

Genetic parameters of average milk flow recorded electronically from milking parlours and automatic milking systems in Estonian Holstein dairy cows

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ABSTRACT: The objective of this study was to investigate the feasibility of recording electronically average milk flow rate (AFR) from milking parlours (MP) and automatic milking systems (AMS), and to estimate heritability of AFR and genetic correlations with other traits in Estonian Holstein. AFR data were available for 11,001 cows at the beginning of their first lactation from 23 farms with AMS and from 34 farms with MP. The genetic correlation between AFR, measured by AMS and MP treated as two different traits, was 0.918. AFR had moderately high heritability (0.495). There was a positive genetic correlation with milk yield and a negative correlation with both fat and protein contents. The genetic correlation of AFR with SCS was 0.27, which decreased to 0.147 at the end of the first lactation, and increased (to 0.233) at the beginning of the second lactation.

Keywords: Genetic parameters, Estonian Holstein, Milk flow rate

Introduction

Milking characteristics, or milkability, have economic importance for modern dairy systems (Boettcher et al. (1998)), mainly associated with increasing herd size and the use of automatic milking systems (Berry et al. (2013)).

The implementation of modern milking systems is rapidly increasing: in Estonia 174 automatic milking system (AMS) devices have been installed (milking about 12% of cows according to national recording data) and at least 35% of cows recorded are milked in modern milking parlours (MP) with automatic cow identification and measurement of production and milking time (Ilves Kaivo, personal communication, (2014)). Milking parlour and AMS efficiency is strongly influenced by the milking duration time of individual cows (Carlström et al. (2013); Edwards et al. (2014)).

Several traits and methods of data collection have been proposed and used for recording and for the genetic evaluation of milking efficiency. Milking speed can be subjectively assessed by farmers for Holstein Friesian cows in most countries, it is recorded with a stop-watch for Simmental and Brown Swiss cows in Germany and Austria and it is recorded with electronic milk meters the Italian Brown Swiss population (Berry et al. (2013)).

The choice of data collection method depends on costs and the requirements of the quality of the data: recording

with electronic milk meters is usually much more expensive compared with subjective scoring, but it gives more accurate data for genetic evaluation.

Modern milking systems offer opportunities for on-line recording of several milkability traits. Carlström et al. (2014) showed that Average Milk Flow Rate (AFR, kg/min) is the main trait that can be available for both AMS and MP, and can be used for routine recording of milkability. They reported a moderately high heritability (0.42-0.54), high repeatability among data within the same lactations (0.63-0.77) and a high genetic correlation across lactations (0.93-0.99).

The objectives of the present study were: i) to compare the quality of electronically recorded AFR data from milking parlours and automatic milking systems; ii) to estimate the genetic parameters of AFR in Estonian Holstein dairy cows at the beginning of first lactation; iii) to estimate the genetic correlations between AFR and milk yield and milk quality traits recorded in the first and second lactations, and the genetic correlation of AFR with udder conformation traits.

Materials and Methods

Data. Data in this study are collected as part of the BioCC project 1.1, with the aims of applying genetic evaluation for milkability in Estonian Holstein cows. Average milk flow rate (kg/min) was collected by the Estonian Animal Recording Centre (Tartu, Estonia), on an online query form, from July 2010 to December 2013 from AMS and MP farms.

In AMS, daily average AFR was recorded and for MP the weekly average was used to minimize possible recording errors caused by device (eg. teat cup drop off) or operator (incorrect udder or device handling).

Only one data value during an official phenotypic recording between 60 and 90 days in milk for primiparous cows was registered. The total records from 11,001 Estonian Holstein cows, from 23 farms with AMS and from 34 farms with MP, were available for the present study.

Records of milk yield and milk quality traits on the day of AFR recording were available for all cows. For a portion of the cows the milk yield and milk quality traits records were available from 270–330 days in milk in the first lactation (6,669 cows), from 5–60 days in the second lactation (4,752 cows), and udder conformation traits

(5,736 cows) were scored on a scale of 1–9 from 8–305 days in milk in the first lactation.

Statistical analysis. A preliminary data editing process was used in order to remove abnormal records. An AFR of more than 5.5 kg/min was discarded, and a minimum of five animals per farm were considered. Somatic cell counts were log-transformed into Somatic Cell Scores ($SCS = 3 + \log_2(SCC/100.000)$). Initially a bivariate animal model was used to evaluate the genetic correlation between AFR recorded by AMS and MP, treated as two different traits:

$$y_{ijkl} = \mu + HR_i + YR_j + MO_k + a_l + e_{ijkl}$$

where y_{ijkl} is the AFR (kg/min) recorded by AMS or MP; μ is the model intercept; HR_i is the fixed effect of the i^{th} herd (1–23 for AMS and 1–34 for MP); YR_j is the fixed effect of the j^{th} year of recording (2010–2013); MO_k is the fixed effect of the k^{th} month of recording (1–12); $a_l \sim N(0, A\sigma_a^2)$ is the random additive genetic effect of animal l depending on pedigree; $e_{ijkl} \sim N(0, I\sigma_e^2)$ is the random residual term.

A second approach was applied where AFR collected from AMS and MP were considered the same trait, and several bivariate models were fitted to evaluate the genetic correlations between AFR and other traits recorded.

To estimate the correlation with milk yield and quality traits at different stage of lactation and parity, the following model was used:

$$y_{ijkl} = \mu + HR_i + YR_j + MO_k + a_l + e_{ijkl}$$

where y_{ijkl} is the dependent variable; μ is the model intercept; HR_i is the fixed effect of the i^{th} herd (1–57); YR_j is the fixed effect of the j^{th} year of recording (2010–2013); MO_k is the fixed effect of the k^{th} month of recording (1–12); $a_l \sim N(0, A\sigma_a^2)$ is the random additive genetic effect of animal l ; $e_{ijkl} \sim N(0, I\sigma_e^2)$ is the random residual term.

To estimate the correlations between AFR and udder conformation traits the same model, with an additional fixed effect of days in milk of the conformation evaluation (ten 30 days classes from 5–305 days in milk), was used.

The number of animals in the additive genetic relationship matrix was 44,689, and included all cows with a phenotypic record, and their ancestors up to three generations back. Pedigree information was supplied by the Estonian Animal Recording Centre (Tartu, Estonia). Estimates of heritability and genetic correlation coefficients were obtained with the software package VCE-6 (Groeneveld et al. (2008)).

Results and Discussion

Means and standard deviations of AFR recorded by AMS and MP were comparable (Table 1). The genetic correlation between AFR measured by AMS and MP was 0.918 (s.e. 0.054). An even higher result (0.97) was

reported by Carlström et al. (2014) in Swedish Holsteins. Due to this high correlation, in subsequent analyses the AFR recorded from both AMS and MP were treated as the same trait.

Table 1. Descriptive statistics of average milk flow rate recorded by milking parlours and automatic milking systems

Milking system [†]	No. of farms	No. of cows	Average Flow, kg/min			
			Mean	SD	Min	Max
AMS	23	2,626	2.12	0.78	0.30	5.40
MP	34	8,375	2.14	0.75	0.08	5.50

[†]AMS= Automatic Milking System; MP= Milking Parlour

The results of genetic estimation confirmed that AFR had a moderate-high heritability (0.495, Table 2), which is in agreement with Carlström et al. (2014), but higher than the results of Berry et al. (2013) and Edwards et al. (2013).

A positive genetic correlation with milk yield and negative correlations with fat and protein contents is in agreement with previous studies by Berry et al. (2013). Genetic correlations between AFR and milk yield, protein and fat contents measured at the beginning of the first lactation were higher compared to genetic correlations at the end of the first lactation and at the beginning of the second lactation. Genetic correlation of AFR with somatic cell score was 0.271. At the end of the first lactation this was 0.147, and at the beginning of the second lactation 0.233.

The genetic correlations between AFR and udder conformation traits showed almost no or a moderate relationship depending on the trait. Rear udder height and teat length showed the stronger correlation (+0.327 and -0.202, respectively). The correlation with overall udder score was 0.093 and with teat placement 0.086 but both with high standard errors.

Conclusion

This study aim was to show the feasibility of using on-line electronically recorded AFR records for estimation of genetic parameters. The AFR measured by AMS and MP can be considered same trait as there is a high genetic correlation between them. In future the relationship between different milking system brands needs to be explored. Average flow rate recorded at the beginning of the first lactation showed a high heritability and it seems to be a good method for routine recording of AFR for genetic evaluation. In our opinion a potential genetic index for milkability should include, in addition to AFR, also SCS and some udder conformation traits, but further genetic response simulation is needed in order to be more convincing.

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Table 2. Heritability and genetic correlations of average milk flow rate (standard errors in parenthesis) for milk production and udder conformation traits

Trait ¹	N	h ² (s.e.)	r _{gen} (s.e.) with AFR
First parity cows recorded at 60-90 days in milk			
AFR, kg/min	11,001	0.495 ² (0.032)	-
Milk, kg/d	10,989	0.251 (0.031)	0.408 (0.065)
Fat, %	10,872	0.213 (0.026)	-0.248 (0.069)
Protein, %	10,904	0.364 (0.035)	-0.166 (0.067)
SCS	10,909	0.062 (0.015)	0.271 (0.107)
First parity cows recorded at 270-330 days in milk			
Milk, kg/d	6,669	0.394 (0.048)	0.165 (0.075)
Fat, %	6,624	0.396 (0.044)	-0.121 (0.074)
Protein, %	6,632	0.550 (0.049)	-0.045 (0.067)
SCS	6,634	0.076 (0.019)	0.147 (0.039)
Second parity cows recorded at 5-60 days in milk			
Milk, kg/d	4,752	0.103 (0.033)	0.164 (0.131)
Fat, %	4,695	0.158 (0.041)	-0.041 (0.111)
Protein, %	4,708	0.147 (0.033)	0.053 (0.113)
SCS	4,707	0.067 (0.027)	0.233 (0.152)
Udder conformation traits			
OUS	5,736	0.315 (0.044)	0.093 (0.085)
FUA	5,736	0.197 (0.035)	0.007 (0.101)
Udder depth	5,736	0.390 (0.047)	0.003 (0.081)
Rear udder height	5,736	0.273 (0.041)	0.327 (0.088)
Udder cleft	5,736	0.188 (0.034)	0.039 (0.104)
Teat placement	5,736	0.303 (0.046)	0.086 (0.086)
Teat length	5,738	0.354 (0.046)	-0.202 (0.081)

¹AFR= Average Milk Flow Rate; SCS= Somatic Cell Score; OUS = Overall Udder Score; FUA = Fore Udder Attachment
²mean value from bivariate models