Estimation of genetic parameters for test-day somatic cell count in UK Holstein Friesian dairy herds

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Introduction Somatic cell count (SCC) is used widely as an indicator trait for both clinical and subclinical mastitis, and was introduced into genetic evaluations in the UK in 1998. The present evaluations of SCC are based upon a single trait repeatability lactation average model using the first five lactations. The test-day model is now widely adopted for routinely recorded traits, thus the objective of this study was to estimate genetic parameters for SCC using a test-day model.

Materials and methods Log_e SCC (LSCC) was analysed from a dataset consisting of 1,220,344 SCC tests from 43592 Holstein/Friesian cows during their first three lactations that calved between the years 1997 and 2009, and sired by 1654 bulls. Cows required records for all three lactations and a minimum of eight herd-test days were required for lactations one and two, and a minimum of six herd-test day records for lactation three. Lactations were analysed separately and mean LSCC for lactations one, two and three were 11.66. 11.91, and 12.22, respectively. The dataset was analysed in ASReml (Gilmour *et al*., 2006) with a sire random regression model fitting Legendre polynomials of order 2 for sire effect and permanent environmental effect of the cow. Residual variances for four classes were estimated according to lactation stage: 4-24, 25-49, 50-249, and 250-305 days in milk.

Results Daily heritability (h^2) estimates for LSCC tended to increase with increased days in milk and the average daily h^2 increased with increased lactation. The average daily h^2 for lactations one, two, and three were 0.07, 0.10, and 0.11, respectively. Daily h^2 estimates for lactations one, two, and three ranged from 0.06 to 0.10, 0.06 to 0.17, and 0.07 to 0.18, respectively. Permanent environmental variances for LSCC were at their highest at the start of lactation, generally decreased with stage of lactation, and increased with lactation number. Similarly, residual and phenotypic variances decreased with stage of lactation / days in milk and estimates were higher with increased lactation number. Phenotypic variances for LSCC ranged from 0.75 to 1.42, 0.74 to 1.71, and 0.83 to 2.01 for lactations one, two and three, respectively. Mean phenotypic variances for LSCC were 0.87, 1.01, and 1.20, respectively. As expected genetic and permanent environmental correlations were highest when days in milk were closest to each other (Table 1). Genetic and permanent environmental correlations between days in milk for LSCC tended to be higher in lactation one. Within lactations the genetic and permanent environmental correlations between days in milk had very similar values for lactations two and three.

Table 1 Heritabilities (on diagonal), genetic correlations (below diagonal), and permanent environmental correlations (above diagonal) on selected days for LSCC in the first two lactations.

	Lactation 1							Lactation 2						
Days in milk	4	54	104	154	204	254	304	4	54	104	154	204	254	304
4	**0.07**	0.89	0.65	0.47	0.37	0.35	0.35	**0.06**	0.89	0.64	0.42	0.29	0.23	0.21
54	0.94	**0.08**	0.93	0.81	0.72	0.63	0.47	0.90	**0.08**	0.92	0.78	0.66	0.53	0.31
104	0.76	0.94	**0.07**	0.97	0.91	0.79	0.55	0.71	0.94	**0.09**	0.96	0.89	0.73	0.40
154	0.56	0.81	0.96	**0.06**	0.98	0.88	0.63	0.54	0.84	0.97	**0.10**	0.97	0.85	0.51
204	0.43	0.69	0.89	0.98	**0.07**	0.96	0.75	0.42	0.72	0.89	0.97	**0.10**	0.94	0.66
254	0.38	0.61	0.79	0.91	0.97	**0.09**	0.91	0.32	0.57	0.73	0.85	0.95	**0.14**	0.87
304	0.38	0.53	0.67	0.77	0.86	0.96	**0.10**	0.23	0.36	0.48	0.61	0.77	0.93	**0.17**

Conclusions Heritability estimates were generally low, but increased with stage of lactation and parity, and were in the range of those previously reported (Mrode *et al,* 2001; Mrode and Swanson, 2003). The increase in daily h^2, particularly for lactations two and three, with increased days in milk were not solely due to increased genetic variances, but also due to reduced permanent environmental variances, and residual variances with increased stage of lactation. A model that accounts for the changes in h^2 and genetic correlations with days in milk should produce more accurate evaluations.

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