

\\EFFECTS OF HERD MEAN AND STANDARD DEVIATION
ON COW INDEXES FOR MILK, AND
ADJUSTMENTS OF COW INDEXES FOR THESE EFFECTS

by

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Dissertation submitted to the Faculty of the
Virginia Polytechnic Institute and State University
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

in

Animal Science (Dairy Genetics)

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December 1984
Blacksburg, Virginia

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Dairy Science

(ABSTRACT)

Lactation records of cows born since 1964 were used to compute Cow Indexes (CI) for 581,519 Holsteins and 352,758 Jerseys. CI were used to predict Modified Contemporary Deviations (MCD) of daughters at three levels each of herd mean (μ) and standard deviation (σ), and regressions were compared to expected values. For Holsteins, regressions were greater than expected in herds with average μ or high σ , suggesting that heritability (h^2) should be higher for cows in those herds. Heritability estimates agreed with observed regressions for herd σ (h^2 of .178, .193, and .206 as herd σ increased) but not for herd μ (h^2 of .222, .163, and .206). For Jerseys, regression results indicated that h^2 should increase with herd μ , but there was no trend for herd σ . Heritability estimates agreed with the observed regressions for μ (h^2 of .246, .291, and .331) but not for σ , as h^2 increased substantially (.254, .293, and .371) as

herd σ increased.

Eight adjustments were made for CI: two varied h^2 to adjust for genetic effects, two adjusted MCD for environmental effects, and four were combinations of these. For Holsteins, regressions of daughter MCD on dam CI were greater than expected for all CI, but regressions of son MCD on dam CI were less than expected. Rankings of CI, based on R^2 , differed considerably for the three groups examined (all daughters, daughters of elite cows, and sons). For Jerseys, CI of elite dams predicted offspring MCD as expected, but for several CI, regressions for all daughters were less than expected. There were smaller differences in rankings of CI than for Holsteins.

Under the assumption that large true breed differences are unlikely, the best CI for both breeds had MCD standardized to a common variance, with h^2 of .20. This was nearly optimal for Jersey groups, although less than optimal for Holsteins. This CI adjusted for environmental effects of herd σ , ignoring differences in genetic variation. It decreased differences among CI for cows in high variance herds, and increased differences in low variance herds.

ACKNOWLEDGEMENTS

The author would like to give special thanks to Dr. W. E. Vinson, for serving as committee chairman, and for his guidance, support, and friendship throughout her years as a graduate student.

Thanks are due to Dr. R. E. Pearson, for suggestions and encouragement, and for serving on her graduate committee.

The author would also like to thank Dr. B. G. Cassell for encouragement, and Drs. M. L. McGilliard, K. H. Hinkelmann, and J. M. White for suggestions, and for serving on her graduate committee.

The author would like to gratefully acknowledge the Animal Improvement Programs Laboratory, United States Department of Agriculture, for their interest in this project and for providing the data, and especially would like to thank Dr. R. L. Powell, for his help and suggestions and for serving on her graduate committee.

Finally, the author would like to thank her parents,
, for their tremendous support.

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INTRODUCTION

The Cow Index (CI) is a measure of the genetic merit of a cow, expressed as her transmitting ability for a trait. Its major use is in the selection of cows to be dams of young bulls to enter progeny testing programs. United States Department of Agriculture--Dairy Herd Improvement Association CI currently are computed using information on 1) the cow, 2) her paternal half sibs, and 3) her dam and maternal grandsire. This information is included, respectively, as the cow's Modified Contemporary Deviation (MCD), her sire's Predicted Difference (PD), and her dam's CI. Each source of information is weighted by the appropriate selection index weight based on the amount of information and the genetic relationship to the cow. The best cows in the breed for CI are designated elite and are considered for use as bull mothers.

If there are any errors in CI, there can be potentially serious problems as a result. The first, and most obvious, is that the CI would be less accurate than it should be. Cows could be misranked compared to their true genetic merits. The best cows would not necessarily be chosen as bull mothers, so the most genetic progress would not be made. The second problem is that this error would be carried over into the next generation. The CI contains the

dam's CI in its pedigree portion. If the dam's CI is inflated, for example, by some error, then her daughter's CI would also be inflated, although to a lesser extent. This is more of a problem than a similar situation would be in a bull's PD. In a PD, the weight for the pedigree portion approaches zero as the bull gains more daughter information. However, a cow cannot gain as much additional information through her own records as can a bull through records of his daughters. With large numbers of records, the weight given to the MCD approaches .35, so the pedigree portion's weight can only decline to about .65, still much larger than zero. Because the MCD has a much larger range than the pedigree, the relative weight of a cow's record actually is much larger than 35% and of the pedigree less than 65%, but the pedigree weighting still does not approach zero. Thus any error in a CI will be perpetuated in the daughter's CI and beyond.

A potential source of error is any genetic or environmental effects that are not accounted for adequately in the CI procedure. Several effects are presently adjusted for in calculations. Fixed effects of age, month, region, length of record, and times milked per day are adjusted for with correction factors. The herd in which the record is made is accounted for in calculating the MCD, which is the cow's record minus the average of records of contemporaries

(CTP), plus the average PD of sires of those CTP. Deviating records from CTP removes additive effects common to all cows in the herd. The PD of sires is a measure of the genetic merit of the CTP, and accounts for the genetic level of the herd.

The adjustments for the herd are additive, but there may be some other effects of the herd that are nonadditive in nature which would not be removed. Herds differ from each other for both means and variation for production, MCD, and CI. The differences in variation, in particular, may not be accounted for adequately. In that case, magnitude of CI would be affected by the herd in which the cow made her records, resulting in misranking of cows. Also, in setting up selection index equations to compute the weights, it is assumed that all cows with the same amount of information have the same variance of MCD. If there are herd differences in variation that are not accounted for, this assumption may not be valid. The calculated weights would not necessarily be the correct index weights for the cow, and the resulting CI would be less accurate than its computed reliability indicates.

CI may need to be adjusted for these effects of herd mean and variation. The appropriate adjustment would depend on whether the effects are genetic or environmental in nature.

Differences among herds for means and variation could be expected to be partly genetic. Cows within a herd are related to one another, and are subject to similar selection pressure and sire usage, resulting in genetic differences among herds. Numbers and genetic merits of sires used can affect genetic variation in the herd. Also, variances of daughter records are not homogeneous across sire groups, and the sire may have an effect on the variation of his daughters. Thus herds using one group of sires could have more genetic variability than herds using other sires. Measures of the fraction of differences among herds that are genetic have varied, ranging from a very small fraction to 33%. Differences among herds for genetic variation and heritability (h^2) also have been seen, with both increasing as herd production increases.

Thus at least some of the differences among herds for variation likely are genetic in nature. However, most of the differences in variation would be environmental. As a result, although herds with high variation would have more cows with high enough CI to be on the elite list, they would not necessarily be better genetically than herds with low variation. Genetically superior cows would not always have high CI, and some cows that should be bull mothers could be missed when selections are made.

CI can be adjusted to remove the effects of differences

in herd variation. To adjust for genetic differences among herds, h^2 could be varied according to herd mean or variance. This would affect the index weights, but not the MCD or pedigree portion of the CI. Adjustments for environmental variation should decrease variation in high variance herds and increase it in low variance herds. Potential adjustments include standardizing records to a common within herd variance, and log transformation of records. These would affect the MCD, but not the index weights or the pedigree portion of the CI.

Differences among herds for variation are likely partly genetic and partly environmental, not either alone. Both types of adjustments can be considered valid, but they have opposing effects on CI. A combination of the two types may be the best method to remove herd effects.

There is concern about the herd differences for mean and variation which are not accounted for in current CI procedures, and which appear to be making CI inaccurate. The extent to which there is a problem has not been fully determined. Any potential adjustments to CI for the herd effects need to be examined before they can be incorporated into calculation procedures; if they do not improve the CI much, they may not be worth the added computational costs.

The objectives of this study were:

1. to determine what problems exist with CI, particularly

involving herd mean and variation, and

2. to examine several methods of adjusting CI for these herd effects.

REVIEW OF LITERATURE

The Modified Contemporary Comparison Cow Index

CI for milk production have been calculated using Modified Contemporary Comparison (MCC) procedures since 1974, when that system first was implemented. These CI included information on the cow herself and her paternal half sibs. The cow's records were included as her MCD and sib records were included as the PD of the cow's sire (24). Each was weighted by the appropriate selection index weight, where w was the weight given to the MCD, such that

$$CI = .5[w(MCD) + (1-w)(PD_{sire})]$$

In calculations, records of the cow and her CTP are expressed as mature equivalent records. These have been adjusted, using correction factors, for fixed effects of age, month, region, length of record, and times milked per day. The MCD for a lactation is calculated as the cow's record minus the average of her modified CTP, plus the average PD of sires of those CTP (24). Deviating records from CTP removes additive environmental effects common to all cows in the herd. The PD of sires is a measure of the genetic merit of the CTP, and accounts for the genetic competition the cow faces in the herd.

A weighted average of MCD for the cow is taken to calculate the overall MCD for all records of the cow. The

weighting, LACTWT, depends on the amount of information each lactation's MCD contains. This is determined by the lengths of the records of the cow and her CTP, the numbers of CTP and sires of CTP, and the repeatability (RPT) of CTP sires (7). The larger each of these measures is, the larger will be the weight given to the lactation MCD; with more information, the MCD will be a better indicator of the cow's genetic ability.

The weightings given to overall MCD and PD_{sire} in the CI formula, w and $1-w$, are the appropriate selection index weights. They depend on the h^2 of the trait (.20 for milk), the sum of LACTWT for the cow's records, and the RPT of the sire's PD (24).

The CI formula was revised in 1981 to include the dam's CI, changing the formula to

$$CI = .5[w(MCD) + (1-w)(PD_{\text{sire}} + CI_{\text{dam}})]$$

The weights now also depend on the RPT of the dam's CI. This CI resulted in a substantial increase in accuracy, with little additional computational effort (20). If no dam information was available, the original CI formula would be used (21). In July 1981, this was changed so that if the dam's CI was unavailable, half of the PD of the maternal grandsire would be used in its place, when possible; this also would affect w (21).

One additional revision has been made. MCC evaluations

are computed with a fixed genetic base, allowing PD or CI calculated at different times to be compared directly. In 1984, the genetic base for PD and CI was changed, so that the average PD of sires of cows calving for the first time in 1982 was set to zero (21). The CI formula was adjusted to account for this base change, resulting in

$$CI82 = .5[w(MCD + ADC_y) + (1-w)(PD82_{sire} + CI82_{dam})]$$

ADC_y was an adjustment for genetic merit of dams of CTP, where the subscript y is the birth year of the cow. ADC varies by birth year to account not only for the base change but also for differences in merit of dams of CTP over time (21). Merit of dams of CTP had not been considered previously in CI, and as a result cows had generally been underevaluated relative to bulls (21). ADC puts CI back on the same genetic base as PD. If there was no information on the dam, the CI would be computed as

$$CI82 = .5[w(MCD + ADC_y) + (1-w)(PD82_{sire} + ADC_{y-5})]$$

ADC_{y-5} , the ADC for 5 years prior to the birth of the cow, was used in place of the dam's CI, and assumes the dam was 5 years old when the cow was born (22).

Repeatability of CI, analogous to RPT of PD, is a measure of the reliability or accuracy of the CI. As a cow gains more records, along with accurate pedigree information, the RPT of her CI can approach about .55. This is much lower than RPT of PD, which can approach 1, making

CI less reliable measures of genetic merit than PD.

Any error in CI could affect its accuracy. As a result, cows could be misranked compared to their true generic merits, and thus the best cows would not necessarily be chosen as bull mothers. One potential source of error is the herd the cow is in. The environmental and genetic levels of the herd are adjusted for in calculating the MCD. These adjustments are additive, but there may be other effects of the herd that are nonadditive in nature which would not be removed. Bereskin and Freeman (1) found that the herd-year-season (HYS) component of variance, as a fraction of the variation within HYS, was reduced when records were deviated from a Regressed Adjusted Herdmate Average, so the deviation did remove much of the effects of HYS. However, they noted that the deviation may not remove all biases. Herds differ from each other for both means and variation for production, MCD, and CI. The differences in variation, in particular, may not be accounted for adequately.

Adjustment of CI for these other herd effects may be possible. The appropriate adjustment to be made would depend on the nature of these herd effects, whether they are genetic or environmental. Many researchers have examined the extent to which differences among herds for means and variances are genetic or environmental.

Genetic differences among herds

Differences among herds could be expected to be partly genetic. One reason is that cows within a herd are related to one another. Freeman and Henderson (10) found an average additive relationship of .040 for cows within the Holstein herds examined. The relationship results in a genetic covariance among cows in a herd, and thus is a cause of genetic variation among herds. In addition, cows within a herd are subject to similar selection pressure and sire usage, resulting in genetic differences among herds (10,19,30).

Genetic variation may also be influenced by sires used in the herds. First, herds have different numbers of sires used with different averages for genetic merit (15,31). As a result, there could be different genetic variabilities from one herd to the next. Second, variances of daughter records are not homogeneous across sire groups (5,12,32,33,35). Johnson (12), in 1945, concluded that the sire had only a small effect on the uniformity of his daughters, while the herd was much more important. However, this was prior to widespread use of artificial insemination (AI) and frozen semen, which allowed bulls to be used in large numbers of herds. Later researchers came to different conclusions. Based on repeatabilities, Van Vleck (32) suggested that 40-60% of differences in variance of daughter

records were due to effects contributed by the sire. Clay et al. (5) reported nearly equal contributions of the herd and the sire to daughter variability, so a considerable part of the variability was associated with the sire. They also found a low to moderate h^2 of daughter variance, so daughter variability is determined partly by the sire.

Many researchers have attempted to quantify the fraction of differences among herds that is genetic. Estimates have varied for different populations, and have had a fairly wide range.

At the low end of the range, Robertson and Rendel (27) concluded that little of the variation between herds was genetic. Pirchner and Lush (18) found h^2 of herd differences for fat yield to be about .10 with large standard errors, so differences among herd averages were only slightly caused by genetic differences among the herds. In Canada, only 2.05% of herd differences were found to be genetic (29). For herds in England, Wiener (36) found that $24 \pm 18\%$ of variation between herds was due to genetics, and suggested that nearly all of the differences were environmentally caused. There were breed differences, however, and a genetic cause of differences would be more likely for Friesians than for Ayrshires. Miller (16) also found breed differences in the h^2 of herd average. Less of the differences among herds were genetic for Holsteins than

for Jerseys. Morillo and Legates (17) compared herds on the Estimated Breeding Value of sires produced in the herd but tested elsewhere. The genetic portion of herd differences was found to be small but real.

Brumby (2) examined Jersey herds in New Zealand. These cows were selected for fat yield, and feeding was by grazing only. The high production group of herds was more genetically diverse than the low group, but the variation of heifers was higher in the low group, likely due to a genotype by milking technique interaction. For milk yield, the difference between the high and low groups was nearly all due to management. However, for fat yield, 10-17% of differences between herds were genetic.

Other researchers have found a similar fraction of differences among herds to be genetic. Plum (19) suggested that up to 40% of differences among herds for fat yield may be genetically caused. Henderson et al. (11) found the intrasire regression of daughter record on CTP herd average to be .6. This regression approaches 1 if there is no genetic relationship among herdmates, and approaches .5 as herdmates are more closely related; thus a regression of .6 implies that some of the differences among herds are genetic. Mao et al. (14) reported a pooled estimate of 17% for the percent of total variance among herds due to additive genetic causes. They also noted that the relative

herd genetic variance was declining over time, so herds were becoming more homogeneous genetically and/or more heterogeneous environmentally over time. Finally, Spike and Freeman (31) found that 10% of the variation associated with HYS was genetic.

In addition, genetic variation and h^2 have been found to vary with herd yield. Legates (13) divided herds into 5 production levels and calculated intra-herd-sire h^2 by daughter-dam regression. For Jerseys, h^2 increased as herd level increased. This was seen for Holsteins also, except for the highest herd level, where h^2 declined. Guernseys showed no trend. However, none of these h^2 were different from the pooled h^2 for the breed. Burnside and Rennie (3) calculated intraherd h^2 from the correlation among paternal half sibs (PHS), for 7 herd levels. Heritabilities tended to increase as herd level increased, with the h^2 fitting a quadratic curve, with h^2 lowest at both extremes. Sire rank was the same at all herd levels. Danell (6) examined first lactation Swedish Red and White cows at 3 levels of production. Genetic variation increased as herd level increased, and genetic standard deviations for herds were more variable from one year to the next at the high level. Heritabilities also increased as herd level increased. Sires ranked the same at all herd levels.

Powell and Norman (23) found the within herd regression

of first lactation milk yield on sire PD to be higher for high yield herds than for low yield herds. This could be explained by higher h^2 and/or higher variance in the high yield herds. Holstein herds were stratified by herd yield. Heritabilities of first lactation yield were calculated from the correlation among PHS and from the regression of daughter MCD on dam MCD within sire of the daughter. Heritabilities were found to increase with herd average yield; daughter-dam h^2 increased 50% and PHS h^2 doubled.

Thus at least some of the differences among herds are genetic in nature. However, most of the differences in variation would be environmental.

Environmental differences among herds

Phenotypic variance has been found to increase as herd level increased (6,13,23), and the correlation between herd mean and variance was reported to be .46 (13). Powell et al. (26) divided herds into 5 discontinuous levels for milk yield and 5 levels for PD milk of sires used in the herd. Average MCD increased as PD increased, and increased slightly as herd average increased within PD level, so PD may not be a sufficient measure of the genetic level of the herd. Within herd standard deviation was similar within yield classes across PD, but increased as yield class increased within all PD levels. It appears that much of

this increased variation would be environmental rather than genetic.

Differences in variation among herds will affect the percent of the herd designated elite. Herds with high variation (high σ herds) would have the most cows with CI high enough to be on the elite list. When differences in variation are environmentally caused, cows in high σ herds would be called elite, but they would not necessarily be better genetically than cows from low σ herds.

Powell et al. (26), with herds stratified by yield and PD of sires, examined the percent of elite cows in the herds. If environmental variation has no effect on CI, percent elite should be the same for all yield levels within a PD class. However, the percent elite cows was found to increase not only as PD increased but also as yield increased. High PD-high yield herds had 5.4% elite cows, while high PD-low yield herds had only .2% elite cows. Average yield of the herd was as important as average CI in explaining percent elite. Thus environmental variation, which increased as yield increased, had an effect on CI.

Everett et al. (8) stratified herds by within herd variation. Low σ herds had the highest percent AI cows and the most years on Dairy Herd Improvement testing, so they should be better genetically than high σ herds. However, low σ herds had the lowest percent elite cows, .2% elite

compared to 10% elite in the highest σ herds. In addition, bulls at Eastern AI Cooperative were divided into two groups based on the variation of the herds they came from. Bulls from low σ herds had higher Northeast AI Sire Comparisons than those from high σ herds. It appeared that low σ herds were genetically superior to high σ herds, although they had fewer cows on the elite list.

Adjustment of Cow Indexes

CI can be adjusted to remove these effects of herd variation. Because some of the differences among herds for variation appear to be genetic, records of cows in high σ herds should be weighted more heavily than records made in low σ herds. Heritability increases as herd yield increases, so it has been suggested (26) that a higher h^2 could be used for the higher producing herds. Herd production and variation are positively correlated, so this is roughly equivalent to using higher h^2 in higher σ herds. This will affect the index weights, such that, in high σ herds, more weight is given to the cow's own records and less to the pedigree.

However, most of the differences among herds appears to be environmental. Records in high σ herds should then be adjusted so the resulting σ would be lower, and records in low σ herds adjusted so the resulting σ would be higher.

Ways to make the adjustment include standardizing records to a common within herd variance, and log transformation of records. These would not affect the index weights, and thus would not affect the pedigree portion of the CI, but would affect the MCD that is multiplied by that weight.

Differences among herds for variation are likely partly genetic and partly environmental, not either alone. The two types of adjustments, for genetic differences and for environmental differences, can both be considered valid, but they have opposing effects. A combination of the two types may be the method of adjustment that would work best to remove herd effects.

MATERIALS AND METHODS

Current Cow Indexes

Lactation records of Holstein and Jersey cows born after January 1, 1964, were obtained from the Animal Improvement Programs Laboratory, United States Department of Agriculture (USDA). Records were all those available for Jerseys and a sample of about 10% for Holsteins, the latter including all records made in herds with a herd code ending in "4." In the records, production of the cow and CTP were expressed as 305 day, 2X, mature equivalent, and information on CTP and CTP sires were weighted averages, weighted by the amount of information available on each CTP. Numbers of cows and lactations are summarized in Table 1.

Several edits of the data were made. Records designated as not usable for sire summary, as well as records with negative or zero cow or CTP production, were deleted. All usable lactations of a cow were included in calculations.

MCD for each lactation was computed as the cow's record minus the average of her modified CTP plus the average PD of CTP sires. Overall MCD for the cow was a weighted average of these lactation MCD. LACTWT was the weighting used for this, and was calculated as described in (7). CI82 was computed as

Table 1. Numbers of lactations, herd-years, and cows.

	Holsteins	Jerseys
<hr/>		
Lactations:		
original data	1,612,453	1,162,578
after edits on records	1,575,554	1,123,403
Herd-years:		
after edits on records	48,659	34,808
Cows:		
after edits on records	631,283	410,347
with Cow Index	581,519	352,758
daughter-dam pairs	229,366	175,046
<hr/>		

$$CI82 = .5[w(MCD + ADC_y) + (1-w)(PD82_{sire} + CI82_{dam})]$$

or as

$$CI82 = .5[w(MCD + ADC_y) + (1-w)(PD82_{sire} + ADC_{y-5})]$$

when the dam was not in the data set. Note that when the dam was not in the data set, no maternal grandsire identification was available, and thus half of his PD could not be used in place of the dam's CI in calculations. Index weights w and $1-w$ were calculated as described in (20), and depended on the h^2 of milk yield (.20), the sum of LACTWT for the cow's records, and the RPT of the sire's PD and the dam's CI. RPT of CI was also calculated as described in (20), and depended on w and the RPT of the sire's PD and the dam's CI. PD82 of sires were obtained separately from USDA. Any cows without this sire information were deleted from the data set. As a result, CI were computed for 581,519 Holsteins and 352,758 Jerseys.

The dam's CI was evaluated as a predictor of her daughter's MCD by examining regressions of daughter MCD on dam CI. Of interest was how well high index cows predicted their daughter's performance compared to average or below average cows. If high CI are due in part to the environment, rather than genetics, they would not predict daughter performance as well as average CI which better reflect true genetic differences. Also, CI of dams may predict performance of daughters in the same herd better

than that of daughters in different herds, because they would be subject to similar herd conditions, including within herd variance.

Regressions of daughter MCD on dam CI were calculated with the sire of the daughter absorbed. The regression coefficient theoretically should equal 1.0, and was used as a measure of how well the dam's CI predicted her daughter's performance. Squared multiple correlations (R^2) for various groups cannot be compared directly across groups, because groups contained different numbers of observations.

Dams were divided into various groups for calculation of these regressions, to make comparisons between groups. The groupings made were:

1. Daughter-dam pairs in the same herd were compared to those in different herds.
2. Dams were divided into 4 groups by magnitude of their CI, which would be equivalent to truncation selection on dam CI.
3. Dams were classified into 3 categories for both herd μ (M) and herd σ (S) for average production of modified CTP (MCA). Herds were designated as above, at, or below average, and there were spacings between the categories (categories were discontinuous). Magnitude of spacings were 320 kg in μ and 80 kg in σ for Holsteins, and 225 kg in μ and 60 kg in σ for Jerseys. Spacings were smaller

for Jerseys because magnitude and ranges of herd μ and σ were smaller than for Holsteins. Dams in herds with fewer than 10 cows were deleted, because herd σ based on such small numbers would be unreliable. In addition, dams were designated as being above or below average for birth-year-adjusted CI (2 categories for D). Birth-year-adjusted CI were used to remove genetic trend. Dams born in the 1960's have lower CI than dams born in the 1970's because of genetic trend. With unadjusted CI, older dams would be called below average and younger dams would be above average. Birth-year-adjusted CI were used to more adequately designate which cows were above or below herd average when their records were made. Dams were grouped based on these M and S categories, with and without the additional D classification, both together (MxS groups) and separately (marginal M or S groups).

Heritability at levels of herd mean and variance

One potential adjustment to CI would involve varying h^2 as herd μ changes. An adjustment of this type was attempted by Powell et al. (26). Their procedure was to divide the cow's MCA by 7500, and multiply the result by the current h^2 of .20 to give the new h^2 to use for that cow. It was uncertain whether 7500 was an appropriate value to use for this study. Also, this value was suggested for Holsteins,

and a value for Jerseys would likely be very different. A better idea of what the adjustment should be was needed for both breeds. In addition, changes in h^2 as herd variation increases have not been examined by other researchers. Therefore, h^2 of milk yield were computed for 3 levels of herd μ and 3 levels of herd σ for MCA, for both Holsteins and Jerseys. Having more than 3 levels would have been desirable to better examine h^2 changes, but this was not feasible due to prohibitive computer costs.

Herd μ and σ were calculated using MCA from all usable records of cows. Data for h^2 computations were first usable records which were initiated prior to 40 months of age. Cows in herds with fewer than 10 cows were deleted in order to have more reliable estimates of herd variation.

Cows were grouped by herd μ and σ separately. Herds were designated as low, average, or high for μ and σ of MCA. Initial numbers of sires in groups were too large for computations. Edits were first made by constricting the ranges of herd μ and σ for the groups, increasing the spacing between groups, to remove cows. An alternate method for reducing numbers would be to increase the number of daughters/sire required for a sire to remain in the data set. However, it was felt that this would result in a more selected data set, which could have an effect on the analysis. Therefore, numbers were first reduced to a

reasonable amount by changing the ranges of herd μ and σ . Then at least 25 daughters/sire for Holsteins and 20 daughters/sire for Jerseys were required for a sire to be included in h^2 calculations. It was felt these values were small enough for selection not to be much of a factor but large enough to give accurate estimates for each sire. As a result of edits, there were no more than about 400 sires in each group, which was nearing computational limits.

Paternal half-sib h^2 for milk yield were estimated using a mixed model including fixed effect of herd-year and random effects of sire and error. Herd-years were absorbed, and sire and error variance components were used to estimate h^2 .

Adjustment of Cow Indexes

Several adjustments of CI were attempted. These were:

1. Standardization of records to a common within herd variance. This adjustment for within herd variance assumes differences among herds for variation are environmentally caused. This adjustment was made to the deviation (DEV) of a cow's record from the average of her CTP.

DEV was adjusted instead of MCD, because MCD contains DEV plus the genetic merit of CTP sires. The genetic merit of sires should not be adjusted, because it is a measure of

the genetic merit of the animals to which the cow is being compared. Adjusting MCD would affect genetic differences among cows, while the adjustment is trying to remove environmental effects. Therefore it would be more appropriate to adjust DEV, rather than MCD, and then to add the genetic merit of sires to adjusted DEV to form the new MCD.

The adjustment was

$$DEV' = \sigma * (DEV - \mu_{HY})/\sigma_{HY} + \mu_{HY}$$

where μ_{HY} = herd-year mean for DEV

σ_{HY} = within herd-year standard deviation for DEV

σ = overall within herd-year standard deviation for DEV.

Subtracting μ_{HY} from DEV and dividing by σ_{HY} standardizes the record, expressing it as the number of σ_{HY} units above or below herd-year average. This is multiplied by σ , which scales the record by the overall within herd-year σ for all herds. Adding μ_{HY} yields a form similar to DEV as it is used in the current CI system. As a result of the adjustment, each herd's average remains unchanged (μ_{HY}), and all herd-year variances will be changed to a constant σ^2 .

Ideally, DEV might be adjusted to a common variance within CTP group and year, or a variance of CTP in the herd for that year. This would be similar to herd-year-season variance. However, this would result in a problem with

small numbers. Some cows have very few CTP in a given year, and these variances would be unreliable. Use of herd-year variance, the variance of all cows in the herd with records that year, would result in more practical numbers, and was the variance chosen for this adjustment. It assumes that the variance is constant across all seasons and across all ages in the same herd and year; i.e. that age adjusted records of cows calving in certain months are not more variable in production than those calving at other times, and that age adjusted records of cows of different ages are similar in variability.

Herd-year μ and σ for DEV were calculated from all usable lactations made in each herd-year. Overall within herd-year σ was the average σ for DEV for all herd-years with at least 10 cows, and was 1247.8 kg for Holsteins and 867.3 kg for Jerseys.

Individual lactation DEV were adjusted, and average PD of CTP sires was added to give MCD. These MCD were combined in the usual way, as described in the previous section, to calculate each cow's overall MCD and CI.

2. Log transformation of records. This is a second way to adjust for within herd variance, which also assumes differences among herds for variation are environmentally caused. In addition, because it adjusts for variation indirectly by using herd averages, using a multiplicative

model, it is assuming that the correlation between herd mean and standard deviation for production is 1.0.

A log transformation adjustment is used in the Northeast AI Sire Comparison (NEAISC) procedure. Records are transformed using natural logs, and are untransformed at the end of the sire evaluation procedure using the average production of 2 year olds that freshened in 1982 (9); the genetic merit of these 2 year olds is the genetic base for the NEAISC. The analogous method for use in MCC procedures would be to first calculate

$$R = \ln(\text{Record}) - \ln(\text{CTP Avg}) + \ln(\text{AVG})$$

where Record = cow's record

CTP Avg = average of CTP

AVG = the equivalent of the NEAISC's average production level of 2 year olds freshening in 1982.

The antilog of R is the adjusted production record for the cow. AVG is subtracted from this, and the resulting value is DEV", used in place of DEV in the MCD. This procedure is equivalent to

$$\text{DEV}'' = \text{AVG} * \text{Record} / \text{CTP Avg} - \text{AVG}.$$

Before this could be done, a value for AVG needed to be determined. It was decided that the appropriate AVG would make the variance of DEV" equal to the variance of DEV, the unadjusted deviation. So

$$\text{Var}(\text{AVG} * \text{Record} / \text{CTP Avg} - \text{AVG}) = \text{Var}(\text{Record} - \text{CTP Avg})$$

$$\text{or } \text{AVG}^2 * \text{Var}(\text{Record} / \text{CTP Avg}) = \text{Var}(\text{Record} - \text{CTP Avg}).$$

The two variances were computed from all usable records of cows. Resulting AVG were 7317.9 kg for Holsteins and 4653.9 kg for Jerseys.

Individual lactation DEV were adjusted, and average PD of CTP sires was added to give MCD. These MCD were combined in the usual way, as described in the previous section, to calculate each cow's overall MCD and CI.

3. Varying h^2 with the cow's MCA. This adjusts for changes in h^2 as herd average changes. It assumes some of the differences among herds for their averages are genetic in nature.

Adjustment was by a regression, predicting h^2 at a given level of production. For Jerseys, the regression equation was determined based on the h^2 calculated in this study. However, for Holsteins, h^2 results were very unlike those from previous studies. Therefore values from the literature (3,6,13,23) were used. Regressions of h^2 on herd level were calculated for each study's h^2 estimates, and the coefficients were averaged to give one regression coefficient to use in the adjustment. Intercepts of the regression lines for each breed were the values which gave h^2 of .20 at average MCA, because .20 is the h^2 used in current CI calculations. Equations used for determining h^2

for the adjustment were:

$$h^2 = .00001416 * MMCA + .0955 \quad \text{for Holsteins, and}$$

$$h^2 = .00001684 * MMCA + .1197 \quad \text{for Jerseys,}$$

where MMCA is the average MCA for the cow. MMCA is a value for the cow, not for the herd, so h^2 could be different for different cows in the same herd. These h^2 were used in calculating w in the CI.

4. Varying h^2 with σ of MCA for the herd. This adjusts for changes in h^2 as herd variation changes. It assumes some of the differences among herds for variation are genetic.

This h^2 adjustment was also by a regression. Heritabilities computed in this study were used to determine the equations. Again, the intercept of the regression line was the value which gave h^2 of .20 at the average level of herd σ for MCA. Equations used for determining h^2 for the adjustment were:

$$h^2 = .00002619 * SMCA + .1837 \quad \text{for Holsteins, and}$$

$$h^2 = .00014199 * SMCA + .1311 \quad \text{for Jerseys,}$$

where SMCA was the standard deviation of MCA for the herd. SMCA were computed from all usable records of cows in the herd. Thus h^2 was the same for all cows in a herd. These h^2 were used in calculating w in the CI.

5. Combinations of the adjustments. The four adjustments discussed can be classified in two categories. The first two affect DEV and MCD, and the other two affect h^2 and w . As well as using each adjustment alone to calculate CI, the four combinations of adjustments were used. These were:

- 1) h^2 by MMCA + standardized DEV
- 2) h^2 by MMCA + log transformation
- 3) h^2 by SMCA + standardized DEV
- 4) h^2 by SMCA + log transformation.

For all adjustments, records made in herd-years with fewer than 10 cows were deleted to have reliable measures of herd-year variation. This edit was required only for the standardized DEV adjustment, but was used for all adjustments so resulting CI and MCD could be compared. In addition, the same data were used to compute current CI for comparison. All MCD and CI were calculated for 563,853 Holsteins and 339,568 Jerseys.

From a practical standpoint, the log transformation and h^2 based on the average of CTP are the easiest to implement. They use information which currently is incorporated in MCD, and which therefore is readily available on all cows, to make the adjustment. The standardized DEV and h^2 based on herd variance adjustments, however, require μ and σ for the herd or herd-year to be computed first. This makes them

more difficult and more costly to implement for national CI evaluations.

Comparison of Cow Index adjustments

The relative performance of each of the nine CI types was examined by comparing R^2 and regression coefficients from various regressions of offspring MCD on dam CI. Several regression equations were fit for each of the nine CI types. These regressions resulted from combinations of three offspring MCD (all daughters, sons, and daughters of high CI dams), two regression models (linear only and linear plus quadratic effects of dam's CI), and two options of using either individual observations or group averages for CI and offspring MCD in regression models. Regressions of average offspring MCD on average dam CI for groups of relatively narrow range in CI (1, 5, and 10 kg for all daughters, daughters of high CI dams, and sons, respectively) were to examine accuracy of predicting average offspring MCD from CI of dams with similar estimated transmitting abilities. These analyses primarily were to compare R^2 rather than regression coefficients.

Regressions of individual daughter MCD on individual dam CI, with sire of daughter absorbed, were calculated for each CI type. The appropriate daughter MCD was used for each CI type; e.g. if CI with h^2 of .20 and log transformed

MCD was being examined, then the daughter's log transformed MCD was used in calculating the regression. Regression coefficients and R^2 were used to compare the 9 CI types.

Average dam CI also was used to predict average daughter MCD. Each dam CI group consisted of dams which had the same CI, rounded to the nearest kg. Because dams in these groups had identical CI (to the nearest kg), the situation was one of predicting the average MCD of offspring of dams with identical transmitting ability. Groups were formed separately for each CI type. Dams at the extremes, more than 3.5 standard deviations above or below the mean, were put into one group for each extreme. For each group, dam CI, the appropriate daughter MCD, and sire PD were averaged. Two multiple regression models were used to predict daughter MCD. In the first model, average sire PD and average dam CI were the independent variables. In the second model, the quadratic form of dam CI, averaged for the group, was also included. Regression coefficients were examined, and R^2 were used to compare the 9 CI types. A t-test for differences between simple correlations was used to compare, pairwise, the square roots of R^2 . It was assumed that if these R were significantly different, then the R^2 were also significantly different.

The ability of CI to predict individual MCD of sons was examined. MCD was used rather than PD because of part-whole

relationships between son PD and sire PD (sire PD is included in the son's PD) and between son PD and dam CI (PD of the dam's sire, the maternal grandsire of the son, is in both evaluations). Son information was the latest USDA MCC sire evaluation through July 1984. MCD of sons was not directly available, but could be calculated from the components of the PD. The PD is calculated as

$$PD = RPT * MCD + (1 - RPT) * (\text{Ancestor Merit}).$$

MCD was obtained as

$$MCD = [PD - (1 - RPT) * (\text{Ancestor Merit})] / RPT.$$

There were 2971 Holstein and 1796 Jersey son-dam pairs available. These dams should be the best cows of the breed, for some combination of selection criteria. Regression of son MCD on dam CI, with sire of son absorbed, were computed for each CI type. Son MCD were those calculated by USDA, and were not adjusted in any way. Regression coefficients and R^2 were used to compare the 9 CI types.

Additionally, average dam CI was used to predict average son MCD for all CI types. The procedure used was similar to that described above for daughter-dam pairs, except that groups were 10 kg of dam CI in size, and extreme dam CI were defined as those more than 2.0 standard deviations from the mean. Also, some sons had sires with no valid PD information available, and these were deleted from the data set for this analysis. As a result, there were

2921 Holstein and 1737 Jersey son-dam pairs used for averages. The same two regression models were used, in this case to predict average son MCD. R^2 were used to compare the CI types, and regression coefficients were also examined.

A further examination was made of elite cows, those which could have been chosen as dams of bulls to enter AI service. Prediction of daughter MCD from elite dams was to determine whether any differences between daughter-dam and son-dam relationships were from using son MCD as the dependent variable, or from using CI of selected, elite dams as the independent variable. Dams forming this data set had CI at least 2.0 standard deviations above the average CI for their year of birth. There were 6844 Holstein and 4379 Jersey daughter-dam pairs available. Dams were 1.2% of all cows with CI, and 3% of all daughter-dam pairs.

Regressions of daughter MCD on dam CI, with sire of daughter absorbed, were computed for each CI type, using the appropriate daughter MCD for that CI. Again, as described previously, average daughter MCD was predicted from average sire PD and average dam CI, using two regression models. Here 5 kg dam CI groups were formed, and extreme dam CI were defined as those more than 3.0 standard deviations above average (because of the truncation selection used, no CI were 3.0 standard deviations below average; the distribution

of CI was skewed). R^2 and regression coefficients were used to compare the CI types.

RESULTS AND DISCUSSION

Current Cow Indexes

Means and standard deviations for cows and their CTP for lactations usable in calculations are listed in Table 2 for both Holsteins and Jerseys. Standard deviations for days in milk and milk yield were lower for CTP than for cows, because standard deviations for cows were for individual records, while those for CTP were for means.

Cow milk yield was slightly lower than CTP yield for both breeds. Mean PD of CTP sires was negative for both breeds because of the many older cows included in the data set. Their CTP would have old sires whose PD would be expected to be negative relative to the 1982 genetic base due to genetic trend since they were born. Average RPT of CTP sires was higher for Holsteins. For both breeds, cows had on average about 24 modified CTP (number of true CTP plus 1) sired by 12 to 13 different bulls.

Means for CI are in Table 3 for all cows with CI and for daughter-dam pairs. Holsteins averaged 2.50 records, while Jerseys averaged slightly higher. In both breeds, cows had up to 15 records. MCD and CI had negative means for both breeds, and RPT of CI averaged about 40%.

For daughter-dam pairs, daughters had slightly fewer records than the average for all cows, while MCD and CI were

Table 2. Means and standard deviations (SD) of measures for lactations after edits on records.

Measure ^a	Holsteins		Jerseys	
	Mean	SD	Mean	SD
Cow Days in Milk	275.41	59.59	272.45	61.69
CTP Days in Milk	274.65	28.96	271.59	30.63
Cow ME Milk	7357.56	1626.13	4721.35	1164.55
CTP ME Milk	7380.18	1105.80	4736.56	811.59
CTP Sire PD Milk	-288.16	191.12	-276.16	183.85
CTP Sire RPT	82.08	17.02	69.05	18.83
No. Modified CTP	23.28	32.92	25.24	28.00
No. CTP Sires	13.36	12.92	12.08	9.85
N	1,575,554		1,123,403	

^aCTP=Contemporary, ME=Mature Equivalent, PD=Predicted Difference, RPT=Repeatability; milk values are in kg.

Table 3. Means and standard deviations (SD) for cows with Cow Indexes (CI) and for daughter-dam pairs.

Measure ^a	Holsteins		Jerseys	
	Mean	SD	Mean	SD
All cows:				
No. records	2.50	1.66	2.75	1.89
MCD	-385.01	1209.14	-334.96	850.34
CI	-335.19	210.33	-323.46	187.39
RPT of CI	40.54	6.59	40.15	7.09
N	581,519		352,758	
Pairs:				
Dau No. records	2.46	1.60	2.67	1.78
Dau MCD	-316.21	1233.15	-267.76	869.10
Dau CI	-285.74	225.28	-264.13	194.02
Dau RPT of CI	44.89	5.39	43.66	6.02
Dam No. records	4.07	2.10	4.44	2.32
Dam MCD	-307.94	1036.93	-264.82	731.39
Dam CI	-370.30	193.92	-347.62	169.40
Dam RPT of CI	43.77	5.62	43.24	6.11
N	229,366		175,046	

^aMCD=Modified Contemporary Deviation, RPT=Repeatability; milk values are in kg.

higher and CI had a higher RPT. Their dams averaged slightly more than 4 records, with MCD and RPT similar to their daughters but with lower CI.

Regressions of daughter MCD on dam CI with sire of daughter absorbed are in Table 4. For Holsteins, the regression coefficient was 1.154, and was significantly different ($P < .01$) from the theoretical value of 1.0. The coefficient was similar when daughters and dams were in the same herd and larger when they were in different herds. Both coefficients were different from 1.0, but neither was different from the coefficient for all cows. Thus for Holsteins, when dams had negative CI (as most did), their daughters' MCD were less than expected based on the theoretical regression of 1.0, and when dams had positive CI, their daughters' MCD were higher than theoretically expected.

For Jerseys, the regression coefficient was 1.007, much lower than for Holsteins, and was not different from 1.0 ($P > .05$). As for Holsteins, the coefficient was similar to that for all cows when pairs were in the same herd and larger when pairs were in different herds. However, for Jerseys none of the coefficients were different from 1.0 ($P > .05$). Thus daughters' MCD were close to what the dams' CI would predict them to be, based on the theoretical value of the regression.

Table 4. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index with sire of daughter absorbed.

Group		Holsteins	Jerseys
All cows	b	1.154 ^a	1.007
	SE	.014	.013
	N	229,366	175,046
Same herd	b	1.151 ^a	1.002
	SE	.014	.015
	N	218,916	127,924
Different herds	b	1.291 ^a	1.045
	SE	.073	.026
	N	10,450	47,122

^aSignificantly different from 1.0 ($P < .01$).

^bSignificantly different from 1.0 ($P < .05$).

For both breeds, the coefficient differed more from 1.0 when daughters were in different herds than their dams, although regressions for pairs in different herds were not different ($P > .05$) from the other regression coefficients for the breed. Coefficients more different from expected values for pairs in different herds could be anticipated if herd mean or variation have an effect on CI and MCD. Daughter and dam records made in the same herd would have been subject to the same herd conditions, while records made in different herds may have been affected by very different herd conditions. CI of dams in one herd may not predict MCD of daughters in other herds as well as if the daughters were in the same herd as the dam. Although regression coefficients are expected to be more different for pairs in different herds, the expected direction of the difference is debatable. Powell et al. (25) found the correlation between daughter and dam MCD to be higher in the same herd than in different herds. This implies that the regression coefficient should be lower in different herds. In this study, however, the coefficient was higher in different herds. This may be due to pairs in different herds being a special group of cows. One of the pair had been sold into another herd, so these were likely superior cows (for some trait), and there would be the potential for preferential treatment of both daughters and dams. As a result, the

correlation, and thus the regression, could be higher for pairs in different herds.

Regressions with dams grouped by their CI are in Table 5. For Holsteins, the groups near the mean (groups 2 and 3) had regression coefficients that were not different ($P > .05$) from 1.0, while for the extreme groups coefficients were larger and were different ($P < .05$) from 1.0. Thus a problem with CI seemed to exist for Holstein dams with extreme CI values. Many dams in group 4 (high CI) had positive CI, and MCD of their daughters were greater than indicated by dam's CI. Conversely, dams in group 1 (low CI) had negative CI, and MCD of their daughters were lower than expected from their dams' CI. Overall for Holsteins, the range of daughters' MCD was greater than expected from the range of dams' CI, suggesting that CI generally were conservative (closer to zero) estimates of dams' genetic merit. These results might be expected from computing CI using h^2 (.20) less than the true h^2 , by failure to use h^2 appropriate to specific subpopulations of the data (if differences in true h^2 exist), or by failure to account for effects of differences in herd variation on dams' CI or daughters' MCD. For Jerseys, regressions were not different ($P > .05$) from 1.0 for any of the CI groups. This result suggests either that h^2 is constant at about .20 throughout the Jersey population, or that there are counteracting effects of

Table 5. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index (CI) with sire of daughter absorbed, and dams grouped by CI.

Group ^a		Holsteins	Jerseys
1	Dam CI	<-506	<-466
	b	1.125 ^c	1.014
	SE	.058	.056
	N	56,205	45,215
2	Dam CI	-506 to -370	-466 to -348
	b	1.047	1.050
	SE	.125	.114
	N	61,048	44,926
3	Dam CI	-370 to -235	-348 to -229
	b	.961	1.011
	SE	.136	.122
	N	57,424	42,480
4	Dam CI	>-235	>-229
	b	1.345 ^b	1.059
	SE	.056	.050
	N	54,689	42,424

^aGroups 1 and 2 are below the mean and groups 3 and 4 are above the mean; CI values are in kg.

^bSignificantly different from 1.0 (P<.01).

^cSignificantly different from 1.0 (P<.05).

varying h^2 and differences in herd variation.

Dams next were classified into 3 categories for both herd μ (M) and herd σ (S) for Modified CTP Average. Dams also were designated as being above or below herd average for CI. Dams averaged slightly negative for their deviation from herd average CI. Therefore, to have more reasonable numbers of observations in the various groups, dams whose CI exceeded this average deviation were designated "above average," while dams with CI less than the average deviation were designated "below average."

Regressions for Holstein M and S groups, including all dams, are in Table 6. It was expected that regression coefficients would increase as the M level increased, because it has been found that h^2 increases as herd average increases (3,6,13,23). This trend was only partly seen for the marginal M groups; low M had a coefficient not different ($P > .05$) from 1.0, while average and high M groups had larger coefficients that were different ($P < .01$) from 1.0 and essentially equal to each other. A consistent trend of increasing coefficients as M increased was not seen within any of the S levels, and generally the coefficient for average M was largest. For marginal S groups, coefficients increased as S increased, with all coefficients different ($P < .01$) from 1.0, and the coefficient for low S different ($P < .01$) from the other two. As S increased within the M

Table 6. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index with sire of daughter absorbed, and dams grouped by herd mean (M) and standard deviation (S) for Modified Contemporary Average, for Holsteins.

		S low (<515)	S average (595 to 710)	S high (>790)	Across all S
M low (<6915)	b	1.034	1.076	1.298 ^b	1.030
	SE	.048	.065	.119	.030
	N	19,690	11,746	4,410	52,677
M average (7235 to 7715)	b	1.158 ^a	1.265 ^a	1.262 ^a	1.205 ^a
	SE	.060	.060	.062	.028
	N	13,176	13,505	13,001	58,213
M high (>8035)	b	1.140	1.109	1.259 ^a	1.200 ^a
	SE	.079	.063	.058	.030
	N	8,721	13,215	14,856	53,733
Across all M	b	1.079 ^a	1.181 ^a	1.228 ^a	
	SE	.029	.029	.032	
	N	55,239	55,683	45,882	

^aSignificantly different from 1.0 (P<.01).

^bSignificantly different from 1.0 (P<.05).

levels, the coefficient for high S was generally largest, and within low and high M levels it was the only coefficient different ($P < .05$) from 1.0.

Regression coefficients for the 9 MxS classifications indicate that problems with CI are occurring for herds with average μ and/or high σ . Regression coefficients for these herds were all larger than 1.0, so the range of daughters' MCD was greater than expected from their dams' CI, based on the theoretical value of the regression. The conservative nature of these dams' CI suggests that true h^2 is higher for these herds than the constant .20 currently used in calculations. Thus the problem at high σ suggests that true h^2 is higher in high σ herds, while a h^2 of .20 still may be appropriate for low and average herds. This implies that much of the differences among herds for variation are genetic rather than environmental, which is in contrast with results of Everett et al. (8), whose results implied differences among herds for variation were environmentally caused. The problem at average μ suggests a similar explanation of h^2 of .20 being inappropriate for this herd level. However, this implies that h^2 should be higher for average μ herds than for extreme herds, which is in contrast with previous h^2 computations (3,6,13,23), which found h^2 to increase as herd average increased.

Regressions for Holstein dams below herd average CI are

in Table 7 by categories of M and S for herd MCA. For marginal M groups, regression coefficients increased as herd average increased similar to the trend for all dams. As M increased within S levels, results were again similar to the trend for all dams, with coefficients for average M tending to be largest. For the marginal S groups, coefficients increased as S increased, as for all dams, except that here the low S coefficient was not different ($P>.05$) from 1.0. As S increased within the M levels, the coefficient for high S was largest in each case.

Regressions for Holstein dams above herd average CI are in Table 8. For marginal M groups, regression coefficients increased as herd average increased. However, there was no consistent trend as M increased within any of the S levels. For marginal S groups, coefficients increased as S increased. This was seen also within low and high M levels, but within the average M level, the average S group had the highest coefficient.

Thus, for Holsteins, a general increase was seen in regressions of daughter MCD on dam CI as either herd M or S increased. Further, the general increase in regressions affected dams both above and below herd average for CI.

Regressions for Jersey M and S groups, including all dams, are in Table 9. One previous study (13) had shown that h^2 increased as herd average increased for Jerseys as

Table 7. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index (CI) with sire of daughter absorbed, and dams grouped by herd mean (M) and standard deviation (S) for Modified Contemporary Average, for Holstein dams with CI below herd average.

		S low (<515)	S average (595 to 710)	S high (>790)	Across all S
M low (<6915)	b	1.019	1.016	1.352 ^b	.997
	SE	.080	.100	.176	.044
	N	7,647	5,492	2,325	23,217
M average (7235 to 7715)	b	1.148	1.305 ^a	1.310 ^a	1.180 ^a
	SE	.094	.080	.082	.038
	N	6,280	7,650	7,517	31,464
M high (>8035)	b	1.085	1.052	1.199 ^b	1.183 ^a
	SE	.109	.084	.081	.041
	N	4,789	7,649	8,410	30,407
Across all M	b	1.047	1.149 ^a	1.235 ^a	
	SE	.044	.040	.044	
	N	25,210	30,070	25,989	

^aSignificantly different from 1.0 (P<.01).

^bSignificantly different from 1.0 (P<.05).

Table 8. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index (CI) with sire of daughter absorbed, and dams grouped by herd mean (M) and standard deviation (S) for Modified Contemporary Average, for Holstein dams with CI above herd average.

		S low (<515)	S average (595 to 710)	S high (>790)	Across all S
M low (<6915)	b	1.038	1.148	1.425 ^b	1.042
	SE	.065	.094	.194	.041
	N	12,043	6,254	2,085	29,460
M average (7235 to 7715)	b	1.199 ^b	1.216 ^b	1.170	1.220 ^a
	SE	.084	.099	.103	.043
	N	6,896	5,855	5,484	26,749
M high (>8035)	b	1.190	1.257 ^b	1.367 ^a	1.274 ^a
	SE	.128	.107	.091	.047
	N	3,932	5,566	6,446	23,326
Across all M	b	1.111 ^a	1.225 ^a	1.258 ^a	
	SE	.040	.044	.051	
	N	30,028	25,613	19,893	

^aSignificantly different from 1.0 (P<.01).

^bSignificantly different from 1.0 (P<.05).

Table 9. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index with sire of daughter absorbed, and dams grouped by herd mean (M) and standard deviation (S) for Modified Contemporary Average, for Jerseys.

		S low (<355)	S average (415 to 530)	S high (>590)	Across all S
M low (<4400)	b	.957	.949	.996	.916 ^a
	SE	.043	.061	.146	.028
	N	18,703	9,160	2,268	41,548
M average (4625 to 5020)	b	1.048	1.090	1.019	1.017
	SE	.063	.053	.058	.026
	N	9,016	11,324	9,584	44,087
M high (>5245)	b	1.190 ^b	1.123 ^b	1.073	1.088 ^a
	SE	.074	.055	.047	.028
	N	6,363	12,198	14,371	42,247
Across all M	b	1.027	1.025	1.010	
	SE	.026	.026	.031	
	N	46,340	47,974	33,094	

^aSignificantly different from 1.0 (P<.01).

^bSignificantly different from 1.0 (P<.05).

for Holsteins. Thus it was anticipated that coefficients would increase as M increased. For marginal M groups, this trend was seen, with coefficients increasing from less than 1.0 at low M to greater than 1.0 at high M. The same trend, although not as strong, was seen as M increased within the S levels. This suggests that h^2 varies with herd μ , such that h^2 of .20 is appropriate for average μ herds while lower h^2 should be used for low μ herds and higher h^2 for high μ herds. For marginal S groups, coefficients declined slightly as S increased, but none were different ($P > .05$) from 1.0. A similar trend was seen as S increased within the M levels, although for the high M level coefficients did decline as S increased.

Results for Jersey dams with CI below herd average are in Table 10 for categories of M and S for herd Modified CTP Average. For marginal M groups, the coefficient increased as M increased, as for all dams. The same trend was generally seen as M increased within the S levels, although here most coefficients were not different ($P > .05$) from 1.0. For marginal S groups, coefficients increased as S increased, with the coefficient for high S different ($P < .05$) from 1.0. This was the reverse of that seen for all dams. As S increased within the M levels, coefficients increased within low and average M and declined within the high M level, although again most coefficients were not different

Table 10. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index (CI) with sire of daughter absorbed, and dams grouped by herd mean (M) and standard deviation (S) for Modified Contemporary Average, for Jersey dams with CI below herd average.

		S low (<355)	S average (415 to 530)	S high (>590)	Across all S
M low (<4400)	b	.848 ^b	.887	1.031	.886 ^b
	SE	.076	.092	.234	.046
	N	6,103	4,056	971	16,074
M average (4625 to 5020)	b	1.107	1.108	1.127	1.060
	SE	.104	.078	.079	.038
	N	3,618	5,608	5,311	21,710
M high (>5245)	b	1.158	1.132	1.119	1.128 ^a
	SE	.101	.076	.064	.038
	N	3,494	6,574	7,538	22,593
Across all M	b	.985	1.028	1.095 ^b	
	SE	.042	.037	.042	
	N	18,180	23,945	17,408	

^aSignificantly different from 1.0 (P<.01).

^bSignificantly different from 1.0 (P<.05).

($P > .05$) from 1.0.

Regressions for Jersey dams above herd average for CI are in Table 11. Results were very similar to those for all Jerseys, except that the marginal low M coefficient was not different ($P > .05$) from 1.0.

In general, there appeared to be an effect of herd μ and σ for Modified CTP Average on the relationship between CI of dams and MCD of daughters for Holsteins. Regressions of daughter MCD on dam CI consistently exceeded 1.0, with an overall increase in regressions as either herd μ or σ increased. The increase in regressions affected dams with above and below herd average CI. Results suggest that h^2 used in computing CI for Holsteins is less than the true h^2 , and that h^2 may vary with herd μ and σ , specifically with highest h^2 being appropriate for average μ or high σ herds.

Jerseys showed a strong effect of variation in herd μ for Modified CTP Average on the relationship between dam's CI and daughter's MCD, but little effect of herd σ . Thus h^2 may vary with herd μ for Jerseys. Regressions of daughter MCD on dam CI generally were less than for Holsteins, and many were not different ($P > .05$) from the expected regression of 1.0.

Heritability at levels of herd mean and variance

Heritabilities of milk yield for cows grouped by herd μ

Table 11. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation on dam Cow Index (CI) with sire of daughter absorbed, and dams grouped by herd mean (M) and standard deviation (S) for Modified Contemporary Average, for Jersey dams with CI above herd average.

		S low (<355)	S average (415 to 530)	S high (>590)	Across all S
M low (<4400)	b	1.016	.969	1.103	.930
	SE	.055	.087	.204	.037
	N	12,600	5,104	1,297	25,474
M average (4625 to 5020)	b	1.043	1.142	.940	1.002
	SE	.083	.080	.096	.039
	N	5,398	5,716	4,273	22,377
M high (>5245)	b	1.317 ^a	1.212 ^b	1.028	1.094 ^b
	SE	.121	.086	.075	.043
	N	2,869	5,624	6,833	19,654
Across all M	b	1.068	1.059	.962	
	SE	.035	.038	.048	
	N	28,160	24,029	15,686	

^aSignificantly different from 1.0 (P<.01).

^bSignificantly different from 1.0 (P<.05).

for MCA are in Table 12 for both breeds. High mean herds tended to be larger in size, so the number of herd-years was greater for the low mean groups than for the high mean groups.

For Holsteins, h^2 was lowest at average μ and higher at the extremes. This is the reverse of the trend seen for regressions in the previous section (Table 6), where within each level of herd σ , the regression coefficient was highest for average μ . This suggests that the trend seen for regressions is not entirely due to differences in h^2 in the herds, but also is caused by other effects of the herd average. Additionally, it may be affected somewhat by herd variance, because of a correlation between herd μ and σ . As well as being different from regression results, these h^2 are in contrast with results of previous researchers (3,6,13,23), who found h^2 to increase as herd μ increased. It is uncertain why these results are so different. There may be something peculiar about cows in the extreme herds, making h^2 for low and high groups unusual. The results may have looked more reasonable if more groups had been examined; a general increasing trend may then be seen, although the extreme groups may not follow the trend exactly. However, this does not explain the low h^2 for the average μ group.

For Jerseys, h^2 increased markedly as herd μ increased.

Table 12. Heritabilities and approximate standard errors (SE) of milk yield for Holsteins and Jerseys grouped by herd mean for Modified Contemporary Average.

	Group		
	Low	Average	High
Holsteins:			
Range (kg)	<6100	7285 to 7425	>8610
No. Cows	16,185	17,892	22,690
No. Herd-years	3,804	2,491	1,559
No. Sires	325	322	348
Heritability	.222	.163	.206
SE	.029	.021	.021
Jerseys:			
Range (kg)	<3960	4680 to 4860	>5580
No. Cows	22,717	27,227	25,316
No. Herd-years	4,373	2,688	1,638
No. Sires	357	382	292
Heritability	.246	.291	.331
SE	.027	.027	.032

This agrees with the results of a previous study (13). All three h^2 calculated were larger than the .20 used in CI calculations. The trend agreed with the trend seen for regressions (Table 9), although the regressions implied that h^2 of .20 would be appropriate for average μ .

Heritabilities of milk yield for cows grouped by herd σ for MCA are in Table 13 for both breeds. For Holsteins, h^2 increased slightly as herd σ increased. This trend was the same for regressions, although for regressions the trend was stronger. Other effects of herd σ may also have some impact on the regressions, resulting in the stronger trend.

For Jerseys, h^2 increased substantially as herd σ increased. This was unlike the results for regressions, where no trend was seen. Thus other effects of herd σ are counteracting the differences in h^2 , resulting in constant regression coefficients. If CI of Jerseys are adjusted for differences in h^2 , an additional adjustment for herd σ would appear to be necessary.

Adjustment of Cow Indexes

To simplify the discussion of CI adjustments, a system of subscripts for 'CI' will be used to describe each CI type. The first symbol in the subscript will designate the h^2 used in the calculations: - is .20 as in the current CI system, M is h^2 by mean MCA for the cow, and S is h^2 by σ of

Table 13. Heritabilities and approximate standard errors (SE) of milk yield for Holsteins and Jerseys grouped by herd standard deviation for Modified Contemporary Average.

	Group		
	Low	Average	High
Holsteins:			
Range (kg)	<405	655 to 685	>935
No. Cows	20,574	15,227	20,013
No. Herd-years	2,556	1,736	3,101
No. Sires	406	268	338
Heritability	.178	.193	.206
SE	.020	.025	.023
Jerseys:			
Range (kg)	<290	460 to 505	>675
No. Cows	24,279	15,167	24,204
No. Herd-years	2,438	1,816	2,608
No. Sires	379	247	332
Heritability	.254	.293	.371
SE	.025	.035	.035

MCA for the herd. The second symbol will designate the MCD used: - is the current MCD, σ is MCD standardized to a common within herd variance, and \ln is log transformed MCD. Thus $CI_{-,-}$ is CI as calculated currently, while $CI_{M,\ln}$ used h^2 based on mean MCA for the cow with log transformed MCD. The nine CI types are summarized in Table 14. Similarly, the three types of MCD will be described as MCD_{-} , MCD_{σ} , and MCD_{\ln} , with the subscripts as described above.

Means for all cows for the three types of MCD and for change in MCD with the adjustments are listed in Table 15 for both Holsteins and Jerseys. Mean MCD were similar for MCD_{-} and MCD_{σ} , and were lower for MCD_{\ln} . Standard deviations were highest for MCD_{-} and lowest for MCD_{σ} . This adjustment tended to adjust extreme MCD toward the mean, resulting in lower variation and a smaller range. Standard deviations for MCD_{\ln} were slightly lower than for MCD_{-} , and the lower limit of the range was closer to zero, but the upper limit of the range was extremely high, particularly for Holsteins where the upper limit of the range more than doubled in magnitude.

This was a substantial difference between the two MCD adjustments, even though both are intended to adjust for herd variation. This is because MCD_{σ} used herd variance directly, while MCD_{\ln} adjusted for herd mean and only indirectly for herd variance, with the assumption that the

Table 14. Notation used for description of usual and adjusted Cow Indexes (CI).

CI	h^2 used ^a	MCD ^b used
CI _{-, -}	.20	current
CI _{-, σ}	.20	standardized
CI _{-, ln}	.20	log transformation
CI _{M, -}	mean MCA	current
CI _{M, σ}	mean MCA	standardized
CI _{M, ln}	mean MCA	log transformation
CI _{S, -}	σ of MCA	current
CI _{S, σ}	σ of MCA	standardized
CI _{S, ln}	σ of MCA	log transformation

^aMCA=Modified Contemporary Average.

^bMCD=Modified Contemporary Deviation.

Table 15. Means, standard deviations (SD), minimum (min), and maximum (max) values for usual and adjusted Modified Contemporary Deviation (MCD), and change in MCD.^a

MCD ^b	Mean	SD	Min	Max
-----Holsteins-----				
Usual	-381.69	1209.50	-7208.56	6256.92
σ	-380.92	1135.97	-5646.31	5237.00
ln	-364.86	1193.40	-6022.89	14801.76
Actual change:				
σ	.77	235.40	-3371.41	3466.18
ln	16.83	183.20	-2130.37	9256.08
Absolute value of change:				
σ	148.15	182.93	.00	3466.18
ln	113.70	144.63	.00	9256.08
-----Jerseys-----				
Usual	-343.24	849.41	-5342.47	6639.30
σ	-342.37	796.43	-3971.92	5761.48
ln	-330.29	834.07	-4106.09	9305.09
Actual change:				
σ	.88	167.52	-3284.48	2349.73
ln	12.95	145.99	-2073.11	3311.52
Absolute value of change:				
σ	102.79	132.27	.00	3284.48
ln	90.44	115.34	.00	3311.52

^aChange=Adjusted MCD - Usual MCD; values are in kg.

^bUsual=MCD as currently calculated, σ =standardized to a common within herd variance, ln=log transformation.

correlation between mean and variance is 1.0. An example, using an extreme cow, illustrates the difference between the two methods. This cow had 1 record, producing 9362 kg, while CTP production was 2985 kg, and average PD of CTP sires was -831 kg. Thus this cow produced substantially above herd average, with MCD_{\cdot} of 5546 kg. To calculate MCD_{σ} , the required σ_{HY} for DEV was computed as 1842 kg. This was higher than σ_{HY} for the average herd, as would be expected from the large range of milk yield which apparently existed in that herd. Standardizing to a common variance will act to decrease the variation in this herd, adjusting DEV closer to zero. The resulting MCD_{σ} for this cow was 3567 kg, much lower than MCD_{\cdot} . The log transformation uses the average of CTP, 2985 kg, as the herd level. Because this is very low, it assumes the herd variance is also very low, and acts to adjust DEV farther from zero. The resulting MCD_{ln} for this cow was 14802 kg, substantially larger than MCD_{\cdot} and the largest MCD for any cow in the data set. Thus the two adjustments for MCD, although intending to do the same thing, could instead act very differently in some cases.

However, this cow is an extreme one, the exception rather than the rule. Most cows' MCD changed relatively little. Average actual change in MCD was near zero for both adjustments and both breeds, with standard deviation of

change about 210 kg for Holsteins and 155 kg for Jerseys. Absolute value of the change averaged 90 to 148 kg.

Means for the 9 CI types for all cows are in Table 16 for both breeds. Holstein CI averaged slightly lower than Jersey CI, and had larger standard deviations and ranges. Means and standard deviations were very similar for all CI types, within a breed. Ranges varied slightly for the different CI, with largest ranges for CI using MCD₋. There was less variation in CI than implied by ranges in MCD, primarily because cows with extreme MCD tended to have single records, so their MCD were weighted less heavily in calculating CI.

Means for change in CI for Holsteins are in Table 17. Actual change in CI averaged close to zero for all CI, with standard deviations less than 22 kg. Ranges varied for the different CI, with the smallest range for CI_{S,-} and largest ranges for CI_{S,ln} and CI_{-,ln}. Absolute value of change also averaged close to zero for all CI types, with all means less than 15 kg. Standard deviations were also low. Ranges were smallest for CI_{S,-} and largest for CI_{S,ln} and CI_{-,ln}. Smallest and largest ranges differed in size by about 200 kg.

Means for change in CI for Jerseys are in Table 18. Means for actual change were similar to those for Holsteins. Standard deviations were smaller than for Holsteins, but

Table 16. Means, standard deviations (SD), minimum (min), and maximum (max) values for usual and adjusted Cow Indexes (CI).

CI ^a	Mean	SD	Min	Max
-----Holsteins-----				
-, -	-334.01	210.85	-1239.25	716.93
-, σ	-333.94	206.39	-1212.49	628.73
-, ln	-332.08	209.55	-1222.83	715.04
M, -	-334.43	212.33	-1266.38	757.74
M, σ	-334.28	206.80	-1207.97	644.34
M, ln	-332.45	209.58	-1217.57	700.21
S, -	-334.05	211.05	-1242.61	737.68
S, σ	-333.97	206.47	-1213.73	629.83
S, ln	-332.11	209.67	-1224.11	718.53
-----Jerseys-----				
-, -	-322.37	187.69	-1017.60	577.80
-, σ	-322.31	184.58	-928.41	494.78
-, ln	-320.81	186.62	-1008.99	537.33
M, -	-322.61	188.28	-1017.84	621.40
M, σ	-322.51	184.62	-927.97	532.42
M, ln	-321.02	186.35	-1008.88	527.33
S, -	-322.49	187.67	-1028.06	634.22
S, σ	-322.42	184.12	-925.87	492.58
S, ln	-320.93	186.14	-1019.02	586.90

^aThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the Modified Contemporary Deviation (MCD) used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Values are in kg.

Table 17. Means, standard deviations (SD), minimum (min), and maximum (max) values for change in Cow Index (CI)^a for Holsteins.

CI ^b	Mean	SD	Min	Max
Actual change:				
- , σ	.08	21.39	-249.74	239.84
- , ln	1.93	16.69	-174.06	366.17
M, -	-.42	8.84	-184.73	103.71
M, σ	-.26	18.51	-237.66	212.70
M, ln	1.56	9.16	-93.34	174.03
S, -	-.03	2.98	-78.49	75.49
S, σ	.05	21.11	-224.80	230.50
S, ln	1.91	16.57	-174.46	372.40
Absolute value of change:				
- , σ	14.17	16.03	.00	249.74
- , ln	10.98	12.72	.00	366.17
M, -	5.50	6.93	.00	184.73
M, σ	12.32	13.82	.00	237.66
M, ln	6.22	6.90	.00	174.03
S, -	1.76	2.40	.00	78.49
S, σ	14.03	15.79	.00	230.50
S, ln	10.88	12.65	.00	372.40

^aChange=Adjusted CI - Usual CI; values are in kg.

^bThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the Modified Contemporary Deviation (MCD) used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

Table 18. Means, standard deviations (SD), minimum (min), and maximum (max) values for change in Cow Index (CI)^a for Jerseys.

CI ^b	Mean	SD	Min	Max
Actual change:				
- , σ	.06	15.89	-311.44	176.86
- , ln	1.56	13.84	-216.74	224.83
M, -	-.24	5.54	-77.54	111.76
M, σ	-.15	14.22	-289.33	145.94
M, ln	1.34	9.35	-158.55	129.15
S, -	-.12	9.87	-129.19	206.13
S, σ	-.05	16.76	-280.92	154.59
S, ln	1.43	14.61	-183.88	204.69
Absolute value of change:				
- , σ	10.30	12.11	.00	311.44
- , ln	9.14	10.52	.00	224.83
M, -	3.41	4.37	.00	111.76
M, σ	9.30	10.77	.00	289.33
M, ln	6.30	7.04	.00	158.55
S, -	6.01	7.83	.00	206.13
S, σ	11.13	12.53	.00	280.92
S, ln	9.79	10.93	.00	204.69

^aChange=Adjusted CI - Usual CI; values are in kg.

^bThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the Modified Contemporary Deviation (MCD) used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

those which were largest for Holsteins tended to be largest for Jerseys as well. Ranges were somewhat different than for Holsteins, with the smallest for $CI_{M,-}$ and largest for $CI_{-,σ}$. Absolute value of change again averaged close to zero, but differences among CI types were less than for Holsteins. As for actual change, ranges were smallest for $CI_{M,-}$ and largest for $CI_{-,σ}$. Ranges for these two CI changes differed in size by about 200 kg.

All daughter-dam pairs

Means for daughter-dam pairs are in Table 19 for Holsteins. All means for MCD and CI were negative. MCD of daughters and dams were similar, with dams' MCD averaging slightly higher. CI of daughters exceeded the average for all cows (Table 16), while CI of dams were below average, as could be expected due to genetic trend. Dams had lower standard deviations for MCD and CI than daughters. Means and standard deviations were very similar for all CI types. RPT averaged 45% for daughters and 44% for dams.

Means for Jerseys are in Table 20. Means and standard deviations followed the same trends as for Holsteins, but with higher means and lower standard deviations. RPT were slightly lower than for Holsteins, averaging about 44% for daughters and 43% for dams.

Regressions of daughter MCD on dam CI, with sire of

Table 19. Means and standard deviations (SD) for daughter-dam pairs, for Holsteins.

Measure ^a	Daughters		Dams	
	Mean	SD	Mean	SD
MCD -	-313.48	1232.57	-308.06	1038.78
MCD σ	-313.90	1141.13	-304.66	1000.76
MCD ln	-297.40	1185.62	-290.56	1025.82
CI -, -	-285.68	225.44	-370.43	193.99
CI -, σ	-285.65	219.94	-369.91	191.15
CI -, ln	-283.45	222.42	-368.04	192.83
CI M, -	-286.23	227.41	-370.68	195.37
CI M, σ	-286.15	220.89	-370.19	191.58
CI M, ln	-283.96	223.04	-368.36	192.88
CI S, -	-285.71	225.82	-370.37	194.39
CI S, σ	-285.69	220.16	-369.85	191.43
CI S, ln	-283.47	222.66	-367.97	193.15
RPT -	44.90	5.38	43.73	5.64
RPT M	45.16	5.60	43.75	5.92
RPT S	44.97	5.42	43.81	5.70
N	226,132			

^aMCD=Modified Contemporary Deviation, CI=Cow Index, RPT=Repeatability. The first symbol for CI=the symbol for RPT, and defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol for CI=the symbol for MCD, and defines the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Milk values are in kg.

Table 20. Means and standard deviations (SD) for daughter-dam pairs, for Jerseys.

Measure ^a	Daughters		Dams	
	Mean	SD	Mean	SD
MCD -	-266.98	867.98	-264.21	732.61
MCD σ	-266.01	798.68	-263.16	699.31
MCD ln	-252.36	824.64	-251.82	716.56
CI -, -	-264.12	194.04	-347.55	169.45
CI -, σ	-264.08	189.93	-347.43	166.65
CI -, ln	-262.22	191.26	-345.80	167.71
CI M, -	-264.55	195.09	-347.65	170.25
CI M, σ	-264.48	190.37	-347.56	166.94
CI M, ln	-262.63	191.41	-345.98	167.68
CI S, -	-264.31	194.53	-347.75	170.11
CI S, σ	-264.27	189.86	-347.67	166.70
CI S, ln	-262.41	191.14	-346.03	167.76
RPT -	43.68	6.02	43.22	6.10
RPT M	43.93	6.24	43.28	6.44
RPT S	43.52	6.52	43.01	6.88
N	170,455			

^aMCD=Modified Contemporary Deviation, CI=Cow Index, RPT=Repeatability. The first symbol for CI=the symbol for RPT, and defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol for CI=the symbol for MCD, and defines the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Milk values are in kg.

daughter absorbed, are in Table 21. For Holsteins, all coefficients were higher than 1.0, and were significantly different ($P < .01$) from 1.0. Regressions involving MCD_{-} were largest in magnitude (1.151 to 1.157) and had smallest R^2 (which included sums of squares for sires absorbed). Regressions involving MCD_{o} and MCD_{1n} were smaller and were similar in magnitude, with MCD_{1n} coefficients slightly higher. The coefficient for $CI_{,-}$, the current CI, was largest. For all CI, the range in daughter MCD was larger than expected based on the theoretical value of the regression, but for several of the adjustments the range was closer to expected than for $CI_{,-}$. Thus all CI were conservative in their prediction of daughter MCD, but with some adjustments they were less so than $CI_{,-}$.

Similar trends were seen for Jerseys. Regressions involving MCD_{-} were largest, although not different ($P > .05$) from 1.0, and had the smallest R^2 . Those involving MCD_{o} and MCD_{1n} were smaller in magnitude and were different ($P < .05$) from 1.0. As for Holsteins, the coefficient for $CI_{,-}$ was largest, but here daughters' MCD were close to what the dams' CI would predict them to be based on the theoretical value of the regression. Adjustments to MCD reduced regression coefficients in Jerseys as in Holsteins, but yielded coefficients slightly but significantly less than expected, in contrast to Holsteins. Thus ranges in daughter

Table 21. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation (MCD) on dam Cow Index (CI), with sire of daughter absorbed.

CI type ^a	Holsteins			Jerseys		
	b	SE	R ²	b	SE	R ²
-, -	1.157 ^b	.014	.163	1.018	.013	.179
-, σ	1.091 ^b	.013	.166	.969 ^c	.012	.187
-, ln	1.109 ^b	.013	.166	.970 ^c	.013	.187
M, -	1.151 ^b	.014	.163	1.014	.013	.180
M, σ	1.090 ^b	.013	.166	.968 ^b	.012	.187
M, ln	1.111 ^b	.013	.166	.971 ^c	.013	.187
S, -	1.156 ^b	.014	.163	1.011	.013	.179
S, σ	1.090 ^b	.013	.166	.966 ^b	.012	.187
S, ln	1.108 ^b	.013	.166	.966 ^b	.013	.187

^aThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

^bSignificantly different from 1.0 ($P < .01$).

^cSignificantly different from 1.0 ($P < .05$).

MCD were less than predicted for CI with adjusted MCD even though R^2 were slightly higher.

For both breeds, R^2 were very similar for the 9 CI types. This agrees with results of Powell et al. (26), who found small differences in R^2 for prediction of offspring from 4 types of CI. Thus in prediction of MCD of single daughters, there was little difference between CI types. This results partly from the limited accuracy of predicting performance of a single offspring from estimated transmitting abilities of its parents. In an attempt to better identify any differences which might exist in accuracy of CI, dams were grouped based on their CI, and average dam CI and average sire PD were used to predict average daughter MCD. This would be similar to predicting average performance of many daughters, and should be more sensitive to differences among the CI types than the prediction of single daughter MCD.

Results for Holsteins are in Table 22. Daughter-dam pairs were divided into 1290 to 1335 1 kg groups, with the exact number depending on the CI type (those with larger standard deviations could be divided into more groups), and with between 1 and 573 pairs in each group. Results are reported for the model including dam CI in linear form only. Results for the quadratic form were fairly consistent within the breed, and therefore will be discussed but not

Table 22. Regression coefficients (b) and standard errors (SE) for prediction of average daughter Modified Contemporary Deviation (MCD) from average sire Predicted Difference (PD) and average dam Cow Index (CI), for Holsteins.

CI type ^a		Intercept	PD	CI	R ²
-, -	b	286.133	.927	1.102 ^c	.720
	SE	13.786	.095	.041	
-, σ	b	261.940	1.059	.982	.748
	SE	12.478	.100	.045	
-, ln	b	290.391	.886	1.088	.706
	SE	14.312	.107	.047	
M, -	b	296.526	.919	1.111 ^b	.739
	SE	13.312	.103	.042	
M, σ	b	246.158	1.012	.980	.748
	SE	12.305	.101	.044	
M, ln	b	298.465	.906	1.104 ^c	.757
	SE	12.689	.097	.042	
S, -	b	280.448	.642 ^b	1.207 ^b	.703
	SE	14.380	.115	.049	
S, σ	b	251.951	1.247 ^c	.874 ^b	.731
	SE	12.778	.100	.043	
S, ln	b	302.086	.980	1.059	.727
	SE	13.639	.108	.047	

^aThe first symbol defines the h² used: - is .20, M is h² by mean Modified Contemporary Average (MCA) of the cow, and S is h² by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Values are in kg.

^bSignificantly different from 1.0 (P<.01).

^cSignificantly different from 1.0 (P<.05).

specifically included in tables.

For most regressions, the coefficient for average sire PD was not different ($P > .05$) from 1.0. Of the two which were different from 1.0, one was smaller and one was larger than 1.0. The coefficient for average dam CI was different ($P < .05$) from 1.0 for 5 of the CI types, with one of these ($CI_{S,\sigma}$) being less than 1.0. In all cases, the regression coefficient for the quadratic effect of CI was positive, and for 5 of the CI it was different ($P < .01$) from zero. This indicates that there is a larger range in daughter MCD than would be expected from the dams' CI (CI were conservative), and the adjustments did not reduce this effect. However, the indicator of differences among CI of primary importance was the R^2 for the regression models. R^2 includes sums of squares for sires, but these should be similar for all CI types. R^2 varied from .703 for $CI_{S,-}$ to .757 for $CI_{M,ln}$. Six of the CI had R^2 higher than the .720 for the current CI, with the R^2 for $CI_{M,ln}$ significantly larger ($P < .05$) than .720. For this CI, the regression coefficient for predicting single daughter MCD (Table 21) was intermediate at 1.111. Percentage differences in R^2 (less than 8%) suggest modest increases in CI accuracy are possible, with R^2 for $CI_{M,ln}$, $CI_{-, \sigma}$, and $CI_{M,\sigma}$ exceeding that for the usual CI by 4 to 5%.

Results for Jerseys are in Table 23. Daughter-dam

Table 23. Regression coefficients (b) and standard errors (SE) for prediction of average daughter Modified Contemporary Deviation (MCD) from average sire Predicted Difference (PD) and average dam Cow Index (CI), for Jerseys.

CI type ^a		Intercept	PD	CI	R ²
-, -	b	227.375	1.211 ^c	.821 ^b	.725
	SE	12.198	.107	.058	
-, σ	b	188.498	.822 ^c	.911	.797
	SE	9.343	.084	.047	
-, ln	b	199.695	1.439 ^b	.612 ^b	.709
	SE	12.235	.101	.057	
M, -	b	208.718	1.028	.865 ^c	.735
	SE	11.338	.105	.055	
M, σ	b	179.766	.504 ^b	1.045	.748
	SE	10.339	.091	.050	
M, ln	b	202.477	.917	.891 ^c	.761
	SE	10.577	.091	.051	
S, -	b	217.069	.781 ^c	1.031	.750
	SE	11.213	.090	.049	
S, σ	b	203.047	.672 ^b	1.022	.776
	SE	10.030	.091	.050	
S, ln	b	194.054	1.152	.756 ^b	.754
	SE	10.823	.092	.052	

^aThe first symbol defines the h² used: - is .20, M is h² by mean Modified Contemporary Average (MCA) of the cow, and S is h² by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Values are in kg.

^bSignificantly different from 1.0 (P<.01).

^cSignificantly different from 1.0 (P<.05).

pairs were divided into 1078 to 1117 1 kg groups, with between 1 and 462 pairs in each group. Regression coefficients for average sire PD ranged from .504 to 1.439. Four coefficients less than 1.0 and two greater than 1.0 differed significantly ($P < .05$) from 1.0. Coefficients for average dam CI were different ($P < .05$) from 1.0 for five of the CI types, with all of these being less than 1.0. Regression coefficients for the quadratic effect of dam CI were not different ($P > .05$) from zero, except that for $CI_{S,ln}$, which was negative. Thus for Jerseys the curve for prediction of average daughter MCD from average dam CI was linear, except for $CI_{S,ln}$, where there was less range in daughters' MCD than would be expected from the range in dams' CI.

R^2 for Jerseys varied from .709 for $CI_{-,ln}$ to .797 for $CI_{-,σ}$. Seven of the CI had R^2 higher than the .725 for the current CI. Of these, three (for $CI_{-,σ}$, $CI_{S,σ}$, and $CI_{M,ln}$) were significantly larger ($P < .05$) than .725. As for Holsteins, percentage differences in R^2 (less than 13%) suggest modest increases in CI accuracy are possible, with the three largest R^2 exceeding that for the usual CI by 5 to 10%.

Son-dam pairs

Means for son-dam pairs are in Table 24 for both

Table 24. Means and standard deviations (SD) for son-dam pairs.

Measure ^a	Holsteins		Jerseys	
	Mean	SD	Mean	SD
SON: MCD	-255.79	467.56	-186.04	359.72
PD	-262.53	260.57	-199.71	229.35
RPT	38.86	20.17	37.43	18.50
DAM: MCD -	437.84	1291.32	525.02	899.75
MCD σ	371.42	1160.24	441.31	776.21
MCD ln	433.13	1295.65	480.03	827.62
CI -, -	-275.48	223.87	-231.71	198.50
CI -, σ	-283.21	211.07	-243.39	184.54
CI -, ln	-276.92	217.33	-238.07	187.13
CI M, -	-273.35	228.41	-228.56	203.56
CI M, σ	-281.77	213.91	-240.98	188.13
CI M, ln	-275.70	219.53	-236.01	189.89
CI S, -	-274.78	225.10	-229.98	204.94
CI S, σ	-282.66	211.92	-242.55	188.58
CI S, ln	-276.31	218.32	-237.21	190.80
RPT -	43.56	5.70	45.07	5.06
RPT M	44.00	6.15	45.53	5.52
RPT S	43.68	5.81	45.25	6.30
N	2971		1796	

^aMCD=Modified Contemporary Deviation, PD=Predicted Difference, RPT=Repeatability, CI=Cow Index. The first symbol for CI=the symbol for RPT, and defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol for CI=the symbol for MCD, and defines the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Milk values are in kg.

breeds. Mean MCD and PD of sons were negative for both breeds. RPT averaged 39% for Holsteins and 37% for Jerseys, which is low for PD. All sons had at least 10 daughters, but many had daughters in only one herd, resulting in low average RPT. Average dam MCD were positive, and CI were negative but higher than means for daughter-dam pairs (Tables 19 and 20). This is to be expected, because dams of sons should be among the best cows of the breed, and should have above average CI. RPT of CI averaged 44% for Holsteins and 45% for Jerseys. The Jersey average RPT was slightly higher than for daughter-dam pairs (Table 20).

Regressions of son MCD on dam CI with sire of son absorbed are in Table 25. For Holsteins, regression coefficients ranged from .369 to .402, and all were significantly different ($P < .05$) from the theoretical regression of .5 (the theoretical regression is .5 rather than 1.0 because the son's MCD is the average MCD of his daughters, which are granddaughters of his dam). Regression coefficients for predicting son MCD and daughter MCD (Table 21) for Holsteins agree with results of Powell et al. (26), who saw regressions higher than the expected 1.0 for predicting daughter MCD and lower than the expected .5 for predicting son MCD from usual and adjusted CI. Other researchers have found lower than expected correlations between sons and dams. Rothschild et al. (28) found the

Table 25. Coefficients (b) and standard errors (SE) for regression of son Modified Contemporary Deviation (MCD) on dam Cow Index (CI), with sire of son absorbed.

CI type ^a	Holsteins			Jerseys		
	b	SE	R ²	b	SE	R ²
-, -	.377 ^b	.043	.385	.505	.046	.454
-, σ	.401 ^c	.045	.385	.571	.050	.458
-, ln	.379 ^b	.044	.384	.530	.049	.452
M, -	.369 ^b	.042	.385	.491	.045	.453
M, σ	.399 ^c	.045	.385	.561	.049	.458
M, ln	.380 ^b	.043	.384	.526	.048	.453
S, -	.376 ^b	.042	.385	.477	.044	.452
S, σ	.402 ^c	.045	.385	.548	.048	.456
S, ln	.379 ^b	.044	.384	.513	.048	.452

^aThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

^bSignificantly different from .5 ($P < .01$).

^cSignificantly different from .5 ($P < .05$).

correlation between dam CI and son PD to be lower than expected. Butcher and Legates (4) found the correlation between son Breeding Value (BV) and the BV of his dam based on all records to be lower than expected, although it was closer to expected if only first records of the dam were included in BV. Also, Van Vleck and Carter (34) found a less than expected correlation between the dam's average record and the son's PD. This implied that within groups of selected dams, differences among performance of dams are of limited value in predicting a son's daughter superiority. Thus, for Holsteins, although the range in daughters' MCD was more than expected from the range in dams' CI, the range in sons' MCD was less than expected.

For Jerseys, however, coefficients were from .477 to .571, and none differed ($P > .05$) from .5, so range in son MCD was as expected from range in dam CI. CI with higher coefficients for Holsteins tended also to have higher coefficients for Jerseys. The rank of coefficients from highest to lowest was similar for the two breeds.

As for daughter-dam pairs, R^2 were very similar for the 9 CI types. There was little difference between the CI in their ability to predict MCD of individual sons. Again, this agrees with results of Powell et al. (26), who found little difference in R^2 for prediction of son MCD from four CI types.

Dams of sons then were grouped based on their CI, and regressions of average son MCD on average dam CI computed. Results for Holsteins are in Table 26. Son-dam pairs were divided into 86 to 92 10 kg groups, depending on σ of CI, with between 2 and 71 son-dam pairs in each group. Regression coefficients for average sire PD ranged from .410 to .652, with none different ($P > .05$) from .5. Coefficients for dam CI were all lower than .5, with three significantly different ($P < .05$) from .5. Coefficients for the quadratic effect of dam CI were all positive, and all but two ($CI_{M,-}$ and $CI_{S,ln}$) were different ($P < .05$) from zero. For most CI, there was a somewhat larger range in son MCD than expected from the range in dam CI, due to the positive quadratic effect. The exceptions were $CI_{M,-}$ and $CI_{S,ln}$, whose regressions were linear. R^2 (which included sums of squares for sire PD) for the regressions ranged from .679 for $CI_{-, \sigma}$ to .781 for $CI_{-, ln}$. Two CI types, $CI_{-, ln}$ and $CI_{S,-}$, had R^2 higher than $CI_{-, -}$ (.749), but neither was significantly larger ($P > .05$).

Results for Jerseys are in Table 27. Son-dam pairs were divided into 75 to 83 10 kg groups, with between 1 and 55 son-dam pairs in each group. For average sire PD, one coefficient, which was less than .5, was significantly different ($P < .05$) from .5. Coefficients for average dam CI were different from those for Holsteins, which were all less

Table 26. Regression coefficients (b) and standard errors (SE) for prediction of average son Modified Contemporary Deviation (MCD) from average sire Predicted Difference (PD) and average dam Cow Index (CI), for Holsteins.

CI type ^a		Intercept	PD	CI	R ²
-, -	b	-99.447	.531	.347	.749
	SE	14.856	.158	.079	
-, σ	b	-93.991	.559	.346	.679
	SE	18.512	.169	.090	
-, ln	b	-102.755	.643	.305 ^b	.781
	SE	13.567	.130	.067	
M, -	b	-113.528	.452	.348 ^c	.724
	SE	14.157	.136	.067	
M, σ	b	-70.905	.410	.459	.708
	SE	18.646	.194	.101	
M, ln	b	-94.710	.460	.396	.741
	SE	15.904	.183	.092	
S, -	b	-110.296	.587	.305 ^b	.779
	SE	13.151	.137	.068	
S, σ	b	-85.722	.652	.333	.715
	SE	18.379	.156	.085	
S, ln	b	-104.878	.428	.381	.744
	SE	14.844	.164	.083	

^aThe first symbol defines the h² used: - is .20, M is h² by mean Modified Contemporary Average (MCA) of the cow, and S is h² by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Values are in kg.

^bSignificantly different from .5 (P<.01).

^cSignificantly different from .5 (P<.05).

Table 27. Regression coefficients (b) and standard errors (SE) for prediction of average son Modified Contemporary Deviation (MCD) from average sire Predicted Difference (PD) and average dam Cow Index (CI), for Jerseys.

CI type ^a		Intercept	PD	CI	R ²
-, -	b	33.603	.379	.677 ^b	.873
	SE	13.145	.090	.069	
-, σ	b	38.144	.476	.629	.899
	SE	12.288	.105	.079	
-, ln	b	40.639	.630	.549	.894
	SE	12.278	.100	.070	
M, -	b	11.034	.270 ^b	.662 ^b	.822
	SE	14.511	.101	.076	
M, σ	b	45.697	.512	.631	.862
	SE	14.902	.123	.091	
M, ln	b	35.839	.448	.637 ^b	.898
	SE	12.002	.089	.066	
S, -	b	7.979	.269	.667 ^b	.832
	SE	14.103	.118	.078	
S, σ	b	31.844	.550	.575	.856
	SE	14.601	.116	.084	
S, ln	b	30.182	.521	.572	.848
	SE	14.924	.121	.090	

^aThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Values are in kg.

^bSignificantly different from .5 ($P < .05$).

than .5. For Jerseys, all coefficients exceeded .5, with 4 significantly different ($P < .05$) from .5. None of the coefficients for the quadratic effect of dam CI were different ($P > .05$) from zero. Thus all CI showed a linear relationship to MCD of sons. For the CI with coefficients different from .5, there was a larger range in son MCD than expected from the range in dam CI, particularly for $CI_{,-}$ which had the largest regression coefficient. The other adjustments showed ranges in son MCD not significantly different than expected from dam CI. Only 3 CI had R^2 higher than that for $CI_{,-}$ (.873), and none were significantly larger ($P > .05$). Of these three, two ($CI_{,-\sigma}$ and $CI_{,-ln}$) had regression coefficients not significantly different from .5, while one ($CI_{M,ln}$) was different (.637).

For both breeds, results for averages of son-dam pairs (Tables 26 and 27) differed considerably from those for averages of daughter-dam pairs (Tables 22 and 23). This is apparent if CI types are ranked based on their R^2 . The most striking difference concerns $CI_{,-\sigma}$ and $CI_{,-ln}$. For Holsteins, daughter regressions on dam's $CI_{,-\sigma}$ yielded the highest R^2 and $CI_{,-ln}$ one of the lowest, while son regressions on $CI_{,-\sigma}$ had lowest R^2 and $CI_{,-ln}$ the highest. For Jerseys, daughter MCD was predicted most accurately by $CI_{,-\sigma}$ and least accurately by $CI_{,-ln}$, while both $CI_{,-\sigma}$ and $CI_{,-ln}$ were among the most accurate CI for predicting sons.

One possible explanation of these differences is selection. Dams of daughters are relatively unselected compared to dams of sons. Most cows would have daughters which would themselves later have records, while relatively few would have sons which are progeny tested. Dams of sons are, or should be, a very select group of cows, the elite of the breed.

The selection of cows as bull dams would have been based at least partly on the cow's CI_{1,1}, the CI currently calculated by USDA, rather than one of the other CI examined. However, the 8 other CI are correlated with CI_{1,1}. Selection on CI_{1,1} may change its relationship to the other CI, and also the relationship among the 8 other CI. This could result in one CI being relatively more accurate for predicting daughter performance (unselected group) than for predicting son performance.

One way to examine the impact of selection is to compare correlations among CI for selected and unselected cows. Large differences between the two sets of correlations would suggest selection is having an important effect.

Correlations among CI for Holsteins are in Table 28. For each pair of CI, two correlations are given. The first is for all cows for which these CI were calculated, and the second is for cows which were dams of sons. Correlations

Table 28. Correlations among Cow Index (CI) types for all cows and for dams of sons,^a for Holsteins.

CI ^b	-, σ	-,ln	M,-	M, σ	M,ln	S,-	S, σ	S,ln
-,-	.995 .993	.997 .995	.999 .999	.996 .994	.999 .998	1.000 1.000	.995 .993	.997 .995
-, σ		.996 .993	.992 .989	.999 .999	.996 .994	.995 .992	1.000 1.000	.996 .992
-,ln			.993 .989	.994 .990	.999 .999	.997 .994	.996 .993	1.000 1.000
M,-				.995 .993	.997 .995	.999 .999	.992 .989	.993 .989
M, σ					.996 .993	.996 .994	.999 .999	.994 .990
M,ln						.999 .998	.996 .994	.999 .999
S,-							.995 .993	.997 .995
S, σ								.996 .993

^aFor each pair of CI, the correlation on top is for all cows (N=563,853) and the correlation beneath it is for dams of sons (N=2921).

^bThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

were all extremely high, between .989 and 1.000. Correlations generally were slightly lower for the selected group, but the difference between correlations for selected and unselected cows were not more than .004.

Correlations for Jerseys are in Table 29. Results are similar to those for Holsteins. Correlations were extremely high, between .983 and 1.000, and there was not more than .011 difference between correlations for selected and unselected cows.

Thus selection did not appear to be a cause of the different rankings of CI types in predicting performance of daughters and sons. An alternative explanation for differences in results for predicting performance of daughters and sons is that when daughters were predicted, their MCD were adjusted in the same way as their dams', while sons' MCD were those calculated by USDA (MCD_). However, Powell et al. (26), when examining three adjustments for CI, found no difference in prediction of daughter MCD when those MCD were adjusted or unadjusted. Another possible reason for the difference between prediction of sons and daughters is that son MCD is an average of several of his daughters generally across several herds, while daughter MCD is an average of records of a single cow generally in one herd.

Table 29. Correlations among Cow Index (CI) types for all cows and for dams of sons,^a for Jerseys.

CI ^b	-, σ	-,ln	M,-	M, σ	M,ln	S,-	S, σ	S,ln
-,-	.996 .990	.997 .994	1.000 .999	.997 .992	.999 .998	.999 .995	.996 .988	.997 .992
-, σ		.997 .991	.995 .987	1.000 .999	.997 .992	.994 .983	.999 .995	.996 .986
-,ln			.995 .989	.996 .988	1.000 .999	.995 .987	.996 .986	.999 .995
M,-				.996 .990	.997 .994	.999 .996	.995 .987	.995 .989
M, σ					.997 .991	.995 .985	.999 .996	.995 .985
M,ln						.997 .991	.996 .988	.999 .995
S,-							.996 .991	.997 .995
S, σ								.997 .991

^aFor each pair of CI, the correlation on top is for all cows (N=339,568) and the correlation beneath it is for dams of sons (N=1737).

^bThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

Daughter-dam pairs for high Cow Index dams

The differences between the results for predicting MCD of sons and daughters could have resulted from factors peculiar to son MCD (e.g. son's MCD was not adjusted as was dam's, or son MCD was from different cows in different herds), or because the dams used in predicting sons were elite cows. Therefore a third group was examined in regression equations. This group consisted of daughter-dam pairs, where the dams had high CI for their years of birth. The CI for milk yield of these dams were sufficient to qualify them as dams of sons, but they may not necessarily have actually had any sons which eventually were progeny tested. However, these elite cows likely would have had daughters, and the CI of these dams were used to predict the MCD of their daughters.

Means for these daughter-dam pairs are in Table 30 for Holsteins. Means for MCD and CI were positive for both dams and daughters. MCD were substantially larger for dams, and CI were also larger for dams. Standard deviations for MCD and CI were larger for daughters, due to the truncation selection used to choose dams for the data set. All means were higher than those for all daughter-dam pairs (Table 19) and for son-dam pairs (Table 24). Means for Jerseys are in Table 31. Trends were similar to those for Holsteins, although MCD and CI means were lower than for Holsteins and

Table 30. Means and standard deviations (SD) for daughter-dam pairs, for Holstein dams with high Cow Indexes (CI).

Measure ^a	Daughters		Dams	
	Mean	SD	Mean	SD
MCD -	367.94	1369.93	1737.68	787.81
MCD σ	302.09	1181.92	1541.91	662.08
MCD ln	339.16	1250.32	1646.20	769.21
CI -, -	18.30	203.37	84.24	92.40
CI -, σ	3.19	190.63	61.51	84.39
CI -, ln	11.28	193.62	73.85	87.53
CI M, -	20.91	208.76	90.70	98.19
CI M, σ	4.83	194.16	66.28	86.81
CI M, ln	12.71	196.91	78.11	88.02
CI S, -	19.17	204.21	86.13	93.00
CI S, σ	3.85	191.10	63.06	84.43
CI S, ln	12.00	194.17	75.49	87.63
RPT -	45.43	4.79	46.87	4.44
RPT M	46.13	4.97	47.47	4.71
RPT S	45.56	4.84	47.05	4.54
N	6844			

^aMCD=Modified Contemporary Deviation, RPT=Repeatability. The first symbol for CI=the symbol for RPT, and defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol for CI=the symbol for MCD, and defines the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Milk values are in kg.

Table 31. Means and standard deviations (SD) for daughter-dam pairs, for Jersey dams with high Cow Indexes (CI).

Measure ^a	Daughters		Dams	
	Mean	SD	Mean	SD
MCD -	262.38	974.23	1255.19	666.11
MCD σ	219.05	826.54	1082.56	527.92
MCD ln	237.60	840.63	1122.45	612.20
CI -, -	7.85	151.37	56.38	81.57
CI -, σ	-5.28	141.81	34.35	74.12
CI -, ln	-1.80	141.54	39.47	75.43
CI M, -	9.64	155.76	62.64	86.62
CI M, σ	-4.26	144.43	39.02	76.24
CI M, ln	-1.07	143.66	43.56	75.98
CI S, -	9.59	155.75	62.80	92.14
CI S, σ	-4.44	144.11	38.70	79.19
CI S, ln	-1.05	143.65	43.64	79.88
RPT -	45.21	5.27	48.12	3.99
RPT M	46.12	5.42	48.96	4.29
RPT S	45.74	5.90	48.87	5.17
N	4379			

^aMCD=Modified Contemporary Deviation, RPT=Repeatability. The first symbol for CI=the symbol for RPT, and defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol for CI=the symbol for MCD, and defines the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Milk values are in kg.

several daughter CI had slightly negative means. Means for CI of dams indicate that these dams were selected more intensely for CI milk yield than dams which actually had progeny tested sons (Table 24).

Regressions of individual daughter MCD on individual dam CI with sire of daughter absorbed are in Table 32. For Holsteins, all coefficients were greater than 1.0, but only 3 were significantly different ($P < .05$) from 1.0. These 3 also had the highest regression coefficients for all daughter-dam pairs (Table 21). For Jerseys, most coefficients exceeded 1.0, unlike results for all daughter-dam pairs (Table 21), but none were significantly different ($P > .05$) from 1.0. As seen previously, there was little difference in R^2 (which includes sums of squares for sires absorbed) for the 9 CI types. However, R^2 were lower for Jerseys than for Holsteins, which was in contrast to results for all daughter-dam pairs and for son-dam pairs.

Dams with high CI then were grouped based on their CI. Results for regressions to predict average daughter MCD are in Table 33 for Holsteins. Daughter-dam pairs were divided into 87 to 99 5 kg groups, with between 1 and 222 pairs in each group. For average sire PD, only the regression coefficient for the CI_{,-} model was less than 1.0, but all coefficients except 3 were not different ($P > .05$) from 1.0. For average dam CI, the largest coefficient (1.675) was for

Table 32. Coefficients (b) and standard errors (SE) for regression of daughter Modified Contemporary Deviation (MCD) on dam Cow Index (CI), with sire of daughter absorbed, for dams with high CI.

CI type ^a	Holsteins			Jerseys		
	b	SE	R ²	b	SE	R ²
-,-	1.450 ^b	.219	.322	1.274	.217	.246
-, σ	1.102	.205	.323	1.114	.203	.250
-,ln	1.187	.206	.327	1.040	.201	.251
M,-	1.457 ^b	.208	.322	1.251	.204	.247
M, σ	1.165	.201	.324	1.146	.197	.251
M,ln	1.297	.207	.328	1.093	.199	.252
S,-	1.469 ^b	.218	.322	1.048	.190	.245
S, σ	1.116	.205	.323	.989	.189	.250
S,ln	1.204	.206	.327	.900	.188	.250

^aThe first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

^bSignificantly different from 1.0 ($P < .05$).

Table 33. Regression coefficients (b) and standard errors (SE) for prediction of average daughter Modified Contemporary Deviation (MCD) from average sire Predicted Difference (PD) and average dam Cow Index (CI), for Holstein dams with high CI.

CI type ^a		Intercept	PD	CI	R ²
-, -	b	255.957	.668	1.675	.501
	SE	69.025	.377	.358	
-, σ	b	435.961	1.967 ^b	.082 ^b	.568
	SE	55.464	.299	.346	
-, ln	b	455.632	1.904 ^c	.332 ^c	.444
	SE	59.199	.402	.332	
M, -	b	303.137	1.266	1.428	.629
	SE	64.785	.258	.316	
M, σ	b	358.654	1.336	.726	.602
	SE	52.360	.268	.316	
M, ln	b	343.855	1.221	1.004	.436
	SE	72.430	.410	.391	
S, -	b	396.714	1.582 ^c	.801	.623
	SE	56.097	.277	.291	
S, σ	b	335.186	1.177	.668	.415
	SE	67.973	.342	.414	
S, ln	b	329.365	1.122	.990	.583
	SE	48.874	.313	.266	

^aThe first symbol defines the h² used: - is .20, M is h² by mean Modified Contemporary Average (MCA) of the cow, and S is h² by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Values are in kg.

^bSignificantly different from 1.0 (P<.01).

^cSignificantly different from 1.0 (P<.05).

CI_{,-,-}. Two extremely low coefficients were .082 for CI_{,-,σ} and .332 for CI_{,-,ln}, both of which were different (P<.05) from 1.0. These coefficients were associated with significantly greater than expected regressions for sire PD. All coefficients for dam CI in quadratic form were positive, but only that for CI_{,-,ln} was different (P<.05) from zero. Thus for most CI there was a linear relationship between daughter MCD and dam CI. Although several coefficients differed considerably from 1.0, few differences were significant due to relatively large standard errors. The regression of daughter MCD on dam CI_{,-,σ} was not different (P>.05) from zero, with no quadratic trend, and was of little value in predicting daughter MCD after accounting for sire PD. R² for the CI ranged from .415 for CI_{S,σ} to .629 for CI_{M,-}. Five CI had higher R² than CI_{,-,-}, which was intermediate at .501. However, no R² were different (P>.05) from .501.

Results for Jerseys are in Table 34. Daughter-dam pairs were divided into 78 to 93 5 kg groups, with between 1 and 169 pairs in each group. Coefficients for average sire PD were extremely variable. Three of these, -.375 with CI_{S,-}, .180 with CI_{S,ln}, and 2.127 with CI_{,-,σ}, were significantly different (P<.05) from 1.0. Two coefficients for average dam CI also were different (P<.05) from 1.0 (-.390 for CI_{,-,σ} and .362 for CI_{,-,ln}). These coefficients

Table 34. Regression coefficients (b) and standard errors (SE) for prediction of average daughter Modified Contemporary Deviation (MCD) from average sire Predicted Difference (PD) and average dam Cow Index (CI), for Jersey dams with high CI.

CI type ^a		Intercept	PD	CI	R ²
-, -	b	274.231	1.033	.737	.209
	SE	68.804	.598	.483	
-, σ	b	325.621	2.127 ^c	-.390 ^b	.295
	SE	56.822	.481	.475	
-, ln	b	240.240	.628	.362 ^c	.191
	SE	36.680	.343	.294	
M, -	b	310.226	1.594	.458	.245
	SE	69.709	.558	.432	
M, σ	b	217.601	.755	.628	.337
	SE	32.554	.282	.270	
M, ln	b	216.991	.346	.646	.218
	SE	39.304	.356	.324	
S, -	b	169.901	-.375 ^b	1.301	.179
	SE	58.291	.395	.335	
S, σ	b	229.516	.630	.633	.187
	SE	55.636	.462	.451	
S, ln	b	208.434	.180 ^b	.718	.192
	SE	37.085	.274	.284	

^aThe first symbol defines the h² used: - is .20, M is h² by mean Modified Contemporary Average (MCA) of the cow, and S is h² by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation. Values are in kg.

^bSignificantly different from 1.0 (P<.01).

^cSignificantly different from 1.0 (P<.05).

also were different from 1.0 for Holsteins. Most coefficients for dam CI in quadratic form were positive, and only one, for $CI_{M,-}$, was different ($P < .05$) from zero. Thus $CI_{M,-}$ showed a larger range in daughter MCD than expected, particularly at the upper end of the range in dam CI. Regressions for other CI indicated linear relationships between daughters and dams. R^2 were lower than for Holsteins, ranging from .179 for $CI_{S,-}$ to .337 for $CI_{M,\sigma}$. Four CI had R^2 higher than $CI_{-,-}$, which was intermediate at .209, but none were significantly different ($P > .05$) from .209.

Rankings of CI based on R^2 were different for these elite dams than for all daughter-dam pairs and for son-dam pairs. This suggests that son-dam rankings of CI based on R^2 were different from all daughter-dam rankings both because son rather than daughter performance was predicted, and because dams were selected.

Comparison of Cow Index types

A comparison of R^2 for regression models, from prediction of average offspring MCD, is in Table 35 for Holsteins. With the three sets of R^2 seen together it is obvious that there is no uniform answer to the question of which CI is "best," in the sense of highest R^2 for predicting performance of offspring. Often, adjustments

Table 35. Comparison of R^2 for regression models, for all daughter-dam pairs (ALL DAU), son-dam pairs (SON), and daughter-dam pairs where dams had high Cow Indexes (HIGH DAU), for Holsteins.

ALL DAU		SON		HIGH DAU	
CI ^a	R ²	CI	R ²	CI	R ²
M, ln	.757 ^b	-, ln	.781 ^b	M, -	.629 ^b
-, σ	.748 ^{bc}	S, -	.779 ^b	S, -	.623 ^b
M, σ	.748 ^{bc}	-, -	.749 ^b	M, σ	.602 ^{bc}
M, -	.739 ^{bc}	S, ln	.744 ^b	S, ln	.583 ^{bcd}
S, σ	.731 ^{bcd}	M, ln	.741 ^b	-, σ	.568 ^{bcd}
S, ln	.727 ^{cd}	M, -	.724 ^b	-, -	.501 ^{bcd}
-, -	.720 ^{cd}	S, σ	.715 ^b	-, ln	.444 ^{cd}
-, ln	.706 ^d	M, σ	.708 ^b	M, ln	.436 ^{cd}
S, -	.703 ^d	-, σ	.679 ^b	S, σ	.415 ^d

^aCI=Cow Index. The first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

^{bcd}For R^2 with different superscripts, the higher R^2 is significantly larger ($P < .05$) than the lower R^2 .

which were best for one offspring group were intermediate or relatively poor for the other groups.

An example of this is $CI_{-,ln}$. This CI was best for predicting sons but relatively poor for predicting daughters for Holsteins. This may have been because of the large effect the log transformation had on MCD of some cows. Perhaps the log transformation overadjusted for the problem of within herd variance, and as a result $CI_{-,ln}$ was relatively poor for predicting daughter MCD_{ln} . Recall also that cows with extreme MCD_{ln} did not tend to have very extreme $CI_{-,ln}$, because they usually had few records. $CI_{-,ln}$ was not as affected as MCD_{ln} , but was changed enough that $CI_{-,ln}$ was relatively good at predicting MCD of sons, which were MCD_{-} . $CI_{-,ln}$ may have been better at predicting daughter MCD_{-} than daughter MCD_{ln} .

$CI_{-,σ}$, the adjustment that was intending to do the same thing as $CI_{-,ln}$, had the reverse result. It was relatively good for all daughter-dam pairs, intermediate for elite daughter-dam pairs, and worst for son-dam pairs. This was perhaps because it worked in the opposite way from the log transformation for the extreme cows. This MCD adjustment may have done a good job at reducing effects of herd variation, which affected dams and daughters, making it relatively good as a predictor of daughter MCD_0 . However, because son MCD is an average of daughters across herds,

CI_{-,σ} may not have been as useful in prediction of son MCD, and CI_{-,σ} were changed enough to make it relatively poor for prediction of son MCD.

CI_{-,σ}, the current CI, was better for predicting sons than for predicting daughters, relative to the other CI. However, only in the case of all daughter-dam pairs was there a CI with a significantly higher R² than that of CI_{-,σ}.

Results for Jerseys were quite different than for Holsteins. Based on earlier regression and h² results, it was not expected that CI_{S,-} would work well. Recall that although h² was found to increase substantially as herd variance increased, there was no difference in regression coefficients (daughter MCD on dam CI; Table 9) as herd variance increased. Thus it was concluded that if h² by herd σ was used in the CI, an adjustment of MCD would also be needed, and varying h² only should not predict offspring performance as well.

A comparison of R² for Jerseys is in Table 36. CI_{S,-} was one of the worst CI for prediction of sons and daughters of elite dams, and was intermediate for all daughter-dam pairs. For all three sets of predictions, use of an adjusted MCD with the h² by herd σ resulted in a modest improvement relative to CI_{S,-}. As for Holsteins, CI_{-,ln} was relatively better for prediction of son MCD than for

Table 36. Comparison of R^2 for regression models, for all daughter-dam pairs (ALL DAU), son-dam pairs (SON), and daughter-dam pairs where dams had high Cow Indexes (HIGH DAU), for Jerseys.

ALL DAU		SON		HIGH DAU	
CI ^a	R^2	CI	R^2	CI	R^2
-, σ	.797 ^b	-, σ	.899 ^b	M, σ	.337 ^b
S, σ	.776 ^{bc}	M,ln	.898 ^b	-, σ	.295 ^b
M,ln	.761 ^{cd}	-,ln	.894 ^{bc}	M,-	.245 ^b
S,ln	.754 ^{cde}	-, -	.873 ^{bc}	M,ln	.218 ^b
S,-	.750 ^{cde}	M, σ	.862 ^{bc}	-, -	.209 ^b
M, σ	.748 ^{cde}	S, σ	.856 ^{bc}	S,ln	.192 ^b
M,-	.735 ^{def}	S,ln	.848 ^{bc}	-,ln	.191 ^b
-, -	.725 ^{ef}	S,-	.832 ^{bc}	S, σ	.187 ^b
-,ln	.709 ^f	M,-	.822 ^c	S,-	.179 ^b

^aCI=Cow Index. The first symbol defines the h^2 used: - is .20, M is h^2 by mean Modified Contemporary Average (MCA) of the cow, and S is h^2 by σ of MCA for the herd. The second symbol is the MCD used: - is the current MCD, σ is standardized to a common within herd variance, and ln is log transformation.

^bcdef For R^2 with different superscripts, the higher R^2 is significantly larger ($P < .05$) than the lower R^2 .

daughter MCD. However, rankings of CI for the three groups were more uniform than for Holsteins.

The choice of a single CI which is "best" for both Holsteins and Jerseys must assume that a large true difference between the breeds is not likely. There may be some breed differences, but they should not be expected to be large enough to warrant the use of different procedures to calculate cow transmitting abilities. This is justifiable from a practical standpoint as well, because it would be difficult for USDA to implement different systems for different breeds, and because it would be difficult for dairymen to understand as well.

Under this assumption, the "best" CI for the two breeds is $CI_{-, \sigma}$. For Jerseys, this was a nearly optimum CI, as it was relatively best or near best for all three groups of offspring. This CI was less optimal for Holsteins. It was relatively good for all daughter-dam pairs, intermediate for elite daughter-dam pairs, and worst for son-dam pairs. This relatively poor result for predicting son MCD is the weakest point for this CI, but this may be considered an aberration, because of its relatively good results for Jerseys and for the other two Holstein groups, and because its R^2 was not significantly smaller than the other R^2 for Holstein son-dam pairs.

For both breeds, it was less effective to adjust for

differences in h^2 as herd μ increased. There had been large differences in h^2 as herd σ changed, so genetic variation increased as herd σ increased, but it was more important to adjust for environmental effects of herd variation than for the genetic differences. The adjustment chosen acted to increase CI of elite dams in low variance herds and to decrease CI of elite dams in high variance herds. This agrees with the adjustment suggested by Everett et al. (8) to be necessary.

Again, this was under the assumption that a large true breed difference is not likely. However, it instead may be accepted that true breed differences exist, and that these may be large enough for use of different procedures for the two breeds to be justified. This does not change the conclusion for Jerseys. CI_{σ} was relatively best or near best for all three groups. Thus it was most important to correct for environmental causes of differences in variation among herds.

However, for Holsteins the CI chosen as "best" most likely would be $CI_{S,-}$. This CI was relatively accurate for predicting sons and daughters of elite dams, although worst for predicting all daughters. However, the major use of CI is for choosing dams of bulls to enter progeny testing programs. The cows of most interest are the elite cows. Thus a CI that is relatively best for prediction of

offspring of elite dams would be the logical optimum choice (although, of course, one that worked well for all three groups would be most desirable, but no such choice was available here).

The choice of this CI indicates that differences among herds for genetic variation are important and need to be accounted for. This CI acts to increase CI of elite cows in high variance herds, and decrease CI of elite cows in low variance herds. This is the reverse of results for Jerseys. Adjustments of MCD to correct for environmental differences among herds for variation were not as effective for Holsteins. Thus it appears that it was more important in Holsteins to correct for genetic differences than for environmental differences when primarily interested in elite cows.

CONCLUSIONS

Results of this study indicate that CI of Holsteins and Jerseys differ in their ability to predict MCD of offspring, as measured by comparisons with expected values of those regressions. Generally, if regressions were equal to their expectations for one breed, they would differ from expectations for the other breed. Heritability for levels of herd μ also differed for the two breeds. Thus results for one breed cannot automatically be assumed to hold for another breed. It is unknown at this time, however, why these differences should exist.

For Holsteins, CI overall tended to be conservative in prediction of daughter MCD, with range in daughter MCD larger than expected from range in dam CI. Regressions were significantly different from their expectations for cows in herds with average μ or high σ . The conservative nature of CI in those herds suggested that h^2 used in calculations should be higher than .20 for cows in those herds. Heritabilities computed at levels of herd σ agreed with this, showing highest h^2 in high σ herds. Adjusting for differences among herds for genetic variation may be needed. The situation with herd μ was less straightforward for Holsteins. Heritabilities did not follow a linear trend as herd μ increased, and h^2 was lowest at average μ . This

suggested that nongenetic effects associated with herd μ were having an impact on prediction of daughter MCD from dam CI. Thus adjustments for genetic effects of herd μ may not be effective unless environmental effects are adjusted for as well.

When adjustments to CI of Holsteins were made, CI were still conservative in prediction of daughter MCD, but CI had the opposite effect when predicting son MCD. Range in son MCD was significantly less than expected from range in dam CI. There were large differences in the relative ranking of CI types, based on R^2 , depending on which offspring group was examined (all daughters, daughters of elite dams, or sons). For example, $CI_{-,ln}$ was best for predicting sons but relatively poor for predicting daughters, perhaps because of the large effect the log transformation had for some cows. $CI_{-,o}$, which was intending to do the same thing as $CI_{-,ln}$, had the reverse result, as it was relatively good for all daughters, intermediate for daughters of elite cows, and worst for sons. This adjustment tended to act in the opposite way from the log transformation for the extreme cows.

Results for Jerseys differed substantially from those for Holsteins. Overall, prediction of daughter MCD was as expected based on the theoretical value of the regression. For some levels of herd μ , however, regressions did not

follow expectations. Regressions showed a strong increase as herd μ increased, and indicated that while h^2 of .20 was good for average μ herds, h^2 used in calculations should be lower for low μ and higher for high μ herds. Heritabilities computed also increased as herd μ increased, although all estimates were larger than .20. Regressions as herd σ increased, unlike for Holsteins, showed no trend. However, h^2 increased substantially as herd σ increased. This indicated that adjustments for h^2 by herd σ would be important, but further adjustments for herd σ would also be necessary. Thus, for Jerseys, adjustments for h^2 by herd μ appeared to be important. However, if adjustments for herd σ were implemented, both genetic and environmental adjustments would need to be considered.

When adjustments to CI were made for Jerseys, CI of elite dams predicted offspring MCD as expected based on the theoretical value of the regression. However, for all daughters, some CI resulted in ranges of predicted daughter MCD significantly smaller than expected. When comparing CI types for the three sets of offspring predictions, there were smaller changes in ranking, based on R^2 , than for Holsteins. For example, as for Holsteins, $CI_{-,ln}$ was relatively better for prediction of son MCD than daughter MCD, but $CI_{-, \sigma}$ was relatively good for all offspring groups. Other CI also tended to be more stable in their relative

rankings than for Holsteins. As had been expected from regression and h^2 results, $CI_{S,-}$ was relatively poor for predictions for Jerseys. It was one of the worst CI for prediction of progeny of elite dams and intermediate for all daughters. Use of an adjusted MCD while varying h^2 by herd σ resulted in a modest improvement relative to $CI_{S,-}$. CI varying h^2 by herd μ were fairly good, particularly $CI_{M,ln}$.

The CI which was "best" for both breeds, in the sense of highest R^2 for prediction of progeny, was $CI_{-, \sigma}$. This was best or near best for all offspring groups for Jerseys. For Holsteins, it was less than optimal, as it was relatively good for all daughters, intermediate for daughters of elite dams, and worst for sons. The poor result for sons may be considered an aberration, due to the relatively good results for the other groups. This CI adjusted only for environmental effects of herd σ , and ignored differences among herds for genetic variation. It acted to decrease CI of high producing cows in high σ herds, and increase CI of high producing cows in low σ herds.

Choice of this CI as best for both breeds assumes that large true differences between the breeds are not likely. There may be some breed differences, but these are assumed to be small enough that use of different CI for the breeds would not be justified. Differences between the breeds were seen in this study, particularly in how closely the

regressions agreed with expectations. These differences probably were small enough for this assumption to hold.

However, it may be argued that true breed differences exist. This changes the choice of a "best" CI for Holsteins. For Jerseys, $CI_{-, \sigma}$ was nearly optimum. For Holsteins, however, $CI_{S, -}$, which varied h^2 by herd σ , was a better choice. This CI was near best for predicting MCD of sons and MCD of daughters of elite dams, although worst for predicting all daughters. Because CI has its major use in selection of dams of bulls to enter progeny testing programs, a CI that is relatively good for elite dams is a reasonable choice. This CI, however, works in the opposite way from $CI_{-, \sigma}$ by increasing CI of high producing dams in high σ herds and decreasing CI of high producing dams in low σ herds. This indicates that, for Holsteins, it would be more important to adjust for genetic effects than for environmental effects, particularly when interested in elite cows. This difference from Jerseys would seem to be a large difference between the breeds, and tends to substantiate the idea that large differences exist.

Whichever assumption truly holds, it should be noted that the CI which were the "best" choices are not among the easiest to implement. In both cases, a measure of herd σ is needed. Unlike the measures of herd μ used for some other adjustments, these herd σ are not readily available. For

CI_{-,σ}, herd-year μ and σ for deviation from CTP is needed. This would need to be updated each year, although values from previous years would still be valid. For CI_{S,-}, an overall measure of herd σ for MCA is needed. The cost of these changes may be too great to justify their implementation, particularly because these CI were not significantly better than the CI currently used.

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