



Genetic evaluation of milking speed for Slovenian Holstein cattle regarding to different scoring approaches

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ABSTRACT

The objective of this research was to determine differences between estimated variance components and heritability of milking speed for Slovenian Holstein cattle regarding to different scoring approaches. Milking speed was scored by two different scoring approaches. From year 1989 to 2004, milking speed was scored on scale of 1–3, while from year 2004, scale of 1–5 was applied in scoring of milking speed. For analysis, from both approaches, 71.757 records were available. For genetic evaluation of milking speed univariate model and multi-trait model was used. In univariate model milking speed data on scale of 1–3 was evaluated, while in multi-trait model, both, milking speed data on scale of 1–3 as one trait, and milking speed data on scale of 1–5 as second trait, was evaluated. Herd and residual variances were lower in multi-trait model in comparison with variances in univariate model, while genetic variance was higher in multi-trait model. Variances for all random effects in multi-trait model were higher for new trait (MS 5) than for old trait (MS 3). Heritability for MS 5 was considerably higher than heritability for MS 3 estimated from both models. Breeding values for MS 5 had almost three time greater standard deviation in relation to breeding values for MS 3 in multi-trait. Appliance of new scoring approach resulted in genetic variance increase, which finally resulted in higher heritability value, which would enable faster selection response. Further investigation based on revalorisation of economic value for milking speed in calculation of Total Merit Index is needed.

(Keywords: genetic evaluation, milking speed, scoring approaches, cattle)

INTRODUCTION

Milking speed of dairy cows is economically important trait. Dairy cows with longer period of milking duration require more time and energy for milking. However, to fast milking speed potentially increase possibility for development of udder diseases that could finally result in culling. Milking speed could be measured with a LactoCorder within official Milk Recording, when data are recorded as average milking speed in kg per minute, or scored on scale 1–3 and 1–5 within Linear Scoring (*Rensing and Ruten*, 2005). Heritability for milking speed scored on scale 1–5 for Canadian Holstein was 0.20 (*Blair*, 2003). *Rensing and Ruten* (2005) reported that heritability for German Holstein for measured milking speed was 0.28, while for owners scored milking speed heritability was 0.10. The objective of this research was to determine differences between estimated variance components and heritability of milking speed for Slovenian Holstein cattle regarding to different scoring approaches.

MATERIALS AND METHODS

Milking speed was scored by two different scoring approaches. From year 1989 to 2004, milking speed was recorded within Linear Scoring of first lactation cows. The linear scoring expert asked the owner to score milking speed on scale of 1–3 (where: 1–slow, 2–average, 3–fast). From this scoring approach, 51.111 records were available for genetic evaluation. From year 2004, scale of 1–5 (where: 1–very slow, 2–slow, 3–average, 4–fast, 5–very fast) was applied in scoring of milking speed. Data on milking speed were recorded within Milk Recording of first lactation cows. For genetic evaluation, from this approach, 20.646 records were available. Data used for evaluation were from Central data base of Agricultural institute of Slovenia. Descriptive statistics for milking speed are reported in *Table 1* for old data and in *Table 2* for new data.

Table 1

Descriptive statistics for data collected from 1989 to 2004

trait	n	mean	SD	CV	min	max
milking speed (3)	51.111	2.227	0.478	21.453	1.000	3.000
age at calving (days)	51.111	863.89	106.67	12.35	506	1.200
age at scoring (days)	51.111	1.021.19	124.67	12.20	588	1.497
period from calving to scoring	51.111	157.29	64.22	40.83	5	365

Table 2

Descriptive statistics for data collected from 2004 to 2005

trait	n	mean	SD	CV	min	max
milking speed (5)	20,646	3.744	0.767	20.483	1.000	5.000
age at calving (days)	20,646	857.78	109.59	12.78	488	1200
age at scoring (days)	20,646	927.81	112.02	12.07	563	1426
period from calving to scoring	20,646	70.03	23.64	33.75	5	326

Descriptive statistic show that mean values for milking speed are in both cases over expected theoretical mean value. The age of first calving is not very different in comparison of this parameter in both system of scoring. In new system the cows are just six days younger at first calving. One of main things in case of changes of scoring system is also differences in period from calving to scoring. In old system the linear scoring expert goes to farm in main cases just twice per year and for this reason the mean value for period from calving to scoring is nearly half year. In new system of scoring milking speed the mean value of period from calving to scoring is more than twice smaller in comparison with this parameter in old system. This change we can explain with scoring within Milk Recording in most cases at second and third milk control.

According to age at first calving, cows were divided into five groups, S1 (<750 days), S2 (750–810 days), S3 (810–870 days), S4 (870–930 days), S5 (>930 days). Additionally, according to period from calving to scoring, cows were divided into five groups, D1 (<60 days), D2 (60–90 days), D3 (90–120 days), D4 (120–150 days), D5 (>150 days). For genetic evaluation of milking speed univariate model and multi-trait

model was used. In univariate model milking speed data on scale of 1–3 was evaluated, while in multi-trait model, both, milking speed data on scale of 1–3 as one trait, and milking speed data on scale of 1–5 as second trait, was evaluated.

The statistical model for milking speed was the same in all cases:

$$y_{ijkl} = OL_i + T_j + SD_k + h_l + a_{ijkl} + e_{ijkl} \quad (1)$$

where:

y_{ijkl} – records of milking speed (on scale of 1–3 or on scale of 1–5) assumed normally distributed,

OL_i – concatenated effects of expert and year of scoring,

T_j – calving season,

SD_k – concatenated effects of classes of age at first calving and classes of period from calving to scoring,

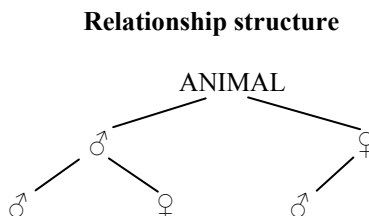
h_l – random effect of herd,

a_{ijkl} – random additive genetic effect of animal,

e_{ijkl} – random residual effect.

In covariance estimation relationship structure as shown in *Figure 1* was used. Animal, shown on *Figure 1*, presents each first calving cow with score of milking speed.

Figure 1



For statistical analysis the SAS/STAT package was used (*SAS Institute Inc.*, 2000), while for estimation of variance components and heritabilities MTC program (Fortran) was used. For breeding values estimation MTJAAM program (Fortran) was used.

RESULTS AND DISCUSSION

As it was expected, based on material analysis, differences in estimated dispersion parameters between models were considerable (*Table 3*). Residual variance, in univariate model, was considerably higher in comparison with genetic and herd variances. Relationship between those variances resulted in low heritability, which in case of univariate model was only 0.026 (*Table 4*). Herd and residual variances were lower in multi-trait model in comparison with variances in univariate model, while genetic variance was higher in multi-trait model (*Table 3*). Variances for all random effects in multi-trait model were higher for new trait (MS 5) than for old trait (MS 3). In all cases covariances were low which means that correlation between traits was close to zero.

Due to differences between variances according to models, difference between heritabilities was also expected. Although covariances between new and old trait were low, heritability for MS 3 in multi-trait model considerably increased in relation to heritability for MS 3 in univariate model. Heritability for milking speed scored on scale of 1–5 (MS 5)

was considerably higher than heritability for milking speed scored on scale 1–3 (MS 3) estimated from both models (*Table 4*). Similar results of heritability value for milking speed scored on scale 1–5 for Canadian Holstein were obtained by *Blair* (2003), while *Erf et al.* (1992) and *Boettcher et al.* (1998) reported considerably lower heritability.

Table 3

Variance and covariance components for random effects

model	trait		variance	
univariate model			herd	0.008275
			animal	0.002895
			residual	0.100233
			MS (5)	MS (3)
multi-trait model	herd	MS (5)	0.006037	0.000365
		MS (3)	0.000365	0.004541
	animal	MS (5)	0.035060	0.000724
		MS (3)	0.000724	0.009179
	residual	MS (5)	0.096899	-0.001232
		MS (3)	-0.001232	0.067850

Table 4

Heritabilities according to models

model	trait	heritability
univariate model	milking speed (3)	0.026
multi-trait model	milking speed (3)	0.116
	milking speed (5)	0.254

Figure 2 and *3* show relations between standardised breeding values estimated on old way of scoring and breeding values estimated with multi-trait model. With purpose of standardisation of breeding values standard deviation of 12 point and mean value of 100 point were used. In case of breeding value for milking speed standard deviations of breeding values were: 0.0201 for old MS, 0.0363 for new MS 3 and 0.0978 for new MS 5. This results shown us that breeding values were more variable in multi-trait model. Higher variability of breeding values for MS 3 in multi-trait model in relation to breeding values for MS 3 in univariate model indicate that new scoring approach (scale 1–5) induce higher variability.

Breeding values for MS 5 had almost three time greater standard deviation in relation to breeding values for MS 3 in multi-trait. Although the differences in variability of breeding values for milking speed scored on scale 1–3 were relatively high, the differences between rang of animals according to breeding value between univariate and multi-trait model were small (*Figure 2*).

Relationship between old breeding values and breeding values estimated with multi-trait model for milking speed scored on scale 1–5 was negligible (*Figure 3*) which means that, from statistical point of view, MS 5 and MS 3 are different traits, despite of that, from biological point of view MS 5 and MS 3 are same trait.

Figure 2

Relation between old breeding value and new breeding value estimated with multi-trait model for MS 3

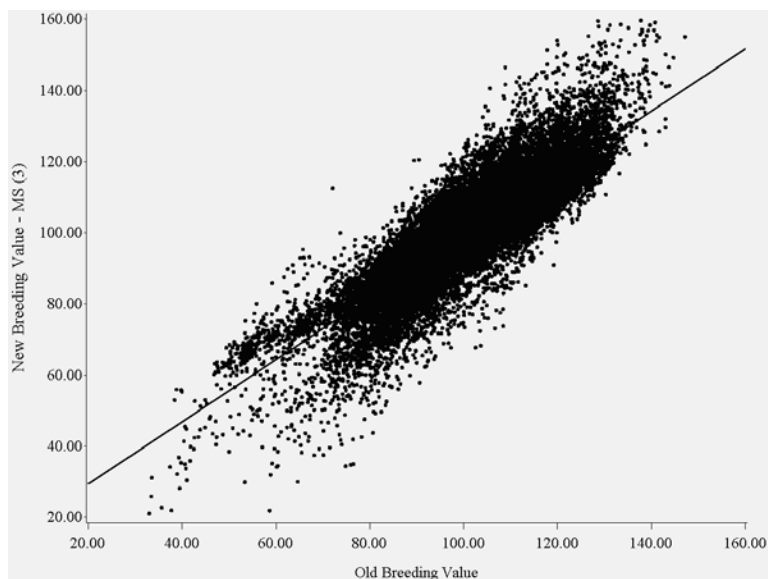
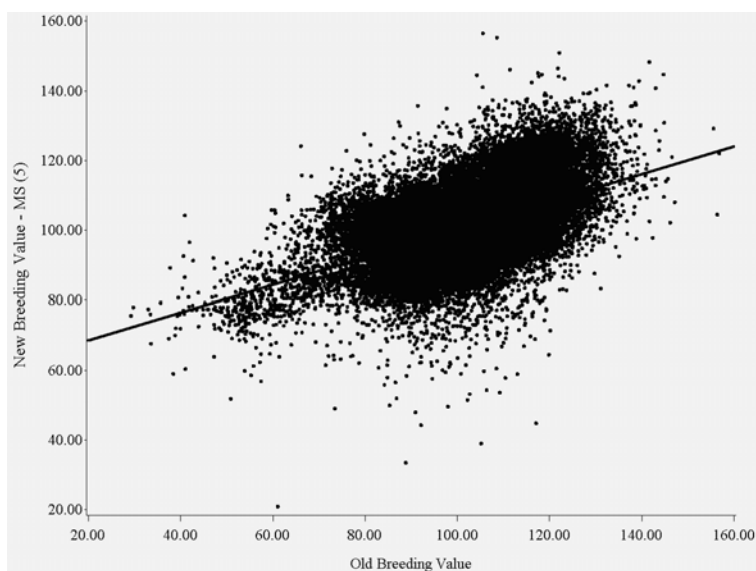


Figure 3

Relation between old breeding value and new breeding value estimated with multi-trait model for MS 5



CONCLUSIONS

With introduction of new scoring approach for milking speed in year 2004, changes in results were expected. Changes in estimated breeding values were also expected. Appliance of new scoring approach resulted in genetic variance increase, which finally resulted in higher heritability value. Higher heritability values enables faster selection response. So far, economic value for milking speed in calculation of Total Merit Index was 0.03, but selection for mentioned trait was not successful because of low heritability value. Therefore, further investigation should be based on revalorisation of economic value for milking speed in calculation of Total Merit Index.

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