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Disciplines

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Comparison of Single and Multiple-Trait Selected Sires. Response in Mastitis Traits.^{1,2}

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ABSTRACT

Estimated somatic cell counts and incidence of clinical mastitis were measured on 163 daughters of two groups of bulls selected by two alternative criteria. Yield bulls were selected solely on progeny test for milk in first lactation; Merit bulls were selected by independent culling levels on fat-corrected milk yield, percent daughters culled in first lactation, and udder type conformation of daughters. Daughters of Yield sires exceeded daughters of Merit sires by 685 kg milk in first lactation. Groups did not differ significantly in measures of clinical mastitis or in measures of estimated cell counts of milk. Also, groups did not differ in kilograms milk discarded because of antibiotic treatment for mastitis, in spite of the large difference in total milk yield. Mean milk discarded per lactation completed was 171 kg, representing 64,243, and 207 kg for parities one, two, and three.

INTRODUCTION

Mastitis losses of US dairymen exceed \$1.5 billion annually (2). No available information

indicates whether the frequency of mastitis infections per cow is changing. Average milk per cow is increasing steadily (17). This increased milk yield is believed to add stress on the cow's udder.

Evidence of association between milk yield and incidence of mastitis is based largely on correlation. O'Bleness et al. (15) reported a genetic correlation of .44 between milk yield and incidence of clinical mastitis. Wilton et al. (23) reported genetic correlations between milk yield in first lactation and mastitis incidence in later lactation that averaged around .30.

More numerous reports have dealt with the phenotypic association between milk yield and various measures of mastitis. Moxley et al. (14) reported a correlation of $-.14$ between herd average somatic cell count and milk yield; regression of milk yield on cell count was -59 kg milk per 100,000 cells/ml. Braund et al. (4) found that cows producing less than 9 kg milk per day were more frequently positive on California Mastitis Test (CMT) than were cows producing over 9 kg/day. Afifi (1) reported a negative relationship between somatic cell counts and milk yield of heifers but inconsistent associations in older cows. Grootenhuis et al. (8) reported a correlation of $-.39$ between somatic cell count and milk yield in Friesians but nonsignificant negative correlations in two local Dutch breeds. Rendel and Sundberg (18) found production of heifers infected in first lactation nonsignificantly lower than that of uninfected heifers. Schmidt and Van Vleck (22) found a small positive correlation between milk yield and infection rate. Dodd and Neave (6) found a positive relationship between milk yield and mastitis incidence. Analyses by Legates and Grinnells (13) suggested a near-zero intraherd, intrabreed correlation between mastitis incidence and milk yield in first lactation. Phenotypic correlations between milk yield in first lactation and mastitis in later lactation

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reported by Wilton et al. (23) were negative and near zero.

Thus, two studies suggested positive genetic relationship between milk yield and mastitis incidence, but phenotypic results are conflicting. Associations involving cell counts and milk yield appear to be negative. Correlations of milk with clinical mastitis and with bacteriological tests tend to be positive or near zero.

Most of the studies cited involved milk yield for total lactations as the production measure. Interpretation of such analyses is uncertain because of the confounding effects of mastitis upon subsequent milk yield. Crossman et al. (5) reported yield or quarters treated for mastitis shows little recovery until the next lactation. The result is that subsequent milk yield of cows is depressed after infection. Such a result leads to negative relationship between infection rate and milk yield. If the relationship between susceptibility and yield potential is positive, the effect of infection upon the milk secreting tissue could mask the true relationship.

An alternative for establishing the genetic relationship between milk-producing ability and mastitis susceptibility is to select for milk yield and observe whether frequency of infection changes according to the selection applied. Numerous reports of heritabilities have indicated a genetic basis for several mastitis-related traits. Reports by Fostad (7), Grootenhuis et al. (8), and Kleinschroth et al. (12) have indicated breed differences in mastitis incidence or cell counts. However, Hickman (10) reported a correlated response in teat length when selection was for protein yield, which may have been related to frequency of mastitis.

The purpose of this study was to determine whether mastitis incidence in two groups of cows was related to the criteria of sire selection in forming the groups.

MATERIALS AND METHODS

Two groups of cows were produced in an experiment in which were different criteria of selection for choice of sires for the two groups. Details of the experiment have been given by Pearson et al. (16). Briefly, Yield sires selected annually were the two active AI bulls with the highest Predicted Difference (PD) for milk in first lactations of daughters, with repeatability exceeding 40%. Merit or multiple-trait sires selected annually were the two with the highest

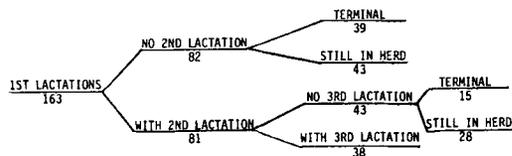


Figure 1. Distribution of data.

udder type index (based on Holstein-Friesian Association percentage acceptable for four descriptive traits) from among those bulls that had a PD (4% FCM) greater than 181 kg, repeatability greater than 40%, and less than 10% of their daughters culled in first lactation. Foundation cows were assigned randomly to the two selection groups and remained in a group for all subsequent matings. Matings were made by Design B of Hickman and Freeman (11), which provides for some bulls used initially to be returned to service in the latter stages of the experiment. Matings began in 1970, and first calvings were in 1973; the data included lactations completed through December 1, 1978.

Sixteen sires were selected in each group. The data described here are preliminary and include progeny of only 12 sires in each group. Figure 1 describes the in-progress nature of the data. A total of 282 lactations of 163 cows were available. The experimental design allowed cows to have a maximum of three lactations. Cows were culled only if they became unfit for normal management.

Table 1 defines the traits used to summarize mastitis incidence. The first eight traits are based on the observation of clinical mastitis: physical signs such as udder inflammation or clotty milk accompanied by the intramammary application of antibiotic. Systemic treatments were not included. The MDIS represents the total milk discarded during lactation because of prior treatment with antibiotics. Two traits were based upon Wisconsin Mastitis Test (WMT) results — MWMT is the mean of monthly tests and WMT1 is the WMT score obtained in the 1st mo of lactation (7 to 38 days after calving). A few lactations lacked a WMT test within the first 38 days, and these were excluded from analyses on MWMT and WMT1.

The basic statistical model was

$$y = X\beta + Z\mu + e,$$

TABLE 1. Definition of traits.

Abbreviation	Definition
INF	Infected = 1; not infected = 0.
DAY1	Days elapsed from calving to first mastitis treatment.
SLF	Number of treatments in left-front quarter.
SLR	Number of treatments in left-rear quarter.
SRF	Number of treatments in right-front quarter.
SRR	Number of treatments in right-rear quarter.
SUM	Sum of number of treatments in all quarters.
IND	Ratio of DAY1 to total days in milk.
MDIS	Milk (kg) discarded due to mastitis treatments.
MWMT	Average of monthly Wisconsin Mastitis Test (WMT) scores.
WMT1	WMT score on first monthly test after calving.

where y contains the traits measured, X and Z are known incidence matrices, β contains fixed effects of selection group, parity (lactation number), and month of calving, μ contains random effects for sires within groups and cows within sires, e contains the random error effects (the random effects have means zero,

variances σ_s^2 , σ_c^2 , and σ_e^2 , and zero covariances). The general least-squares analyses were by SAS (20) and Harvey (9) computational packages. Expected mean squares are in Table 2. Differences between selection groups were tested against the mean square for sires within group.

Since nonnormality of error terms was suspected for all traits in Table 1, numerous transformations were utilized to normalize distributions to fulfill that assumption required for tests of hypothesis. Transformations were: square root for SLF, SLR, SRF, SRR, and SUM; arc sine for IND; and \log_e for MWMT and WMT1. The INF was not transformed; as suggested by Legates and Grinnells (13), average infection rates generally are near .5, in which case a transformation would have little value. Decisions regarding significance of mean differences (groups, parities, months) generally were not changed by these transformations. Because of the similarity of results and to aid in interpretation, all means in the tables are in original scales of measure.

RESULTS AND DISCUSSION

Table 3 compares sire progeny tests with actual daughter performance in the experiment for traits related to selection criteria. These results illustrate expected and actual differences between the two groups of cows. Progeny tests are unweighted arithmetic means of the 16 sires selected in each group. Daughters' performance (first lactation) does not include progeny of all sires and is an unweighted least-squares mean. Table 3 shows that milk yield was 685 kg

TABLE 2. Expected values of mean squares.

Source	E(MS)
Group (c)	$\sigma_e^2 + 1.21 \sigma_c^2 + 9.27 \sigma_s^2 + Q(G)$
Sires (group) (s)	$\sigma_e^2 + 1.26 \sigma_c^2 + 8.20 \sigma_s^2$
Cows (sires) (c)	$\sigma_e^2 + 1.61 \sigma_c^2$
Parity (P)	$\sigma_e^2 + Q(P)$
Month (M)	$\sigma_e^2 + Q(M)$
Error (e)	σ_e^2

TABLE 3. Comparison of population progeny test evaluations to actual selection results in Beltsville herd.^a

	Progeny test evaluation		Beltsville performance	
	Merit	Yield	Merit	Yield
Milk (kg)	174	522	7,113	7,798
Fat (kg)	274	280
Final Score	+39	-.68	71.1	69.4

^a240 daughters with yield results, 133 daughters with type appraisals.

higher in the Yield group, which was nearly twice as much as the difference in sire evaluations. Thus, the two groups of cows differed distinctly in milk yield. Average type score was low in this herd because there was no selection of cows on type.

Estimates of means of selection groups for the 11 traits are in Table 4. These estimates are from a reduced model omitting the cow random effect, rather than the full model (means or desired estimable functions were not obtainable from the complete model). Tests of significance, however, were upon results from the full model. With the exception of INF, selection groups were not significantly different. Comparison of mean squares for INF gave an approximate F of 4.74 ($P < .05$). However, as in Table 2, the inequality of coefficients in expectations of the group and sire/group mean squares requires the Satterthwaite procedure (21). When this procedure was used, the selec-

tion group difference for INF was nonsignificant.

The INF mean difference indicating 6% more lactations infected in the Yield group may tempt one to believe that a tendency is developing that may prove to be real when additional data are obtained. Susceptibility to mastitis is not expressed fully until second or third lactation. Only 23% of the 163 cows had three lactations. For the number of times treated during a lactation (SUM), the Merit group exceeded the Yield group by 1.22 treatments, but this was nonsignificant. In interpreting the means for SUM, SLF, SLR, SRF, SRR, and MDIS, uninfected lactations were included as zero. Because uninfected lactations were included, the number of treatments in lactations actually infected was greater than indicated in Table 4.

The MDIS was virtually identical in the two groups. This is surprising, particularly in view of the large difference in yield between the groups

TABLE 4. Estimable functions for selection group effects (averaged over other effects in model).^a

Trait ^b	Merit		Yield	
	\bar{X}	SE	\bar{X}	SE
INF	.41	.06	.47	.07
DAY1	211	16	211	18
SLF	.82	.27	.76	.29
SLR	.92	.39	.98	.43
SRF	1.92	.41	.93	.46
SRR	1.57	.40	1.34	.45
SUM	5.23	.88	4.01	.97
IND	.67	.05	.66	.06
MDIS (kg)	170	40	172	38
MWMT	6.8	.3	6.9	.3
WMT1	7.2	.9	7.3	.8

^aModel = μ + group + sires (group) + month + parity.

^bDefinition of traits in Table 1.

(685 kg). Even with an equal rate of mastitis infection, the Yield group would be expected to have more discarded milk. Perhaps the greater number of treatments per lactation in the Merit group counterbalanced the higher production in the Yield group. In an attempt to interpret comparisons of MDIS between the two selection groups, an analysis added a linear regression of MDIS on total milk yield in the lactation. The regression was $-.03$ ($P < .05$), but the selection groups still did not differ in milk discarded.

The traits mean WMT (MWMT) and WMT at first test (WMT1) are estimates of the somatic cell content of milk. Means of these cell count estimates were almost identical for the selection groups and were not significantly different. The WMT in the 1st mo was .4 unit larger in each group than the average WMT during lactation. Results of Ruffo et al. (19) suggested higher cell counts in late lactation but not in early lactation.

The results in Table 4 suggest that the difference in milk yield in this selection experiment was not accompanied by an increase in mastitis frequency as expressed by estimated somatic cell counts, milk discarded, or clinical incidence. It is tempting to conclude from these results that selection for higher milk yield will not increase incidence of mastitis. Sire selection in this experiment is, however, only one of

many ways in which a group difference of 685 kg milk yield could be achieved. This is particularly true of the sires selected to form the Merit group where several criteria were used. Another reason for caution in interpreting these results is the limited sampling of environmental conditions pertaining to mastitis. Frequency of mastitis is below average in this herd. Because antibiotic treatment has been applied liberally in this herd, *Streptococcus agalactiae* is relatively infrequent in comparison with *Staphylococcus aureus*, other streptococci, and coliforms (3). Finally, our report is based primarily on first lactations, so that full opportunity for expression of animal differences in susceptibility did not exist.

Table 5 gives estimates of means for parities 1 through 3. Means for the clinical mastitis traits agree with (13, 18, 22, 23) indicating lower frequency in first lactations. For example, SUM increased from 2.48 in first lactation to 5.16 in second. Increases from second to third parity were smaller.

Table 5 contains an estimate of milk discarded from antibiotic treatment in the first three parities. Discarded milk was 243 kg per completed lactation in parity 2 but only 64 kg in parity 1. The mean dropped to 207 kg in parity 3. With a milk price of 22¢ per kg, losses would be approximately \$14, \$54, and \$46 for each lactation in parities 1, 2, and 3.

TABLE 5. Estimable functions for parity effects (averaged over other effects in model).^a

Trait ^b	Parity 1	Parity 2	Parity 3
INF ^c	.34	.44	.49
DAY1	231	200	201
SLF	.42	1.04	.90
SLR	.66	1.28	.91
SRF ^c	.59	1.48	2.21
SRR	.80	1.37	2.20
SUM	2.48	5.16	6.22
IND	.73	.62	.64
MDIS (kg) ^c	64	243	207
MWT ^c	5.5	7.0	8.0
WMT1 ^c	6.3	6.6	8.7
Number of lactations	163	81	38

^aModel = μ + group + sires (group) + month + parity.

^bSee Table 1 for definition of traits.

^cMeans differ at $P < .05$.

Parity differences in WMT scores agree with (1, 4), indicating lower cell counts in first parity. Changes in WMT1 with parity were erratic with only a slight increase (.3) from first to second parity.

Month of calving was not a significant source of variation in any of the traits.

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