

Effect of Bimonthly Sampling on Genetic Parameters and Evaluation for Somatic Cell Count

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Introduction

In countries with no recording schemes for mastitis incidence, somatic cell count (SCC) remains the major genetic tool for the reduction of mastitis incidence through indirect selection. However, Shook and Schutz (1994) indicated that the increasing prevalence of environmental pathogens as causes of mastitis, which tend to produce very high SCC responses for relatively short duration, could reduce the effectiveness of SCC as an indirect selection tool. The continued downward trend in milk price in the UK is focussing attention on cost reduction with many farmers opting for cheaper milk recording schemes with fewer recordings. The concern is that bimonthly sampling will miss short frequency mastitis infections when compared with monthly sampling. It is not clear what effect this might have on genetic parameters and evaluations. This paper reports on the effect of bimonthly recording on genetic parameters and evaluations for SCC.

Materials and Methods

Genetic Parameters

The data consisted of the first lactation log_e SCC of 31,236 Holstein heifers which calved between 1991 and 1995. These were the progeny of 481 sires. Genetic parameters were estimated using a sire random regression (RR) model. The fixed effects were herd-test-day and fixed regressions, nested within nine subclasses of age at calving by season of calving. The fixed regressions represented fixed lactation curves modelled by orthogonal polynomials of order 4 for days in milk (DIM). Quadratic functions were used to model random sire and permanent environment (cow) effects using orthogonal polynomials for DIM. Residual variances were estimated for 3 different classes of DIM. In the first analysis (analysis A) with this model, all heifers had 10 test day (TD) records.

The effect of bimonthly recording was examined by deleting even numbered TD SCC of the daughters of certain bulls. It was assumed that certain herds, which were previously recording on a monthly basis, switched over to bimonthly recording. This created three categories of sires. Category I consisted of 120 bulls, representing sires which had no new daughters after the switch and therefore all daughters had monthly TDs. Category II consisted of 240 bulls, representing sires with daughters before and after the switch, therefore a proportion of their daughters had bimonthly TDs. The even-numbered TDs were therefore deleted for 25% of the daughters of the first 120 bulls in this category and 50% for the remaining 120 bulls. The last group of bulls (Category III) was made up of 121 bulls and represented sires used only after the switch, with all daughters having bimonthly TDs. Therefore, all daughters of these bulls had their even-numbered TDs deleted. The assignment of bulls to each category was such that progeny group size varied from 10 to greater than 200 daughters in each category. Analysis B used all data in categories I to III to estimate genetic parameters using the same model as in analysis A.

In a third analysis (analysis C), representing the worst case scenario, the even numbered TDs of all heifers in the data were deleted. Using the same model as in analysis A, genetic parameters were estimated. The genetic parameters from analyses B and C were compared with those from analysis A to evaluate the effect of bimonthly recording.

Genetic Evaluations

The first 3 lactation SCCs from the data set used for the national evaluation of SCC for Holsteins in the UK in November 2001, were re-analysed (analysis D) using a test day model (TDM). The model used for the TDM genetic evaluation was similar to that in analysis A, except that a linear function was fitted for animal effects in place of

the sire effects and the 3 lactations were analysed as different traits. The genetic parameters used were described by Mrode and Swanson (2001). A summary of the data is given in Table 1.

Gauss Seidal iteration with over-relaxation was employed to solve the mixed model equation, iterating on the data. Predicted Transmitting Abilities (PTAs) for 305-day SCC were computed for the bulls from the RR coefficients for animal effect after convergence. Reliabilities for bulls were calculated using the method described by Jamrozik et al (2001) but modified to account for the effects of herd-test-day.

To study the effect of bimonthly sampling on genetic evaluations for bulls, it was assumed that a proportion of herds switched over to bimonthly recording in the more recent years. All herds in the data set with cows born in 1997 or later were selected. About 30% of these herds (2,800 herds) were then randomly chosen and assumed to have opted for bimonthly recording, commencing with cows born in 1997. The even-numbered TDs of all cows born in 1997 or later in these 2,800 herds were deleted to mimic bimonthly recording. These herds had a total of 124,203 cows with 1,300,719 TDs, of which 622,266 were deleted. Evaluations of bulls from the analysis (analysis E) using this modified data were compared with those from analysis D.

Results

Genetic Parameters

The estimates of daily heritability (h^2) from analyses A, B and C, for different stages of lactation, are in Figure 1. The inclusion of bimonthly TDs for a proportion of the bulls'

daughters (analysis B) slightly increased daily h^2 at the beginning and end of the lactation relative to analysis A. These slight increases in daily h^2 were due to an increased daily genetic variance. When all daughters of bulls have bimonthly TDs (analysis C), daily h^2 estimates were slightly lower in early and late lactation compared with analysis A.

The estimates of daily pe variances were very similar for analyses A and B but were lower for C in early stages of lactation and higher in late stages of lactation. The increase in daily pe variances in the later stages of lactation resulted in the slightly lower daily h^2 towards the end of lactation.

The within lactation genetic correlations (r_g) were examined by calculating the r_g between the 7th DIM, 154th DIM and 301st DIM with different days throughout the lactation. The r_g between day 7, 154 or 301 with days 7–305 of the lactation were generally higher in analysis C (all even-numbered TDs deleted) compared with analysis A. A similar trend was observed for analysis B for r_g between day 301 and other days throughout the lactation. However, the r_g were lower in analysis B compared with analysis A between day 154 and days in early lactation (7-70 DIM) and between day 7 and mid lactation (91-217 DIM). The largest difference in r_g between analyses A and B was 0.05, between 301 DIM and 49-70 DIM. The difference of 0.08 between 154 DIM and 7 DIM was largest between analyses A and C.

The correlations between pe effects at various stages of lactation were similar in analyses A and B. In analysis C, the correlations between 301 DIM and the rest of the lactation were lower than in analyses A and B.

Table 1. Summary of Holstein data used for genetic evaluation.

Lactation	No. of Cows	No. of Test Days
1	1,287,930	11,920,882
2	691,650	6,342,101
3	416,035	3,787,796

Genetic Evaluations

Simple and rank correlations between bull PTAs from using all TDs (analysis D) and bimonthly TDs (analysis E) are in Table 2. For bulls with at least 20 daughters, bimonthly sampling has little effect on bull PTAs when less than 80% of their daughters have bimonthly TDs (bi-TDs). For instance, with 25% or less daughters with bimonthly TDs, the simple and rank correlations between PTAs from analyses D and E for bulls with at least 20 daughters were essentially 1. However, these correlations dropped to 0.91 (0.90 for rank correlation) for bulls with 80-100% of their daughters with bimonthly TDs and progeny group sizes of 20-50 daughters. For bulls with more than 50 daughters and the same proportion with bi-TDs, the correlations were 0.94. In

addition, for this group of bulls, average reliability dropped by 7-8% in analysis E with bi-TDs compared with analysis D. The distribution of differences in PTAs from analyses D and E, for those bulls with 80-100% of their daughters with bi-TDs, indicates bimonthly sampling resulted in both over and under-prediction of bull evaluations by about $\pm 8\%$.

It might be argued that a fixed regression model (FRM) that treated TD records as repeated measurement, might be more suitable for SCC when bi-TDs are available. Preliminary analysis not presented in this paper, showed that FRM gave similar results to the RRM in terms of re-ranking of bull proofs with bi-TDs.

Table 2. Simple correlations and rank correlations (in brackets) between bull evaluations calculated from monthly and bimonthly test day records.

% DTR*	Bulls with 20-50 daughters		Bulls with greater than 50 daughters		
	No of bulls	Correlations		No of bulls	Correlations
1-25	427	0.99	(0.98)	795	1.00 (1.00)
26-79	262	0.97	(0.97)	325	0.98 (0.97)
80-100	100	0.91	(0.90)	106	0.94 (0.94)

* % DTR = percentage of total daughters of bulls with bimonthly test day records.

Conclusion

Bimonthly sampling resulted in only slight increases or decreases in daily heritability and genetic variances. When all daughters of bulls have bimonthly TDs, variances of permanent environment were reduced in early lactation. Within lactation, genetic correlations among DIM tended to increase with bimonthly sampling. In general, bimonthly sampling did not significantly influence genetic parameters. However, significant re-ranking of bull proofs occurred when 80-100% of daughters of bulls had bimonthly TDs compared with monthly TDs, as a result of over and under prediction. This was accompanied by a 7-8% average reduction in accuracies of bull proofs. Bimonthly sampling would have a significant effect on the proofs of young bulls with few daughters undergoing test.

References

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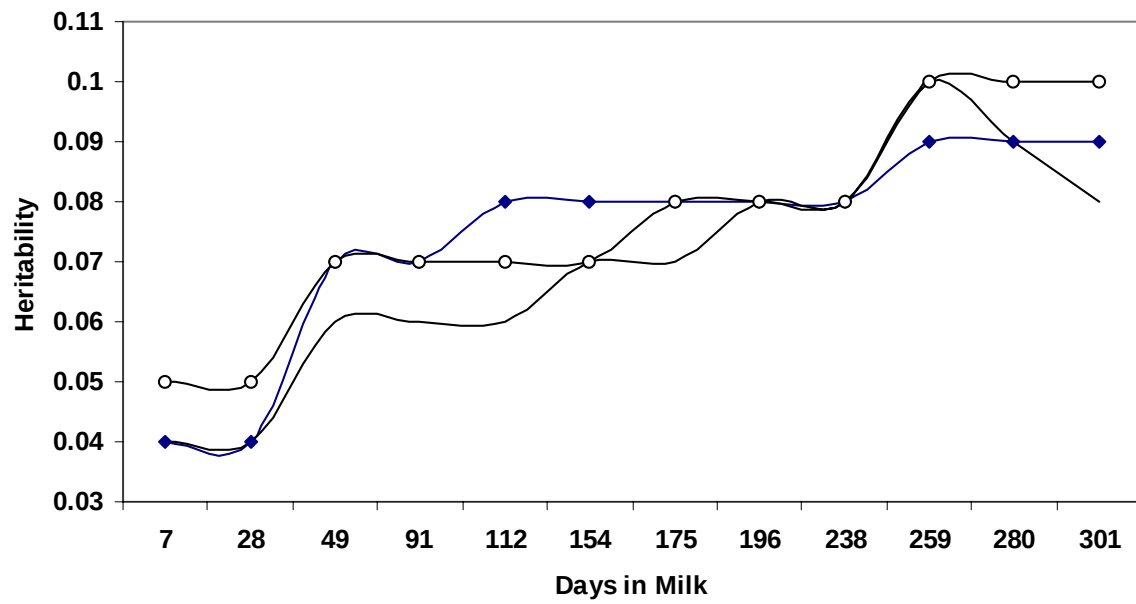


Figure 1. Daily heritabilities when all heifers have 10 TDs (◆), a proportion of heifers with bimonthly TDs (○), and all heifers have bimonthly TDs (—).