

A COMPARISON OF HERDMATE, ITERATIVE, AND MIXED MODEL
SIRE SUMMARIES FOR TYPE IN HOLSTEIN CATTLE,

by

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INTRODUCTION

Since yield and other economically important traits in dairy cattle are sex limited and generally have low heritabilities, progeny testing has been utilized to evaluate the genetic merit of dairy bulls. Selection decisions using progeny tests are based on the comparison of the average merit of a bull's offspring to the average performance of the progeny of contemporary sires.

In 1971 the Holstein Friesian Association of America (HFAA) introduced a progeny test procedure, predicted difference type (PDT) to evaluate the transmitting abilities of Holstein sires for final classification score. The method utilized the average deviation of bull's progeny from breed average for final score to evaluate genetic merit of Holstein sire for conformation. A breed average system was implemented since dairy geneticists contended that environmental differences between herds had little relative effect on classification score. However further investigation demonstrated that herd differences did affect sire evaluation and a herdmate comparison was adopted by HFAA in 1976.

Hermate comparisons or modifications have been used since 1954 as a means of accurately estimating genetic transmitting abilities of dairy sires for production traits. The herdmate comparison like other evaluation procedures developed from genetic theory generally have several simplifying assumptions. One of the basic assumptions underlying the herdmate comparison is that progeny of different bulls are

compared to herdmates of equal genetic merit.

In 1974 the United States Department of Agriculture (USDA) implemented the Modified Contemporary Comparison (MCC) that accounted for the genetic merit of herdmates' sires since systematic errors were included in sire summaries for yield traits. Adoption of the MCC was due to differential use of high predicted difference bulls for milk. Another change in sire evaluation procedure for milk yield that occurred in 1974 was the use of contemporary deviations instead of herdmate deviations in the calculation of sire summaries. The adoption of a contemporary comparison removed bias created by comparing young cows to their more heavily culled herdmates and also reduced dependence on age correction factors.

The specific purposes of this project were:

1. to determine whether the failure to adjust for genetic merit of herdmates' sires produces systematic errors in sire evaluation for conformation,
2. to determine the effect of using a herdmate versus a contemporary comparison for PDT calculation, and
3. to consider the feasibility of refinements in the current sire evaluation method for type to correct for biases and improve accuracy of estimating sires' transmitting abilities.

LITERATURE REVIEW

Sire Evaluation for Conformation

Historically dairymen and industry personnel have placed a great deal of emphasis on selection for type traits. In 1973 Cassell et al. (14) showed that bulls with above average type proofs were used more extensively than other bulls to sire sons. In another study in the same time period, Miller et al. (45) found that the average predicted difference for milk yield was near zero for the bulls siring sons. While this problem concerning sires of sons is not as dramatic today (30), recent studies on semen pricing (4, 15, 55) have indicated conformation continues to play a major role in sire selection decisions by dairymen. Therefore dairy cattle geneticists have examined the sources of variation in type traits to determine the feasibility of selection for these traits and the best methods for use for this selection.

A major source of variation in type score and one of primary interest to dairy geneticists is that due to herd differences. If herd effects and other environmental components are large, then a herdmate method of sire evaluation is necessary. However, if herd effects are small, then other means of breeding value estimation can be used. Harvey and Lush (21) used a nested analysis and found herd differences to account for 18% of the total variation in type score. In a study involving official Jersey data, Norman et al. (50) found herd effects to represent 15% of the total phenotypic variation in final score and, slightly less, 9 - 13% of the variation in the descriptive codes. Similar results were previously reported by Specht et al. (63) for both

final score and descriptive codes, Vinson et al. (70) for final score, and Legates (32) for descriptive traits. Three studies (54, 69, 73) reported herd differences of less than 10% for descriptive traits. However one (69) did find larger herd components of variance (14 to 20%) in the mammary traits. Higher estimates of herd effects have been reported. Jamieson et al. (27) estimated the herd component for final score to be 19% using official Holstein-Friesian data, and Legates (32) found estimates of 23 to 35% for final score and the scorecard traits. These studies utilized cows of all ages, while other studies used only first classification scores. This could explain differences in the estimates. Discrepancies in the magnitude of the herd component have also been attributed to variation among herds in selection intensity for type (70).

In most studies, the herd components of variance are much smaller than those of approximately 30 to 50% for milk yield. These results indicated to several researchers (9, 69, 71) that little would be gained by using a herdmate comparison for type evaluation. However more recent studies indicated that herdmate comparisons are feasible and are more accurate than breed average evaluation. Vinson et al. (70) reported a significant herd by classifier interaction for final score and the descriptive traits. This component indicated there is variation in standards of classifiers among herds. Norman et al. (50) reported a significant herd by year interaction, which accounted for 21% of the variation in final score and 14 to 18% in the descriptive codes. This estimate was the largest component of variation reported in their

study. From these findings, Norman et al. (50) recommended that sire summaries for type should be calculated within herd-year.

Jamieson et al. (27) evaluated the usefulness of initial type summaries in predicting later proofs and examined several alternative methods of PDT calculation. The models¹ included one based on breed average deviations, four herdmate comparisons with combinations of corrections for herdmate average and dams, and a daughter-dam method. Correlations between initial and later proofs ranged from .49 to .77 and were similar for the breed average and herdmate models, but were less for the daughter-dam method. While the breed average model was as accurate a predictor of future daughter performance as other models studied, the correlation between PDT and average scores of mates on which a bull was initially used was sizeable (.39). Similar correlations for the herdmate deviation models were near zero. They concluded that there was a positive association between the type of mates (or herds) in which a bull is initially used and later herd useage. Correlations between breed average PDTs and adjusted herdmate average were also high, .5 or greater, indicating the quality of herds greatly influenced PDTs calculated in this manner. These findings led to their recommendation that a herdmate comparison would increase accuracy of PDT.

Correlations between the present PDT, which includes an adjustment for dams, and adjusted herdmate average were negative in the study by Jamieson et al. (27). This finding may be indicative of a slight negative bias due to the positive association between dam's

scores and genetic merit of competition (herdmates). This hypothesis is true if there is a positive correlation between herd average and genetic level of herds. This idea is supported by the fact that adding a correction for genetic level of herdmates resulted in changing correlations from negative to positive in all instances in their study.

Studies (31, 42) involving the accuracy of prediction of type proofs from pedigree information indicate that the herdmate comparison PDT has alleviated several of the problems of the breed average calculation, such as reducing the weight attributed to dams of young sires in predicting future PDTs. However no significant increase in accuracy was observed by using herdmate instead of a breed average model. These findings are in agreement with Jamieson et al. (27).

Regression of Daughter Performance on Herdmate Average

The herdmate comparison (HC) was designed to reduce the effects of non-genetic variation in breeding value calculation in sire evaluation of traits with large environmental components of variance. Since the inception of the herdmate comparison in the early 1950's, scientists recognized that genetic differences between herds existed and these differences could cause biases in sire proofs. To alleviate this problem, Henderson et al. (25) introduced the intra-sire regression of daughter yield on herdmate average to adjust daughter deviations for genetic differences among herds. They estimated the regression coefficient to be approximately .6. However they recalculated the coefficient several years later using a more extensive data set and obtained an estimate of .911 (24).

While Henderson et al. (25) first recommended the use of intra-sire regression of daughter yield on herdmate average in sire evaluation, Robertson and Rendel (59) first proposed this regression as a method of determining genetic differences among herds. They stated the estimate would approach unity if there were no genetic differences between herds and would be approximately .5 if the differences between herds were entirely genetic in nature. Pirchner and Lush (56) also used this procedure to measure the additive genetic variance due to herd differences. They used the value $2(1 - b)$, where b is the intra-sire regression of daughter records on herdmate average, as an estimate of the proportion of herd differences which are additive genetic in nature. Touchberry (66), as referenced by Miller (43), also concurred with earlier interpretations of the regression. Henderson, as cited by Van Vleck (68), expressed reservations concerning the use of this method to measure genetic differences among herds. However, Van Vleck (68) tested assumptions that the regression is linear and that the regression is the same for each sire group. The assumptions were found to be valid except for extreme cases where the herdmate average deviated greatly from breed average.

Jamieson et al. (27) estimated the intra-sire regressions of daughter score on herdmate average by year and obtained values ranging from .70 to .61 for the five years studied. These values appeared to be intuitively low (73). Using these estimates, Jamieson et al. (27) calculated that 61 - 78% of the variation between herds was due to additive genetic differences.

Many estimates of the intra-sire regression of daughter milk yield on herdmate average have been reported (3, 16, 17, 34, 43, 56, 59, 62). They range from .71 to 1.08. Miller (43) attributed part of these discrepancies to differences in the definition of herdmate average since variations of both herdmate and contemporary averages were used.

Several studies have investigated breed differences in the regression coefficient. Henderson and Carter (24) reported small breed differences, while others (43, 59) have noted greater regression estimates for Holsteins and Guernseys than the other breeds. Therefore genetic differences appeared greater among herds in the colored breeds than in Holsteins, and deviation of herdmate average from breed average should receive greater weight in sire evaluation.

Age is also a source of variation in the regression coefficient. Studies (3, 16, 43) have consistently shown that regression based on first lactations only are less than values estimated from second and later lactations. These findings are in agreement with the higher heritability estimates found in later lactations than estimates based on first records (43). Genetically, cows in second and later lactations are less variable than cows in first lactation since poor producers are culled before completing subsequent records.

Bereskin (5) found, as cited by Miller (43), that adjusting for numbers of herdmates increases the regression coefficient. Findings of Allaire (2) supported this point. Allaire (2) also found that regression of daughter yield on unadjusted herdmate average increased as the number of herdmates increased.

Mao et al. (34) examined trends in the estimates of intra-sire regression of daughter records on herdmate average. No significant time trends were detected. However the regression coefficients for the artificially sired population suggested that the relative additive genetic variation among herds is decreasing about 1% per year. This result is in agreement with Pirchner and Lush (56), who stated that artificial insemination (AI) will eventually remove genetic differences among herds. However Mao et al. (34) pointed out that these results could be due to different samples of herds each year in their study.

Findings of Miller (43) and Mao et al. (34) suggest that errors in age adjustment factors tend to increase the regression coefficient. These results are contrary to those of Gaunt et al. (17).

Sources of Bias in Sire Evaluation

One of the major assumptions underlying the HC is that herdmates of different bulls' progeny are random samples of the population and have the same average genetic merit. During the early 1960's, studies (38, 39, 46) suggested that this condition held true and that the adjustment using the intra-sire regression of daughter yield on herdmate average was sufficient. However with the widespread use of AI, dairymen were better able to implement their different selection goals and the assumption became questionable.

Variation in the genetic merit of herdmates' sires has been well documented. McDaniel et al. (41) examined the genetic merit of sires of herdmates by geographical region, bull stud, age of bulls, and year. They found that the average predicted difference of the herdmates'

sires varied by 134 kg. between the highest and lowest regions and by 173 kg. between the extreme AI organizations. In another study involving regional variation, Miller (43) regressed daughter yield on herd-mate average within sire for milk, fat, and fat percent and found significant regional differences for all traits. Since this regression has been used as a measure of genetic differences between herds, Miller's study indicated potential biases in sire evaluations due to regional variation in genetic merit of herds.

Norman et al. (51) calculated regressions within sire and year of calving of daughter yield, herd-mate and contemporary averages, and daughter deviation from herd-mate average on the average PD of herd-mates' sires. They found a positive association between the average PD of herd-mates' sires and daughter and herd-mate averages. However they reported that daughter deviation from herd-mate average declined as genetic merit of herd-mates' sires increased. Their results demonstrated that sire evaluations calculated from average daughter deviation from herd-mates were affected by the genetic merit of herd-mates' sires.

Another assumption underlying the HC is that there is no genetic trend in the population. Genetic improvement in the yield traits has been well documented (20, 26, 28, 57), and various studies (20, 57, 58) have shown that genetic trend biases herd-mate comparison studies. These results led to the adjustment for genetic progress in the modified contemporary comparison (MCC) used by United States Department of Agriculture (USDA) by standardizing deviations to a base year. Genetic

trend in conformation, final score in particular, would be immeasurable, although it probably exists, since evaluation criteria of the breed associations change over time and the associations attempt to maintain a fixed average for the breed. Therefore adjustment for genetic trend in conformation is not practical at this point.

The present PDT system includes an adjustment for the dams of daughters included in the proofs (75). Type proofs are adjusted by a factor, $.5h^2$, of the deviation of dam's score from her herdmate average, where h^2 is the heritability of final classification score. The heritability estimate used in PDT computation is .30 and was calculated by Cassell et al. (13). An adjustment for mates of sires in sire evaluation for milk yield has been investigated by several geneticists (26, 44, 46, 47). However the consensus opinion was that the adjustment was not economically justified and the bias, although present, did not appreciably influence sire proofs. However several researchers (6, 36) felt that this bias tended to prolong the use of older well-proven sires beyond a justifiable period since they were usually mated to above average dams. Therefore an adjustment may be warranted in the future.

Recently two sire evaluation methods for milk yield have been designed and implemented to replace the HC. The methods are the MCC, adopted by USDA for national sire summaries (1), and the Best Linear Unbiased Prediction (BLUP) procedure, proposed by Henderson (23) in 1966 and used in the Northeast AI sire summary since 1971. These procedures removed the dependence on some of the underlying assumptions

of the herdmate method and reduced biases in sire evaluation.

The MCC is an iterative procedure. This technique utilizes repeated estimates of genetic merit of each sire to adjust for competition level provided by herdmates (1). This adjustment replaced the approximation, .1 (herdmate average - breed average), used previously in the HC. The old correction factor assumed that herdmates producing above breed average were genetically better than breed average, which is not always correct since herd management levels may disguise or enhance genetic potential. Adjustment for the genetic merit of herdmates' sires by iteration more accurately accounts for genetic level of competition and also accounts for differences among bulls due to genetic trend (1).

The BLUP procedure effectively accounts for genetic base, transmitting ability of herdmates' sires, and herd-year-season effects by using a series of simultaneous equations. Estimates of herd-year-season effects and sire differences are obtained by solving the equations. This system allows for both direct and indirect comparisons between bulls. Another feature of the procedure is the addition of a relationship matrix. Relationships between sires are used to improve predictions and provide ties between bulls of different generations and groups. However a major disadvantage of the BLUP system is the computer space required to store and solve the equations. This requirement has limited the use of BLUP in sire evaluation, particularly as a national sire summary model.

The current national sire summary for yield, the MCC, utilizes

pedigree indexing as a method of grouping bulls for evaluation. The usefulness of pedigree indices as a relative estimate of a bull's breeding value has been verified (7, 67). From selection theory, a pedigree index is as reliable as production records on six daughters, each in a different herd. Researchers (11, 37) have also demonstrated that most pedigree information contains as much information as most non-AI proofs and is especially useful in increasing accuracy of sire proofs based on limited numbers of progeny. Pedigree indices for type are also accurate predictors of future PDTs (31, 42). However the correlations between pedigree information and PDT are not as large as expected and indicate possible problems with the present PDT system.

The Use of Herdmate Vs. Contemporary Comparisons :

Another change made in sire evaluation procedures by USDA in 1974 was the implementation of a contemporary comparison. Many dairy geneticists (3, 20, 33, 35, 40) have addressed the possibility of using contemporaries, non-paternally related cows of the same parity, instead of herdmates and advocated that cows be compared only with contemporaries due to bias introduced by comparing first lactation cows to more highly selected herdmates. Allaire and Gaunt (3) reported selection biases of nearly -120 kg. due to comparing first lactation cows with cows of all ages. Hargrove and Legates (20) and McAllister and Allaire (35) reported less bias of -75 and -42 kg. respectively. McDaniel et al. (40) found biases of 86 kg. and 115 kg. in Jersey and Brown Swiss breeds and relatively small ones, less than 10 kg., for the other breeds. Another major advantage

of a contemporary comparison over a herdmate procedure, is the reduction of dependence on age correction factors (36).

There are several disadvantages of a contemporary comparison. One of the major problems is the loss of progeny information due to lack of contemporaries. McDaniel et al. (40) reported that this loss prompted the replacement of a contemporary comparison with a herdmate comparison in Canada. They also cited a 75% increase in the number of bulls qualifying for evaluation after the adoption of the herdmate method. McDaniel et al. (40) examined this loss in five U.S. breeds and found from 6 to 23% of the first lactation AI sired cows and 9 to 25% of the non-AI sired cows lacked first parity contemporaries. They also reported slightly higher percentages, between 10 to 28% and 15 to 29%, for cows in second lactation. Their results compare favorably to the 11% loss of records found by Fairchild et al. (16) and 14% decrease obtained by Tomaszewski et al. (65).

In addition to the loss of progeny, cows generally have 20 to 33% fewer contemporaries than herdmates (16, 40, 65). Having fewer numbers of contemporaries relative to herdmates increases the sampling variation of a contemporary comparison relative to one based on herdmates. McDaniel et al. (40) examined the effects of increased sampling variation, which was 5 to 40%, and found the contemporary comparison to be a less precise predictor of sires' genetic merit. However in most cases, they found the approximate confidence limits on the prediction to be only slightly lower (<10%) when herdmates were used instead of

contemporaries. Therefore they concluded that this disadvantage was not severely critical and could be accepted if selection biases were removed.

The disadvantage of a strict contemporary comparison caused USDA to adopt a modified form which utilizes records of all progeny with one or more herdmates of any age, but weights herdmates of the same parity group more heavily (1). However with the implementation of an adjustment for genetic merit of herdmates' sires, some of the positive effects of using a contemporary comparison are reduced. Bulls with high transmitting abilities tend to have a higher percentage of daughters that survive to later lactation (8). Therefore adjusting for the genetic level of competition removes part of the selection bias from sire evaluation (40).

Comparison of Evaluation Procedures

Several investigators have examined the effectiveness of the MCC in removing biases inherent with the herdmate comparison (HC). Norman et al. (52) found the average PD for milk of bulls with ten or more daughters changed -8, 33, 13, -20, and -8 kg. in Ayrshire, Brown Swiss, Guernsey, Holstein, and Jersey breeds, respectively. The standard deviations of change ranged from 76 to 118 kg. Adjustment for pedigree grouping accounted for most of this change, 49 to 73%, while genetic merit of herdmates' sires accounted for 26 to 39%. However, the large effect of pedigree was probably due to low average repeatability, under 40%, for bulls in the study. The importance of adjustment for genetic level of competition increased with higher

repeatabilities, accounting for 41 to 83% of the change in bulls with over 80% repeatability.

McDaniel (36) and Norman et al. (51) showed that sire evaluations on 2/3 of the summarized Holstein bulls contained errors of less than 23 kg. due to differences in PD's of herdmates' sires. Although some bulls changed greatly with the adjustment, the number was small in comparison to the total number summarized. Norman et al. (51) found that correlations between adjusted and unadjusted summaries were high due to the relatively small amount of bias compared to actual genetic differences between bulls. McDaniel (36) found that correlations between unadjusted herdmate comparisons and a least squares method of sire evaluation was 80 to 85% of the expected value. However adjusting for genetic merit of herdmates' sires increased the correlation to over 90% of the theoretical correlation.

Schaeffer et al. (61) found that accounting for genetic differences of herdmates increased sire proof variance by 22%. Their results correspond to a 19 - 58% relative increase in variation in PDs when comparing MCC to HC methods reported by Norman et al. (52).

Norman et al. (52) examined correlations of PD milk by both MCC and HC methods with daughter information added after the 1974 summarization date. Correlations were .04 to .15 higher with MCC than HC summaries. However they found MCC had the greatest advantage over HC procedures when bulls had small numbers of daughters due to inclusion of pedigree information in MCC proofs. Correlations of PD milk and additional daughter yield were .13 higher with bulls having ten or

less daughters and were only .04 higher than HC values with bulls having more than 100 progeny. The accuracy of MCC proofs in predicting future daughter performance was also demonstrated by Cassell and Norman (10).

Tomaszewski et al. (65) examined summaries of bulls calculated from two independent sets of progeny to measure how repeatabilities between evaluations were affected by adjustment for variation in herdmaters' sires' PDs. Adjusting for genetic average of herdmaters' sires increased correlations between independent sets of progeny tests only .01 to .02. They attributed this small increase to the high correlation (.80) between Predicted Differences (PDs) of herdmaters' sires in the two progeny groups and concluded the adjustment increased accuracy more than the correlations indicated. From the high correlations between PDs, they also concluded that large numbers of progeny do not guarantee unbiased evaluation since large numbers do not insure that a bull will be compared to a random sample of bulls.

In another study by Norman et al. (49), sires accounted for a larger percentage of the variation in modified contemporary deviations (MCD) than herdmate deviation (HD), 95.4% compared to 89.7%. These greater values suggested that MCC procedures reduced environmental and residual effects in sire evaluation. The effectiveness of the MCC in removing bias due to genetic trend was also tested. While year of calving was a significant source of variation in HD, it was not significant for MCD. This study (49) and others (10, 52) demonstrated that individual proofs computed from herdmate methods generally declined with time due to genetic trend and increased genetic merit of herdmaters. However

MCC proofs in the studies were as likely to increase as decrease over time.

Only a few researchers have compared MCC proofs with BLUP estimates. Rothschild et al. (60) found that MCC evaluations resembled Northeast AI summaries more than did the HC. Rankings of the MCC and the Northeast comparison were similar and the results indicated that MCC removes a substantial portion of bias favoring natural service sires and older sires in the HC. However the range of differences between groups of bulls was smaller with the MCC than the Northeast procedure. This difference may be due to the use of multiple records in MCC calculation. However the results may suggest errors in pedigree grouping or the failure to remove all the genetic differences between herds. Rothschild et al. (60) concluded that incorrect age factors may have caused these differences, but this is unlikely since dependence on age factors was greatly reduced in the MCC.

Norman et al. (53) examined mixed model, MCC, and HC methods of sire evaluations and found higher correlations between mixed model and MCC estimates than with HC proofs. Correlations increased with the consideration of only AI bulls and with the inclusion of pedigree grouping. However correlations between HC and mixed model estimates declined when pedigree grouping was used. These results show little differences between mixed model and MCC estimates.

Zelinger and Jensen (76) also compared mixed model estimates calculated from Wisconsin DHIA data and USDA MCC proofs. Rank correlations between Holstein mixed model and MCC proofs were .86 for 614

sires with over 50 daughters. Correlations were slightly less for bulls with fewer progeny. Their study gave no indication of significant differences between mixed model and MCC procedures and substantiated the work of Norman et al. (53).

Two studies have examined methods to remove biases in cows' Estimated Transmitting Abilities (ETA). Spike and Freeman (64) compared several methods of adjusting ETAs for genetic difference between herds and found adjustment for the average ETA of herdmates to be the superior method, accounting for 60% of the genetic differences among herd averages contained in the estimates. Other methods included several mixed model estimates and a method similar to the MCC. Hansen and Everett (19) compared herdmate and BLUP ETAs and found correlations of .87 to .78 for all cows, and higher estimates, .83 to .90 for AI populations. Standard deviations for herdmate ETAs were approximately twice those of the BLUP estimates.

MATERIALS AND METHODS

Data Source

Data used in this study consisted of 1,085,161 official type classification records on cows classified between 1-1-67 and 12-31-76. Records were edited for erroneous type scores and identification information with 14,147 records being deleted.

Age is a significant source of variation in final score with older cows generally classifying higher than younger animals (12, 50, 71). Classification records were age adjusted using correction factors developed by Kliewer (29). These factors were computed from classification scores of Holstein cows classified in 1973 through 1975. These factors are currently used by the Holstein-Friesian Association and are shown in Table 1.

Herdmate averages were computed using age adjusted data. Herdmates were defined as those cows, excluding paternal half-sisters, that were in the same herd and classified on the same day. Herdmate averages were adjusted for number of herdmates by the method developed by Heidhues et al. (22). The regression value is calculated as

$$b = \frac{N}{N + \sigma_e^2 / \sigma_h^2}$$

where N is the number of herdmates, σ_e^2 is the within herd variance, and σ_h^2 is the among herd variance.

Estimates for the among and within herd variances, calculated by Jamieson et al. (27), were 3.04 and 12.71. Using these estimates, the regression factor reduced to approximately $\frac{N}{N + 4}$. The herdmate

Table 1. Factors for Age Adjusting Final Classification Scores to Maturity

<u>Age in Months</u>	<u>Age in Years and Months</u>	<u>Adjustment Factor</u>
Less than 24	Less than 2-0	1.07
24 to 25	2-0 to 2-1	1.06
26 to 28	2-2 to 2-4	1.05
29 to 30	2-5 to 2-6	1.04
31 to 35	2-7 to 2-11	1.03
36 to 41	3-0 to 3-5	1.02
42 to 49	3-6 to 4-1	1.01
50 to 123	4-2 to 10-3	1.00
124 to 133	10-4 to 11-1	0.99
134 to 141	11-2 to 11-9	0.98
142 to 168	11-10 to 14-0	0.97
More than 168	More than 14-0	0.96

average was regressed toward the population mean using the following formula:

$$\text{adjusted } \overline{HM} = \overline{B} + \left[\left(\frac{N}{N + 4} \right) (\overline{HM} - \overline{B}) \right]$$

where \overline{B} is the mature breed average (81.5 points). An animal was required to have five or more herdmates to be included in her sire's summary. A total of 27,506 records were deleted due to lack of sufficient number of herdmates.

Cows in each herd were divided into two contemporary groups, first classification and later classifications. Individual contemporary averages were calculated and adjusted for numbers of contemporaries. The first classification group consisted of those cows less than 36 months of age and the later classification group consisted of all other cows in the herd. Cows with less than five contemporaries were deleted from the contemporary data set.

Dam information was added to the daughter record if available. Approximately half the daughters, 527,995, had classified dams in the data file. Herdmate and contemporary averages for the dams were calculated in the same manner as daughters and were placed under the same restrictions. If dam information was not available, the dam's score was assumed to be herd average.

After herdmate and contemporary averages were calculated, the data set was edited to delete duplicate observations on individual

cows by using first available classification on each animal. This deletion left 775,744 records in the data set. The records were then grouped by sire registration number and PDTs were calculated for bulls with at least ten daughters. A total of 6,816 bulls were summarized.

Transmitting abilities for type were estimated using the following formula employed presently by HFAA:

$$PDT = R[(\overline{FS_p} - \overline{HM_p}) - .15(\overline{FS_d} - \overline{HM_d})]$$

where R is the repeatability of progeny test, $\overline{FS_p} - \overline{HM_p}$ is the average deviation of a bull's progeny from their respective herdmate average, .15 is the phenotypic correlation ($h^2/2$) between classification scores of daughters and dams, and $\overline{FS_d} - \overline{HM_d}$ is the average deviation of the dams of a bull's progeny from their respective herdmate average.

Repeatabilities (R) were computed using a formula developed by Plowman and McDaniel (58).

$$R = \frac{Ne h^2}{4 + (Ne - 1)h^2 + \frac{4\sum n_i(n_i - 1)C^2}{Ne}}$$

where Ne is the total number of progeny of a bull, h^2 is heritability (.30) of final score, 1/4 is the relationship between paternal half-sibs, n_i is the number of daughters in the ith herd, and C^2 is the environmental correlation among half-sibs in the same herd.

The C^2 value, .18, used in this study was estimated by Yao et al. (75) and is presently used by HFAA. This procedure for adjusting proofs for accuracy takes into account both the number of progeny and

their distribution across herds, giving more weight to daughters in additional herds than additional progeny in the same herds.

The PDT formula used by HFAA corrects for the non-random genetic merit of dams with respect to sires, but does not account for genetic differences between herds. Three methods of adjusting for these differences were used in this study. Two were iterative procedures and the other, a mixed model method developed by USDA for the American Jersey Cattle Club (AJCC).

The first iterative procedure involved adjusting the deviated records for the average PDT of the herdmates' sires. The following equation was used:

$$PDT = R[(\overline{FS}_p - \overline{HM}_p + \overline{PDT}_p) - .15(\overline{FS}_d - \overline{HM}_d)]$$

where \overline{PDT}_p is the average PDT of the herdmates' sires.

This formula differs slightly from a similar adjustment used by USDA in the MCC. USDA utilizes the average modified contemporary deviation (MCD) of the herdmates' as a measure of genetic merit of competition while the average PDT of herdmates' sires was used in this study.

The other iterative model involved adjusting the herdmate deviations for the average cow index of the herdmates. Cow indices for type were calculated for each cow using methods developed by Kliever et al. (29). Formulas used in the calculations are listed in Table 2. The model is as follows:

$$PDT = R[\overline{FS}_p - \overline{HM}_p + 2(\overline{CI}_p)] - .15(\overline{FS}_d - \overline{HM}_d)]$$

Table 2. Cow Indexes for Type Using Various Combinations of Information

Cow, Sire and Dam Available

$$CI_1 = b_{11}(FS_c - HM_c) + b_{12}(PDT) + b_{13}(FS_d - HM_d)$$

$$b_{11} = \frac{.555 - .15R}{3.91 - .3R}$$

$$b_{12} = \frac{1.4}{3.91 - .3R}$$

$$b_{13} = \frac{.2125}{3.91 - .3R}$$

Cow and Sire Available

$$CI_2 = b_{21}(FS_c - HM_c) + b_{22}(PDT)$$

$$b_{21} = \frac{.6 - .15R}{4 - .3R}$$

$$b_{22} = \frac{1.4}{4 - .3R}$$

Cow and Dam Available

$$CI_3 = b_{31}(FS_c - HM_c) + b_{32}(FS_d - HM_d)$$

$$b_{31} = .1419$$

$$b_{32} = .0537$$

FS_c = Final score of cow being indexed (age adjusted)

PDT = Predicted Difference Type of cow's sire

FS_d = Final score of dam of cow (age adjusted)

HM_c = Adjusted herdmate average for cow

HM_d = Adjusted herdmate average for dam

R = Repeatability of sire's PDT

where CI is the average cow index of herdmates. Spike and Freeman (64) utilized a similar method to adjust cow indices for milk yield for the average transmitting ability of herdmates. They found this method to be superior to 13 other adjustments, including several MCC and mixed model methods.

Herdmate comparisons were used to compute the average PDT of herdmates' sires and the average cow index of herdmates for the first iteration. Sires with less than ten daughters were not summarized and their PDTs were assumed to be zero when calculating the average PDT of herdmates' sires. Less than 5% of the records did not have sire PDTs. PDTs used in calculating the genetic merit of herdmates in subsequent iterations were the solutions obtained from the previous round. Iteration continued until changes in PDTs between consecutive rounds were less than .05. This figure was less than 1/10 standard deviation of PDT. Four rounds of iteration were usually needed for bull proofs to settle to this point.

Genetic theory has demonstrated that pedigrees contain information that can be utilized in the calculation of transmitting abilities of individuals to increase the accuracy of predicting genetic merit, particularly when a bull has few progeny. In 1974 USDA began utilizing information on a bull's sire and maternal grandsire, in addition to his daughters' yield, in the calculation of PDs. Bulls were grouped by pedigree index and the average MCD of bull's daughters in each group was calculated. This information was included in summarization by multiplying the group average by the factor, $1 - \text{Repeatability of the}$

progeny test, and adding the result to the iterated estimate of transmitting ability.

Pedigree information has been shown to be an accurate predictor of future type proofs (31, 43), even though the accuracy is not as high as expected in most instances. Additional type proofs were calculated utilizing PDTs of both sire and maternal grandsire similar to the addition of pedigree information in yield proofs. Bulls were ranked on the basis of their pedigree estimate, $PI = 1/2 \text{ sires' PDT} + 1/4 \text{ maternal grandsire's PDT}$, and then divided into genetic groups. Grouping was partially subjective and was based on numbers of bulls in a group and the range of their pedigree indices. Pedigree indices and genetic group averages were computed using the two iterative PDTs. The group averages used in PDT calculation are shown in Table 3. If no pedigree information was available on a sire, additional PDTs that included pedigree grouping were not calculated. There were 2444 bulls with pedigree information.

The BLUP PDT estimate was calculated using programs developed by Norman et al. (48) for AJCC. The following model was utilized in the calculation of PDT using mixed model methodology:

$$Y_{ijklm} = h_{ij} + g_k + s_{kl} + (hs)_{ikl} + c_{iklm} + e_{ijklm}$$

where,

Y_{ijklm} is the type score of the mth daughter by the lth sire in the kth genetic group in the jth classification round and ith herd;

Table 3. Genetic Group Averages by Pedigree Index Intervals Used in Adjusting Iterated PDTs for Pedigree.

<u>Pedigree Index</u>	<u>Number of Bulls</u>	<u>Genetic Group Averages</u>	
		<u>Iterated on Avg PDT of HMs' Sires</u>	<u>Iterated on Avg CI of HM</u>
> 1.01	595	.057	.088
.76 - 1.00	695	-.011	.023
.51 - .75	646	-.091	-.064
.26 - .50	791	-.170	-.148
.01 - .25	957	-.239	-.216
-.26 - .00	840	-.392	-.353
-.51 - -.25	523	-.418	-.366
<u>≤</u> -.5	460	-.593	-.548

- h_{ij} is a fixed effect common to all observations in the jth classification round in the ith herd;
- g_k is a fixed effect common to daughters of sires in the kth genetic group;
- s_{kl} is a random effect common to daughters of the lth sire in the kth genetic group;
- (hs) $_{ikl}$ is a random effect common to daughters of the lth sire in the ith herd in the kth genetic group;
- c_{iklm} is a random cow effect of the mth daughter of the lth sire in the ith herd in the kth genetic group;
- e_{ijklm} is the unexplained variation associated with the type score of the mth daughter of the lth sire in the kth genetic group that appears in the ith herd and jth classification round.

There was an additional restriction placed on all mixed model summaries. Only classifications on cows less than 43 months of age were used in computing BLUP PDTs. However no restriction was placed on the number of daughters needed to calculate mixed model proofs. Another feature of mixed model proofs was that the average PDT of bulls summarized was forced to zero. Since grouping was necessary for the mixed model, bulls were placed into either non-AI or AI groups. Additional mixed model proofs utilizing pedigree information were also computed. Group averages were calculated by pedigree index intervals for the AI and non-AI groups. Unlike the iterative pedigree groups

there was a group average for bulls with no pedigree information. Group averages used for the mixed model calculations are shown in Table 4. Pedigree indices and genetic group averages were obtained using BLUP PDTs.

Comparison of Evaluation Methods

Type proofs are reported for the 3392 bulls with ten or more daughters with at least five herdmates using the present herdmate method, the two iterative procedures, and the mixed model method. To compare the methods of evaluation, product-moment and rank correlations were calculated. Differences and absolute differences between PDTs calculated by the different methods were also examined. Correlations between procedures were also calculated for those bulls with 80% repeatability or more. PDTs adjusted for pedigree for those sires available with pedigree information were also reported. The effects of considering the genetic merit of herdmates' and pedigree grouping on the differences in PDTs from the present HM comparison and the two iterative methods were examined. Correlations squared (R^2) between pedigree index and PDT were used to measure relative importance of pedigree group in accounting for the differences.

To determine the effect of genetic level of competition on sire evaluation, cows were divided into three groups based on their herdmate average. The low group contained cows with herdmate averages less than 79.75, the middle group, individuals with herdmates averaging between 79.75 and 81.75, and the high group, those with herdmate averages of 81.75 or more. There were 225,293, 358,217, and 277,091

Table 4. Genetic Group Averages for AI and Non-AI Proven Sires by Pedigree Index Intervals Used in Adjusting Mixed Model PDTs for Pedigree

<u>Pedigree Index</u>	<u>Number of Bulls</u>	<u>Genetic Group Average</u>
	<u>AI - Proven Sires</u>	
≥ .80	269	.66
.40 - .79	316	.22
.0 - .39	388	.13
< 0	335	- .33
No Pedigree	569	- .32
	<u>Non-AI Proven Sires</u>	
≥ 1.20		.81
1.0 - 1.19		.66
.80 - .99		.45
.70 - .79		.29
.60 - .69		.07
.50 - .59		.22
.40 - .49		.12
.30 - .39		.08
.20 - .29		- .05
.10 - .19		- .22
0 - .09		- .31
- .10 - - .01		- .40
- .20 - - .11		- .44
- .30 - - .21		- .90
- .40 - - .31		- .91
- .50 - - .41		-1.09
≤ .61		-1.20
No Pedigree		- .19

cows in the three groups respectively. Herdmate averages are not the most accurate indicator of genetic merit of herdmates since there are large environmental effects for type scores. However herdmate average was assumed to be indicative of genetic merit of the herd and was the best measure of genetic level without using PDT itself as a basis of grouping. This use would be unsatisfactory since errors in the evaluation system would also be expressed in grouping.

Herdmate comparisons were computed in the three levels for bulls with at least 20 daughters in a respective herdmate average group. Proofs were calculated for 1519, 1792, and 1301 bulls in the low, middle, and high groups respectively. There were 778 bulls with at least 20 daughters in all three groups. Large discrepancies between PDTs calculated in the three groups would denote biases due to genetic level of competition or herdmate average. Product-moment and rank correlations were also obtained for sire proofs calculated in the three levels.

Proofs in the three levels were also computed using the two iterative procedures and the BLUP comparison. Herdmate comparisons, calculated for each level, were used in the first iterative round to compute average PDT of herdmates' sires and cow indices of herdmates. PDTs were assumed to be zero when not available. There were 20 to 23% of the records in the three groups without sire PDTs. The same iterative procedure used in the overall data set was employed in the three groups. BLUP PDTs were calculated on all sires without any restrictions on daughter numbers and only records of cows less than 43 months

of age were used. However PDT averages in the three levels were not forced to zero as in the overall data set. Pedigree grouping was not used in the three herd levels. However the mixed model proofs do include AI-non-AI grouping since some type of grouping was necessary for the model. Proofs on 670 bulls with at least 20 daughters in the herd-mate and iterative PDTs and at least ten daughters in the mixed model estimates are reported. The differing restrictions were used to guarantee ample numbers for comparison. Differences in restrictions and assumptions between the methods makes any direct comparison between proofs calculated in the herd levels difficult. However the systems can be evaluated to test their relative effectiveness in reducing differences in sires' PDTs calculated in the three levels.

Another test of the effectiveness of adjustment for genetic competition and pedigree grouping involved examining sire summaries on two sets of progeny that were independent of herd level. Cows were placed in one of two progeny groups on the basis of their herd codes. Progeny in herds having a last digit of less than 5 for their herd identification code were included in the first sample and the second group were daughters from herds with codes ending with the numbers 5 through 9. Summaries were calculated for 663 bulls with at least 20 daughters in both progeny groups. Correlations were estimated between evaluations in the two groups to measure the repeatability of independent progeny tests on the same bull. The effects of adjustment for competition on the repeatabilities were also examined. Mixed model estimates were not calculated for the two independent sets.

Contemporary Vs. Herdmate Comparison for Type

To examine the feasibility of changing from a herdmate to a contemporary comparison, contemporary and herdmate averages were calculated and compared. Any consistent difference between contemporary and herdmate deviations would denote a bias. The existence of systematic errors would favor the adoption of a contemporary comparison. However, there are two major disadvantages inherent with the use of such a comparison. They are the loss of progeny information due to the lack of sufficient numbers of contemporaries, and the increased sampling variation in sire estimates due to the reduced numbers of contemporaries relative to herdmates. The percentage of cows lacking contemporaries, but having herdmates was determined for the overall data set and for first and later classification groups.

RESULTS AND DISCUSSION

Comparison of Sire Evaluation Methods for Type

Means and standard deviations of PDTs calculated using herdmate, iterative, and mixed model comparisons are listed in Table 5. Means for 934 sires with greater than 80% repeatability are listed in parentheses. Average repeatabilities, number of daughters, and ranges of the evaluations are also shown. There were 3392 bulls with evaluations calculated by the three methods. The mean mixed model PDT was near zero, $-.01$, while the other means were negative. This was due to adjusting the mixed model to zero. Therefore mixed model evaluations were consistently higher than PDTs calculated by the other methods throughout the study. Averages for the herdmate comparison were $-.18$ using first available record and slightly less, $-.24$ using the most recent classification. The later method is the one currently used by HFAA. Differences in the means of the two herdmate comparisons may be due to a bias in favor of younger cows due to over age adjustment since using first available records would increase the proportion of young animals in the summary compared to the use of most recent score. However results to be described later refuted this explanation and the different means are probably due to sampling. The mean iterative PDTs were $-.24$ and $-.19$ using average PDT of herdmates' sires and average cow index of herdmates respectively. The slightly higher PDT iterated on average cow index of herdmates compared to iteration on PDTs of herdmates' sires was consistent throughout this study. This trend was probably due to the possibility that cow indices may be a more accurate

Table 5. Means and Standard Deviations of PDTs Calculated by Three Evaluation Methods

	<u>Mean PDT</u>	<u>Standard Deviation</u>	<u>Mean no. Daughters</u>	<u>Mean Repeatability</u>	<u>Range PDTs</u>
<u>Herdmate Comparison</u>					
First available score	-.18 ^a (-.32) ^b	.64 (.86)	169.7 (530.9)	.56 (.92)	-3.19 to 2.28 (-3.19 to 2.28)
Most recent score	-.24 (-.42)	.67 (.88)	169.7 (530.9)	.57 (.92)	-3.46 to 2.11 (-3.46 to 2.11)
<u>Iterative Comparison</u>					
Avg PDT of herdmates' sires	-.24 (-.48)	.77 (.99)	169.7 (530.9)	.57 (.92)	-3.71 to 2.18 (-3.71 to 2.18)
Avg Cow Index of herdmates	-.19 (-.48)	.73 (.94)	169.7 (530.9)	.57 (.92)	-3.41 to 2.24 (-3.41 to 2.17)
<u>Mixed Model</u>	-.01 (.01)	.60 (.81)	89.6 (275.5)	.47 (.69)	-2.99 to 2.51 (-2.62 to 2.51)

^a3992 bulls with at least 10 daughters in all evaluations

^b934 bulls with 80% repeatability or greater for the two iterative and herdmate comparisons

indicator of genetic competition than PDTs of the herdmates' sires since they include actual performance of herdmates.

While the means of the herdmate and iterative comparisons are similar, adjusting for the level of genetic competition increased the variation. This point was demonstrated by higher standard deviations for the iterative procedures, .77 and .73, as compared to .67 and .64, the standard deviations of PDTs calculated by the herdmate comparison. There was less variation in BLUP PDTs than in the other methods. This may be due to the additional qualification that a cow must be less than 43 months of age to be included in the mixed model summary which resulted in lower repeatabilities in the BLUP estimates. Hanson and Everett (19) reported smaller standard deviations for BLUP ETAs than herdmate estimates. However in a study by Norman et al. (53), there were no consistent differences in variances for mixed model milk proofs compared to MCC and HC methods.

The mean PDTs for the more repeatable data set were generally lower than for the overall set. This can be explained by the negative correlation between milk and type found by Grantham et al. (18) and, also shown in Table 6, and that the smaller set containing AI bulls has been selected more intensely for milk improvement. Jamieson et al. (27) found that sires are initially proven in above average herds and are used over a wider range of herd conditions with later useage. Results from this study indicated that type proofs in high scoring herds were less variable than proofs calculated in other herd levels. The inclusion of

Table 6. Correlations Between Herdmate, Iterative, and Mixed Model Evaluations for Type^a

	<u>Hermdate</u>		<u>Iterative</u>		<u>Mixed Model</u>	<u>PD Milk</u>
	<u>First Available</u>	<u>Most Recent</u>	<u>Avg PDT of HMs' Sires</u>	<u>Avg CI of HM</u>		
<u>Hermdate</u>						
First Available	1.00 ^b	.97	.97	.98	.81	-.21
Most Recent	.99	1.00	.94	.95	.77	-.23
<u>Iterative</u>						
Avg PDT of HMs' sires	.98	.97	1.00	1.00	.81	-.25
Avg CI of HM	.99	.97	1.00	1.00	.82	-.24
<u>Mixed Model</u>	.87	.87	.90	.90	1.00	-.11
PD milk	-.28	-.31	-.30	-.29	-.21	1.00

^aCorrelations for 3392 bulls above diagonal, correlations for 934 bulls with >80% repeatability below diagonal

^bAll correlations statistically significant (P<.01)

non-AI proofs in the complete data set may also partially explain the differences in variance. Norman et al. (53) reported larger standard deviations in sire evaluations of AI bulls compared to non-AI bulls.

Correlations between sire evaluations for type calculated from the three methods are shown in Table 6. Correlations for 3392 bulls with evaluations in all three methods are shown above the diagonal, while correlations for 934 bulls with greater than 80% repeatability are shown below the diagonal. In the larger data set correlations between the mixed model PDT and the other procedures, herdmate-first available and the two iterative methods, are .81, .81 and .82 respectively. This similarity was surprising since one would expect the correlations between the two iterative procedures that adjust for genetic differences in competition and the mixed model method that also accounts for genetic merit of herd mates to be higher than the correlation between the herd-mate comparison that included no adjustment for level of competition. However correlations in the more repeatable data set were slightly higher for the iterative methods and BLUP PDT than HC and BLUP estimates. While the correlations in the larger set are surprising, Norman et al. (53) found similar results in a study comparing sire evaluation methods for milk. They reported similar correlations between MCC and mixed model proofs and between HC and mixed model evaluations respectively. However they also found a larger correlation, .92, for MCC and mixed models than HC and mixed models in a set containing only AI bulls.

The correlations for herdmate-most recent comparisons were

consistently lower than for other methods. This result was anticipated since the other procedures used first classification or first available score and utilized a higher proportion of the same records in summarization. However the correlation between the herdmate-most recent comparisons and the mixed model evaluations was .87, which equalled the corresponding correlation for the other herdmate proof. The two iterative procedures were highly correlated.

Correlations between the type proofs and PD milk, which was the January 1978 USDA MCC proof, are also listed in the table. Correlations are consistently higher for the mixed model estimate and PD milk than the other methods and are consistently lower for the high repeatability set than the overall data set. The lower correlations for the more repeatable set can be explained due to selection, with a higher percentage of bulls being plus proven for milk in this group compared to the complete set. Correlations are similar to these reported by Grantham et al. (18) using the old breed average PDT method.

Rank correlations are reported in Table 7. Bulls appeared to rank more consistently between the two iterative procedures and mixed model methods than between herdmate and mixed model evaluations. This trend was shown in both data sets. These results are in agreement with studies (53, 60) that compared correlations between HC, MCC and mixed model evaluations for milk yield. Rank correlations were similar for the two iterative proofs and were consistently higher in the 80% repeatability set.

Mean and frequency distributions of the differences between PDTs

Table 7. Rank Correlations Between Herdmate, Iterative, and Mixed Model Evaluations for Type^a

	<u>Hermdate</u>		<u>Iterative</u>		<u>Mixed Model</u>
	<u>First Available</u>	<u>Most Recent</u>	<u>Avg PDT of HMs' Sires</u>	<u>Avg CI of HM</u>	
<u>Hermdate</u>					
First Available	1.00	.96	.97	.98	.76
Most Recent	.99	1.00	.93	.94	.73
<u>Iterative</u>					
Avg PDT of HMs' sires	.98	.96	1.00	1.00	.78
Avg CI of HM	.99	.97	1.00	1.00	.78
<u>Mixed Model</u>	.87	.84	.89	.89	1.00

^aCorrelations for 3392 bulls above diagonal, correlations for 934 bulls with >80% repeatability below diagonal.

^bAll correlations statistically significant (P<.01)

are listed in Table 8. The PDTs were adjusted for the respective means to make comparisons between evaluation procedures. The results indicated that 76% of the PDTs calculated using most recent records exceeded those using first-available scores after adjustments were made for the respective means. However 47% of the proofs differed by less than .10 with a mean difference of $-.02$.

Adjustments for genetic level of competition generally increased PDTs with 56% and 49% of the PDTs iterated on average PDTs of herdmates' sires and average cow index of herdmates respectively, exceeding the herdmate comparison estimates. The iterative procedure based on cow indices resulted in less change compared to using PDTs of herdmates' sires. Fifty-three percent of the herdmate comparisons exceeded mixed model proofs. Similar percentages, 53 and 52, of PDTs calculated by the two respective iterative procedures exceeded mixed model estimates. However the average difference between mixed model and proofs calculated using the other procedures was zero or near zero for all cases. PDTs were more variable when comparing proofs to the BLUP procedure than comparisons against the herdmate-first available PDT as shown by the standard deviations of differences in Table 8. This was expected due to the smaller variance of BLUP PDTs compared to the other methods.

Means and frequency distributions of absolute differences between proofs are listed in Table 9. There appeared to be relatively small absolute differences between herdmate-first available comparisons and the herdmate-most recent proofs. Sixty-three percent of the proofs changed less than .10 with an average difference of .11. Similar

Table 8. Means and Frequency Distributions of Differences Between Proofs^a

PDTs COMPARED	DISTRIBUTION OF DIFFERENCES BY INTERVALS						Mean differ- ences	Standard deviation of differences
	<-.5	-.49 to -.10	-.09 to .00	.01 to .10	.11 to .50	>.5		
<u>HM(First)</u> - ^b								
HM(Recent)	.00	.29	.47	.15	.26	.01	-.02	.16
IT(\overline{PD})	.00	.24	.32	.20	.22	.01	.00	.18
IT(\overline{CI})	.00	.18	.31	.27	.23	.00	.01	.15
<u>MM</u> - ^c								
HM(First)	.07	.35	.11	.10	.26	.09	-.01	.38
HM(Recent)	.09	.34	.10	.10	.24	.13	.00	.43
IT(\overline{PD})	.11	.33	.09	.08	.25	.13	.00	.45
IT(\overline{CI})	.09	.33	.10	.09	.27	.11	.00	.42

^aadjusted for differences in the overall means of methods

^b6816 bulls included in comparison

^c3392 bulls included in comparison

Table 9. Means and Frequency Distributions of Absolute Differences Between Proofs^a

PDTs COMPARED	DISTRIBUTION OF ABSOLUTE DIFFERENCES BY INTERVALS						Mean Absolute Differences	Standard Dev. of Differences
	<.05	.06 to .10	.11 to .25	.26 to .50	.51 to 1.0	>1.0		
<u>HM(First)-^a</u>								
HM(Recent)	.23	.40	.27	.08	.01	.00	.11	.11
IT($\overline{\text{PD}}$)	.27	.26	.35	.10	.01	.00	.13	.12
IT($\overline{\text{CI}}$)	.34	.25	.32	.08	.01	.00	.11	.10
<u>MM-^b</u>								
HM(First)	.11	.11	.29	.32	.15	.02	.30	.24
HM(Recent)	.09	.11	.26	.32	.20	.02	.34	.27
IT($\overline{\text{PD}}$)	.09	.09	.26	.31	.22	.03	.35	.28
IT($\overline{\text{CI}}$)	.09	.10	.28	.31	.18	.02	.34	.27

^aadjusted for differences in the overall means of methods

^b6816 bulls included in comparison

^c3392 bulls included in comparison

results were found comparing the herdmate-first available PDT to the iterative procedures. Comparing the mixed model procedures to the other methods yielded larger absolute differences. Seventeen percent of the bulls had absolute differences between herdmate-first available and mixed model proofs of .5 or greater with an average absolute difference of .30. The average absolute difference between the two respective iterative methods and the mixed model procedure were .35 and .34.

To determine if genetic level of herdmates affected the present sire summaries, regressions of final score, herdmate average, and deviation from herdmates on the two measures of competition, average PDT of herdmates' sires and average cow index of herdmates, were calculated. The regressions within sire and within year of classification are in Table 10. The regressions of final score and adjusted herdmate average on average PDT of herdmates sires were 1.47 and 2.52 respectively, while the corresponding regressions on average cow index of herdmates were 1.19 and 2.23. These findings suggest a positive association between herd average and genetic merit of competition. The regressions of daughter deviation from herdmate average on both measures of genetic caliber of herdmates were negative. Negative regression coefficients indicated that deviations of individual daughters from herdmates are affected by the quality of bulls that sired the herdmates. Therefore variation in sires of herdmates would also affect sire summaries since deviations are used in calculating type proofs. Norman et al. (51) calculated similar regressions for milk yield and found the same trends.

Correlations between the two measures of genetic merit of

Table 10. Regressions^a of Daughter Score, Herdmate Average, and Deviation from Herdmates on Two Measures of Genetic Merit of Herdmates

	<u>Daughter Final Score</u>	<u>Adjusted Herdmate Average</u>	<u>Daughter Deviation From Herdmate Average</u>
Average PDT of Herdmates' : Sires	1.47 ± .04 ^b	2.52 ± .01	-1.05 ± .04
Average Cow Index of Herdmates	1.19 ± .03 ^b	2.23 ± .02	- .83 ± .03

^aWithin sire, year classified

^bStandard errors

herdmates, final score, and herdmate average are listed in Table 11. The high correlations between average PDT of sires of herdmates, average herdmate cow index and adjusted herdmate average support the contention that cows in high scoring herds are subjected to stiffer competition and that not accounting for differences in genetic merit of herdmates would bias herdmate comparisons for type.

Regressions of PDT calculated from herdmate, iterative, and BLUP comparisons on herdmate average are listed in Table 12. The regression for the herdmate comparison, .06, was less than the corresponding coefficients obtained for the other evaluation methods. The higher coefficients for the methods that accounted for competitive level reflected the positive association between herdmate average and genetic merit of herdmates reported earlier.

Regression of Daughter Score on Herdmate Average

While the intra-sire regression of daughter records on herdmate averages have been primarily used for adjustments for herd differences in the herdmate comparison, others (27, 43, 56, 59, 64) have used the regression as a measure of the genetic differences between herds. The value $2(1 - b)$, where b is the intra-sire regression of daughter record on herdmate average, estimated the proportion of herd differences due to additive genetic differences. Jamieson et al. (27) estimated the regression of final score on herdmate average by year of classification and found the coefficient to range from .70 to .61. They interpreted that approximately 61 to 78% of the variation between herds was due to genetic differences. The intra-sire regression of final score on

Table 11. Correlations Between Variables Included in Sire Evaluation

	<u>Final Score</u>	<u>Adjusted Herdmate Average</u>	<u>Average PDT of Herdmates' Sires</u>	<u>Average Cow Index of Herdmates</u>
Final Score	1.00	.38	.17	.16
Adjusted Herdmate Average		1.00	.48	.45
Average PDT of Herdmates' Sires			1.00	.92
Average Cow Index of Herdmates				1.00

Table 12. Regression of PDTs Calculated From Different Methods on Adjusted Herdmate Average^a

<u>PDT Method</u>	<u>b</u>
<u>Herdmate</u> ^b	
First Available	.06 ± .01
<u>Iterative</u> ^b	
Average PDT of herdmates' sires	.11 ± .01
Average Cow Index of herdmates	.12 ± .01
<u>Mixed Model</u> ^c	.10 ± .01

^aFirst available scores used.

^b6816 bulls included.

^c4416 bulls included.

adjusted herdmate average was calculated in this study and found to be $.80 \pm .01$, which is higher than the estimate reported earlier.

Many researchers have studied factors that affect the intra-sire regression of daughter milk record on herdmate average. Miller (43) and Mao (34) found that errors in age correction factors inflated the estimates for milk yield. Use of different sets of age correction factors in the two studies may explain part of the differences. If there were errors in age factors calculated by Kliewer (29), the regression value obtained in this study could be overestimated. However the average score of cows in this study was 81.5 which is breed average. Data used by Jamieson et al. (27) contained a larger percentage of older cows. Since older cows are more alike genetically than younger cows, one would expect a larger estimate from the earlier study. Pirchner and Lush (56) stated that the regression would be .5 if all the differences between herds were due to additive genetic effects. The estimate, .6, obtained for several years by Jamieson et al. (27) was close to this value and seems intuitively low since environment has an effect on type score. If data used in this study were subjected to increased selection for type, compared to the earlier study, differences in selection intensity could explain discrepancies in the coefficients.

Comparison of Proofs Calculated in Herd Average Groups

In an attempt to determine the effects of genetic level of competition on sire evaluation for type, bulls were summarized in three progeny groups based on the daughters' herdmate averages. Summaries were

calculated using herdmate and iterative comparisons for those bulls with at least twenty daughters in each group. The requirement for summarization using mixed model method was at least ten daughters. A lower number of daughters was required for summarization using mixed model methodology in order to increase the number of sires with proofs calculated by all three comparisons. This reduction in numbers required was necessary since only cows less than 43 months of age were used in calculating BLUP PDTs, while first available records with no requirement on age were used in other PDT computations. Means and standard deviations of the PDTs calculated by the various procedures are presented in Table 13. Average repeatabilities and daughters per sire are also listed.

If genetic level of competition has no effect on sire evaluation for type, the summaries calculated using the herdmate comparison in the three herd levels should be the same. However if large differences between the proofs in the three levels exist, then adjustment for the genetic caliber of herdmates is warranted to improve accuracy of evaluation.

The average herdmate comparisons for the 670 sires were .12, -.28, and -.45 for low, middle and high herdmate average groups respectively. The difference between the extreme means was .57 indicating that herd average influences sire evaluations and creates a positive bias in favor of bulls proven in below average herds.

Mean PDTs adjusted for the average PDT of sires of herdmates were .17, -.20, and -.23 for the three respective levels. While this

Table 13. Means and Standard Deviations of PDTs Calculated by Herdmate, Iterative, and Mixed Model Comparisons in Three Herdmate Average Groups^a

<u>Herdmate</u> (first available)	<u>Mean</u> <u>PDT</u>	<u>Standard</u> <u>Deviation</u>	<u>Mean no.</u> <u>Daughters</u>	<u>Mean</u> <u>Repeatability</u>	<u>Range</u> <u>PDTs</u>
low	.12	.93	210.5	.87	-3.04 to 2.49
mid	-.28	.86	327.20	.90	-3.33 to 2.26
high	-.45	.78	250.69	.86	-3.09 to 1.94
<u>Iterative</u> (avg PDT of HMs' sires)					
low	.17	.98	188.64	.86	-3.15 to 2.62
mid	-.20	.85	307.19	.90	-3.38 to 2.43
high	-.23	.77	239.29	.85	-2.72 to 2.11
<u>Iterative</u> (avg CI of herdmates)					
low	.10	.96	188.64	.86	-3.02 to 2.52
mid	-.17	.84	307.19	.90	-3.28 to 2.49
high	-.20	.77	239.29	.85	-2.71 to 2.12
<u>Mixed Model</u>					
low	.11	.76	91.01	.51	-2.82 to 2.42
mid	.08	.67	155.95	.61	-2.33 to 2.32
high	.03	.59	126.49	.52	-2.65 to 2.07

^a670 bulls with at least 20 daughters in the herdmate and iterative PDTs and at least 10 daughters in mixed model proofs

adjustment reduced the differences in the three groups, it appears that evaluations in the below average herds are still biased upward. The adjustment increased the means in the groups by .05, .08, and .22 respectively. Increases in all three herd levels indicated that better than average bulls for conformation are used in each group. However dairymen with high herd averages appear to have selected more intensively for PDT.

The other iterative procedure adjusting for average cow index of herdmates, yielded means of .10, -.17, and -.20 for the respective groups. This adjustment decreased average PDT in the low group by .02, while increasing the mean PDTs in the middle and high groups by .11 and .23 respectively. The slight decline in means in the low group suggests that females in this level are not selected intensively for conformation. Increased average PDTs in both the middle and high levels using this adjustment compared to the other iterative model suggested that female selection for type was practiced in these herd levels.

Means for the mixed model estimation were .11, .08, and .03 for the groups. Repeatabilities were less, .51 to .61, compared to the other procedures due to the added age requirement. Even with mixed model proofs, proofs computed in below average herds appear to be biased upward. BLUP estimates in the herd levels, like those in the overall data set, are generally higher than proofs estimated from the other procedures.

One interesting point that may explain part of the discrepancies between proofs in the three herd groups was the decreasing standard

deviation of the type proofs from low to high levels. This trend was observed in all four procedures. Decreased variance in proofs, along with earlier results involving adjustment for average cow index of herd-mates, suggested a positive association between herd average and selection intensity on type. Intensive selection reduced variation in final score within a herd. This reduction results in a smaller range in deviations from herd-mates for cows in these herds relative to deviations of cows of equal genetic merit in herds where type selection is not practiced. These lower deviations are reflected in lower proofs of bulls sampled in these herds. If differing selection intensities are responsible for most of the differences between PDTs in the various herd levels, sires used primarily in high averaging herds will be biased downward with any of the procedures. An adjustment for differing selection intensities for type would be almost impossible to calculate since poor type individuals are generally culled before classified.

Correlations between PDTs calculated by different methods in the three herd-mate average levels are listed in Table 14. An unusual result from the correlations was the slightly higher correlations between the three herd-mate PDTs than the procedures that adjusted for genetic competition. These findings may be due to the larger variation in proofs adjusted for genetic level of herd-mates. The two iterative procedures are highly correlated as expected. Correlations between the three mixed model proofs were less than the corresponding correlations between proofs calculated by the other methods. This result can be explained by the lower repeatabilities of the BLUP estimates and

Table 14. Correlations Between PDTs Calculated by Different Methods in Herdmate Average Levels^a

	Herdmate (first available)			Iterative (avg PDT of HMs' sires)			Iterative (avg CI of HM)			Mixed Model		
	Low	Mid	High	Low	Mid	High	Low	Mid	High	Low	Mid	High
<u>Herdmate (first available)</u>												
low	1.00 ^b	.86	.80	.97	.84	.78	.98	.85	.79	.83	.74	.68
mid		1.00	.85	.84	.98	.82	.84	.98	.83	.72	.85	.71
high			1.00	.77	.84	.97	.78	.85	.97	.67	.73	.80
<u>Iterative (avg PDT HMs' sires)</u>												
low				1.00	.84	.75	1.00	.84	.75	.84	.74	.68
mid					1.00	.83	.84	1.00	.83	.72	.86	.72
high						1.00	.75	.83	1.00	.65	.71	.80
<u>Iterative (avg CI of HM)</u>												
low							1.00	.84	.76	.84	.74	.68
mid								1.00	.83	.72	.86	.72
high									1.00	.66	.72	.80
<u>Mixed Model</u>												
low										1.00	.66	.63
mid											1.00	.68
high												1.00

^a670 bulls included

^ball correlations statistically significant (P<.01)

lower theoretical expectations. The two iterative procedures were slightly more correlated with the mixed model proofs than the herdmate comparisons. Rank correlations are listed in Table 15. Results are similar to the product-moment correlations. All correlations were statistically significant at the .01 level.

Means and frequency distributions of the differences between proofs calculated in the herd levels are shown in Table 16. Eighty-three percent of the herdmate comparisons calculated in below average herds exceeded herdmate PDTs in high herds, and 78% of the low PDTs were greater than those computed in the middle group. Approximately 71% of the middle level HC proofs exceeded their corresponding estimates in high herds. Iteration on the average PDT of herdmates' sires reduced the advantage of PDTs in low herds. After the adjustment about 75% of the low proofs exceeded those estimated in the middle level and about 70% exceeded those in high averaging herds. This adjustment particularly reduced the advantage of proofs calculated from middle group over those in the high average level. After the adjustment only 50% of the middle proofs exceeded the high herd average evaluations.

Adjustment for the average herdmate cow index appeared to remove more of the biases than the other iterative procedure. Only 69% and 68% of the low PDTs were greater than those estimated in the high and middle groups respectively. Like the other adjustment, iteration on average cow index of herdmates removed most of the biases in favor of proofs calculated in middle levels compared to high group proofs.

The mixed model procedure was most effective in reducing biases

Table 15. Spearman Rank Correlations Between PDTs Calculated by Different Methods in Herdmate Average Levels^a

Herdmate (first available)	Herdmate (first available)			Iterative (avg PDT of HMs' sires)			Iterative (avg CI of HM)			Mixed Model		
	Low	Mid	High	Low	Mid	High	Low	Mid	High	Low	Mid	High
low	1.00 ^b	.84	.79	.97	.83	.77	.98	.83	.78	.80	.69	.66
mid		1.00	.83	.82	.98	.80	.83	.98	.81	.68	.81	.68
high			1.00	.77	.83	.96	.77	.83	.97	.64	.70	.77
Iterative (avg PDT HMs' sires)												
low				1.00	.82	.74	1.00	.82	.75	.82	.71	.67
mid					1.00	.81	.82	1.00	.81	.68	.83	.69
high						1.00	.74	.81	1.00	.63	.67	.77
Iterative (avg CI of HM)												
low							1.00	.82	.75	.81	.71	.67
mid								1.00	.81	.68	.83	.69
high									1.00	.63	.68	.78
Mixed Model												
low										1.00	.62	.59
mid											1.00	.63
high												1.00

^a670 bulls included

^bstatistically significant (P<.01)

Table 16. Means and Frequency Distributions of Differences Between Proofs Calculated in Herdmate Average Levels

<u>PDTs Compared</u>	<u>Distribution of Differences by Intervals</u>						<u>Mean Difference</u>	<u>Standard Deviation of Difference</u>
	<u><-.5</u>	<u>-.49 to -.10</u>	<u>-.09 to .00</u>	<u>.01 to .10</u>	<u>.11 to .50</u>	<u>>.5</u>		
<u>Herdmate (first available)</u>								
Low-High	.06	.08	.02	.04	.24	.55	.52	.61
Low-Mid	.05	.13	.05	.06	.30	.41	.36	.53
Mid-High	.09	.18	.06	.09	.37	.22	.15	.48
<u>Iterative (avg PDT of HMs' sires)</u>								
Low-High	.12	.13	.05	.04	.23	.43	.33	.70
Low-Mid	.07	.14	.05	.06	.29	.39	.32	.57
Mid-High	.16	.22	.11	.06	.29	.15	.00	.50
<u>Iterative (avg CI of HM)</u>								
Low-High	.14	.15	.04	.04	.25	.37	.24	.68
Low-Mid	.08	.16	.07	.06	.31	.31	.24	.56
Mid-High	.16	.24	.10	.07	.29	.14	.00	.50
<u>Mixed Model</u>								
Low-High	.16	.21	.06	.06	.27	.24	.08	.60
Low-Mid	.17	.23	.07	.08	.26	.19	.03	.59
Mid-High	.13	.25	.08	.09	.28	.18	.05	.51

in favor of bulls' proven in below average herds. Only 57% and 53% of the sires had proofs calculated in the below average group that were greater than corresponding estimates from the high and middle levels. Means and frequencies of absolute differences between proofs calculated in the three herd levels are listed in Table 17.

Directional changes in PDTs after adjustment for competitive level of herdmates are included in Table 18. Sixty-two percent of the PDTs in the low group increased with adjustment for average PDT of herdmates' sires, while 71% and 92% of the PDTs in the middle and high levels increased.

The corresponding percentages for the adjustment for average cow index of herdmates were 51, 78, and 96% for the three respective herd-mate average levels. While PDTs calculated by the two iterative procedures are highly correlated, adjustment using average cow index of herdmates removed more of the bias due to genetic competition. This finding was expected since cow indices are more indicative of genetic superiority of an individual than the PDT of animal's sire.

Mixed model estimates calculated in the herd levels were generally greater than corresponding herdmate HC proofs. This finding was not surprising since mean mixed model PDTs were consistently higher than mean PDTs estimated from the other methods.

Intra-sire regressions of final score on adjusted herdmate average were calculated for the three herd levels. The coefficients were $.77 \pm .02$ for the low and middle herdmate average groups and larger, $.93 \pm .01$ for the higher scoring group. The larger coefficients in high herd

Table 17. Means and Frequency Distributions of Absolute Differences Between Proofs Calculated in Herdmate Average Levels

<u>PDTs Compared</u>	<u>Distribution of absolute differences by intervals</u>						<u>Mean Absolute Difference</u>	<u>Standard Deviation of Difference</u>
	<u><.05</u>	<u>.06 to .10</u>	<u>.11 to .25</u>	<u>.26 to .50</u>	<u>.51 to .50</u>	<u>>1.0</u>		
<u>Herdmate (first available)</u>								
Low-High	.03	.03	.11	.21	.37	.22	.67	.43
Low-Mid	.25	.04	.09	.21	.31	.10	.36	.53
Mid-High	.07	.08	.24	.31	.25	.05	.40	.31
<u>Iterative (avg PDT of HMs' sires)</u>								
Low-High	.04	.05	.13	.23	.36	.19	.63	.44
Low-Med	.06	.05	.18	.26	.34	.11	.52	.39
Med-High	.09	.09	.24	.28	.27	.04	.39	.31
<u>Iterative (avg CI of HM)</u>								
Low-High	.04	.06	.15	.23	.36	.16	.58	.42
Low-Mid	.06	.07	.19	.29	.31	.08	.48	.37
Mid-High	.09	.08	.25	.28	.27	.04	.39	.31
<u>Mixed Model</u>								
Low-High	.05	.08	.19	.29	.30	.09	.48	.37
Low-Mid	.07	.07	.22	.28	.26	.10	.46	.37
Mid-High	.07	.09	.23	.29	.27	.04	.40	.31

Table 18. Means and Frequency Distributions of Changes After Adjustment for Genetic Level of Competition

PDTs COMPARED	DISTRIBUTION OF CHANGE BY INTERVALS						MEAN CHANGE	STANDARD DEV. OF CHANGE
	<u><-.5</u>	<u>-.49</u> to <u>-.10</u>	<u>-.09</u> to <u>.00</u>	<u>.01</u> to <u>.10</u>	<u>.11</u> to <u>.50</u>	<u>>.5</u>		
<u>Herdmate-Iterative</u> <u>(First Available) - (Avg PDT of HMs' sires)</u>								
Low	.00	.45	.17	.13	.23	.02	-.03	.23
Mid	.02	.43	.26	.14	.15	.00	-.07	.19
High	.08	.66	.17	.06	.02	.00	-.22	.19
<u>Herdmate-Iterative</u> <u>(First Available) - (Avg CI of HM)</u>								
Low	.00	.29	.22	.17	.31	.01	.03	.19
Mid	.02	.47	.28	.10	.11	.00	-.10	.17
High	.08	.66	.17	.06	.02	.00	-.25	.18
<u>Herdmate-Mixed Model</u>								
Low	.15	.24	.08	.10	.27	.14	.01	.52
Mid	.38	.35	.05	.05	.10	.03	-.35	.46
High	.49	.30	.05	.04	.09	.02	-.48	.47

levels indicated greater genetic resemblance between cows in these herds compared to cows in lower classifying herds.

Using the regression values to estimate the proportion of total variation among herds in the different groups attributed to additive genetic differences, 14% of the variation between herds was additive genetic in nature in high herd levels. A greater portion, 46%, of the differences between herds in the other groups were due to genetic differences. These findings supported the contention that cows in high averaging herds are subjected to increased selection for type since selection reduced variation in herds and increases the genetic likeness among herdmates.

These results are supported by the means and standard deviations for final score, herdmate average, and the two measures of genetic merit shown in Table 19. The average scores in the respective groups were 78.96, 80.77, and 82.79 while the corresponding standard deviations were 4.54, 3.81, and 3.58. The declining variation in final score can be attributed to a combination of using higher PDT bulls and heavier culling for type in higher scoring herds. The average PDT of herdmates' sires were $-.23$ for the low group, $-.05$ for the middle group, and $.13$ for the high herdmate level. The differences between herd levels in emphasis placed on sire selection for type was even greater when the mean PDT of the bulls in the groups was considered. The average PDT of bulls in the low group was $.07$ compared to $-.28$ and $-.45$ for the middle and high levels respectively. There was also more variation in average PDT of sires of herdmates in the lower group than in the two higher

Table 19. Means and Standard Deviations of Final Score, Herdmate Average, Average PDT of Herdmates' Sires, and Average Cow Index of Herdmates by Herdmate Average Groups

	<u>Final Score</u>		<u>Adjusted Herdmate Average</u>		<u>Average PDT of Herdmates' Sires</u>		<u>Average Cow Index of Herdmates</u>	
	<u>Mean</u>	<u>Standard Deviation</u>	<u>Mean</u>	<u>Standard Deviation</u>	<u>Mean</u>	<u>Standard Deviation</u>	<u>Mean</u>	<u>Standard Deviation</u>
LOW	78.96	4.54	78.69	.98	-.23	.32	-.24	.35
MID	80.77	3.81	80.77	.96	-.05	.27	-.06	.30
HIGH	82.79	3.58	82.86	.94	.13	.25	.13	.28

groups.

These findings confirmed that more selection pressure for type was practiced in high averaging herds than lower scoring ones. This increased selection intensity in the high group created a negative bias for bulls proven primarily in high scoring herds. The part of this bias attributed to sire selection can be removed by accounting for the average PDT of herdmates' sires. Adjusting for average cow index of herdmates can remove additional differences in female selection for type. However since cow indices are computed using herdmate deviations, the lower variation in final score in the higher averaging herds was also reflected in deviations of lower magnitudes in the high scoring group. This fact reduced cow indices computed in high herds relative to indices' of individuals of equal genetic merit in lower herds.

These lower deviations from herdmates in high scoring herds compared to low herds due to increased selection for body conformation in high herds are also used in PDT computation and cannot be removed from sire evaluation.

Pedigree Grouping in Sire Evaluation for Type

Means and standard deviations of PDTs calculated using herdmate, iterative, and mixed model comparisons with and without pedigree grouping are listed in Table 20. Results are shown for those bulls with pedigree information and a subset, bulls with greater than 80% repeatability. The grouping procedure used by USDA in calculation of mixed model proofs included a grouping for bulls with no pedigree information. However no corresponding group was used in the iterative

Table 20. Means and Standard Deviations (SD) of Sire Evaluations for Type from Herdmate, Iterative, and Mixed Model Comparisons for Bulls with Pedigree Information

	<u>All Bulls^a</u>		<u>Bulls >80%^b Repeatability</u>	
	<u>Mean</u>	<u>SD</u>	<u>Mean</u>	<u>SD</u>
Herdmate (first available)	-.18	.63	-.34	.84
<u>Iterative</u> <u>(avg PDT of HMs' sires)</u>				
without pedigree grouping	-.25	.76	-.50	.96
with pedigree grouping	-.33	.77	-.52	.97
<u>Iterative</u> <u>(avg CI of HM)</u>				
without pedigree grouping	-.19	.73	-.42	.92
with pedigree grouping	-.26	.74	-.43	.93
<u>Mixed Model</u>				
without pedigree grouping	-.01	.59	.01	.81
with pedigree grouping	.04	.71	.04	.86

^a2444 bulls with pedigree information

^b666 bulls with >80% repeatability

procedures and only bulls with at least a sire's PDT are compared. Mean proofs calculated using the iterative methods declined with the inclusion of grouping, while mixed model PDTs increased slightly. However the decline in mean PDT was not as great for the higher repeatability set. The average change in herdmate proofs compared to iterative procedures with grouping was $-.17$ and $-.11$ for adjustment on average PDT of herdmates' sires and average cow index of herdmates respectively, while the corresponding changes were $-.18$ and $-.09$ for the high repeatability group. Proofs declined with grouping even though the average pedigree index was $.26$ and $.29$ for the two respective iterative procedures. This point can be explained by negative average of PDTs for bulls with pedigree indices in that range as shown in Table 3. The studies of Lee et al. (31) and McNeil et al. (42) also support this contention. Biases due to differing selection intensities may have caused the problems associated with lower than expected correlations between pedigree indices and herdmate deviation PDTs.

Simple correlations squared were used to measure the relative importance of pedigree grouping. Pedigree information accounted for 43 - 46% of the change in iterative proofs and less, 23 - 24% of the change in the high repeatability set. Similar trends were reported by Norman et al. (52) examining the relative contribution of pedigree and genetic level of competition in MCC milk proofs. However they found higher portion (57 - 73%) of change due to pedigree for all bulls studied and about the same percentage (26%) due to pedigree grouping in high repeatability sires. The increased percentage of

change accounted by pedigree grouping for milk yield compared to grouping for type was due to increased accuracy of pedigree prediction of PD milk compared to PDT prediction.

Correlations between proofs are listed in Table 21. Correlations for the complete set are shown above the diagonal and correlations for the restricted set are below the diagonal. Mixed model proofs without pedigree grouping are more highly correlated with other proofs compared to mixed model comparisons that included pedigree information. This was not surprising since the inclusion of pedigree grouping generally lowers iterative PDTs while slightly increasing mixed model proofs. This point may be due to more accurate prediction with the use of mixed model procedures or may be due to differences in the mean PDTs among the procedures.

Correlations Between Proofs Calculated From Independent Progeny Groups

Progeny of bulls were divided into two independent sets based on the last digit of the herd identification code. Herdmate and iterative proofs were calculated in the two groups for bulls with more than twenty daughters in each group in order to examine how repeatabilities of independent progeny tests were affected by adjustment for genetic level of competition. Means and standard deviations are listed in Table 22. There were no differences in means calculated in the two groups. As in previous work, adjustment for genetic differences increased variation in PDT. Summaries in the two independent levels had repeatabilities averaging 87 and 88% respectively.

Table 21. Correlations Between Herdmate, Iterative, and Mixed Model Comparisons for All Bulls With Pedigree Information and Those With 80% Repeatability or Greater^a

	<u>Hermate (First available)</u>	<u>Iterative (avg PDT of HMs' sires)</u>		<u>Iterative (avg CI of HM)</u>		<u>Mixed Model</u>	
		<u>w/o pedigree</u>	<u>w/ pedigree grouping</u>	<u>w/o pedigree</u>	<u>w/ pedigree grouping</u>	<u>w/o pedigree</u>	<u>w/ pedigree grouping</u>
<u>Hermate (first available)</u>	1.00	.97	.96	.98	.97	.81	.75
<u>Iterative (avg PDT of HMs' sires)</u>							
w/o pedigree	.98	1.00	.99	1.00	.99	.81	.77
w/ pedigree	.98	1.00	1.00	.99	1.00	.82	.81
<u>Iterative (avg CI of HM)</u>							
w/o pedigree	.99	1.00	1.00	1.00	.99	.82	.77
w/ pedigree	.99	1.00	1.00	1.00	1.00	.83	.81
<u>Mixed Model</u>							
w/o pedigree	.88	.90	.90	.90	.90	1.00	.92
w/ pedigree	.85	.88	.89	.88	.89	.99	1.00

^aCorrelations for 2444 bulls with pedigree information above diagonal, correlations for 666 bulls with 80% repeatability or greater below diagonal

Table 22. Means and Standard Deviations of PDTs Calculated by Herdmate^a and Iterative Comparisons in Two Independent Sets of Progeny

	<u>Mean PDT</u>	<u>Standard Deviation</u>	<u>Mean Number of Daughters</u>	<u>Mean Rpt</u>
<u>Herdmate (first available)</u>				
one	-.25	.87	292	.87
two	-.23	.87	336	.88
<u>Iterative (avg PDT of HMs' sires)</u>				
one	-.36	.95	292	.87
two	-.35	.96	336	.88
<u>Iterative (avg CI of herdmates)</u>				
one	-.29	.93	292	.87
two	-.28	.93	336	.88

^a731 bulls included

Correlations between proofs of the 731 bulls summarized in the two groups are listed in Table 23. Adjustment for competitive level of herdmates increased the correlations between independent sets of progeny by .02 for the two iterative methods. This increase corresponded to the .02 increase in correlations estimated by Tomaszewski et al. (65) when comparing milk proofs calculated in independent sets. Their increase was not as great as expected, however Tomaszewski et al. (65) found a high correlation between PDs of herdmates' sires in the two groups. The same was probably true for type proofs with the PDTs of herdmates sires in the two independent sets being highly correlated. Adjustment for genetic merit of herdmates was more effective than was indicated by the increase in correlations between the two sets. These bulls were high repeatability sires and were probably used across a wide variety of herd levels. Adjustments for genetic merit of herdmates were more effective when bulls are not compared to random samples of herdmates.

The Use of Herdmates Vs. Contemporaries in Sire Evaluation For Type

Many breeders have advocated the use of contemporary comparisons instead of herdmate methods. Comparing young cows to their more heavily selected herdmates may create biases in sire proofs. However there are several disadvantages in the use of contemporary comparison. They include the loss of information due to lack of sufficient number of contemporaries and increased sampling variation due to comparing cows to fewer animals. A summary of first and later classification records lacking five or more herdmates and contemporaries are

Table 23. Correlations Between Herdmate and Iterative Comparisons Calculated in Two Independent Sets of Progeny^a

	<u>Herdmate (first available)</u>		<u>Iterative (avg PDT of HMs' sires)</u>		<u>Iterative (avg CI of herdmates)</u>	
	one	two	one	two	one	two
<u>Herdmate (first available)</u>						
one	1.00 ^b	.83	.99	.83	.99	.83
two		1.00	.83	.98	.83	.99
<u>Iterative (avg PDT of HMs' sires)</u>						
one			1.00	.85	1.00	.85
two				1.00	.85	1.00
<u>Iterative (avg CI of herdmates)</u>						
one					1.00	.85
two						1.00

^a731 bulls included

^bAll correlations statistically significant P(<.01)

listed in Table 24. Only 2.6% of the cows lacked sufficient numbers of herdmates. However, 36.8% of the cows under 36 months of age did not have five or more contemporaries. Relatively few older animals, 2.3%, lacked the required number of contemporaries.

In a study comparing the use of herdmates to contemporaries in milk proofs, McDaniel et al. (40) found that .9% of Holsteins lacked herdmates while 6.2 and 12.7% of the first and second lactation cows lacked contemporaries. The higher percentage of first classification animals was due to the fact that five contemporaries were required in this study and only one contemporary was required in the milk study.

Consistent differences between herdmate and contemporary deviations would denote a bias. Differentials between herdmate and contemporary deviations are listed in Table 25. No consistent biases appeared in the first classification group since 50.5% of the contemporary deviations exceeded deviations from herdmates. However, 54.5% of the herdmate deviations for the older group were greater than contemporary deviations.

This finding may illustrate that first classification cows are slightly overadjusted, however it was surprising that a reciprocal increase was not found in the younger group. Selection biases for type within herds due to comparing younger cows to more heavily selected herdmates did not appear to be a problem since animals in both age groups with poor conformation are probably culled before classification.

Use of contemporary deviations would reduce the dependence on

Table 24. Summary of First and Later Classifications Lacking Five Herdmates or Contemporaries

	<u>Number of Records</u>		<u>Records Without Sufficient Numbers of Herdmates (Contemporaries) (%)</u>
	<u>With Herdmates</u>	<u>Without Herdmates</u>	
All cows	1043508	27506	2.6
	<u>With Contemporaries</u>	<u>Without Contemporaries</u>	
First (<35 mths)	134900	78684	36.8
Later (>35 mths)	810626	19298	2.3

Table 25. Differentials Between Herdmate and Contemporary Deviations of First and Later Classifications by Intervals

<u>Herdmate- Contemporary Deviation</u>	<u>First Classification (≤ 36 Months)</u>	<u>Later Classifications (> 36 Months)</u>	<u>Total</u>
< -2.6	2.2%	.1%	.4%
-2.50 to -1.1	16.2	2.2	4.2
-1.0 to - .1	32.1	43.2	41.6
0 to .9	31.0	52.7	49.6
1.0 to 2.4	15.4	1.8	3.7
≥ 2.5	3.0	.0	.4

age correction factors.

Means and standard deviations for 5668 bulls with both herdmate and contemporary comparisons are shown in Table 26. There did not appear to be any difference in the means or standard deviations of the two comparisons. However the average number of daughters declined with the use of contemporaries. A comparison of contemporary and herdmate methods showed 51% of the contemporary PDTs exceeded herdmate PDTs using either first available or most recent record.

Unless age adjustment factors are incorrect and favor one or the two contemporary groups, there did not appear to be any advantage in using a contemporary comparison for sire evaluation for type.

Table 26. Means and Standard Deviations of Herdmate and Contemporary Comparisons for Type^a

	Mean PDT	Standard Deviation	Average Number of Daughters	Average Repeatability	Range
<u>First Available Record Used</u>					
Herdmate	-.18	.61	109	.49	-3.19 to 2.37
Contemporary	-.18	.61	92	.47	-3.30 to 2.28
<u>Most Recent Record Used</u>					
Herdmate	-.22	.63	109	.49	-3.46 to 2.49
Contemporary	-.22	.63	96	.48	-3.46 to 2.48

^a 5668 bulls with at least 10 daughters in both comparisons.

SUMMARY AND CONCLUSIONS

The present PDT procedure is biased due to failure to account for the non-random use of sire and differential culling rate for type among herds. Correlations between herdmate average and the two measures of genetic merit of herdmates, average PDT of herdmates' sires (.48), and average cow index of herdmates (.45) indicated that high PDT sires were used more heavily in higher scoring herds than lower classifying herds.

The results of the herdmate level portion of this study also substantiated the variation in sire use and its effect on sire summaries. The average PDT of herdmates' sires in the low, medium, and high herdmate average groups were -.23, -.05, and .13 respectively. The standard deviations for the respective means were .25, .27, and .37, indicating that high scoring herds consistently used high PDT sires. The effects of failure to account for the genetic quality of herdmates was shown by calculating independent PDTs in the three levels. The average PDT of 670 bulls in the three herdmate respective groups using the current system were .12, -.28, and -.45.

Variation in the genetic merit of herdmates can be removed by adjusting the proofs for the average PDT of herdmates' sires and by adjusting for average cow index of herdmates or by mixed model methodology. However proofs calculated in the low herdmate average group were still favored in the three alternative evaluation procedures that adjusted for the level of genetic competition. While differential use of sires can be removed from sire evaluation, some of the effects of differing selection pressures in herds cannot be

removed.

Selection resulted in lower variation, as expected. Reduction in variation decreased the relative magnitude of deviations from herd-mates in herds that select heavily for conformation compared to herds where little selection pressure was applied. This cumulative selection for type affected sire evaluation more than expected. The effect of cumulative selection pressure on sire evaluation in other traits warrants further investigation.

A contemporary comparison was also examined in this study. The results indicated that no benefit would be gained by the implementation of a contemporary sire summary for type. However the arbitrary use of 36 months as division between first and later classifications may have contributed to the results. Age correction factors, particularly at young ages, may be inflated and this point would not be detected with this study. Therefore further investigation of age correction factors is warranted.

The mixed model comparison appeared to be the most desirable method of sire evaluation for type. It had several properties, such as lower variance, considered desirable by dairy geneticists. The mixed model method also removed more of the bias due to genetic differences among herds than the two iterative procedures.

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A COMPARISON OF HERDMATE, ITERATIVE, AND MIXED MODEL

SIRE SUMMARIES FOR TYPE IN HOLSTEIN CATTLE

by

Benny Ray Bell

(ABSTRACT)

Herdmate comparison used currently by Holstein-Friesian Association of America to calculate predicted difference type was compared to two iterative procedures, adjusting for average PDT of herdmates' sires and average cow index of herdmates respectively, and a mixed model method. PDTs were calculated using the different methods for 6816 bulls with ten or more daughters. Mean PDT for the herdmate comparison was $-.18$ while means for the two respective iterative procedures were $-.24$ and $-.19$. Mixed model proofs sum to zero. Adjustments for average PDT of herdmates' sires increased variance of proofs compared to the other systems. Mixed model PDTs were least variable.

Correlations between herdmate average and two measures of genetic merit of herdmates, average PDT of herdmates' sires and average cow index of herdmates, were $.48$ and $.45$. Positive regression coefficients of final score and herdmate average on two measures of genetic merit of herdmates also indicated a positive association between herd average and level of competition.

The effects of failure to account for genetic merit of herdmates under present system was examined. Progeny were divided into low, middle, and high herdmate average groups and summaries were calculated

for 778 sires with at least 20 daughters in each of three groups. Mean PDTs calculated by the herdmate comparison were .12, -.28, and -.45 for the low, middle, and high groups respectively. Eighty-three percent of the low herdmate comparison PDTs exceeded summaries in high group and 70% of low group evaluations were greater than respective middle group PDTs indicating biases in present sire summaries due to failure to account for genetic level of competition. Adjustment for average PDT of herdmaters' sires and average cow index of herdmaters reduced the advantage of PDTs calculated in low levels. The mixed model method appeared to be most effective in reducing biases in favor of bulls proven in below average herds. Summaries in low group were consistently higher than PDTs calculated in the other levels due to inability to completely remove differences in selection intensities among herds. PDTs calculated in high group were consistently less variable than those calculated in low herd levels. Means of final score, average PDT of herdmaters' sires, and average cow index of herdmaters were larger and less variable than corresponding means in low group demonstrating increased selection for type in high scoring herds. Accuracy in sire evaluation for type will be improved by adjusting for genetic merit of herdmaters, however bulls proven primarily in low scoring herds will continue to be favored slightly.