Genetic Parameters for Test Day Somatic Cell Counts for the First Three Lactations Using a Random Regression Model

R A Mrode and G J T Swanson

Animal Data Centre Ltd, Fox Talbot House, Greenways Business Pk, Chippenham, Wilts SN15 1BN, UK

Introduction

The usefulness of somatic cell counts (SCC) as an indirect selection tool for reducing mastitis incidence has been reported in several studies (see Mrode and Swanson, 1996). Genetic evaluations for SCCs were introduced in the UK in 1998 and are currently based on lactation average and analysed using a single trait repeatability model. Only animals with completed lactations are included. However, in order to utilise information from cows with part lactation SCC records and to account for environmental effects in a more accurate way, a test day model (TDM) evaluation is the preferred method of choice. The objective of this study was to estimate genetic parameters for SCC in the first three lactations utilising a random regression (RR) approach and to compare parameter estimates from sire and animal RR models.

Materials and Method

The $\log_e$ SCC (LSCC) of the first three lactations of 31,236 heifers calving between 1991 to 1995, were used in the study. Cows were required to have a completed first lactation record and at least 8 test day SCC records in both lactations 2 and 3. Herd-test days with a minimum of three records and sires with at least 10 daughters were included in the analyses. The data structure and the means of LSCC by parity are in Table 1.

Table 1. Data structure means and standard deviations (in parenthesis) by lactation

	Lactation		
Variable	1	2	3
LSCC	10.94 (0.94)	11.02 (1.08)	11.24 (1.18)
No. of Cows	31,236	25,069	22,305
No. of Tests	308,534	236,277	206,729
No. of Sires	481	481	481

A series of bivariate analyses (A) fitting a sire RR model were carried out using the ASREML package (Gilmour et al., 1999), initially fitting orthogonal polynomials of order 3 for both the sire and permanent environment (Pe) effects. However, there were problems of convergence for the bivariate analysis between parities 2 and 3 due to very high correlations between the quadratic coefficient for sire effects in both parities. Using the bivariate analyses between parities 1 and 2, and 1 and 3, various combinations of the order of orthogonal polynomials for sire and Pe effect were evaluated. Table 2 shows the difference in log likelihood between various models and the one fitting orthogonal polynomials of order 3 for both sire and Pe. From the results in Table 2, orthogonal polynomials of order 2 for sire and 3 for Pe were fitted in all analyses as there was little difference in log-likelihood between this model when compared with fitting polynomials of order 3 for both sire and Pe effects.

Table 2. Differences in log-likelihood from fitting orthogonal polynomials of order 3 for both sire and permanent effects (S3Pe3) and other models

Model	Parity 1 and 2	Parity 1 and 3
S2Pe2	2,969	3,305
S2Pe3	27	18
S3Pe2	2,856	3,181

The sire RR model used for analyses A therefore was:

$$y_{tljik} = htd_l + bd_i + \sum_{r=1}^{5} \beta_{kr} v_{tr} + \sum_{r=1}^{2} \phi_{jtr} a_{jr} + \sum_{r=1}^{3} \phi_{jtr} p_{jr} + e_{tljik}$$

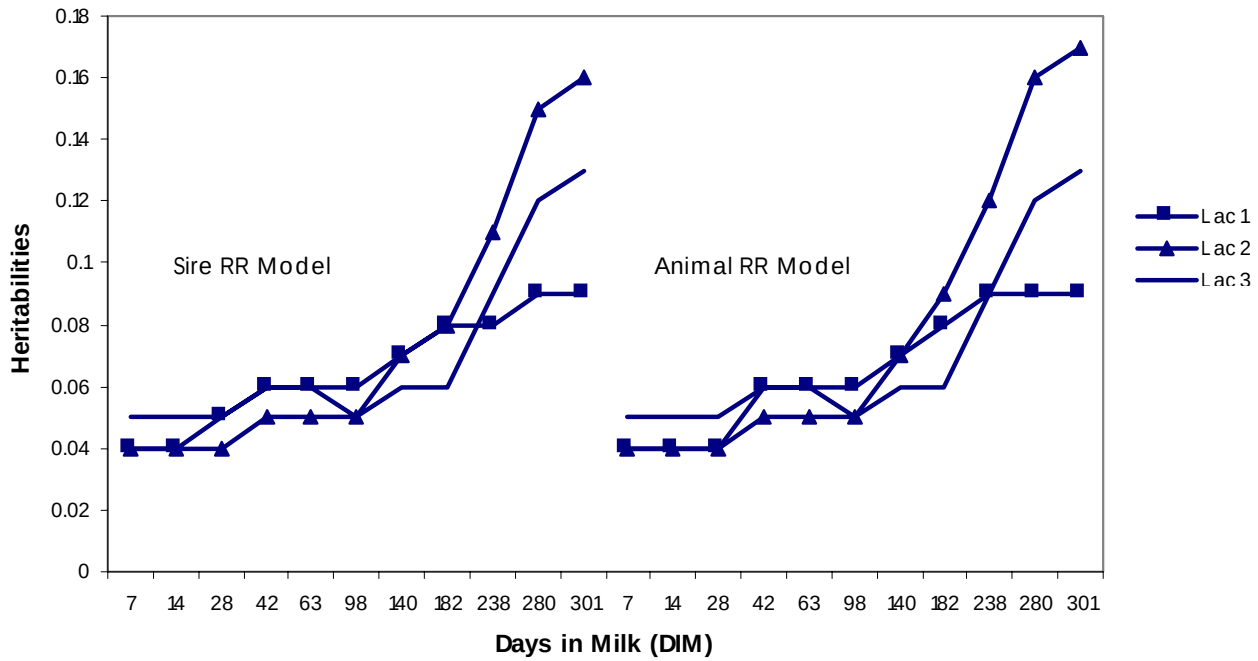
where y_{tljik} is the test day record for cow $_j$ made on day $_t$ within herd-test date (htd) subclass $_l$, for a cow with the bd_i percentage of Holstein genes belonging to subclass $_k$ of age at calving by season of calving; β_k are the fixed regression coefficients specific to the subclass $_k$; v is the vector of the first five polynomials for the $_t$ day in milk; a_j and p_j are vectors of random regressions for sire and Pe effects respectively; ϕ_{jt} is the vector of polynomials for the test day record of cow $_j$ made on day $_t$ and e_{tljik} is the random residual. There were three subclasses of age at calving, nested within 3 subclasses of calving season and nested within parity. Residual variances within parity were estimated for 4 different classes: 4-30, 31-120, 121-240, 241-305 days in milk.

A second analysis (B), in which all 3 lactations were analysed together, were undertaken using Gibbs sampling but an animal model was implemented. A single chain of length 110,000 was implemented with the first 30,000 regarded as the burn-in period. The marginal posterior means obtained in this procedure were used as estimates for the variance components.

Results and Discussion

The estimates of daily heritability (h^2) are in Figure 1. In general, daily h^2 increased with days in milk (DIM) in all parities and were highest in parity 2 at the end of the lactation. Haile-Miriam et al (2001) also observed that daily h^2 increased with DIM in Australian data. The average daily h^2 was 0.07 for parities 1 and 3 and 0.08 for parity 2. The estimates from the animal RR model were essentially identical to those from analyses A, except for parity 2 where they were slightly higher at the end of the lactation.

Figure 1. Daily heritabilities for SCC in the first three lactations (Analyses A and B)



The estimates of daily genetic variances increase with DIM (Figure 2) and were similar in both analyses. This is indicative that the increased daily h^2 values with DIM were due not only to increased genetic variances but also due to a decline in Pe (Figure 3) and residual variances (Table 3) with DIM.

Figure 2. Daily genetic variances (X100) for SCC in the first three lactations (Analyses A and B)

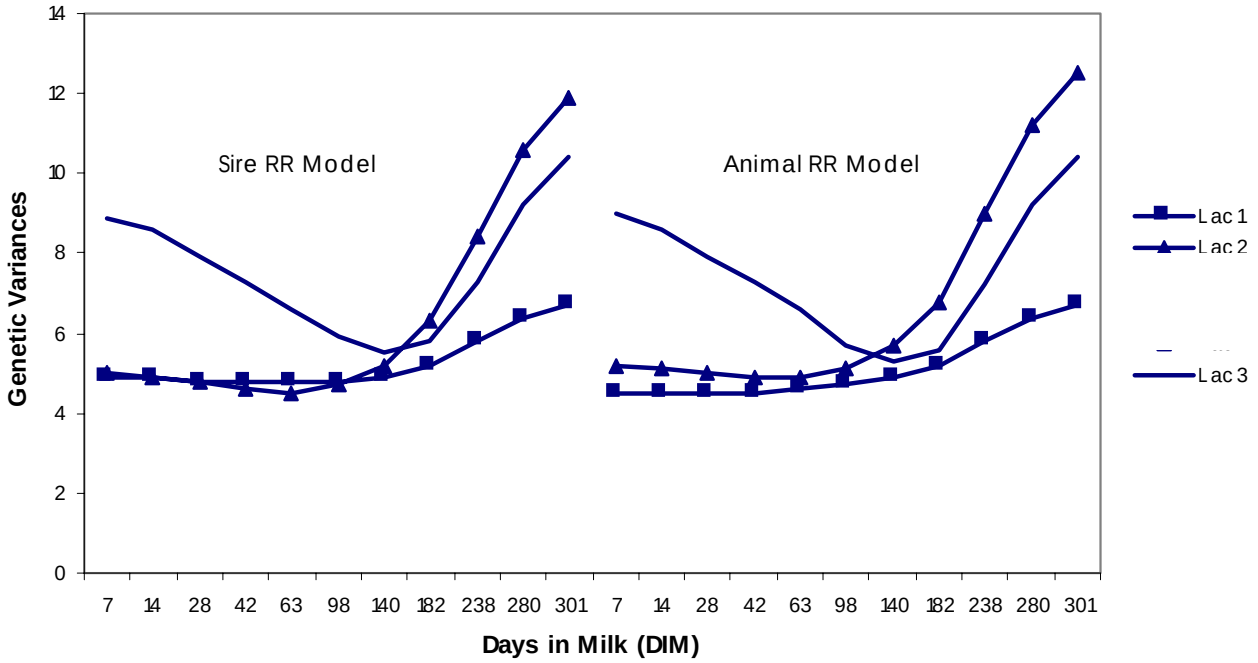
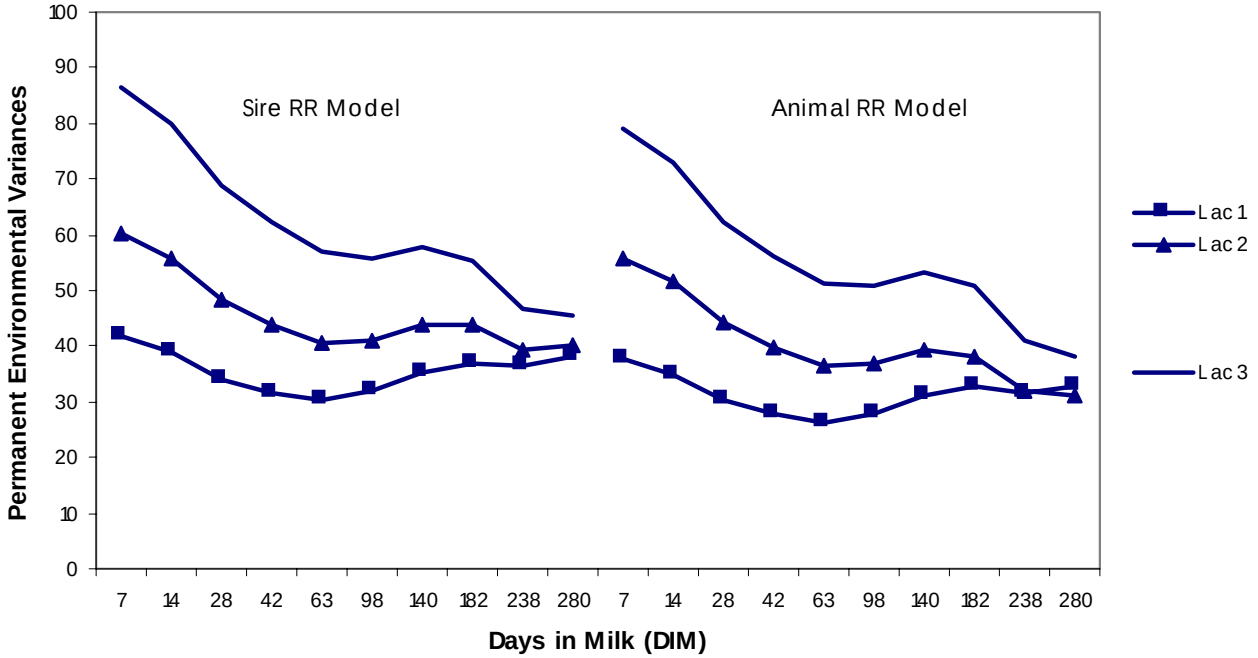


Figure 3. Daily permanent environmental variances (x100) for SCC in the first three lactations



While estimates of residual variances were again similar in analyses A and B, the estimates of daily Pe variances, although similar in trend, were consistently higher in analyses A in all three lactations. This could be due to the fact that three-quarters of the additive genetic variance is included in the estimate of the Pe variance in analyses A. This implies that, if estimates from a sire RR model were to be used in animal TDM evaluations, the co-variance matrix for Pe effect should be adjusted by three-quarters of the genetic variance.

Table 3. Estimates of residual variances from sire (SM) and animal (AM) RR models

	Parities					
	1		2		3	
Classes	SM	AM	SM	AM	SM	AM
4-30	0.686	0.683	0.714	0.709	0.828	0.845
31-120	0.434	0.435	0.536	0.542	0.575	0.574
121-240	0.306	0.305	0.325	0.323	0.333	0.335
>240	0.277	0.281	0.262	0.264	0.262	0.265

The estimates of h^2 for SCCs using completed lactation data (305-day SCC) were about 0.17, 0.16 and 0.13 respectively for parities 1, 2 and 3 from analyses A. Estimates from analyses B were similar at 0.17, 0.18 and 0.12 respectively. These were higher than reported for lactation average SCC using a repeatability model (Mrode and Swanson, 1996).

The genetic correlations (r_g) within each parity were highest between adjacent DIM, usually about 0.97-0.99 and decreased as DIM get further apart. The r_g were particularly high in parity A, even when DIM were far apart. The r_g between days 7 and 301 was 0.73 in parity 1, compared with 0.33 and 0.15 in parities 2 and 3, respectively.

Genetic correlations between parities for the same DIM for parities 1 and 2 (r_{g12}) and parities 1 and 3 (r_{g13}) were of medium size, varying from 0.58 to 0.80 but those between parities 2 and 3 (r_{g23}) were medium to high (0.80 to 0.99). These correlations tended to decline from the beginning of the lactation and were lowest at the end of the lactation for r_{g13}. For r_{g12}, they tended to be highest around the mid-lactation. However, for r_{g23}, the correlations were higher from days 140 to 305 (0.92 to 0.99) but varied from 0.83 to 0.90 between days 7 to 98. The r_{g12}, r_{g13} and r_{g23} computed for 305-day SCC from analyses A were 0.71, 0.73 and 0.94. Corresponding estimates were 0.69, 0.79 and 0.98 from the animal RR model.

Conclusions

Daily heritabilities for LSCC increased with the stage of lactation in the first three parities, averaging about 0.07 within each parity. The heritabilities for lactation SCC from a RR model were higher than estimates from a repeatability model on lactation averages. Heritabilities and genetic variances from a sire RR model were similar to estimates from an animal RR model, except for Pe variances, which were higher with the sire model due to the inclusion of three-quarters additive genetic variances. These would need adjustment if they were to be used employed in animal TDM evaluations. Genetic correlations between the same days in milk in different parities were highest between parities 2 and 3.

References

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