference is possible also at the population level and the change in heritability across lactations is already reported for other traits, such as BCS (Loker et al.,

2011) and SCS (Muir et al., 2007). The change of heritability during lactation for a_{30} was similar during the second and third parity, but different in the first parity. Repeatability estimates for a_{30} had the same change across all parities with higher values after 205 DIM and during the third lactation. The heritability estimates of RCT were higher in the first lactation, and the change during lactation was similar during the second and the third parity. Repeatability estimates of the RCT had a similar change during lactation and very similar values from 50 to 250 DIM throughout all 3 parities.

Estimates of genetic correlations of the milk clotting trait between different parities are not available in the literature. Genetic correlations were found to be 0.91, 0.79, and 0.99 for $\ln(\text{RCT})$ and 0.95, 0.94, and 0.94 for a_{30} between parities 1 and 2, 1 and 3, and 2 and 3, respectively (Figure 3). These results illustrate that RCT and a_{30} are influenced by the same genes in the first, second, and third parity, and, therefore, the regular collection of first lactation records should be sufficient for the genetic evaluation of these milk coagulation traits. These results are in agreement with Tong et al. (1979) and Meyer (1984), who stated that dairy performance of cows in all lactations are determined by more or less the same genes, and first parity milk yield is therefore considered as an efficient selection criterion for lifetime production.

The mean (minimum and maximum) genetic correlations between $\ln(\text{RCT})$ and a_{30} were -0.19 (-0.27 , 0.12), -0.14 (-0.25 , -0.01), and 0.02 (-0.03 , 0.08) for parities 1, 2, and 3, respectively (Figure 4). The shape of genetic correlation curve across DIM was similar for first and second parity, with the minimum negative correlation in the middle of lactation, whereas

Figure 2. Estimates of heritability and repeatability of curd firmness (a_{30}) and log-transformed milk rennet coagulation time [$\ln(RCT)$] for parities 1, 2, and 3 in Holstein cows across DIM.

it was close to zero at the beginning and the end of lactation. For the third parity, the genetic correlation was close to zero for the whole lactation. These genetic correlations suggest that RCT and a_{30} evaluated with the Optigraph are influenced by different genetic loci.

These results are in contrast with other studies where the genetic correlation between RCT and a_{30} was much stronger, ranging from -0.46 to -0.93 (Ikonen et al., 2004; Cassandro et al., 2008; Chessa et al., 2014). This can be explained by different methodologies and instru-

Figure 3. Estimates of genetic correlation between parities and across DIM for curd firmness (a_{30}) and log-transformed milk rennet coagulation time [$\ln(RCT)$].

Figure 4. Estimate of genetic correlation across DIM between curd firmness (a_{30}) and log-transformed milk rennet coagulation time [$\ln(\text{RCT})$] by parities.

ments used for MCP analysis, as demonstrated in the work of Pretto et al. (2011).

The genetic correlation between parities and the quite high heritability in the first lactation for both MCP traits, even though for a_{30} heritability was much higher in third parity ($h^2 = 0.62$), suggest that if a genetic evaluation for MCP is to be developed, regular collection of first lactation MCP records should be sufficient for genetic evaluation, without expenditure on unnecessary costs for milk sample collection and analysis in later lactations.

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