GENETIC PARAMETERS OF TEST DAY SOMATIC CELL COUNTS AND PRODUCTION TRAITS[1]

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SUMMARY

Genetic parameters were estimated for test day log transformed somatic cell scores (SCS) and their relationship with test day production traits and type traits in Holstein dairy cows. Data were analyzed using a multi-trait REML procedure with an animal model. Heritabilities for first lactation individual test day SCS were low (.06 to .10). Genetic correlations between SCS and milk yield and protein yield were positive (.10 to .58), zero between SCS and fat yield, negative between SCS and fat content (-.1 to -.45), negative between SCS and protein content in early lactation (-.08 to -.49), but positive in the last part of the first lactation (.17 to .30). SCS showed desirable negative genetic correlations to some udder type traits, such as fore attachment, rear attachment, median suspensory, and fore teat placement.

INTRODUCTION

Measurements of somatic cell count (SCC) are increasingly used as an indicator trait for selection against mastitis. In comparison to production and type traits, much less is known about the genetic background of somatic cells. The aim of the present study was to analyze test day (TD) log transformed SCC (SCS) and their relationship to production data for first lactation dairy cows. An extension was made to analysis of relationships with udder type traits and to analysis of observations of SCS in second lactation.

MATERIALS AND METHODS

Data consisted of test day records for SCC and production (milk yield, fat%, and protein %) on Ontario Holstein cows with calving years from 1986 to 1990. Edits were done for days in milk (DIM, first test day between 4 and 75 DIM, interval between consecutive test days between 14 and 70 DIM) and irregular production records (milk yields were only accepted in a range from 1.5 to 80 kg, fat concentration from 1.5 % to 8.5%, and protein concentration from 1.5% to 7.5%). After edits, data on 28,684 cows remained, with at least 9 test days within the first lactation. Due to computational limitations and in order to improve the data structure, data on 10,777 cows from 529 large herds were used for estimation of variance components. These cows were progeny of 1117 sires (114 sires with more than 9 daughters) and 9814 dams. Due to the short time period of 4.5 calving years, only 491 dams also had a first lactation record in the data file. For each test day, linear somatic cell score (SCS) was calculated as follows:

$$SCS = \frac{[\log(SCC/1000)]}{.69315} - 3.6439$$

Genetic and residual (co)variances were estimated using multiple trait REML. The following animal model was used for each trait, using a canonical transformation (Meyer, 1985) and specific techniques developed and kindly provided by Misztal et al. (1992):

$$y_{ijk} = HYS_i + b(AGE) + a_j + e_{ijk}$$

where y_{ijk} is the observed SCS or production trait for test day 1 to 9; HYS_i is a fixed herd-year-season effect (two seasons per year); $b(AGE)$ is a covariate of age at calving on trait y_{ijk}; a_j is a random animal additive genetic effect; and e_{ijk} is a residual effect.

Pedigree information for cows in the data file was completed for sire, dam and maternal grandsire. A total of 2126 sires with daughters or granddaughters with observations were found, 238 sires of these sires completed the pedigree on the male side for several generations. Seven phantom groups for unknown parents were defined according to year of birth and sex. 75 - 90 rounds of iteration were carried out until convergence of the estimated variance components.

RESULTS

Some characteristics of the dataset and the estimates of heritability, genetic and residual variances are in Table 1. SCS for TD1 to TD 9 and milk yield for TD1 to TD9, resulting in 18 traits, were analyzed in one estimation run. Heritabilities for SCS were much lower than for milk yield. Heritabilities for individual test days were, as expected, lower than for an average SCS over the first lactation, which was .124 for the described dataset and model.

Table 1. Phenotypic means and variance components for individual test day SCS and milk yield

Trait	Test day	Average DIM	Mean of trait	Variance Residual	Genetic	Heritability	approx. SE of h²
SCS	1	25.4	2.5	2.30	.17	.07	.06
	2	60.8	2.1	2.05	.23	.10	.06
	3	96.4	2.2	2.20	.18	.08	.06
	4	132.1	2.3	2.04	.17	.08	.06
	5	167.8	2.4	2.08	.13	.06	.06
	6	203.5	2.5	1.89	.18	.09	.06
	7	239.4	2.6	1.84	.15	.07	.06
	8	275.4	2.7	1.81	.16	.08	.06
	9	311.4	2.9	1.75	.17	.09	.06
Milk	1	25.4	24.5	14.76	1.56	.10	.06
yield	2	60.8	25.7	11.92	1.90	.14	.06
(kg)	3	96.4	24.5	10.20	2.70	.21	.05
	4	132.1	23.1	8.93	3.80	.30	.05
	5	167.8	21.9	8.41	4.01	.32	.04
	6	203.5	20.7	7.87	4.67	.37	.04
	7	239.4	19.6	8.07	4.43	.35	.04
	8	275.4	18.1	9.01	3.95	.31	.04
	9	311.4	15.8	11.09	4.71	.30	.05

Genetic and residual correlations from the 18 trait REML analysis are in table 2. For brevity, results from test days 2, 4, 6, and 8 were omitted in further tables. Genetic correlations between adjacent test days within a trait were high and decreased with increasing distance between test days. Positive genetic correlations between SCS and milk yield showed an undesirable relationship. Highest

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genetic correlations between SCS and milk yield were found for the middle of the lactation, whereas at the end of the lactation, genetic correlations were close to zero or slightly negative.

Table 2. Heritabilities (diagonal), genetic (above diagonal) and residual (below diagonal) correlations between test day observations for SCS and milk yield.

Trait	TD	SCS					Milk yield				
		1	3	5	7	9	1	3	5	7	9
SCS	1	.07	.87	.72	.51	.55	.29	.19	.14	.19	.12
	3	.30	.08	.89	.71	.59	.58	.37	.37	.37	.33
	5	.25	.51	.06	.91	.77	.57	.37	.38	.31	.32
	7	.22	.42	.54	.07	.85	.46	.38	.33	.20	.17
	9	.18	.36	.45	.55	.09	.43	.29	.15	-.03	-.17
Milk	1	-.22	-.01	.01	.00	.02	.10	.73	.68	.53	.43
yield	3	.00	-.13	-.05	-.05	-.02	.42	.21	.95	.83	.55
	5	-.03	-.15	-.17	-.11	-.07	.30	.57	.32	.94	.73
	7	-.03	-.15	-.13	-.18	-.10	.26	.48	.60	.35	.88
	9	-.01	-.13	-.12	-.14	-.25	.15	.35	.40	.52	.30

Genetic correlations between SCS and fat yield were close to zero for all test days. Genetic and residual correlations between SCS and protein yield were very similar to the correlations between SCS and milk yield displayed in Table 2.

Test day records for fat concentration showed negative genetic correlations with SCS (in the range of -.15 to -.45) for all test days. Table 3 shows that genetic correlations between SCS and protein concentration were negative only for the first 5 to 6 test days, but became positive towards the end of lactation.

Table 3. Heritabilities (diagonal), genetic (above diagonal) and residual (below diagonal) correlations between test day observations for SCS and protein concentration.

Trait	TD	SCS					Protein %				
		1	3	5	7	9	1	3	5	7	9
SCS	1	.06	.80	.61	.53	.59	-.17	-.21	-.18	-.06	-.03
	3	.31	.07	.88	.80	.65	-.49	-.25	-.17	-.18	-.20
	5	.25	.51	.05	.92	.80	-.36	-.07	-.08	.00	-.02
	7	.22	.42	.54	.07	.85	-.26	.00	.17	.17	.22
	9	.18	.35	.45	.55	.08	-.02	-.02	.13	.24	.30
Protein	1	.33	.05	.02	.01	-.02	.18	.68	.56	.59	.57
%	3	.00	.16	.07	.06	.03	.09	.36	.96	.86	.63
	5	.01	.09	.12	.06	.02	.10	.46	.45	.92	.73
	7	.01	.11	.07	.11	.05	.05	.34	.46	.47	.90
	9	.00	.07	.05	.02	.14	.03	.30	.34	.45	.37

Some studies have reported changes in genetic correlations between SCS and production traits from first to later lactations from positive to negative (Monardes and Hayes, 1985; Heuven et al., 1988, Banos and Shook, 1990). Culling during or after first lactation of cows with low milk yield and (or) high mastitis incidence might contribute to the change in genetic correlation. Due to the short time period of 4.5 calving years only few of the cows with first lactation also had a second and higher lactation in the current data set. Thus the data set was not well suited for analysis of the relationship of SCS to production traits within second or later lactations. However, on a subset of the described dataset, records from 4813 cows with a complete second lactation (TD 1 to TD 9 required) were taken to estimate variance components between SCS and production traits to get preliminary results for a following study. Heritabilities for SCS were slightly higher for all test days than for the corresponding test days in first lactation. For early test days genetic correlations between SCS and production traits were similar to those from first lactation. In the second half of the lactation, genetic correlations between SCS and milk yield became negative to a high negative correlation of -.79 on test day 9.

Of the 10,777 cows with a completed first lactation 8450 also had observations for type traits. The same model as described previously was used for this analysis. Type traits analyzed were restricted to udder traits: udder-texture, median-suspensory, fore attachment, fore teat placement, rear attachment, and rear teat placement. Precorrection for stage of lactation was done for type traits, with factors from routine evaluation. Classification of herds is usually done only once per herd-year-season, thus the effect of the classifier should be accounted for in the model. Genetic correlations between the 9 test day SCS observations and four of the six type traits were negative (desirable), with a tendency of larger (more negative) values in the middle of the lactation. Genetic correlations were around -.3 with fore-attachment and of -.45 with rear attachment. Genetic correlations of SCS to median-suspensory and fore teat placement were in a range from -.15 to -.20. Genetic correlations of SCS to udder texture and rear teat placement were close to zero.

DISCUSSION

Analysis of test day data from cows in first lactation showed an undesirable positive genetic correlation of SCS to milk and protein yield. Selection for protein yield in first lactation will result in an increase of SCC and therefore mastitis susceptibility. The dataset was not well suited for an analysis of later lactations because of the short time period of calving years. However, the analysis of test day data of second lactation showed a change of the genetic correlations between SCS and milk yield to negative values towards the end of the lactation. The restriction of the dataset to cows with a complete first and second lactation might have introduced some bias in the estimation of variance components for the second lactation. The results for first lactation should be unaffected by selection because of the low incidence of mastitis in first lactation. Further studies will be undertaken for data with a higher percentage of second and later lactations and considering missing values in later lactations.

Selection for udder health should also include some type traits because of their desirable relationship to SCS. Investigation of relationship between SCS and objectively measured type traits, that were introduced recently in Canada, is recommended.

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