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Genetic parameters estimation for milking speed in Croatian Holstein cattle

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Abstract

Milking speed (MS) has a growing importance from a dairy management standpoint. Cows with slow MS require more labour, while cows with fast MS could be in greater risk for udder diseases. Although MS is considered as a trait of importance, little attention has been given to estimate genetic components for MS and its relationship with other traits. The objectives of this study were: 1) to estimate genetic parameters for MS in Croatian Holstein cattle; 2) to use them for the prediction of breeding values; and 3) to estimate proof correlations of MS with production and conformation traits in order to understand the interrelationships among traits. Data included 129,723 test-day records for 35,908 first calving cows taken from the central database of the Croatian Agricultural Agency. Pedigree file consisted of 85,605 animals. In order to improve the normality, logarithmic transformation for MS was used. Variance components were estimated by REML method using VCE-6 program. Statistical model included calving season, milking time, and milk yield class as fixed class effects, while age at first calving and days in milk were fitted as covariates. Random effects were: common herd-test day, permanent environmental and direct additive genetic effect. Common herd-test day and permanent environmental effect accounted 27 % and 15 % of variability. Direct additive genetic effect explained another 14 % of phenotypic variation for MS. Analysis of proof correlations between bulls and cows BV for MS with production and conformation traits showed low to moderate relationships. Most of these proof correlations were positive with an exception of teats length. Genetic evaluation for MS provide useful tool for breeding decisions due to moderate heritability of MS and the trait should be included in the total merit index in the future. In order to determine the appropriate economic weights for MS in the overall index, genetic correlations among MS and production and conformation traits should be estimated.

Key words: milking speed, Holstein breed, test-day records,
genetic parameters, proof correlations

Introduction

Milking speed (MS) or milkability or workability belongs to the group of functional traits which hold an increasing importance in dairy cattle due to its influence on the farmers' production costs (Groen et al., 1997). The trait is defined as the cow's capacity to give completely and

in short time milk produced in the udder gland (Dodenhoff et al., 1999; Ordloff, 2001). In the breeding programs, MS is the trait of interest due to its relationship with udder health and labour efficiency (Göft et al., 1994). Slow milked cows are undesirable for the farmers' because of increased labour time and consequently higher costs for milk

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production. Higher MS is associated with the increased risk of mastitis (Boettcher et al., 1998; Mijić et al., 2004; Zwald et al., 2005). According to Roth et al. (1998) the maximal MS from 3.0 to 4.5 kg/min was considered to be optimal in terms of udder health.

MS could be improved through selection (Boettcher et al., 1998) since it is sufficiently heritable trait which makes breeding reasonable. According to the literature, heritability estimates for MS ranged from 0.03 (Potočnik et al., 2006) up to 0.40 (Dodenhoff and Emmerling, 2009). MS was positively correlated (0.50) with milk production (Santus and Bagato, 1998). Genetic correlations were also positive between MS and protein, fat, and milk yield (0.16, 0.24, and 0.30) in Italian Brown Swiss (Samoré et al., 2010) indicating that high yielding cows tended to be faster in milking. Unfavourable genetic correlation exists between MS and somatic cell count (SCC) since faster milking cows tend to have a higher SCC. Estimated genetic correlations were in range from 0.25 to 0.50 (Luttinen and Juga, 1997; Boettcher et al., 1998; Rupp and Boichard, 1999). Udder confirmation traits also have an effect on MS. Sewalem et al. (2011) reported positive correlations between MS and udder depth (0.24) as well as Wiggans et al. (2007) between MS with rear udder width and rear udder height (0.14 and 0.19) in Brown Swiss. On contrary, Boettcher et al. (1998) estimated negative genetic correlations between MS and rear udder width and teat length (-0.24 and -0.18) in Canadian Holstein.

MS could be assessed using either subjective evaluation of MS which is based on linear scores on a scale from one to five (Sørensen et al., 2000) and objective measurements using stopwatch or electronic flowmeters (Dodenhoff et al., 1999). The advantage of using stopwatch is in easier use and less time consuming compared to flowmeters. However, presence of a technician during milking is required which is the main disadvantage.

In Croatia, MS has been recorded since 2007 using either stopwatch on family farms or electronic flowmeters on large farms. In order to include MS in the genetic evaluation, variance components for MS should be estimated. The objectives of this study were: 1) to estimate genetic parameters for MS in Croatian Holstein cattle; 2) to use them for the pre-

diction of breeding values (BV); and 3) to estimate proof correlations of MS with production and conformation traits in order to understand the interrelationships among traits.

Material and methods

Data for the analysis were provided from the central database of the Croatian Agricultural Agency for the period from January 2007 to July 2016. Recording of MS was conducted by supervisors of Croatian Agricultural Agency according to the ICAR rules (ICAR, 2011). It is performed on two consecutive test-days (2nd and 3rd test-day during the first parity) using stopwatch on family farms and flowmeters on big enterprises. Test-day records from regular alternate scheme (AT) of milk recording (AT4 and BT4 method) together with the pedigree information were included in the analysis. Records were edited according to ICAR guidelines (ICAR, 2011). Holstein cows with records in the first parity between five and 180 days in milk were included in the analysis. Additionally, records were deleted for cows: 1) without birth, calving or test date; 2) with unknown parity, region or herd; and 3) unexpected age at the first calving (younger than 18 months or older than 40 months). Calving season was defined as year-season interaction. Four seasons within year were used as follows: spring (from March to May), summer (from June to August), autumn (from September to November), and winter (from December to February). Furthermore, ten milk yield classes with 5 kg increment were formed based on daily milk yield production (≤ 5 kg the first, >46 kg the last class). Since the milk recording was based on AT, milking time was considered as morning or evening record. After editing, 129,723 test-day records for 35,908 primiparous cows were used in further analysis. In preliminary study, the normality of trait was tested and logarithmic transformation for MS (logMS) was performed. The average MS was 3.15 kg/min (Table 1) which was consistent with the averages (2.21 kg/min and 2.20 min/kg) reported by Fürst (2000) in Austrian and by Dodenhoff (2004) in Bavarian Holstein cows. The average logMS was 3.93 and daily milk yield 26.6 kg/day. Similar averages were reported for Hungarian Holstein breed (Amin, 2007).

All animals with records and their relatives tracing back for five generations were included in the pedigree file (Table 2). The total number of animals involved in the pedigree was 85,605. The proportion of non-base animals was 97.5 %. Among them, 66.1 % had both parents known. Small proportion of animals (2.5 %) was considered as the base population. The average number of progeny per sire was 8.9. Dams had on average 1.8 progenies.

Effects of calving season (S_i), milking time (T_j), and milk yield class (M_k) were considered as fixed class effects. Age at first calving ($x_{ijklmno}$) and days in milk ($t_{ijklmno}$) were used as covariates and were modelled as quadratic regression. Common herd-test day (c_m), permanent environmental (p_{mn}) and direct additive genetic effect (a_n) were included in the model as random effects.

The following model present the best fit for logMS and is shown in scalar notation [1]:

$$y_{ijklmno} = \mu + b_1(x_{ijklmno} - \bar{x}) + b_2(x_{ijklmno} - \bar{x})^2 + b_3(t_{ijklmno} - \bar{t}) + b_4(t_{ijklmno} - \bar{t})^2 + S_i + T_j + M_k + c_m + p_m + a_n + e_i \quad [1]$$

The GLM procedure in the statistical package SAS (SAS Inst. Inc., 2009) based on Least Square Method was used to define the fixed part of the model. The effects were included in the model based on significance level (p-value), degrees of freedom (df), and proportion of variation (R^2) explained by the effects and the model. Milk yield class was modelled as fixed class effect instead as covariable due to considerable increase of R^2 . Least square means were computed for each of the significant fixed effects. Covariance components were estimated by Residual Maximum Likelihood (REML) method using VCE-6 program package (Groeneveld et al., 2008). Estimated genetic parameters were further used to predict BV for MS using a previously defined model. Altogether, BVs were predicted for 79,950 cows, while the number of bulls included in the evaluation was 9,665. Subsequently, proof correlations between BV for MS and BV for production and conformation traits were regularly estimated during the routine national genetic evaluation.

Table 1. Descriptive statistics for production data

Variable	Unit	N	Mean	SD	Minimum	Maximum
MS	kg / min	129,723	2.15	1.27	0.50	14.00
logMS	log-transformed	129,723	3.93	0.68	2.00	6.80
Milk yield	kg	129,723	26.6	7.26	3.0	50.0
Age	months	129,723	26.2	3.26	18.0	40.0
Stage of lactation	days	129,723	93.72	49.32	5.0	180.0

Table 2. Pedigree structure

Item	N
Animals with records	35,908
Non-base animals	83,485
• both parents known	55,163
• only sire known	24,871
• only dam known	3,451
Base animals	2,120
Proportion of base animals (%)	2.5 %
Average number of progenies per sire	8.9
Average number of progenies per dam	1.8
Total number of animals	85,605

Results and discussion

The proportion of variation (R^2) accounted for the fixed part of the model for logMS was 23 %. All fixed effects included in the model were significant ($P < 0.05$). Age at first calving modelled as quadratic regression had significant effect ($P < 0.05$) on average logMS (Figure 1). The highest proportion of calvings was at the age from 23 to 28 months with the average logMS between 4.1 and 4.2. The average logMS decreased when cows became older at the first calving. The proportion of cows that calved between 32 and 40 months was low, as well. An increased trend of logMS by age at calving was observed in the studies of Williams et al. (1984) and Meyer and Burnside (1987) for Holstein cows.

Days in milk (or stage of lactation) affected variation ($P < 0.05$) of logMS. The shape of predicted lactation curve for logMS (Figure 2) suggested that a quadratic regression could be fitted for modelling of the logMS. Relationship between stage of lactation and MS was also modelled by quadratic regression in Canadian Holstein cows (Williams et al., 1984; Meyer and Burnside, 1987). Dodenhoff et al. (1999) used Ali-Schaeffer lactation curve (Ali and Schaeffer, 1987) with four regression coefficients to model the effect of stage of lactation in German Holstein, Fleckvieh, and Braunvieh breed, respectively.

Calving season modelled as year-season interaction had significant effect ($P < 0.05$) on logMS (Figure 3). LogMS had an increasing trend during calving seasons in years from 2007 to 2012. However, in these calving seasons, a smaller number of total records were observed (Figure 3). Winter calving season in 2011 had the highest estimates, while cows calved in winter season of 2015 had the lowest MS. Meyer and Burnside (1987) fitted calving season as interaction with herd effect which accounted considerable proportion of variation in Canadian Holstein cows.

Batra and McAllister (1984) reported positive correlation of MS with milk yield indicating that high-producing cows have a higher MS compared to low producing cows. Differences in MS ($P < 0.05$) were also observed in this study (Figure 4) and MS increased with daily milk production.

Milking time had a significant effect ($P < 0.05$) on logMS. Similar proportion of records, almost

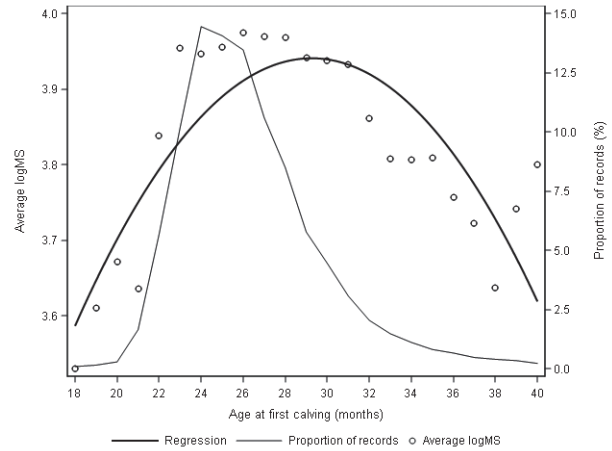


Figure 1. Average logMS and proportion of records by age at first calving

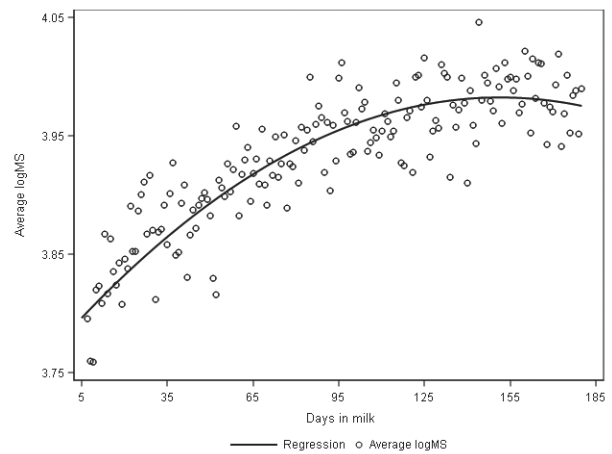


Figure 2. Average logMS by days in milk

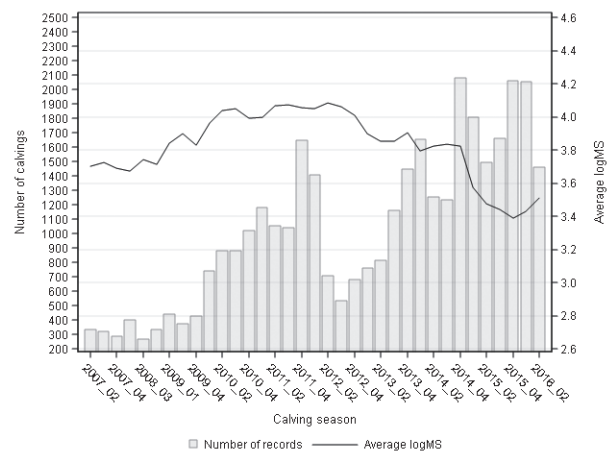


Figure 3. Average logMS by calving season

50:50 (Figure 5) was observed in the analysed data set. Cows milked in the morning had higher logMS (3.87) compared to evening milking cows (3.78).

Estimated heritability was 0.14 for MS (Figure 6) which confirmed the heritability values found from previous studies. The heritability estimated in this work was in accordance with the estimate of 0.14 reported by Sewalem et al. (2011) for Canadian Holstein. Similar heritability (0.15) was estimated in the study of Boettcher et al. (1998), while heritability 0.11 was reported by Zwald et al. (2005). The heritability for MS estimated in this study was lower compared to a heritability value of 0.21 for Canadian Holsteins (Meyer and Burnside, 1987). Estimated MS heritability was 0.22 in the study of Brown Swiss cattle (Wiggans et al., 2007), while in Slovenian Holstein was 0.03 based on univariate and 0.25 on multi-trait model (Potočnik et al., 2006), based on subjective score. Rensing and Rutten (2005) reported heritability of 0.28 for German Holstein, while mean heritability for Hungarian Holstein was 0.20 (Amin, 2007). Estimated heritability for MS in German Fleckvieh ranged from 0.21 to 0.40 based on multiple-trait estimates in the first three lactations (Dodenhoff and Emmerling, 2009) using records measured by milk-recording devices. Differences between heritabilities in reported studies could be attributed to different methods of collecting data related to MS. Sewalem et al. (2011) concluded that these estimates could vary because of differences in the used data and in the applied analytical methods. Furthermore, they stated that the variability in the heritability estimates could be lower if the MS measures were more objective.

The variance ratio for permanent environmental effect (p^2) was 15 % (Figure 6). The estimate was lower compared to the study of Amin (2007) where the same effect explained 52 % of phenotypic variation using fixed multivariate animal model in Hungarian Holstein. Common herd-test day (c^2) effect accounted for another 27 %.

Results of genetic evaluation for MS were expressed as a relative BV with a mean of 100 and a standard deviation of 12. The base group for the mean of 100 was comprised of cows born at year 2010. Proof correlations between BV for MS and different group of traits were calculated in order to provide an understanding of trait interrelationships.

Several studies (Sewalem et al., 2011; Wiggans et al., 2007; Rupp and Boichard, 1999) report relationships among traits BV due to large amount of data which provide reliable results. However, these proof relationships could not be converted to genetic correlations (Rupp and Boichard, 1999). In the current study, separate analysis was carried out for bulls and cows. Proof correlations between MS and production traits (Table 3) included 1,002 bulls born from 1990 to 2012 having ≥ 10 daughters and received an official BV for analysed traits. All together 75,700 cows were included in the correlation analysis. Proof correlations between MS and production traits: daily milk, fat, and protein yields

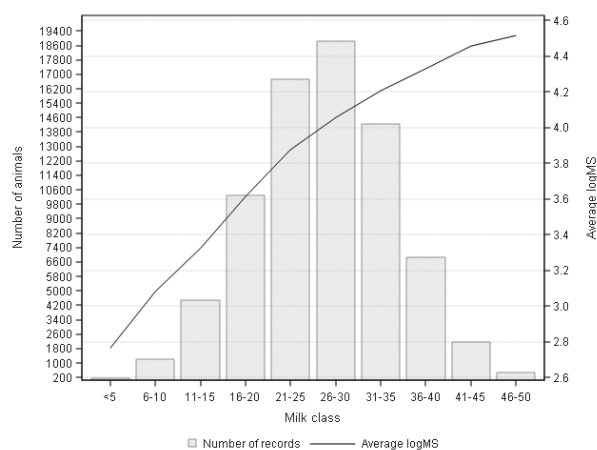


Figure 4. Average logMS by milk yield class

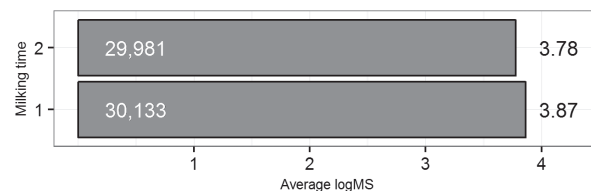


Figure 5. Average logMS by milking time

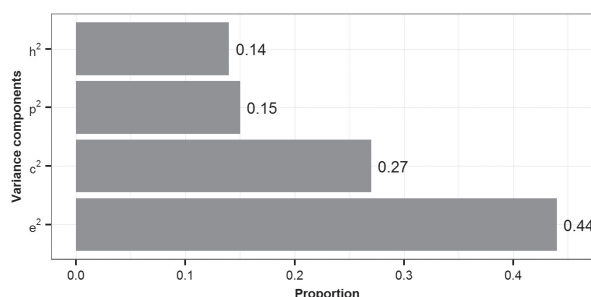


Figure 6. Estimated ratios for MS

were low and positive with values 0.18, 0.18 and 0.16, respectively. Similar trend was observed by Sewalem et al. (2011) in Canadian Holstein. Correlations between MS with fat (0.04) and protein contents (0.00) were not significantly different from zero ($P>0.05$). For cows, proof correlations between MS and yield traits were lower compared to bulls. Slightly higher and significant ($P<0.05$) proof correlations between MS and content traits were observed for cows in comparison to bulls.

Proof correlation of 0.02 was estimated between MT and SCC (Table 3). On contrary, several studies reported positive (i.e., unfavourable) correlation between MS and SCC. Antagonism between MS and SCC comes from the fact that fast milking

cows tend to have higher SCC. Zhang et al. (1994) reported proof correlations of 0.20, 0.02, and 0.11 between MS and SCC in the first, second to fifth, and from all lactations, respectively. Similar trend was observed for the genetic correlation between MS and SCC. Moderate and positive genetic correlations of 0.41 and 0.25 between subjectively measured MS and SCC was reported by Boettcher et al. (1998) for the first and the second parities, respectively. Higher genetic correlation (0.50) was estimated by Luttinen and Juga (1997) in Finnish Holstein-Friesian. Rupp and Boichard (1999) also reported unfavourable genetic correlation of 0.44 between MS and SCC in the first lactation Holsteins. On contrary, a negative genetic correlation

Table 3. Proof correlations between bull and cow BV for MS with production traits and SCC

Trait	Value	
	Bulls	Cows
Daily milk yield	0.18***	0.13***
Daily fat yield	0.18***	0.13***
Daily protein yield	0.16***	0.12***
Fat content	0.04 (n.s.)	0.04***
Protein content	0.00 (n.s.)	0.07***
Somatic cell score	0.02 (n.s)	-0.02***

n.s.= not significant; * $P<0.05$; ** $P<0.01$; *** $p<0.001$

Table 4. Proof correlations between bull and cow BV for MS and conformation traits

Trait	Value	
	Bulls	Cows
Conformation traits		
Udder depth	0.24***	0.08***
Suspensory ligament	0.12***	-0.07***
Fore udder attachment	0.15***	0.03***
Rear udder height	0.17*	0.06***
Rear udder width	0.19***	0.12***
Teats length	-0.16***	-0.11***
Front teats placement	0.20***	0.10***
Rear teats placement	0.18***	0.05***
Angularity	0.10***	0.03***
Stature	0.07***	-0.03***
Body depth	0.10***	0.01***
Foot angle	0.17***	0.07***

* $P<0.05$; ** $P<0.01$; *** $p<0.001$

of -0.15 between MS and SCC was estimated by Zwald et al. (2005). An antagonistic relationship between these traits was also reported in Brown Swiss by Wiggans et al. (2007) and the correlation was not significant. The authors concluded that the negative correlation between MS and SCC may indicate a lower incidence of mastitis with faster MS since slow milking cows were not completely milked out, which could lead to higher SCC.

Proof correlations between MS with conformation traits are shown in Table 4. The number of animals included in the genetic evaluation for conformation traits was lower compared to production traits. Consequently, number of bulls with official BV (≥ 10 daughters) for conformation traits was lower and only 235 bulls were included in correlation analysis. The number of cows was twice lower (30,780) compared to analysis between MS and production traits. The negative proof correlation (-0.16) was estimated between MS and teat length for bulls. Sewalem et al. (2011) also found a negative relationship between MS and teat length (-0.205), as well as Wiggans et al. (1999) who reported a proof correlation of -0.35 in Brown Swiss.

Most of the proof correlations between MS and other conformation traits were positive. Moderate correlations were estimated between MS and traits related to the udder as follows: 0.24 (udder depth), 0.19 (rear udder width), and 0.17 (rear udder height). In agreement with these results, Sewalem et al. (2011) reported correlations between MS and udder depth (0.239). Similar proof correlations between MS and rear udder width and rear udder height (0.14 and 0.19) reported Wiggans et al. (2007) in Brown Swiss. Proof correlation of 0.12 was estimated between MS and suspensory ligament which was consistent with the estimates of 0.128 found by Sewalem et al. (2011). Proof correlations between MS with front and rear teats placement were higher (0.20 and 0.18) compared to values of 0.068 found in the study of Sewalem et al. (2011). MS and angularity proof correlation of 0.10 from the current study was in line with the result from the Sewalem et al. (2011). Proof correlations between MS and conformation traits for cows were lower compared to bulls but in the same direction, with the exception for suspensory ligament and stature.

Conclusions

Estimated genetic parameters for MS were consistent with the results from other studies. Genetic parameters estimated in this study have been applied for genetic evaluation of MS in Croatian Holstein cattle. Proof correlations between bulls' and cows' BV for MS with production and conformation traits showed low to moderate relationships. Most of these proof correlations were positive with an exception of teats length. In the future, MS should be included in the total merit index for Holstein cattle. In order to determine the appropriate economic weights of MS in the overall index, genetic correlations of MS with production and conformation traits should be estimated. It would be important to study a potential lack of antagonism observed between proof correlation of MS and SCC, with the goal to explain their relationship.

Procjena genetskih parametara za svojstvo protoka mlijeka kod holstein pasmine goveda u Hrvatskoj

Sažetak

Svojstvo protoka mlijeka (PM) ima sve veću važnost sa stajališta upravljanja proizvodnjom mlijeka. Kod krava sa sporim PM potrebno je više rada, dok krave s brzim PM mogu biti u većoj opasnosti od pojave bolesti vimena. Iako se PM smatra svojstvom od značaja, malo je pozornosti dano procjeni genetskih parametara za PM i njegovoj povezanosti s drugim svojstvima. Ciljevi ovog istraživanja bili su: 1) procijeniti genetske parametre za PM u populaciji holstein goveda u Hrvatskoj; 2) koristiti izračunate genetske parametre za procjenu uzgojnih vrijednosti (UV) za svojstvo PM; i 3) izračunati korelacije između UV za PM s proizvodnim i sa svojstvima vanjštine kako bi se utvrdili međuodnosi između navedenih svojstava. U analizu je bilo uključeno 129.723 zapisa na kontrolni dan za 35.908 prvotelki holstein pasmine, uzetih iz središnje baze podataka Hrvatske poljoprivredne agencije. Podaci o porijeklu sadržavali su zapise za 85.605 životinja. Logaritamska transformacija podataka za svojstvo PM izvršena je s ciljem dobivanja distribucije slične normalnoj.

Komponente varijance procijenjene su REML metodom u programu VCE-6. Statistički model je uključivao sljedeće fiksne utjecaje s razredima: sezona teljenja, vrijeme mužnje i razredi količine mlijeka, dok su dob kod prvog teljenja i stadij laktacije korišteni kao kontinuirana varijabla. Slučajni utjecaji u modelu bili su: interakcija stado-kontrolni dan, stalni utjecaj okoliša i aditivni genetski učinak. Interakcija stado-kontrolni dan i stalni utjecaj okoliša su pojasnili 27 % i 15 % ukupne varijabilnosti PM. Aditivni genetski učinak je pojasnio dodatnih 14 % fenotipske varijabilnosti PM. Utvrđene su niske do srednje korelacije UV bikova i krava između PM i proizvodnih te PM i svojstava vanjštine. Izračunate korelacije bile su pozitivne s izuzetkom korelacije između UV za PM i duljine sisa. Genetsko vrednovanje za svojstvo PM pruža korisne informacije za donošenje uzgojnih odluka zbog umjerenog heritabiliteta te bi u budućnosti navedeno svojstvo trebalo uključiti u ukupan selekcijski indeks. Da bi se utvrdile odgovarajuće ekonomske težine za PM u ukupnom selekcijskom indeksu, potrebno je prethodno procijeniti genetske korelacije između PM i proizvodnih svojstava te svojstava vanjštine.

Ključne riječi: protok mlijeka, Holstein pasmina, zapisi na kontrolni dan, genetski parametri, korelacije UV

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