Genetic parameters for somatic cell score in the first three lactations of Czech Holstein and Fleckvieh breeds using a random regression model

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ABSTRACT: A multiple-lactation random regression model was applied to test-day somatic cell score (SCS) records from the first three lactations of Czech Holstein and Fleckvieh cows. For Holstein, the data included 26 314 cows, with 244 953, 76 188 and 26 153 test-day records in the first, second and third lactation, respectively. For Fleckvieh, the data included 24 061 cows, with 223 421, 93 358 and 31 305 test-day records in the first, second and third lactation, respectively. The linear model for SCS included the following factors (for the given parity): fixed herd-test date effect, fixed regressions on days in milk within the age-season class, random regressions for the animal genetic and random regressions for the permanent environmental effect of the cow. Third-degree Legendre polynomials were used for all regressions. Gibbs sampling was used to generate samples from the marginal posterior distributions of the model parameters. The resulting daily heritability ranged from 0.08 to 0.11 in the middle part of lactation and it increased only slightly with parity. Extremely high values (0.25, 0.21) observed especially at the beginning and end of the third lactation for Holstein might be caused by the "end-of-range" problem. The average daily heritabilities computed for the part of lactation between 45 and 255 days in milk (DIM) were in the range from 0.10 to 0.14. Daily permanent environmental variances were higher than the genetic variances and daily residual variances decreased with DIM. The residual variances in early lactation increased with lactation number. For both breeds, the highest genetic correlations computed for the part of lactation between DIM 45 and DIM 255 were obtained between the second and third lactation (0.95). The lowest daily genetic correlations of SCS in the same DIM between different lactations occurred at the beginning of lactation, especially between the first and third lactation. The permanent environmental correlations for selected DIM were lower than the respective genetic correlations.

Keywords: test-day somatic cell score; random regression model; genetic parameters; Holstein cattle; Czech Fleckvieh

Mastitis is the most costly disease and a major source of economic loss to dairy farmers, mainly through the increased cost of replacement, veterinary treatments and reduced milk yield (Halasa et al., 2007). Therefore, it is desirable to select against clinical mastitis. Extensive recording of health traits in the Scandinavian countries showed that genetic improvement of mastitis resistance is possible through selection (Heringstad et al., 2000). Wolf et al. (2010) also showed that the number of mastitis cases per lactation is a heritable trait and developed a method for the estimation of breeding value for

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this trait for the Holstein population of the Czech Republic. However, direct selection to reduce mastitis incidence is not often possible due to the lack of recorded data. Somatic cell count (SCC), generally log-transformed into somatic cell score (SCS), can be used as an indirect selection tool for reducing mastitis (Emanuelson, 1988; Mrode and Swanson, 2003). SCS is relatively easy to record and has a higher heritability than mastitis incidence (Mrode and Swanson, 2003). The high genetic correlation between SCS and clinical mastitis (approximately from 0.60 to 0.80; Carlén et al., 2004; Wolf et al., 2010) justifies its use as indirect indicator for both clinical and subclinical mastitis.

In the Czech Republic, the advantages of test-day (TD) model methodology stimulated an increasing interest in the use of original TD measurements instead of aggregated lactation records and in an implementation of test-day model methodology for the genetic evaluation of cattle. The test-day model was first implemented for a routine genetic evaluation for milk production traits. For including SCS in the genetic evaluation, the development of a test-day model for this trait is necessary and the appropriate (co)variance components have to be estimated.

The objectives of this study were therefore to propose a random-regression test-day model for the genetic evaluation of the Czech Holstein and Czech Fleckvieh breeds based on data from the first three lactations, to estimate the (co)variance components for this model and to compare the two cattle breeds with respect to SCS.

MATERIAL AND METHODS

Data

The data consisted of TD records on somatic cell count (SCC) from the first three lactations of Holstein and Fleckvieh cows. They were extracted from the Czech national milk-recording database for cows calved between 1995 and 2003. Cows with the second or third lactations had to have all their preceding lactations in the data set. SCC TD records were required to be recorded between 6 and 305 days in milk (DIM). The number of TD records per lactation ranged from 8 to 10. Records on lactations where the first TD was later than 60 days after calving were excluded. The last TD record was required to be later than 250 days after calving. Age at calving was restricted from 660 to 1000 days in the first, from 1020 to 1420 days in the second, and from 1390 to 1840 days in the third lactation. A minimum of three contemporaries per herd-TD class was required. Cows from sires with fewer than 10 daughters in the data set before editing were excluded. A random selection on herd number was applied to create the final data sets, which were assumed to be representative samples from the whole population of the breed in the considered time interval. A smaller than expected number of records in the second and third parity was a consequence of the structure of the population with SCS recorded and of edits imposed on consecutive lactations.

Summary statistics of the final data sets used for the analyses is given in Table 1. The pedigree files included 63 679 and 59 752 animals for Holstein and Fleckvieh, respectively.

Statistical methods

Monthly TD SCC records, expressed in the value of 1000 cells/ml, were transformed to *SCS* on a logarithmic scale:

$SCS = \log_2(SCC/100) + 3$

The following model equation (the same for both breeds) was used:

Table 1. Summary statistics for the data sets of Holstein and Fleckvieh cows used for the estimation of genetic parameters

Parameter	Holstein			Fleckvieh		
	1	2	3	1	2	3
Average SCS[a]	3.40 (0.003)	3.78 (0.006)	4.13 (0.011)	3.16 (0.003)	3.68 (0.006)	4.01 (0.010)
Number of cows	26 314	8 199	2 804	24 061	10 007	3 355
Number of test days	244 953	76 188	26 153	223 421	93 358	31 305

[a]SCS = somatic cell score (the standard errors are given in parentheses)

$$y_{nkitlj} = \mathrm{HTD}_{ni} + \sum_{m=0}^{3} \beta_{nkm} z_{tm} + \sum_{m=0}^{3} a_{njm} z_{tm} + $$
$$+ \sum_{m=0}^{3} p_{njm} z_{tm} + e_{nkitlj}$$

where:

y_{nkitlj} = l^{th} SCS record on cow j made on day t within herd-test day effect i, for a cow in parity n belonging to subclass k for age and season of calving

HTD_{ni} = fixed herd-test-day effect i within parity n

β_{nkm} = m^{th} fixed regression coefficient specific to sub-class k in parity n

a_{njm} = m^{th} random regression coefficient specific to animal j in parity n

p_{njm} = m^{th} random regression coefficient specific to permanent environmental effect of cow j in parity n

e_{nkitlj} = residual effect for each observation

z_{tm} = covariates associated with DIM, assumed to be the same for both fixed and random regressions

Cows were assigned to one of nine subclasses within parity formed by a combination of three subclasses for age at calving (1st parity: < 800 days, 800 to 900 days, > 900 days; 2nd parity: < 1200 days, 1200 to 1350 days, > 1350 days; 3rd parity: < 1580 days, 1580 to 1760 days, > 1760 days) and three sub-classes for the calving season (February through April, May through September and October through January of the following year).

Third-degree Legendre polynomials (with four coefficients) were used for both the fixed and random regressions on the scale from 7 to 305 DIM. Let $\mathbf{p}_\mathrm{j}$ be the 12 × 1 vector of random permanent environmental regression coefficients (4 regression coefficients for each of the 3 lactations) for cow j with covariance matrix $\mathbf{P}$. Then, the permanent environmental covariance matrix for all cows was assumed to be $\mathbf{I} \otimes \mathbf{P}$ where $\mathbf{I}$ is the identity matrix. Let further $\mathbf{a}_\mathrm{j}$ be the 12 × 1 vector of random regression coefficients for animal j with covariance matrix $\mathbf{G}$. Denoting $\mathbf{A}$ as the additive relationship matrix, then $\mathbf{A} \otimes \mathbf{G}$ was the genetic covariance matrix for all animals. Different residual variances were allowed for different lactations and time periods within lactation, defined as: 7–45 DIM, 46–115 DIM, 116–265 DIM, and 266–305 DIM (Jamrozik et al., 1998). Residual effects on different DIM were assumed to be uncorrelated both within and between cows. The model was a special case of the model of Jamrozik et al. (1998) for the multiple-lactation and multiple-trait scenario.

Bayesian estimation using Gibbs sampling was used to estimate model parameters separately for both breeds. Multivariate normal and inverted Wishart distributions were used for sampling location and dispersion parameters, respectively. For each breed, 55 000 samples were generated and 5000 burn-in samples were discarded. The convergence of the Gibbs scheme and the length of the burn-in period were determined by visual inspection of trace plots for selected parameters.

Estimates of the variance and covariance components were obtained as posterior means of 50 000 samples.

The whole-lactation estimates of genetic parameters referring to average daily SCS were calculated following the procedure described in Jamrozik and Schaeffer (1997). Because of the "end-of-range" problems (occurrence of abnormally high or low variance estimates at the extremes of the studied period) frequently observed when fitting polynomial regressions (Meyer, 2005) we decided to compute the whole-lactation estimates of genetic parameters using only the middle part of lactation, i.e. for the range from 45 to 255 DIM.

Table 2. Additive genetic, permanent environmental (PE) and residual variances and heritabilities of average daily SCS computed for the range from 45 DIM to 255 DIM

Trait or variable	Holstein			Fleckvieh		
	1	2	3	1	2	3
Additive genetic variance	0.24	0.28	0.21	0.19	0.18	0.20
PE variance	0.97	1.12	1.39	0.91	1.01	1.09
Residual variance	0.63	0.63	0.62	0.61	0.58	0.55
Heritability	0.13	0.14	0.10	0.11	0.10	0.10

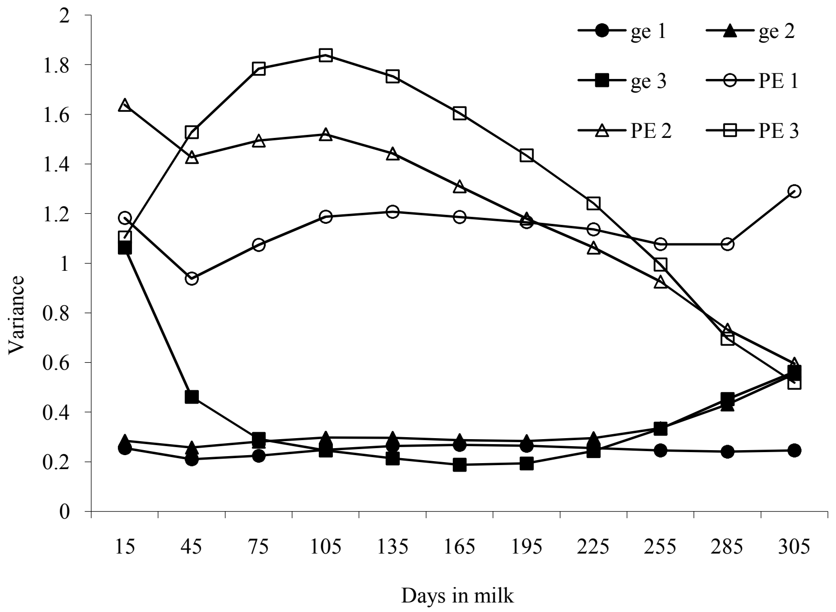

Figure 1. Additive genetic (ge) and permanent environmental daily variances (PE) for somatic cell score in parity 1, 2 and 3 for Holstein

RESULTS

Heritabilities and variances

The average daily variances and heritabilities of SCS computed for the part of lactation between DIM 45 and DIM 255 from the TD RR animal model are presented in Table 2. Additive genetic variances for Holstein cows increased from the first to the second lactation and decreased again in the third lactation below the value in the first lactation whereas in Fleckvieh a slight decrease was observed between the first and the second lactation and the genetic variance had its highest value in the third lactation. A marked increase of the permanent environmental variance with lactation number was found in both breeds. The residual variances decreased with parity for Fleckvieh but remained nearly constant for Holstein cows. The average daily heritability of SCS for Holstein cows was in the range from 0.10 to 0.14 in the first three lactations. The corresponding values for Czech Fleckvieh were somewhat lower (between 0.10 and 0.11).

The estimates of daily additive genetic variances showed a plain trajectory with only small changes over time (Figures 1 and 2) during all lactations and in both breeds. Estimates of variances at the extremes of the studied period were abnormally high in some cases (especially at the beginning of the third lactation for Holstein cows).

The estimated variance components for the permanent environmental effect were higher than the

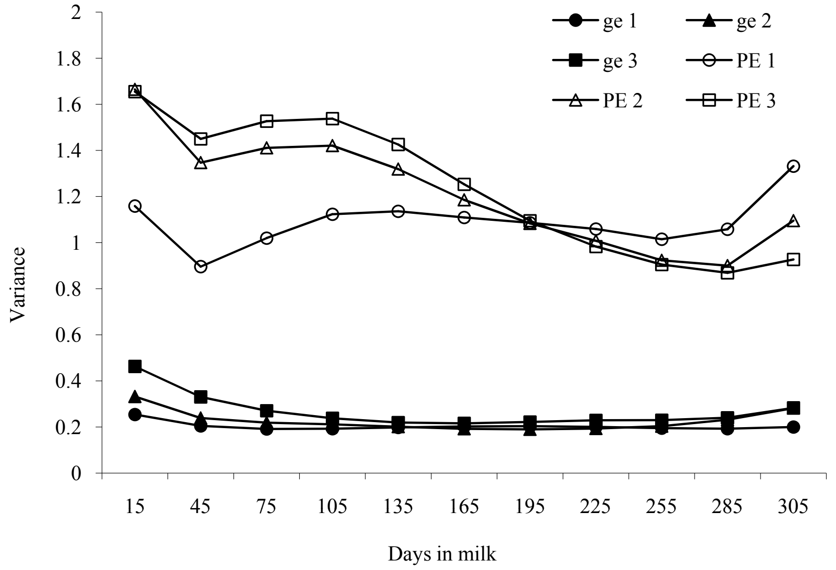

Figure 2. Additive genetic (ge) and permanent environmental daily variances (PE) for somatic cell score in parity 1, 2 and 3 for Fleckvieh

Table 3. Residual variances of test-day SCS in Czech Holstein and Fleckvieh cows for different classes of days in milk in the first, second and third parity

Days in milk	Holstein			Fleckvieh		
	1	2	3	91	2	3
7–45	1.65	1.93	2.10	1.58	1.73	1.71
46–115	1.41	1.56	1.56	1.36	1.47	1.40
116–265	1.07	1.03	1.02	1.04	0.95	0.91
266–305	0.92	0.86	0.96	0.92	0.77	0.78

additive genetic variances in all lactations (Figures 1 and 2). In the inner part of the lactation, they remained relatively constant in the first parity and decreased with days in milk in the second and third parity, whereas the decrease was strongest in third-parity Holstein cows.

The trends of daily residual variances for SCS were similar in all three parities of both breeds (Table 3). The highest values occurred at the beginning of lactations followed by a decrease with DIM. Residual variances in early lactation increased with parity number for both breeds.

Heritability estimates for selected days in milk are presented in Table 4 for Holstein cows and in Table 5 for Czech Fleckvieh cows. These estimates were relatively stable over time and similar for all lactations (in the range from 0.07 to 0.11 for Holstein and from 0.07 to 0.10 for Fleckvieh) during the part of lactation from 45 to 195 DIM. Higher heritability estimates (up to 0.25) occurred at the beginning or end of lactation, especially in the Holstein breed.

Correlations between different lactations

Genetic and permanent environmental covariances and correlations of average daily SCS between different lactations for the range from 45 to 255 DIM are presented in Table 5. Both genetic and permanent environmental covariances were the highest between adjacent lactations. The permanent environmental covariances for SCS between any two lactations were higher than the corresponding genetic covariances. Generally, both types of covariances were higher for the Holstein breed than for Fleckvieh cows.

The genetic correlations for average daily SCS between lactations were very high and almost the same (from 0.94 to 0.95) except the genetic correlation between the first and third lactation of Fleckvieh, which was below 0.90. All permanent environmental correlations between parities for SCS were considerably lower than the respective genetic correlations. The permanent environmental correlations were the highest between the second

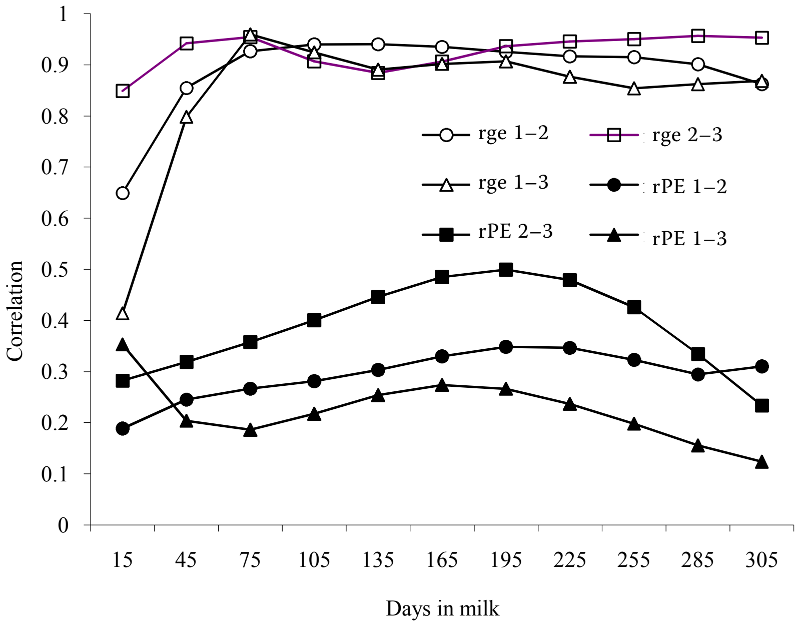

Figure 3. Genetic (rge) and permanent environmental (rPE) correlations for SCS on the same DIM among parities 1, 2 and 3 in Holstein

Table 4. Genetic correlations (above diagonal), heritabilities (on diagonal) and permanent environmental correlations (below diagonal) for SCS on selected days in milk (DIM) in the first three parities of Holstein cows and Fleckvieh cows

Parity	DIM	1					2					3				
		15	45	105	195	285	15	45	105	195	285	15	45	105	195	285
Holstein cows																
1	15	**0.08**	0.91	0.63	0.50	0.41	0.65	0.64	0.52	0.41	0.24	0.41	0.59	0.67	0.51	0.27
	45	0.83	**0.08**	0.89	0.81	0.71	0.77	0.85	0.78	0.68	0.49	0.58	0.80	0.87	0.72	0.52
	105	0.41	0.83	**0.09**	0.95	0.85	0.74	0.92	0.94	0.87	0.73	0.63	0.86	0.92	0.86	0.74
	195	0.27	0.55	0.81	**0.11**	0.95	0.63	0.85	0.94	0.93	0.87	0.55	0.77	0.88	0.91	0.86
	285	0.28	0.43	0.56	0.78	**0.11**	0.45	0.72	0.88	0.91	0.90	0.38	0.62	0.83	0.90	0.86
2	15	0.19	0.22	0.20	0.21	0.26	**0.07**	0.91	0.67	0.60	0.46	0.85	0.90	0.64	0.63	0.56
	45	0.18	0.25	0.27	0.28	0.32	0.89	**0.07**	0.92	0.86	0.65	0.79	0.94	0.85	0.80	0.73
	105	0.15	0.23	0.28	0.33	0.34	0.55	0.86	**0.09**	0.94	0.83	0.62	0.84	0.91	0.87	0.80
	195	0.16	0.20	0.24	0.35	0.34	0.28	0.55	0.82	**0.11**	0.93	0.60	0.77	0.83	0.94	0.90
	285	0.15	0.19	0.20	0.24	0.29	0.37	0.43	0.55	0.86	**0.21**	0.50	0.62	0.66	0.88	0.96
3	15	0.35	0.24	0.11	0.19	0.23	0.28	0.27	0.24	0.19	0.10	**0.25**	0.92	0.45	0.56	0.63
	45	0.23	0.20	0.16	0.22	0.24	0.30	0.32	0.33	0.30	0.21	0.97	**0.11**	0.75	0.69	0.63
	105	0.10	0.17	0.22	0.26	0.27	0.28	0.34	0.40	0.42	0.32	0.85	0.95	**0.07**	0.86	0.64
	195	0.04	0.14	0.23	0.27	0.26	0.29	0.34	0.43	0.50	0.39	0.54	0.68	0.86	**0.07**	0.90
	285	0.15	0.14	0.09	0.10	0.16	0.25	0.29	0.36	0.44	0.33	0.36	0.47	0.66	0.91	**0.21**
Fleckvieh cows																
1	15	**0.09**	0.96	0.79	0.65	0.56	0.84	0.87	0.72	0.49	0.24	0.73	0.78	0.70	0.41	0.22
	45	0.83	**0.08**	0.92	0.83	0.76	0.82	0.92	0.84	0.65	0.40	0.69	0.80	0.81	0.55	0.36
	105	0.40	0.83	**0.07**	0.96	0.87	0.69	0.88	0.94	0.82	0.60	0.54	0.72	0.88	0.72	0.52
	195	0.27	0.54	0.81	**0.09**	0.94	0.58	0.82	0.96	0.89	0.72	0.43	0.63	0.87	0.82	0.63
	285	0.24	0.38	0.51	0.75	**0.09**	0.58	0.77	0.90	0.94	0.83	0.46	0.63	0.86	0.90	0.79
2	15	0.07	0.14	0.18	0.17	0.14	**0.09**	0.92	0.66	0.50	0.20	0.86	0.89	0.74	0.38	0.27
	45	0.10	0.19	0.24	0.25	0.23	0.86	**0.07**	0.89	0.78	0.50	0.77	0.88	0.88	0.60	0.44
	105	0.12	0.21	0.26	0.29	0.29	0.49	0.85	**0.07**	0.89	0.71	0.54	0.72	0.91	0.81	0.65
	195	0.12	0.18	0.24	0.31	0.31	0.28	0.52	0.78	**0.08**	0.91	0.43	0.62	0.86	0.90	0.87
	285	0.08	0.14	0.18	0.24	0.30	0.29	0.37	0.47	0.74	**0.12**	0.19	0.35	0.65	0.88	0.92
3	15	0.05	0.10	0.13	0.11	0.05	0.26	0.28	0.23	0.19	0.19	**0.12**	0.95	0.68	0.34	0.29
	45	0.05	0.12	0.16	0.15	0.11	0.27	0.32	0.30	0.28	0.24	0.89	**0.09**	0.87	0.61	0.39
	105	0.06	0.13	0.17	0.18	0.15	0.23	0.30	0.33	0.35	0.29	0.57	0.87	**0.07**	0.80	0.65
	195	0.10	0.16	0.18	0.20	0.19	0.19	0.26	0.32	0.41	0.39	0.34	0.59	0.83	**0.10**	0.86
	285	0.07	0.12	0.14	0.14	0.21	0.12	0.20	0.25	0.29	0.39	0.33	0.38	0.46	0.77	**0.13**

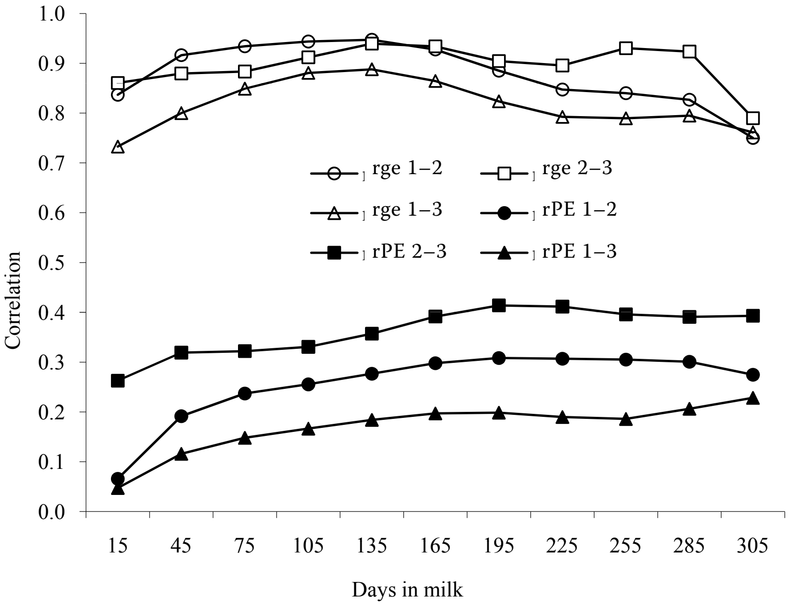

Figure 4. Genetic (rge) and permanent environmental (rPE) correlations for SCS on the same DIM among parities 1, 2 and 3 in Fleckvieh

and third lactation and the lowest between the first and third lactation in both analysed breeds.

The time-dependent estimates of the genetic and permanent environmental correlations for SCS on the same TD among the first three lactations are given in Figures 3 and 4. With the exception of some low values at the beginning of lactation, especially in the Holstein breed, all genetic correlations for both breeds were in the range between 0.8 and 1.0 for the substantial part of the lactation.

The daily permanent environmental correlations were markedly lower than the respective genetic correlations. The strongest relation was found out between the second and third lactation, the lowest between the first and third lactation.

Correlations between SCS on different DIM

The genetic and permanent environmental correlations for SCS among different DIM are presented in Tables 4. The genetic correlations within each parity were the highest between adjacent DIM (0.85–0.95 for Holstein; 0.80–0.96 for Fleckvieh) and they decreased as the DIM got further apart. The differences between breeds were small.

The permanent environmental correlations for SCS among different DIM were similar in pattern to the genetic correlations. They were the highest between adjacent DIM (0.78–0.97 for Holstein; 0.74–0.87 for Fleckvieh) and declined as DIM were further apart. In contrast to the genetic correlations, the permanent environmental correlations were slightly lower for Fleckvieh than for Holstein cows.

DISCUSSION

Time-dependent genetic parameters

Legendre polynomials have been widely used in random regression models for the estimation of genetic parameters and for genetic evaluation of livestock. Polynomials are linear in their parameters and therefore easy to integrate into linear

Table 5. Genetic and permanent environmental covariances and correlations between parities for average daily SCS in Czech Holstein and Fleckvieh cows, estimated for the range from 45 to 255 DIM

Genetic parameter	Holstein			Fleckvieh		
	1–2	1–3	2–3	1–2	1–3	2–3
Genetic covariance	10 740	9 573	10 307	7 795	7 571	8 098
PE covariance	15 974	13 564	26 122	13 464	9 092	18 808
Genetic correlation	0.94	0.95	0.95	0.94	0.88	0.95
PE correlation	0.34	0.26	0.47	0.32	0.21	0.40

Table 6. Estimates of heritability and genetic correlations for whole-lactation SCS from the literature. Unless noted otherwise, the heritability estimates are for the 1st, 2nd and 3rd lactation

Authors	Heritability estimate	Genetic correlations		
		1–2	1–3	2–3
Reents et al. (1995)	0.09, 0.09, 0.11	0.88	0.79	0.95
Liu et al. (2000)	0.20[a]	0.95	0.89	0.97
Mrode and Swanson (2003)	0.17, 0.18, 0.12	0.69	0.79	0.98
Carlén et al. (2004)	0.14, 0.13, 0.10	0.88	0.81	0.98
DeGroot et al. (2007)	0.02–0.06, 0.04, 0.03–0.06			
Miglior et al. (2007)	0.19, 0.27, 0.34	0.54	0.40	0.56
Samoré et al. (2008)	0.18, 0.21, 0.21	0.93	0.87	0.92
Wolf et al. (2010)	0.17[b]			
Yazgan et al. (2010)	0.05, 0.07, 0.03			

[a]approximate value for the first 3 lactations
[b]for all lactations including lactations > 3

models. However, care must be taken when interpreting the results. According to Meyer (2005), "end-of-range" problems are frequently observed for random regression models when fitting polynomial regressions. Van der Werf et al. (1998) stated that although the likelihood of covariance function estimates from random regression models was maximized, variance component estimates in peripheral parts of the trajectory seemed far from realistic values.

Though the "end-of-range" problems have been known since 1901 at least (Runge, 1901), this problem is not taken into account in many studies using random regression models and the mathematical artefacts are misinterpreted as "real values" of genetic parameter estimates. The "end-of-range" problem was the reason why we calculated the whole-lactation parameters only for the interval from 45 to 255 DIM, thus excluding the observations at both ends of lactation. This procedure should give more reliable estimates than using the entire DIM scale.

Many earlier studies, which considered several stages within lactation or used random regression models, observed lower heritability estimates in the initial stage of lactation (Emanuelson et al., 1988; Rogers et al., 1995; Mrode and Swanson, 1996; Haile-Mariam et al., 2001). Except of estimates for the third lactation of Holstein, our findings agree with Liu and Reents (2000), who observed fairly homogeneous heritability estimates throughout the whole lactation length in the first three parities fitting a sire RR model. Due to selection practice in the Czech Republic, the decline in the number of cows from the second to third lactation is enormous. Other factors contributing to this trend could be edits imposed on the consecutive lactations and smaller number of SCS for later parities associated with the beginning of SCS recording in the Czech Republic. Therefore, because of the relatively low amount of information available for the third lactation, the very high heritability estimate of 0.25 at the beginning of this lactation may be a mathematical artefact caused by the "end-of-range" problem.

In the present study, permanent environmental and residual variances until 100 DIM showed higher values for higher parity numbers on the same DIM. This is in agreement with the hypothesis that variation in SCC after calving is largely influenced by differences in environmental factors (Miller et al., 1991) and that this effect seems to be larger for later parities. The same results were published by Liu and Reents (2000) and Mrode and Swanson (2003). As a consequence, the genetic correlations decreased with lactation number. This decrease was observed in Fleckvieh cows to a larger extent than in Holstein cows. Detilleux et al. (1997) suggested that the risk of intra-mammary infection from environmental pathogens, which cause a brief increase in SCC, is high at the beginning of lactation when cows are metabolically stressed. The above facts are consistent with the postulation of Haile-Mariam et al. (2001) that perhaps in early lactation, variations in SCC are due to spikes in SCC as a result of infection, however, later in the lactation, SCC are largely due to responses to infection, which results in more stable elevations of SCC. The differences between the early part and the rest of lactation were confirmed by low values of correlations between SCS for a given DIM and SCS for the completed lactation, especially at the beginning of lactation. Furthermore, mathematical artefacts caused by the "end-of-range" problem may be an additional reason for low correlation estimates.

Genetic correlations between different parities for SCS at the same DIM showed a tendency to be the highest between the second and third parity and the lowest between the first and third parity (Liu and Reents 2000; Haile-Mariam et al., 2001), which is in good agreement with our results. However, Mrode and Swanson (2003) reported slightly lower genetic correlations between the first and second parity than between the first and third parity.

Whole-lactation genetic parameters

Literature estimates of heritability of SCS in the first three lactations are summarized in Table 6. Our results, which were in the range from 0.10 to 0.14, are in good agreement with Reents et al. (1995), Mrode and Swanson (2003), Carlén et al. (2004) and Wolf et al. (2010). Heritabilities around 0.20 estimated by Liu and Reents (2000) and Samoré et al. (2008) are clearly higher than our estimates, but these differences may be explained by differences in populations, statistical models and estimation methods.

However, the estimates of Miglior et al. (2007) for the second and third lactation (0.27 and 0.34) of Canadian Holsteins seem to be extremely large. Possible reasons for the high values might be the use of a selected data set (only cows with data on lactose percentage and milk urea nitrogen were considered) or the inclusion of extreme values at the beginning and end of lactation in the calculation of the whole-lactation heritability ("end-of-range" problem).

On the other hand, DeGroot et al. (2007) and Yazgan et al. (2010) reported very low heritability estimates. DeGroot et al. (2007) explained the low values by the fact that they used a high percentage of non-registered (grade) cows in the analysis. In grade cows, there is a greater chance of misidentification of their sires and dams.

In agreement with our results for Czech Fleckvieh, most authors found that genetic correlations between adjacent lactations were greater than the genetic correlation between the first and third lactation, and the correlation between the second and third lactation was often greater than the correlation between the first and second lactation (Reents et al., 1995; Liuand Reents, 2000; Carlén et al., 2004; Miglior et al., 2007; Samoré et al., 2008). Our results for Holstein cattle did not show this general tendency as all three correlation estimates were very high and did not differ from each other.

Differences between breeds

There are substantial differences between Holstein and Fleckvieh breeds analysed in this study. In Holstein, higher genetic variances give evidence about stronger genetic influences on somatic cell count than those found in Fleckvieh cows. Furthermore, the similarity between different parities is stronger in Holstein than in Fleckvieh, when the correlations for completed lactations are taken into account. There is also a larger fluctuation in variation of SCS in the course of lactation for Holstein cows in comparison with Fleckvieh. The changes in the third lactation of Holstein breed also reflected different selection practices in Holstein herds compared with Fleckvieh. Probably the strong selection pressure on production traits in Holstein is connected with a high level of involuntary culling induced by the low withstand capability of cows. This resulted in a high decrease of the number of completed lactations from the first to third parity. Therefore the results of our study indicate the need of further studying the relationship between SCS and functional traits in Holstein and Fleckvieh cows separately.

CONCLUSIONS

The genetic and permanent environmental parameters found in this study were consistent with commonly published results for other cattle breeds. It can be expected that the application of a test-day model that accounts for genetic and environmental variation in the course of lactation should improve the accuracy of estimated breeding values compared with the animal model for SCS on a lactation basis.

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