Prediction of changes in somatic cell counts due to culling and selection

H. SMIT AND B.W. WICKHAM

Livestock Improvement Division
New Zealand Dairy Board, Hamilton

ABSTRACT

Somatic cell counts are used widely in the dairy industry to provide information on subclinical mastitis and milk quality. The value of this information is related to the benefits that can be obtained by using the somatic cell concentration to predict the presence of mastitis, and to the reduction in somatic cell count concentration that can be achieved by selective breeding.

In this study the reduction in somatic cell concentration that can be achieved by culling and breeding is calculated from data collected under New Zealand conditions.

Selection against logarithm (natural log) somatic cell concentration, without any emphasis on milk production, results in an annual rate of genetic change in log cell concentration of less than 0.6%. This represents the maximum achievable rate of genetic change and is indicative of the small amount of genetic variation observed.

Culling based on log cell concentrations is likely to result in only small reductions in cell concentration. In an average herd, a culling rate of 10% on the basis of their log cell concentration alone is predicted to reduce log cell count in the next lactation by 0.05 (cell concentration change of 20 000/ml).

Keywords: Cows; milk; somatic cells; selection; culling; mastitis; genetic change; heritability; repeatability

INTRODUCTION

Somatic cells are cells which come from the body or blood of the cow. A large variety of different types of cell are included under this heading and they are always present, at least in small numbers, even in normal milk. The tissue in the udder responds to bacterial infection and tissue damage by allowing somatic cells to flow from the blood into the milk in very large numbers. A large percentage of these cells are polymorpho-nuclear leucocytes, which play an important role in the destruction of invading bacteria (Bramley, 1976).

Somatic cells can be counted in milk samples using automatic equipment at the rate of 180 samples/h. A service based upon the use of such equipment, in conjunction with the herd testing of individual cows for milk and fat yields, is provided by the Dairy Board's Livestock Improvement Division.

Somatic cell counts are used as an aid in the control of mastitis and may be useful as a measure of milk value, for both fluid milk and manufacturing milk markets. For these 2 purposes a reduction in cell counts by culling and selective breeding may be desirable.

An extensive analysis of the data collected as part of the somatic cell counting service provided by the Dairy Board has been conducted (Smit and Wickham, 1985a; 1985b). The results provide estimates of environmental factors affecting somatic cell concentration, the phenotypic association between milk yield and somatic cell concentration, as well as heritability and repeatability estimates of somatic cell concentration.

The purpose of this paper is to provide an interpretation of the heritability and repeatability estimates obtained in the study in terms of the responses that could be expected as a result of culling and selection programs being based on somatic cell counts.

TABLE 1 Variance component estimates for log somatic cell count as obtained in a study using field collected data provided by New Zealand Dairy Board. (Table 2 of Smit and Wickham [1985b] with negative values set to zero).

Source of variance	Breed of cow		
	Ayrshire	Friesian	Jersey
Sire	(s) 0.00000	0.00729	0.01985
Herd	(h) 0.19278	0.10376	0.13515
Cow	(c) 0.35968	0.24370	0.24405
Lactation	(l) 0.23234	0.37215	0.30493
Error	(e) 0.66192	0.70343	0.72692
Total	1.44672	1.43033	1.4309

METHOD AND BASE PARAMETERS

A linear model for ln (natural log) of somatic cell concentration, as recommended by Shook (1982), was used. The model has the form:

$$\ln(\text{cell conc.}) = \text{mean} + \text{herd} + \text{sire} + \text{cow/herd-sire} + \text{lact/cow} + \text{error} \quad (1)$$

where, herd, sire, cow within herd sire combination, lactation within cow, and error, are all random variables with means of 0 and variances given by h, s, c, l, and e, respectively. Table 1 contains the estimates of these variances obtained in the earlier study (Smit and Wickham, 1985b).

For this model equations for predicting ln (cell conc.) given previous results, and for predicting changes due to culling and selection were developed using linear model theory (Searle, 1971). Predicted ln (cell conc.) for a further test in the same lactation is given by:

$$c_1 = u + b_1 (y - u) \quad (2)$$

where:

- c_1 ln (cell conc.) being predicted for the next test in the same lactation,
- u herd average ln (cell conc.) for the previous tests,
- y is the cows average ln (cell conc.) for the n tests completed in the lactation,
- and b_1 the regression of ln (cell conc.) in the same lactation on y, the average of n cell counts.

The regression can be expressed in terms of the estimated variance components as:

$$b_1 = (s + c + l) / (s + c + l + e/n) \quad (3)$$

TABLE 2 Change in somatic cell count in a Jersey herd due to culling at various levels of intensity and varying number of tests. This table shows results for current lactation.

Number of tests	Percent culled		
	10	20	30
1	0.09	0.17	0.24
2	0.11	0.20	0.29
3	0.12	0.22	0.31
4	0.12	0.22	0.32
5	0.12	0.23	0.33
6	0.13	0.23	0.34
7	0.13	0.24	0.34
8	0.13	0.24	0.35
11	0.13	0.24	0.35
12	0.13	0.25	0.35
13	0.13	0.25	0.35

Predicted ln (cell conc.) for a test in the next lactation is given by:

$$c_2 = u + b_2 (y - u) \quad (4)$$

where:

- c_2 ln (cell conc.) being predicted for a test in the next lactation,
- $u, y,$ are as defined for (2),
- and b_2 the regression of ln (cell conc.) in the next lactation on the average of n cell counts.

Expressed in terms of the variance components the regression is given by:

$$b_2 = (s + c) / (s + c + l + e/n) \quad (5)$$

The change in ln (cell conc.) in the same lactation and the next lactation due to culling is estimated respectively by:

$s_1 = b_1 * sd$, and
$s_2 = b_2 * sd$,
where, 'sd' is the selection differential.

That is:

$$sd = i * SD \quad (6)$$

where

- i is the standardised selection differential, expressed in standard deviation units,
- and SD is the standard deviation of the ln (cell conc.) used in making the selection decision. This standard deviation depends upon the number of samples (n) for each animal and is given, in terms of the variance components by, $(s + c + l + e/n)^{0.5}$.

The equations giving s_1 and s_2 were used to predict the changes in ln (cell conc.) which would result from the use of cell cencentation alone, based on varying number of tests (n), in culling varying proportions of cows in a herd.

TABLE 3 Change in somatic cell count in a Jersey herd due to culling at various levels of intensity and varying number of tests. This table shows results for the next lactation.

Number of tests	Percent culled		
	10	20	30
1	0.04	0.08	0.11
2	0.05	0.09	0.13
3	0.05	0.10	0.14
4	0.05	0.10	0.15
5	0.05	0.10	0.15
6	0.06	0.11	0.15
7	0.06	0.11	0.16
10	0.06	0.11	0.16
13	0.06	0.11	0.16

Genetic gains due to selection for ln (cell conc.) were calculated for each of the 4 pathways which contribute in traditional cattle breeding programs. The gains were calculated on the assumption that all selection pressure was placed on ln (cell conc.).

Genetic gain per year was calculated as:

$$\text{delta } G = \frac{G(S,S) + G(S,D) + G(D,S) + G(D,D)}{I(S,S) + I(S,D) + I(D,S) + I(D,D)} \quad (7)$$

where

G(,) is the genetic gain/generation on the pathway indicated by the subscripts in the brackets. For example (S,D) is the sire to daughter pathway and (D,S) is the dam to son pathway,

and

I(,) is the generation interval on the pathway indicated by the subscripts in the brackets.

To estimate the genetic gains which can be made in reducing numbers of somatic cells we have examined each of the 4 pathways and calculated expected genetic gains assuming that all selection pressure is placed on reducing ln (cell conc.). Normally an index which combines several traits according to their relative economic values would be used in this type of analysis. This we have not done, because we do not have good estimates of the genetic correlations and because there are no estimates of relative economic value for ln (cell conc.) readily available. The technique used gives an estimate of the upper limit on genetic changes which can be achieved in ln (cell conc.).

Genetic gain on the sire to son, or sire to daughter pathway, assumes a progeny testing approach in which sires are selected on the basis of a progeny test based on m daughters, each tested n times in 1 lactation for ln (cell conc.). Genetic gain/ generation is estimated as:

$$G(S,) = b_3 * i * SD_2 \quad (8)$$

where:

b_3 is the regression of sire breeding value for ln (cell conc.) on the mean ln (cell conc.) of m daughters, tested n times, which in terms of the estimated variance components is given by $(s/[s + c/m + 1/m + e/nm])$,

i is the standardised selection differential,

and SD_2 is the standard deviation of the mean ln (cell conc.) of m daughters each with n tests, which in terms of the estimated variance components is given by, $(s + c/m + 1/m + e/nm)^{0.5}$.

Genetic gains for varying numbers of daughters per bull, m, varying numbers of tests per daughter, n, and varying proportions of sires selected were calculated.

TABLE 4 Genetic gain in log somatic cell counts on sire to son (or daughter) pathway for varying numbers of daughters (m), numbers of tests (n) and selection intensities. Only the Jersey variance components are used as these give the greatest rates of gain.

m	n					
	1	2	3	4	5	10
Selection Intensity = 0.1						
25	0.13	0.14	0.15	0.15	0.15	0.16
50	0.16	0.17	0.18	0.18	0.18	0.19
75	0.18	0.19	0.19	0.20	0.20	0.20
100	0.19	0.20	0.20	0.21	0.21	0.21
125	0.20	0.21	0.21	0.21	0.21	0.22
150	0.20	0.21	0.21	0.22	0.22	0.22
200	0.21	0.22	0.22	0.22	0.22	0.22
Selection Intensity = 0.05						
25	0.15	0.17	0.18	0.18	0.18	0.19
50	0.19	0.20	0.21	0.22	0.22	0.22
75	0.21	0.22	0.23	0.23	0.23	0.24
100	0.22	0.24	0.24	0.24	0.24	0.25
125	0.23	0.24	0.25	0.25	0.25	0.25
150	0.24	0.25	0.25	0.26	0.26	0.26
200	0.25	0.26	0.26	0.26	0.26	0.26

Genetic gains on the dam to son, and dam to daughter pathway were estimated on the assumption that selection of dams is based entirely on her own performance over p lactations each with n tests for ln (cell conc.). Genetic gain/generation is estimated as:

$$G(D,) = b_4 * i * SD_3 \quad (9)$$

where:

b_4 is the regression of dams breeding value for ln (cell conc.) on her average ln (cell conc.) over p lactations each with n tests, which in terms of the variance components estimated is given by $(4s/[s + c + 1/p + e/np])$,

i is the standardised selection differential,

and SD_3 is the standard deviation of the mean of average ln (cell conc.) over p lactations with n tests which is terms of the variance components each estimated is given by, $(s + c + 1/p + e/np)^{0.5}$.

Genetic gains for varying numbers of lactation, p, tests/lactation, n and proportions of animals selected were calculated.

RESULTS

The estimated effect of culling on ln (cell conc.) in the same lactation for varying numbers of tests and varying proportions of cows culled are given in Table 2, for the Jersey based variance components. Virtually

identical results were obtained using the Ayrshire and Friesian variance components. These results represent an extreme situation in which 10%, or more, of cows are culled on ln (cell conc.) alone. At 5 tests/cow, the current situation with the Dairy Board service, the reduction in ln (cell conc.) at the test after culling is estimated to be 0.12 which at a herd average cell concentration of 400000/ml is equivalant to a reduction of 50000/ml. Unless there is clear evidence that somatic cell concentration in milk is of major economic significance the emphasis placed on cell concentration will be much less and the gains likewise much less than these estimates.

The effectiveness of culling on ln (cell conc.) in the subsequent lactation is shown in Table 3. Again there are very small differences between the breeds and only the results for the Jersey parameters are presented. The lower gains, when compared with the results for the same lactation, are a reflection of the relatively high, 0.30492, value of the lactation variance components. At 5 tests and 10% culling on somatic cell concentration alone the reduction of 0.05 ln (cell conc.) units in a herd with an average cell concentration of 400000/ml is equivalent to a reduction of 20000/ml.

Genetic gains on sire to son, or sire to daughter, pathways are in Table 4. At 5 tests/daughter, 50 daughters/sire and selection of the best 5% of bulls on somatic cell concentration alone gives a per generation gain of 0.22 ln (cell conc.) units.

On the dam to son pathway the/generation genetic gain is given by the first part of Table 5 where the best 5% of dams are selected on somatic cell concentration alone. At 2 lactations each with 5 tests the gain is estimated to be 0.23 ln (cell conc.) units.

On the dam to daughter pathway the selection intensity is much lower at 80%, or less, and estimates are given in the lower half of Table 5. At 2 lactations and 5 tests/lactaion the gain is 0.03 ln (cell conc.) units. Clearly there is very little opportunity for making genetic progress on this pathway.

The individual pathway results have been combined according to equation 7 for breeding scheme of a similar design to that currently operated by the Dairy Board as shown in Table 6. The annual rate of genetic gain of 0.02 ln (cell conc.) units is equivalent to a reduction in cell concentration of 8000/ml in a herd with an average cell concentration of 400000/ml.

TABLE 5 *Predicted genetic gain on dam to son pathway for* varying numbers of lactations (p) and tests (n)/lactation. Results are based on Jersey variance components and assume all selection pressure is placed on somatic cell counts.

p	n					
	1	2	3	4	5	10
Selection Intensity = 0.05						
1	0.14	0.16	0.18	0.18	0.19	0.20
2	0.18	0.21	0.22	0.22	0.23	0.24
3	0.20	0.23	0.24	0.25	0.25	0.26
4	0.22	0.24	0.25	0.26	0.26	0.27
5	0.23	0.25	0.26	0.27	0.27	0.28
6	0.24	0.26	0.27	0.27	0.28	0.28
7	0.25	0.27	0.27	0.28	0.28	0.29
Selection Intensity = 0.8						
1	0.02	0.02	0.03	0.03	0.03	0.03
2	0.03	0.03	0.03	0.03	0.03	0.04
3	0.03	0.03	0.04	0.04	0.04	0.04
4	0.03	0.04	0.04	0.04	0.04	0.04
5	0.04	0.04	0.04	0.04	0.04	0.04
6	0.04	0.04	0.04	0.04	0.04	0.04
7	0.04	0.04	0.04	0.04	0.04	0.04

TABLE 6 Estimated genetic gain/generation and/year in log cell count where the breeding programe (selection intensity = i, daughters/sire = m, tests/cow = n, lactations/cow = p) is devoted entirely to reducing cell count.

Generation path		Interval (years)	m	n	p	i	Gain/ generation
S	S	7	75	5	1	1.75	0.20
S	D	7	75	5	1	1.75	0.20
D	S	5		5	2	2.06	0.22
D	D	6		5	2	0.35	0.03
Total		25					0.66

Genetic gain/year = 0.02 log cell count units = 0.57% units/year.

DISCUSSION

Somatic cell concentration, like milk yield or fat yield, is a readily measured trait in dairy cattle. It can be used as part of a culling and breeding program to bring about changes in cell concentration. The magnitude of the changes that can be made through culling and breeding have been quantified in this paper on the assumption that all selection pressure is placed on reducing cell concentration.

The amount of selection pressure justified by the economic value of cell concentration is small. It is thus concluded that the changes in cell concentration likely to result from their incorporation in the breeding scheme will be small and further research effort would be much better directed towards using cell concentration as an aid to mastitis control.

REFERENCES

Bramley A.J. 1976. Variations in the susceptibility of lactating and non-lactating bovine udders to infection when infused with *Escherichia coli*. *Journal of dairy research* **43**: 205-211.

Searle S.R. 1971. Linear Models. Pub. John Wiley & Sons, Inc.

Shook G.E. 1982. Approaches to summarizing somatic cell concentration which improve interpretability. Proceedings National Mastitis Committee, Washington, D.C.

Smit H.; Wickham B.W. 1985a. Environmental factors influencing somatic cell concentration and its association with milk and fat production. Mimeograph, Livestock Improvement Division, New Zealand Dairy Board.

Smit H.; Wickham B.W. 1985b. Heritability and repeatability of somatic cell concentration in milk. Mimeograph, Livestock Improvement Division, New Zealand Dairy Board.