EVALUATION OF CORRECTIVE MATING IN JERSEY CATTLE

by

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(ABSTRACT)

First available appraisals for 67644 Jersey cows were used to estimate relative magnitudes of additive and selected sources of nonadditive genetic variation, and evaluate corrective mating programs for 13 linear type traits scored linearly from 50 to 99 points.

Estimates of additive genetic variances were 11 to 36 percent of within herd-classifier variance, with largest values for stature, strength, rump angle, rump width and udder depth. Dominance components ranged from 2 to 4 times as great as additive components for dairy character, rump width, and the udder traits; fore udder, rear udder height, rear udder width, and suspensory ligament, but were small for the other 7 traits. Maternal effects and the direct additive - additive maternal genetic covariance were unimportant.

Sire predicted differences and four measures of dam's merit (dam's phenotypic score, this score relative to herd average, dam's cow index, and half the maternal grandsire predicted difference) were used to predict offspring scores, deviated from herd average.

Sire regression coefficients were much larger than those for dam's measures, suggesting that sire evaluations should receive more weight than dam measures in a corrective mating context.

Mean squares for effects on offspring scores of interactions between categorical levels of sire predicted differences and dam measures generally were nonsignificant, indicating that additively combining measures is appropriate for predicting offspring performance.

Dam's cow index was found to be superior to dam's score for predicting mean performance of offspring groups (e.g., for large groups of offspring or over time) and is therefore preferred for corrective mating decisions.

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INTRODUCTION

Corrective mating as generally practiced involves both selection and assortative mating; i.e., selected sires and cows are mated in some nonrandom manner with respect to their phenotypes for one or more traits. Assortative mating may be described as "positive", when like phenotypes or estimated genetic values are mated or "negative" for the mating of unlike phenotypes or estimated genetic values. The primary objective of corrective mating frequently is to avoid one or both extremes of phenotypic expression by avoiding "same fault" matings.

Programs of corrective mating are offered by nearly every bull stud, and the number of dairymen interested in having their cattle correctively mated seems to be increasing. However, little is known regarding the efficacy of corrective mating programs or optimum methods for implementing corrective mating programs. Mating decisions can be based on several performance measures of dam's merit, the most effective of which is not known. For example, sires may be paired with specific dams based on the dam's phenotypic score, this score relative to herd average, the dam's cow index, or one half of her sire's (maternal grandsire of offspring) predicted difference. Dam's score probably is used most often, but without logical or empirical justification. Also, it is not known if additive predictions of offspring performance are sufficiently accurate or if interactions between parents need be considered.

Linear type appraisal greatly facilitates the study and application of corrective mating programs as compared to the previous descriptive scoring systems. Using the assumption of completely additive inheritance, linear appraisals provide the opportunity to predict outcomes (with respect to each trait) of specific matings and to examine the accuracy of those predictions.

Allaire (1) has demonstrated that any situation in which scores for one or more traits are related nonlinearly to the selection goal (e.g., some expression of economic returns) may be expected to benefit, at least to some degree, from assortative mating in addition to selection. One source of nonlinear relationships is in the inheritance of the traits themselves. Therefore, the first step toward defining optimum corrective mating programs for linear type traits is to determine the nature of the inheritance of the linear traits, with particular emphasis on the ability of additive models (average performance of parents) to predict offspring performance. The relative magnitude of additive and nonadditive genetic variation for the linear traits must be determined, before efficient breeding programs and mating schemes can be developed. Linear scores provide the opportunity to investigate the mode of inheritance for each trait in order to confirm or refute the apparent nonadditive gene action for several descriptively scored traits.

Hay *et*. *al*. (11) estimated relative magnitudes of additive and several nonadditive sources of genetic variation in 12 descriptive type traits defined by the Holstein Association. Results indicated that estimates of dominance variance were large in comparison to additive components for all 12 traits. However, the nonlinear manner in which traits from Hay's study had been scored may have inflated his estimates of nonadditive genetic variance. Estimates of nonadditive variance components on cattle scored linearly could not be found in the literature.

The objectives of this study were:

(1) To estimate the relative magnitude of additive and selected sources of nonadditive genetic variation for the 13 linear type traits of Jersey cattle.

(2) To determine the accuracy (average error and variation in error) of predicting linear type trait scores of daughters from predicted differences for type traits of sires and various measures of performance for dams.

REVIEW OF LITERATURE

Assortative Mating

Assortative mating can be defined as the mating of sires and dams in a manner which is nonrandom with respect to their phenotypes or estimated genetic values for one or more traits (7, 33). Assortative mating may be described as "positive", when like phenotypes or genetic values are mated or "negative" for the mating of unlike phenotypes or genetic values.

Crow and Kimura (7) have contrasted assortative mating based on phenotypes with inbreeding or outcrossing which represent matings that are nonrandom with respect to genetic relationships. Since individuals of similar phenotypes usually will tend to have similar genotypes, positive assortative mating in small populations will tend to produce results characteristic of mild inbreeding, while negative assortative mating will mimic mild outcrossing. However, since it is possible in larger populations to mate individuals of like phenotypic (or genetic) value while avoiding consanguineous matings, assortative mating is not synonymous with inbreeding or outcrossing.

Wright (33) and Lush (14) have noted that the major effect of assortative mating on population structure is on population variance. Specifically, positive assortative mating is expected to increase population variance while negative assortative mating should reduce population variability. These expected changes in population variance with assortative mating have been shown experimentally in *Nicotiana* by

Breese (5) and in *Drosophila* by McBride and Robertson (16). Breese(5) measured the increase in genotypic variance after one generation of assortative mating in *Nicotiana rustica* and suggested that assorative mating might profitably be used by plant and animal breeders as a means of enhancing genotypic variance and subsequent response to selection. McBride and Robertson (16) also found the expected decrease in population variance with negative assortative mating and demonstrated that the response to selection could be increased by mating selected parents assortatively rather than at randon.

The effect of assortative mating on population variance theoretically may contribute to population improvement in two distinct ways depending upon whether the trait of concern (single or composite) is optimum on some scale at extreme or at intermediate values. Where optimum performance occurs at an extreme, the goal of a breeding program is to direct population mean performance toward that extreme. Positive assortative mating, by increasing variation, should increase potential selection differentials and thereby result in more rapid population improvement. (An alternative, but equivalent, view of the effect of positive assortative mating is that it increases population additive genetic variation.) Where optimum performance occurs at an intermediate value, the goal of a breeding program is to maximize the frequency of individuals at or near the optimum intermediate value. Negative assortative mating, by reducing variation around the population mean (which is directed by selection toward the intermediate optimum), should yield higher frequencies of optimum and near optimum individuals and, consequently, superior mean population performance.

Baker (3) and Soller and Genizi (22) have presented methods for evaluating expected increases in response to selection from positive assortative mating (i.e., as contrasted to selection alone). Baker (3) concluded that positive assortative mating following truncation selection in a breeding program will enhance response to selection by a maximum of 10% with high heritability and low selection intensity and by no more than 4 to 5% under the conditions met with in most breeding programs.

Lush (15) has suggested that within a herd, negative assortative mating is more likely to be encountered than positive, especially if different constituents of net merit are considered separately. Theoretical contributions to genetic improvement from negative assortative mating have not been examined. However, if these contributions are measured in terms of the ability of negative assortative mating to reduce phenotypic variation about some intermediate optimum, they necessarily will be small for traits of low to moderate heritability. Additionally, Lush (15) has addressed a practical breeding problem by noting that assortative mating for several traits simultaneously can be extremely difficult.

Usefulness of Corrective Mating

Corrective mating as generally practiced involves both selection and assortative mating; i.e., selected sires and cows are mated in some nonrandom manner, often based on their type trait evaluations. Genetic improvement in linear type traits, resulting from corrective mating programs likely is due primarily to selection with less than 10% due to assortative mating (3). However, research has shown that attention to specific mating schemes is warranted if selection goals include the improvement of type traits, especially mating schemes which avoid the mating of undersirable extremes.

Hay et. al. (12) found in their study with Holstein cattle that corrective mating was effective as a method of decreasing the frequency of undersirable phenotypes from the female parent generation to the female offspring generation. However, selection alone with predicted difference for overall final score (PDT) as the criterion for sire selection was nearly as effective as sire selection and assortative mating for individual descriptive type traits in improving frequencies of offspring phenotypes relative to breed average frequencies.

Vinson (27) suggested that the primary objective of corrective mating should be to avoid extremes of undesirable type and indicated that selection based on PDT and avoiding "same fault" matings according to individual trait evaluations would be a generally effective method of corrective mating for type. This conclusion was based on results of Hay et. al. (12) and an earlier study (28) in which the efficiency of final classification score, as a selective criterion for improving genetically the 12 components of type descriptively classified by the Holstein Association, was examined. A motivating concern in this study (28) was that the large number of traits in the classification program might dilute selection pressure for important traits and increase the difficulties of establishing and maintaining selective criteria consistent with the predetermined goals of a breeding progrm. Their results (28) indicated that final classification score was an efficient selection criterion for improving individual descriptive components of type. Selection on overall final score would reduce the number of traits considered and therefore the chance of diluting selection pressure over an extensive number of traits. Selection on overall final score was therefore recommended except for situations in which there is an overriding concern for one or a few specific traits. White (30) also addressed the corrective mating issue by suggesting that it be used in conjunction with selection for PDT. The primary decision to use a bull should be based upon his PDT (after attention has been given to PD milk and PD% fat), and then the individual descriptive trait evaluation of the bull could be used to "correctively mate" cows in the herd.

The most logical situations to benefit from nonrandom mating schemes are those characterized by intermediate optima. In such situations where either extreme is sub-optimal, selection and negative assortative mating would tend to produce an intermediate (optimum) mean with minimum variation.

Lush (15) described negative assortative mating as a breeding method to improve a single trait included in total merit where an intermediate has maximum merit. Several traits which logically have intermediate optima currently are scored in linear type evaluation programs for dairy cattle. In work with Jersey type data, Thomas et. al. (23) found that maximum final score occurred at high scores (89 to 99 points) for stature, strength, dairy character, rump width, fore udder, rear udder height and width, and suspensory ligament, but at slightly lower scores (79 to 89 points) for udder depth and at intermediate scores (73 to 79 points) for foot angle, rear legs, rump angle, and teat placement. If a breeder's goal was to maximize final score, as defined in the study of Thomas et. al. (23), a mating scheme involving corrective mating (selection with negative assortative mating) for the four traits with intermediate optima may be useful.

Allaire (1) has demonstrated that intermediate optima for individual traits are not required to expect beneficial results from nonrandom or corrective mating. Rather, any situation in which scores for one or more traits are related nonlinearly to some expression of economic returns may be expected to benefit, at least to some degree, from assortative mating in addition to selection. Allaire demonstrated this with an example in which increased returns from milk production were associated with udders of greater depth and capacity. Beyond a certain point, expenses may be incurred which are related directly to the udder depth and associated characteristics. The net effect may be that economic returns exhibit a curvilinear relationship with depth of udder. With respect to economic returns, the most desirable score for depth of udder was an intermediate value. Allaire further described corrective mating in terms of a multi-trait selection method where at least one trait has a measurement scale nonlinear in its relationship with total merit. If this is the case, maximum improvement in total merit could not be achieved with selection and random mating.

The effectiveness of corrective mating programs has been examined by Hay _et al._ (12), Dishman _et al._ (9), and Burnside _et al._ (6). Hay _et al._ (12) determined frequencies of offspring from all possible combinations of mating types for sires and dams in the Holstein descriptive classification program. Results indicated that corrective mating was effective in increasing frequencies of daughters denoted as desirable, but that most of the improvement was from selection rather than assortative mating. Frequencies of offspring for rear legs, the only trait examined with a logical intermediate optimum, indicated that mating dams with posty hind legs to bulls that had genetic values for extremely sickled hind legs produced fewer cows coded desirable than mating to sires coded ideal for real leg set. However, this may have resulted from the nonlinear categorical nature of the scoring system.

The value of Midwest Breeders Cooperative's corrective mating program for Holsteins was evaluated by Dishman _et al._ (12). Basic form was considered first in mating recommendations with second consideration given to the cow's worst fault along with production and fat test. Their results indicated negative assortative mating (corrective mating) was practiced and that percentages of daughters improved, relative to their dams, in basic form were 5 to 10% higher for matings to recommended sires than for matings to nonrecommended sires. Percentage of daughters improved in their dams' worst fault from recommended as opposed to nonrecommended matings were -1% for heifers and 4% for cows. At least 58% of the daughters scored better than their dams' worst fault for any individual trait.

In a Canadian study of Holstein cattle, Burnside *et al.* (6) examined progeny distributions from sires with significantly different ratings for a given component of conformation, mated to the same cow. Maternal half-sister records were used if the half-sisters were sired by bulls which differed by at least one standard deviation in the type breakdown component under consideration. For each maternal half-sister pair, the sire with the higher proof was termed the "Improver", while the other sire was termed the "Non-Improver." Results were consistent for all type components, indicating that "Improver" sires left significantly greater numbers of high classifying daughters than "Non-Improver" sires when mated to the same cow. Distributions of progeny differed most dramatically for size, rump, dairy character, and body capacity, the traits with higher heritabilities.

Components of Genetic Variance

The total genotypic variation for a trait can be partitioned into components of additive and several nonadditive genetic variances by covariances among relatives. The traditional partitioning into components due to differences in average effects of genes (additive), interaction between pairs of allelic genes (domiance), and interaction between two or more nonallelic genes (epistasis) was augmented by Willham (32) to include additive and nonadditive components of maternal genetic variance and a direct additive - maternal additive covariance. These additional components have proved to be important sources of variation for traits expressed by females in conjunction with parturition and lactation. Results of Willham (32) were used by Eisen (10) to develop efficient mating designs for estimating direct and maternal genetic variances and direct-maternal genetic covariances. These designs have been used sparingly in large animal breeding research due to difficulties in obtaining necessary relatives in non-designed experiments or required numbers of relatives in designed experiments.

Estimates of additive genetic variance are extensive for both production and type traits in dairy cattle (31). Estimates of nonadditive genetic variance have been far fewer in number. Studies to determine the importance of specific combining ability or "nicking" have implied little nonadditive genetic effects for yield (2, 13, 21) and type (19) traits.

Van Vleck and Hart (25) examined covariances among first lactation milk records of Holsteins related as cousins of varying degree, as daughter-dam, as full and maternal sibs, and as aunt-niece of varying degree to estimate the importance of genetic maternal effects. The multiple regression of the expected coefficients of additive direct, additive maternal, dominance direct, and dominance maternal genetic variance components; and additive direct by additive maternal and dominance direct by dominance maternal genetic covariances on the 24 estimated covariances between pairs of relatives gave a multiple correlation coefficient of .95. The regression of actual covariance on the coefficient of additive direct genetic variance gave a correlation of .92. These results suggested that for these data, only additive genetic effects were important for first lactation milk production. Van

Vleck and Bradford (26) were interested in genetic and maternal influence on the first three lactations of Holsteins. Milk records of up to the first three lactations of artificially sired Holstein daughters and their dams were used to estimate heritability from both daughter-dam regression and paternal half-sib correlation. The within-herd estimates from records expressed as deviations from herd-mate average were .37, .30, and .24 from daughter-dam regression for the first three lactations; and the corresponding estimates from half-sib correlation were .24, .21, and .23. These results suggested a large maternal effect in the first lactation, a small amount in the second, and little in the third lactation. Van Vleck and Bradford (26) hypothesized that the higher daughter-dam estimate for the first lactation was due to genetic maternal effects which have smaller effects in succeeding lactations until, at the third lactation, the estimates from both methods are the same and are both derived from direct, additive genetic effects.

The importance of several nonadditive sources of genetic variation for type traits was examined by Hay et al. (11). Traits examined were the 12 descriptive traits defined by the Holstein Association. Variance components resulting from dominance effects appeared to be large in comparison to additive effects for all traits, ranging from 2 to 6 times as large as additive genetic components. However, the nonlinear manner in which the traits had been scored may have inflated estimates of nonadditive genetic variance.

Heritabilities of Linear Type Traits

Estimates of heritabilities for linearly scored type traits are relatively few due to the comparatively recent adoption of linear scoring procedures. Weinberg *et al.* (29) estimated heritabilities for the 13 type traits scored in the Uniform Functional Type Trait Appraisal program using guidelines for scoring recommended by the National Association of Animal Breeders. Cows scored between 24 and 47 months of age were used to calculate heritabilities. The model used included sires (98 with greater than 20 daughters), herd, age, and stage of lactation. Heritabilities (Table 1) ranged from .11 for rear legs to .37 for stature. Heritability estimates from a subset of the data containing cows scored between 48 and 71 months of age did not differ significantly from the estimates of the younger group.

Similar data were used by Norman *et al.* (18). Type scores were adjusted for age and stage of lactation and records were excluded if the sire of the daughter did not have daughters in at least five herds. Heritabilities (Table 1) ranged from .07 to .34, with foot angle having the lowest heritability and stature the highest. Heritabilities were moderate for pelvic angle (.29) and udder depth (.27) and were low for rear legs (.08) and teat placement (.12). These results are similar to heritabilities estimated by Weinberg *et al.* (29). Norman *et al.* (18) concluded that moderate genetic improvement is possible for many type traits if selection is directed to a specific trait; foot angle is an exception.

Table 1. Heritability estimates of linear type traits for Jersey cattle from previous studies.

Trait	Norman (18)	Weinberg (29)
Stature	.34	.37
Strength	.22	.19
Dairy Character	.15	.17
Foot Angle	.07	.12
Rear Legs	.08	.11
Rump Angle	.29	.30
Rump Width	.20	.25
Fore Udder	.15	.17
Rear Udder Height	.14	.14
Rear Udder Width	.14	.14
Udder Depth	.27	.31
Suspensory Ligament	.14	.17
Teat Placement	.12	.15

Heritability estimates of linear type traits for Holstein cattle were computed by Thompson et al. (24) using data from an experimental Holstein linear type appraisal project for traits suggested by the National Association of Animal Breeders. Heritabilities were from .12 (rear view legs and suspensory ligament) to .32 (stature). The authors felt that increased classifier experience with linear scoring may result in larger heritabilities because of decreased residual variation.

In recent work done by Barton et al. (4) heritability estimates for linear type traits in Jersey cattle ranged from .11 to .33. Most estimates were consistent with the results of Weinberg et al. (29) and Norman et al. (18). Heritability estimates were similar for traits evaluated as first and second appraisals except for dairy character, which had higher estimates for first appraisals. It was suggested that within-herd culling may have affected dairy character.

MATERIALS AND METHODS

Data obtained from the American Jersey Cattle Club (AJCC) consisted of first available appraisals for 13 linear type traits on 67644 cows. Cattle were scored linearly from 50 to 99 points between January 1980 and December 1983.

Linear type scores were adjusted for effects of age and stage of lacation using factors developed by Norman (17). There were 8 stage factors, derived from actual days in milk and recorded stage of lactation class (unknown, milking, milking-stale, dry, and dry-springing), and 183 age factors for months of age at classification.

A restriction that cows scored at less than 18 or more than 200 months of age or more than 500 days in lactation would be excluded, was necessary so that all scores in the data set could be age and stage adjusted. Edits also required cows to have valid linear scores between 50 and 99 points for each of the 13 traits.

A second and smaller data set was formed by combining USDA predicted differences for type of Jersey sires from the July 1983 sire summary and cow indexes for type computed in January 1982, with the data set containing linear type appraisals. Each cow was required to have a dam with cow indexes (CI_d) for type, a sire with predicted differences (PD_s) for type, and a maternal grandsire with predicted differences (PD_{mgs}) for type. Cows also were required to be from herds with at least 20 cows appraised and to have dams from such herds.

The number of observations decreased from 67644 to 21453 when data were edited and dams were required to have linear trait scores. The large reduction in numbers probably was because linear scoring recently had been implemented (January 1980). The number of observations decreased to 19349 when PD_s were required. The additional restriciton that required both cow and dam herd sizes to be at least 20, yielded 18578 cows. The final restriction, requiring cows to have CI_d and PD_{mgs}, left 14721 cows in the second data set. Data from the first data set were used to estimate genetic parameters while those in the second were used to evaluate corrective mating procedures.

I. Estimation of Components of Genetic Variance and Covariance

Components of genetic variance and covariance estimated for linear type traits included direct additive, direct dominance and additive maternal genetic variances, and the direct-maternal additive genetic covariance. Components were estimated from covariances among paternal half-sibs, full-sibs, daughters and dams, and maternal half-sibs. Additionally, covariances among single first cousins where sires were full-sibs were examined to estimate first order additive epistatic genetic variances. However, these relatives were dropped due to small numbers, yielding substantial reductions in standard errors for other genetic components.

Covariances among relatives for each of the 13 traits were computed from linear trait scores of those relatives. The basic model included an effect of the herd-classifier subclass plus a random effect of the group that defined the relatives of interest. Sire, full-sib group, and dam (maternal half-sib) variance components were estimated by analysis of variance while daughter-dam covariances were estimated from regression of daughter scores or dam scores.

Covariances among paternal half-sibs were from the model,

$$Y_{ijk} = \mu + HC_i + S_j + e_{ijk}, \text{ where;}$$

Y_{ijk} is the linear trait score on the individual, μ is the overall mean, HC_i is a fixed effect due to the ith herd-classifier subclass, S_j is a random effect due to the jth sire, and e_{ijk} is a random error associated with each individual's score. Cows were included only if their sires had daughters in 10 or more herds, yielding 47106 daughters of 328 sires. The model was solved using GLM procedures of the Statistical Analyses System (SAS) (20), with herd-classifier subclasses absorbed.

Covariances among full-sibs were from the model,

$$Y_{ijk} + \mu + HC_i + FS_{ij} + e_{ijk}, \text{ where;}$$

FS_{ij} is an effect due to the jth full-sib group nested within the i^{th} herd-classifier subclass. A full-sib group was 2 or more full sisters. If full-sibs were in more than one herd, perhaps as a result of embryo transfer, then the herd with the largest number of full-sibs was included, and their full-sibs in other herds were not. This was required for full-sibs to be truely nested within herd-classifier subclasses. The model was solved using the NESTED procedure of SAS.

Covariances between daughters and dams were from the model,

$$D'_{ijk} = \alpha + HC_i + b\,(D_{ij}) + e_{ijk}, \text{ where;}$$

D'_{ijk} is the linear trait score on the daughter, α is the intercept, and $b(D_{ij})$ is the regression coefficient times the linear trait score on the dam. Solution was by SAS GLM with herd-classifier subclasses absorbed.

Covariances among maternal half-sibs were from the model,

$$Y_{ijk} = \mu + HC_i + D_{ij} + e_{ijk}, \text{ where;}$$

D_{ij} is the effect of the j^{th} dam nested within the i^{th} herd-classifier subclass. If a dam had daughters in several herds, then the herd with the largest number of daughters was included, and their maternal sisters in other herds were not. As a result, maternal half-sibs were nested within herd-classifier subclasses. The model was solved using the NESTED procedure of SAS.

These covariances among relatives allowed us to estimate the components of genetic variance and covariance. Matrices were used to solve the system of four equations for each trait shown in Figure 1.

Matrix A contained the covariances among four types of relatives. The amounts of genetic variance and covariance included in the four covariances among relatives are shown in Matrix B. These estimates were from William (32). Each column in the matrix corresponds to one of the four genetic components being estimated (Matrix C). The system of equations was solved for Matrix C for each trait.

Approximate variances for components of covariance among paternal and maternal half-sibs and among full-sibs were computed following Dickerson (8), while those for components of covariance between daughters and dams were from the squared products of regressions of daughters on dams and the within herd variance among dams. Approximate standard errors for components of genetic variance and covariance were square roots of diagonal elements of the matrix formed by the matrix product $\underline{B}^{-1}$ $\underline{V}$ $\underline{B}$, where $\underline{B}$ is the coefficient matrix in Figure 1 and $\underline{V}$ is the vector of approximate variances for covariances among relatives (10).

$$
\begin{bmatrix} COV\ (PHS) \\ COV\ (FS) \\ COV\ (D'D) \\ COV\ (MHS) \end{bmatrix}
=
\begin{bmatrix} 1/4 & 0 & 0 & 0 \\ 1/2 & 1/4 & 1 & 1 \\ 1/2 & 0 & 1/2 & 5/4 \\ 1/4 & 0 & 1 & 1 \end{bmatrix}
\begin{bmatrix} \sigma^2_{Ao} \\ \sigma^2_{Do} \\ \sigma^2_{Am} \\ \sigma_{AoAm} \end{bmatrix}
$$

$$A = B^* \quad C$$

Figure 1

Matrices containing four components of genetic variance and covariance estimated by four covariances among relatives

*Estimates by Willham (32).

Estimates of heritability for the 13 linear type traits were from

$$h^2_i = \frac{\sigma^2_{A_i}}{\sigma^2_{P_i}} \quad , \text{ where;}$$

h^2_i is the hertability of each linear trait

$\sigma^2_{A_i}$ is the additive genetic variance of each trait

$\sigma^2_{P_i}$ is the within herd-classifier phenotypic variance.

II. Evaluation of Corrective Mating

Expected Results of Corrective Mating

The decision to mate a specific sire to a given cow must be based on some expectation regarding the outcome of the mating. Regardless of the objective or goal on any mating, the breeder must predict, at least mentally, the outcomes of various potential matings in order to choose that mating which is optimum relative to his goal. It also seems reasonable that the expectations of breeders will vary according to the average performance of their herds for any given trait. For example, a breeder whose cows are substantially taller than breed average due to favorable environmental effects, likely will expect higher stature scores than the average breeder, from the same type of mating. Expectations from corrective mating therefore were expressed in this study relative to herd average for each specific trait; i.e., the measure of offspring score to be predicted was offspring score as a deviation from herd average.

Linear type appraisals provide the opportunity to predict outcomes of specific matings with respect to each trait in a simple manner using the assumption of completely additive inheritance. For example, offspring performance relative to herd average ($\hat{O}$) might be predicted as,

$$\hat{O} = S + D,$$

where S and D represent some measures of performance for sire and dam. Use of this model to determine optimum matings for specific traits is straight forward. Given the desired offspring score, O^*, and a specific cow to be mated with performance measure, D^*, the required sire has performance measure, S^*, where,

$$S^* = O^* - D^*.$$

Predicted differences of sires (PD_s) for linear type traits are logical choices as measures of sire performance, due to their availability and general acceptance as most accurate available estimates of sire genetic merit. However, several measures for performance of dams are possible. In current practice, most corrective mating decisions probably are based on the phenotypic score of the dam. Alternative measures of dam's performance include her score as a deviation from herd average, her CI_d, and half the predicted difference of her sire, or PD_{mgs} of the offspring. Among these alternatives, the CI_d logically would be preferred as the most accurate estimate of the genetic value received by the offspring from the dam.

Alternative measures of dam's performance were compared for use in corrective mating programs by predicting offspring score using PD_s with each of the four measures of dam's merit listed above and illustrated in Figure 2. Dam's score was expressed relative to breed average and scaled by $.5h^2$ to yield measures similar in mean and variance to CI_d and PD_{mgs}. However, the relative performance of dams (e.g., their rank) is identical for phenotypic score and for the scaled measure actually used. Similarly, dams rank identically relative to herd average regardless of whether their performance is scaled by $.5h^2$ or not.

Means, standard deviations, and ranges for offspring scores predicted from PD_s and each of the four measures of dam's merit (D1 to D4) were computed for all linear traits. Errors of prediction, defined as predicted score minus actual score (e_1 to e_4), also were computed for each method (Figure 2).

$$\hat{O}_1 = PD_s + .5h^2(y-\mu) = PD_s + D1 \qquad e_1 = \hat{O}_1 - O$$

$$\hat{O}_2 = PD_s + .5h^2(y-\bar{H}) = PD_s + D2 \qquad e_2 = \hat{O}_2 - O$$

$$\hat{O}_3 = PD_s + CI_d = PD_s + D3 \qquad e_3 = \hat{O}_3 - O$$

$$\hat{O}_4 = PD_s + .5PD_{mgs} = PD_s + D4 \qquad e_4 = \hat{O}_4 - O$$

Figure 2

Four prediction equations of offspring performance
and corresponding errors of prediction

PD_s = sire predicted difference for each linear trait

h^2 = heritability for the linear trait

y = age and stage adjusted score for each linear trait of the dam

μ = overall mean for each linear trait

O = age and stage adjusted score for each linear trait of the offspring as a deviation from herd average

$\bar{H}$ = dam's herd mean

CI_d = dam's cow index

PD_{mgs} = maternal grandsire predicted difference

Regression of Offspring Scores on Measures of Parental Performance

Four distinct models were used to regress offspring score (relative to herd average) for each trait on measures of parental performance for that trait. Each of the four models was used for each of the four measures of dam's merit, D1 to D4 (Figure 2). In the first model, offspring score was regressed on one of the predictions of offspring performance, $\hat{O}_1$ to $\hat{O}_4$ (Figure 2), computed from PD_S and one of the four measures of dam's merit. In the second model, a quadratic regression was added for $\hat{O}_1$ to $\hat{O}_4$ along with the effect of offspring herd average final score (HAFS) class. Final score class was defined by placing each of the 593 herds represented into one of five classes (60 to 72, 73 to 75, 76 to 77, 78 to 80, and 81 to 90) based on its average (age and stage adjusted) final score. Classes were defined to have a representative number of animals in each class. Each class contained more than 1000 cows.

In the first two models described above, sire and dam measures of performance were weighted equally and combined additively to predict offspring scores. This was according to genetic theory assuming linear scores are partially determined by additive effects of autosomal genes with no maternal effects and random distributions of nonadditive genetic and environmental effects. In the third and fourth models, regressions of offspring score were computed seperately on the measure of sire performance (PD_S) and the measure of dam performance (D1 to D4), to compare partial regression weights with the implicit weights of 1.0 used in the first two models. The third model included only linear regressions of offspring score on parental measures, while the fourth model included linear regressions, quadratic regressions, and the effect of HAFS class.

Quadratic regressions were included in the second and fourth models to detect nonlinear relationships between measures of parents and offspring. Any tendency for offspring scores to plateau at higher measures of parental performance was of particular interest since this may indicate bias in highest scores. The variable, HAFS, was included in the second and fourth models to detect any tendencies to score differently, animals in high or low average final score herds, after accounting for the relative merits of their parents.

Analysis of Offspring Scores by Categorical Levels of Parents

Analysis of variance was used as an alternative to regression analysis for quantitating relationships between measures of parental performance and scores for linear traits of offspring. Expressing performance of parents in a categorical manner allowed computing of least squares means for classes of sire and dam performance and their interaction. This was thought to quantitate, more precisely than results of regression analysis, the results of assortative mating. Due to the similarity of results from regression analysis for dam measures, D1 to D4, categorical levels of dam's performance were defined and evaluated for dam's score (equivalent to D1) and dam's cow index (D3) only.

Five categories of PD_s, dam's score (D1), and CI_d (D3) were defined for each trait, with the requirement that a sufficient number of observations (at least 1000), be in each category. Mean squares from analysis of variance were examined for effects on linear scores of categorical levels of PD_s, D1, or D3, the interaction of sire and dam measures, and HAFS. Least squares (LS) means of offspring scores for categorical levels of HAFS, adjusted for effects of categorical levels of PD_s, D1, or D3, and their interaction were determined. Least squares means of offspring scores for categorical levels of PD_s, D1 or D3, and their interaction, adjusted for effects of categorical levels of HAFS also were computed.

Analysis of Errors of Predicting Offspring Scores

The efficacy of corrective mating can be measured in terms of the accuracy with which the expectation which motivates a particular mating predicts the actual outcome of that mating. In this study, expectations were expressed in terms of additive predictions of offspring, scores for individual linear traits ($\hat{O}_1$ to $\hat{O}_4$) using measures of parental performance (PD_s and D1 to D4). Errors of prediction therefore may be defined as the difference between predicted and actual scores of offspring, e_1 to e_4 (Figure 2).

Means, standard deviations, and ranges of errors of predicted offspring score, using PD_s with one of four measures of dam's merit were computed. Frequencies of errors of a specific magnitude were determined to compare accuracy for different measures of dam's performance. Analysis of errors were also to quantitate the accuracy of corrective mating, or of additive prediction of offspring.

Mean squares from analysis of variance for effects on errors of categorical levels of PD_S, D1, and D3, their interaction, and HAFS were calculated to determine whether errors of prediction were associated with categorical levels of parental performance or final score level of herd. Least squares means for errors similar to those computed earlier for offspring scores, were used to quantitate the magnitude of these effects on errors of prediction.

Extent of Assortative Mating

Correlations between PD_S and the four measures of dam's merit (D1 to D4) were used to determine the extent of assortative or corrective mating. The size of the correlation is an indicator of the degree of assortative mating practiced for the individual linear traits, while the sign of the correlation indicates whether the assortative mating is positive or negative.

RESULTS AND DISCUSSION

I. Estimation of Components of Genetic Variance and Covariance

A logical first step toward defining optimum corrective mating programs is to determine the nature of the inheritance of linear type traits. The relative magnitude of additive and nonadditive genetic variation for each type trait must be determined, before efficient breeding programs and mating schemes can be developed.

Direct additive, direct dominance, and maternal genetic variances and the direct-maternal additive genetic covariance were estimated for each of the 13 linear type traits of Jersey cattle by computing covarinaces among four types of relatives (Table 2). Daughter-dam covariances were estimated differently than the other relatives, whose covariances were estimated by analysis of variance. Daughter scores were regressed on dam scores and the resulting regression coefficients (Table 3) then multiplied by the within herd-classifier variances of the dams' scores to estimate daughter-dam covariances.

For nearly all the traits, covariances (Table 2) among full-sibs were larger than covariances between daughters and dams. The major difference between these covariances is that dominance is present in the full-sib covariance. Covariances among full-sibs were three times as large for dairy character, and two times as large for rump width, fore udder, and rear udder width. Covariances among paternal half-sibs were slightly larger than covariances among maternal half-sibs, for all traits except strength and teat placement. The major difference between

Table 2. Covariances among four types of relatives.[a]

Trait	FS	D'D	PHS	MHS
Stature	5.97	6.36	2.88	2.70
Strength	3.53	2.54	1.34	1.63
Dairy Character	6.56	2.22	1.07	1.04
Foot Angle	1.46	.74	.59	.10
Rear Legs	.98	.99	.61	.33
Rump Angle	3.20	2.73	1.49	.31
Rump Width	4.91	2.59	1.31	.78
Fore Udder	7.17	3.74	1.27	1.19
Rear Udder Height	4.32	2.45	.93	.01
Rear Udder Width	4.63	2.21	1.04	.43
Udder Depth	1.57	1.71	.86	.26
Suspensory Ligament	4.90	3.66	1.35	.13
Teat Placement	2.97	2.26	.91	.97

[a]FS = full-sibs; D'D = daughter-dam; PHS = paternal half-sibs; MHS = maternal half-sibs.

Table 3. Regression coefficients of daughter scores (D') on dam scores (D).

Trait	$b_{D'D}$
Stature	.1825
Strength	.1297
Dairy Character	.1043
Foot Angle	.0340
Rear Legs	.0490
Rump Angle	.1272
Rump Width	.0882
Fore Udder	.1013
Rear Udder Height	.0859
Rear Udder Width	.0745
Udder Depth	.0872
Suspensory Ligament	.0718
Teat Placement	.1014

these two covariances is that the covariance among maternal half-sibs contains maternal effects, although the presence of maternal effects was not indicated for these traits.

Ranges in approximate standard errors of covariances among relatives (Table 4), computed according to Dickerson (8), were similar for paternal half-sibs, daughters and dams, and maternal half-sibs. Standard errors of the covariances among full-sibs were substantially larger, ranging from .45 to 1.30. These large standard errors were due to the smaller numbers of full-sib groups within herd-classifier subclasses.

The four components of genetic variance and covariance for each of the 13 traits, and their approximate standard errors, are shown in Table 5. Estimates of additive effects were approximately ten times their standard errors for all traits. Dominance components ranged from 2 to 4 times as great as additive components for dairy character, rump width, and the udder traits; fore udder, rear udder height, rear udder width, and suspensory ligament. However, dominance effects were small for the other seven traits. Dominance variance was a large proportion, (more than 50%) of the total phenotypic variation for dairy character, fore udder, rear udder height, and rear udder width. These estimates were unexpectedly large, suggesting some source of bias. However, the possibility that estimates of dominance variance were inflated by common environmental components for full-sibs seems unlikely, based on the magnitude of the covariances among maternal half-sibs. That is, since full-sibs in dairy cattle seldom are contemporaneous in time, maternal

Table 4. Ranges in standard errors of covariances.

Relatives[a]	#	Range in SE's
PHS	47106	.06 to .24
FS	3737	.45 to 1.30
D'D	21453	.11 to .28
MHS	64359	.12 to .31

[a]PHS = paternal half-sibs; FS = full-sibs; D'D = daughter-dam; MHS = maternal half-sibs.

Table 5. Components of genetic variance and covariance and their approximate standard errors (SE).[a]

Trait	σ^2_{Ao}	SE	σ^2_{Do}	SE	σ^2_{Am}	SE	σ_{AoAm}	SE
Stature	11.50	.98	1.54	4.97	-1.09	.64	.92	.63
Strength	5.37	.48	2.24	3.34	.67	.43	-.38	.36
Dairy Character	4.28	.40	17.80	4.05	- .16	.43	.13	.34
Foot Angle	2.37	.24	3.06	3.03	- .23	.39	-.27	.28
Rear Legs	2.43	.24	.17	2.95	- .16	.37	-.12	.27
Rump Angle	5.96	.51	5.58	2.79	-1.64	.37	.46	.34
Rump Width	5.23	.47	11.28	3.89	- .85	.48	.32	.39
Fore Udder	5.06	.48	18.83	4.96	-1.73	.57	1.66	.44
Rear Udder Height	3.71	.35	13.53	3.66	-2.33	.44	1.40	.33
Rear Udder Width	4.16	.39	12.64	3.93	-1.19	.48	.58	.37
Udder Depth	3.42	.30	1.82	1.90	- .99	.26	.39	.22
Suspensory Ligament	5.39	.51	13.69	5.36	-3.31	.65	2.10	.50
Teat Placement	3.63	.34	4.36	3.24	- .48	.40	.55	.31

[a]σ^2_{Ao} = direct additive; σ^2_{Do} = direct dominance; σ^2_{Am} = direct maternal; σ_{AoAm} = direct additive-maternal.

half-sibs would appear subject to the same common environmental factors as full-sibs. Additionally, common environmental factors might be expected to cause large estimates of dominance variance for all traits rather than for the subset observed. It therefore seems likely that the large dominance components are real or the result of random sampling errors.

Additive maternal variances were consistently negative, most within two standard errors of zero. These results imply that maternal effects are essentially nonexistent relative to additive and dominance effects. A logical consequence was that components of covariance between direct additive and additive maternal effects were also nonexistent.

Heritability estimates were calculated for each of the 13 traits from the covariances among the four types of relatives. Heritabilities also were calculated from sire, full-sib, and dam components of variance, and daughter-dam regression individually and are shown in Table 6. Only the additive genetic variance was used in these calculations, with other components of genetic variance assumed zero.

Estimates from daughter-dam regression and from sire components of variance were similar for all traits. Estimates from full-sib variance components were consistently largest, while those from dam variance components were smallest. An explanation for the large heritabilities for dairy character, rump width, and several udder traits, estimated from the full-sib variance components, is that dominance variance contributes to the covariance among full-sibs. These same traits were

Table 6. Heritability estimates from sire (σ^2_S), full-sib (σ^2_{FS}), and dam (σ^2_D) components of variance, and daughter-dam regression ($b_{D'D}$).

Trait	$4\sigma^2_S$	$2\sigma^2_{FS}$	$4\sigma^2_D$	$2b_{D'D}$
Stature	.32	.34	.30	.37
Strength	.21	.30	.26	.26
Dairy Character	.17	.46	.16	.21
Foot Angle	.10	.13	.02	.07
Rear Legs	.11	.09	.06	.10
Rump Angle	.29	.33	.06	.25
Rump Width	.19	.36	.11	.18
Fore Udder	.15	.41	.14	.20
Rear Udder Height	.15	.33	.00	.17
Rear Udder Width	.15	.33	.06	.15
Udder Depth	.24	.23	.07	.17
Suspensory Ligament	.14	.26	.01	.14
Teat Placement	.16	.26	.17	.20

described earlier as having large dominance variance components, relative to additive components.

Heritability estimates for each trait, calculated by dividing the additive genetic variance (computed from all covariances among relatives, Figure 1) by the within herd-classifier phenotypic variance are in Table 7. These estimates ranged from .11 for foot angle to .36 for stature and were very similar to those estimated by Weinberg (29) and Norman (18).

Table 7. Heritability (h^2) estimates of linear type traits.

Trait	h^2
Stature	.36
Strength	.23
Dairy Character	.17
Foot Angle	.11
Rear Legs	.12
Rump Angle	.30
Rump Width	.21
Fore Udder	.16
Rear Udder Height	.15
Rear Udder Width	.16
Udder Depth	.27
Suspensory Ligament	.15
Teat Placement	.17

II. Evaluation of Corrective Mating

Expected Results of Corrective Mating

Means and standard deviations for actual (age and stage adjusted) and offspring scores deviated from herd averages (computed from valid scores of cows 18 to 200 months of age and 500 Or less days in lactation) and measures of parental performance are in Table 8. Actual offspring scores (ranging from 69.5 for foot angle to 82.9 for dairy character) were slightly lower than for dams (which ranged from 68.1 for teat placement to 83.1 for dairy character) perhaps as a result of selection. Actual dam scores were slightly higher for all traits except foot angle, rump width, rear udder width, and teat placement. Also, dam's average final score was 79.0, nearly 2 points higher than that for offspring (77.2), indicating selection had occurred.

Means and standard deviations for type traits of Jersey cattle appraised in 1980, computed by Norman et. al. (18) were very similar to actual scores for dams in this study. These results seem reasonable since linear scoring was implemented in 1980, and most dams having daughters in this data set which includes cattle scored between January 1980 and December 1983, would have been in the data set of Norman et. al. (18). Actual offspring scores were similar to overall average computed for each of the 13 traits.

The variability of actual dam scores were larger than offspring scores for 7 of the 13 traits, and similar to those computed by Norman et. al. (18). Standard deviations of actual offspring scores were

Table 8. Means and standard deviations for actual and deviated (from herd average) offspring scores, sire predicted differences (PD) and four measures of dam's merit (D1-D4)[a,b].

Trait	Offspring Score				Sire PD		Dam Measures									
	Actual		Deviated		Sire PD		Actual		D1		D2		D3		D4	
	$\overline{X}$	σ	$\overline{X}$	σ	$\overline{X}$	σ	$\overline{X}$	σ	$\overline{X}$	σ	$\overline{X}$	σ	$\overline{X}$	σ	$\overline{X}$	σ
Stature	74.8	6.66	-.16	6.27	-.02	1.53	75.6	6.60	.13	1.19	.10	1.10	.11	1.62	.08	.76
Strength	80.5	6.28	-.30	5.69	-.03	1.06	81.5	4.71	.08	.54	.06	.53	.05	.84	.02	.47
Dairy Character	82.9	5.58	.21	5.29	.24	.96	83.1	4.96	.05	.42	.03	.39	.01	.70	.00	.44
Foot Angle	69.5	5.36	.47	5.11	-.02	.65	68.6	5.02	-.02	.28	-.02	.26	.00	.47	-.01	.30
Rear Legs	79.3	5.12	-.41	4.86	.04	.70	80.5	4.95	.04	.30	.04	.27	-.03	.50	-.03	.27
Rump Angle	76.9	4.74	-.64	4.55	-.01	1.02	78.5	5.04	.15	.76	.13	.71	.02	.74	-.00	.51
Rump Width	78.7	5.72	.46	5.43	.14	.96	77.9	6.26	-.03	.66	-.03	.61	-.01	.74	.01	.49
Fore Udder	79.3	5.86	.06	5.61	.05	.98	79.6	6.51	.03	.52	.03	.49	.03	.86	-.00	.47
Rear Udder Height	82.3	5.05	.13	4.85	.15	.82	82.5	5.90	.03	.44	.02	.42	.00	.75	-.02	.39
Rear Udder Width	81.0	5.65	.97	5.35	.19	.87	78.9	6.17	-.08	.49	-.08	.46	-.04	.75	-.03	.40
Udder Depth	80.0	3.78	-.21	3.48	.08	.79	80.7	4.81	.07	.65	.07	.61	-.03	.66	-.02	.44
Suspensory Ligament	79.6	5.70	-.07	5.48	.09	.95	80.3	7.63	.05	.57	.05	.55	.00	.81	-.01	.52
Teat Placement	70.1	5.44	.86	5.23	.06	.76	68.1	4.91	-.10	.42	-.09	.41	.01	.50	-.02	.36

[a]D1 = $.5h^2(y-\mu)$; D2 = $.5h^2(y-\overline{H})$; D3 = dams's cow index; D4 = .5 maternal grandsire predicted difference; y = dam's score; μ = overall mean; $\overline{H}$ = herd mean.

[b]Number observations = 14721.

greater than deviated scores, due to the removal of herd effects from the latter. The average deviation ranged from -.64 for rump angle to .97 for rear udder width. There was some tendency for offspring in this data set (n = 14721), which were required to have sire, dam, and maternal grandsire genetic evaluations, to be slightly high in the pins, wide in the rear udder, with closely placed teats relative to their herdmates.

Average sire predicted differences and four measures of the dam for each trait were near zero. Sire predicted differences ranged from -.03 for strength to .24 for dairy character. Sires represented tended to have daughters that are more dairy, have wider rumps, and higher, wider rear udders than sires defining the genetic base for linear traits. Ranges for dam measures were from -.10 to .15 for D1, -.09 to .13 for D2, -.04 to .11 for D3, and -.03 to .08 for D4. Standard deviations were generally higher for sire predicted differences than for the four dam measures. Of the four dam measures, D3 had the largest standard deviations for all traits except rump angle. As was expected, the variability of D1 which contains herd effects, was greater than D2, and D3 greater than D4 which does not include differences among dams by the same sire.

Means, standard deviations, and ranges of predicted offspring scores, using sire predicted differences and four measures of dam's merit are in Table 9. These results are similar to comparisons of D1 to D4 in Table 8, since the predicted offspring scores differ only in contribution from D1 to D4 (i.e. PD_s is constant) . Of the 13 traits,

Table 9. Means, standard deviations and ranges for predicted offspring score using predicted differences of sires with four measures of dam's merit (D1–D4).[a]

Trait	D1				D2				D3				D4			
	$\overline{X}$	σ	MIN	MAX	$\overline{X}$	σ	MIN	MAX	$\overline{X}$	σ	MIN	MAX	$\overline{X}$	σ	MIN	MAX
Stature	.10	1.94	-8.9	7.2	.07	1.85	-8.5	7.5	.08	2.21	-8.3	8.8	.05	1.71	-7.1	6.7
Strength	.05	1.20	-4.8	3.7	.03	1.17	-4.5	3.8	.02	1.35	-5.5	4.5	-.00	1.15	-4.8	4.1
Dairy Character	.29	1.05	-4.4	3.6	.27	1.03	-4.1	3.4	.25	1.20	-6.6	4.2	.24	1.06	-3.4	3.6
Foot Angle	-.04	.71	-2.5	2.4	-.04	.70	-2.4	2.4	-.02	.80	-3.2	3.0	-.02	.71	-2.3	2.1
Rear Legs	.07	.77	-3.6	2.4	.07	.75	-3.6	2.4	.01	.86	-4.5	3.0	.01	.75	-3.0	2.6
Rump Angle	.14	1.28	-4.7	5.0	.12	1.24	-4.8	4.7	.01	1.25	-5.2	4.6	-.01	1.13	-4.5	3.9
Rump Width	.11	1.18	-5.1	3.7	.11	1.13	-5.0	3.5	.13	1.22	-5.7	3.8	.15	1.08	-4.5	3.5
Fore Udder	.08	1.13	-4.5	3.6	.07	1.10	-4.3	3.7	.07	1.33	-6.3	4.5	.05	1.09	-4.3	3.6
Rear Udder Height	.18	.94	-4.5	3.0	.17	.92	-4.5	2.9	.15	1.13	-5.7	4.0	.13	.91	-3.2	3.1
Rear Udder Width	.11	1.02	-4.7	3.3	.11	.98	-4.6	3.1	.15	1.16	-5.3	4.7	.16	.95	-4.7	3.2
Udder Depth	.14	1.02	-5.1	3.9	.15	.98	-5.2	3.7	.05	1.04	-5.1	3.6	.06	.90	-5.0	3.3
Suspensory Ligament	.14	1.12	-5.0	4.1	.13	1.11	-5.0	4.1	.09	1.26	-5.5	4.4	.07	1.07	-4.1	3.7
Teat Placement	-.04	.87	-2.9	4.5	-.03	.86	-2.9	4.7	.06	.91	-2.9	4.8	.04	.83	-2.5	3.1

[a] D1 = $.5h^2(y-\mu)$; D2 = $.5h^2(y-\overline{H})$; D3 = dam's cow index; D4 = .5 maternal grandsire predicted difference; y = dam's score; μ = overall mean; $\overline{H}$ = herd mean.

dairy character had the highest mean across dam measures, and foot angle was consistently negative. Standard deviations of predicted offspring scores were highest for D3, except for rump angle, similar to results in Table 8. Also, the variability of predicted offspring scores for D1 were greater than D2, and D3 greater than D4. Standard deviations of predicted offspring scores were approximately 20 to 30% of the standard deviations of deviated offspring scores (Table 8). The relative size of standard deviations and ranges corresponded roughly to the magnitude of heritabilities of the individual type traits, as expected.

Regression of Offspring Scores on Measures of Parental Performance

Linear and quadratic regression coefficients, and multiple squared correlations (R^2) from regressing offspring score on offspring scores predicted from sire predicted differences and four measures of dam's merit are in Table 10. Traits significantly affected by herd average for final score also are indicated. The first line for each trait corresponds to the model containing the linear regression only, while the second line refers to the model including linear and quadratic regressions and HAFS class. Linear regressions were largest for predicted offspring score from D4 for nine of the 13 traits, and from D2 for three of the remaining four traits. These results may be due to the generally lower variation in predicted offspring scores for D4 and D2 (Table 9).

Linear regression coefficients were nearly equal to the expected value of 1.0 for all traits except strength, udder depth, suspensory

Table 10. Linear (L) and quadratic (Q) regession coefficients, multiple squared correlations (R^2) and significance of herd average final score (FS) for regression of offspring score on offspring score predicted from predicted differences of sires (S) and measures of dam's merit (D1 - D4)[a].

Trait	S + D1				S + D2				S + D3				S + D4			
	L	Q	FS	R^2	L	Q	FS	R^2	L	Q	FS	R^2	L	Q	FS	R^2
Stature	.95			.09	1.03			.09	.89			.10	1.01			.08
	.96	.00[b]		.09	1.03	-.01[b]		.09	.89	.00[b]		.10	1.02	-.02[b]		.08
Strength	1.24			.07	1.18			.06	1.07			.06	1.20			.06
	1.27	-.10		07	1.21	-.09		.06	1.08	-.05		.07	1.23	-.16		.06
Dairy Character	1.07			.05	1.12			.05	.97			.05	1.03			.04
	1.19	-.12	b	.05	1.25	-.15	b	.05	1.00	-.03[b]		.05	1.14	-.13		.05
Foot Angle	.85			.01	.86			.01	.90			.02	1.00			.02
	.84	.03[b]	b	.01	.86	.05[b]	b	.01	.90	-.05[b]	b	.02	1.02	.11[b]	b	.02
Rear Legs	1.03			.03	1.10			.03	1.00			.03	1.16			.03
	1.02	-.03[b]		.03	1.10	.00[b]		.03	1.00	.06[b]		.03	1.15	-.03[b]		.03
Rump Angle	.87			.06	.94			.07	.97			.07	1.00			.06
	.87	.01[b]		.06	.94	.01[b]		.07	.97	.01[b]		.07	.99	-.03[b]		.06
Rump Width	.86			.03	.96			.04	.99			.05	1.06			.04
	.87	-.03[b]		.04	.96	-.04[b]		.04	1.00	-.02[b]		.05	1.07	-.08		.05
Fore Udder	.97			.04	1.04			.04	.89			.04	1.02			.04
	.98	.05	b	.04	1.04	.06	b	.04	.89	.04	b	.04	1.02	.00[b]	b	.04
Rear Udder Height	.99			.04	1.06			.04	.88			.04	1.08			.04
	.99	.02[b]		.04	1.06	.01[b]		.04	.87	.06	b	.04	1.11	-.07[b]	b	.04
Rear Udder Width	.93			.03	1.03			.04	.88			.04	1.09			.04
	.93	-.01[b]	b	.03	1.04	-.04[b]	b	.04	.87	.02[b]	b	.04	1.13	-.07	b	.04
Udder Depth	.67			.04	.72			.04	.74			.05	.81			.04
	.69	.11	b	.04	.75	.13	b	.04	.79	.12	b	.05	.84	.13	b	.05
Suspensory Ligament	.88			.03	.91			.03	.82			.04	.93			.03
	.89	-.01[b]		.03	.92	-.01[b]		.04	.83	.00[b]		.04	.93	-.05[b]		.04
Teat Placement	1.20			.04	1.21			.04	1.26			.05	1.27			.04
	1.19	.03[b]		.04	1.21	.03[b]		.04	1.26	.01[b]		.05	1.27	.02[b]		.04

[a] D1 = $.5h^2(y-\mu)$; D2 = $.5h^2(y-\overline{H})$; D3 = dams's cow index; D4 = .5 maternal grandsire predicted difference; y = dam's score; μ = overall mean; $\overline{H}$ = herd mean.

[b] Not significant; others significant ($P < .05$).

ligament, and teat placement. Coefficients were consistently and unexpectedly high for strength and teat placement, and low for udder depth and suspensory ligament.

Greater than expected regressions for strength and teat placement indicate that larger than expected proportions of parental differences for these traits are reflected in deviated scores of offspring (except for the parental combination, S + D3, for strength, where the regression was near 1.0). This implies that true genetic differences among parents are greater than reflected in their evaluations (i.e., in PD for sires and D1 to D4 for dams). This seems unlikely to have resulted from an under-estimation of heritability since values in the current study are very similar to those reported previously (18, 29). It seems more likely that the parental evaluations used do not reflect fully genetic differences among herds, or that an environmental correlation between offspring and parents exists for these traits.

Less than expected regressions for udder depth and suspensory ligament indicate that smaller than expected proportions of parental differences are reflected in deviated scores of offspring for these traits. Again, this is unlikely to have resulted from the prediction of offspring performance using estimates of heritability which were larger than true values. It seems more likely that sampling variation or environmental biases in parental evaluations are responsible for these results.

Multiple squared correlations were similar across the four measures of dam's performance, being largest for stature, the trait with the highest heritability. These results give no indication that any of the measures of dam's performance is preferred as a more accurate predictor of offspring score.

When quadratic regressions and offspring herd average for final score were added to the model, linear regression coefficients changed little from the linear only model. Linear regression coefficients were significant in both models for all traits using any of the measures of dam's performance (D1 to D4). Quadratic coefficients, were significant across D1 to D4 for strength and udder depth, for all but D3 for dairy character and all but D4 for fore udder. Quadratic coefficients tended to be smallest for D3.

Herd average for final score significantly ($P < .05$) affected all traits for at least one model, except for foot angle, fore udder, rear udder width, and udder depth. It can be concluded that quadratic effects of parental performance and the effect of herd average for final score explained very little of the variation in offspring scores, since R^2's did not increase when these effects were added to the model.

Table 11 contains linear regression coefficients and R^2's for regressions of offspring score which were computed separately for the measure of sire performance (PD_s) and the measure of dam performance (D1 to D4).

Coefficients for sires were always greater than for dams, across D1 to D4. Sire coefficients were much greater than 1.0 for strength, rear legs, and teat placement; somewhat greater than 1.0 for rump

Table 11. Linear regession coefficients and multiple squared correlations (R^2) for regressions of offspring score on predicted differences of sires (S) and measures of dam's merit (D1-D4)[a].

Trait	S	D1	R^2	S	D2	R^2	S	D3	R^2	S	D4	R^2
Stature	1.12	.66	.09	1.14	.80	.09	1.13	.68	.11	1.12	.57	.08
Strength	1.32	.93	.07	1.33	.54	.06	1.33	.66	.07	1.33	.49	.06
Dairy Character	1.14	.77	.05	1.15	.95	.05	1.13	.69	.05	1.13	.58	.04
Foot Angle	1.00	-.04[b]	.02	1.00	-.07[b]	.02	1.02	.67	.02	1.02	.93	.02
Rear Legs	1.22	.01[b]	.03	1.22	.31	.03	1.22	.57	.03	1.23	.72	.03
Rump Angle	1.09	.48	.07	1.10	.62	.07	1.10	.72	.07	1.10	.58	.06
Rump Width	1.17	.19	.04	1.18	.39	.05	1.17	.69	.05	1.17	.63	.05
Fore Udder	1.09	.59	.04	1.09	.82	.04	1.08	.64	.05	1.09	.68	.04
Rear Udder Height	1.16	.41	.04	1.17	.66	.04	1.16	.55	.05	1.17	.69	.04
Rear Udder Width	1.17	.21	.04	1.18	.49	.04	1.17	.50	.04	1.18	.63	.04
Udder Depth	.86	.39	.04	.86	.47	.04	.84	.59	.05	.85	.69	.04
Suspensory Ligament	1.01	.52	.03	1.02	.59	.03	1.02	.55	.04	1.03	.59	.03
Teat Placement	1.34	.73	.04	1.35	.73	.04	1.35	1.04	.05	1.36	.89	.04

[a]$D1 = .5h^2(y-\mu)$; $D2 = .5h^2(y-\overline{H})$; D3 = dams's cow index; D4 = .5 maternal grandsire predicted difference; y = dam's score; μ = overall mean; $\overline{H}$ = herd mean.

[b]Not significant; others significant ($P < .05$).

width, rear udder height, and rear udder width; and less than 1.0 for udder depth. Comparisons of regressions fit separately for sires and dams to regressions in Table 10 for combined estimates of parental performance and suggest that, except for udder depth, larger than expected regressions are associated with inaccuracies in sire evaluations while smaller than expected regressions are due primarily to inaccuracies in measures of dam's performance.

Coefficients for D1 and D2 were extemely small for foot angle and rear legs. All linear regression coefficients were significant except for foot angle and rear legs for D1 and foot angle for D2. No single measure of dam merit yielded consistently higher coefficients than another, however teat placement for D3 was the only coefficient greater than 1.0.

Multiple squared correlations showed no increase over those in Table 10, where sire and dam measures of performance were weighted equally and combined additively to predict offspring scores. There was a tendency for R^2's for models including D3 to be as large or slightly larger (six of the 13 traits) than those for models including D1, D2, and D4. Results in Table 11 indicate that although least squares regression indicate optimum (minimum error sums of squares) prediction is achieved by giving the sire considerably more weight than the dam, the improvement relative to equal weighting of parental measures is not reflected by higher R^2's. The amount the prediction is improved may be small, or R^2 maybe an insensitive measure.

Linear and quadratic regression coefficients, R^2's, and significance of effects of herd average final score for individual measures of parental performance (i.e., sire and dam separately) are in Table 12. Linear regressions for sires and D1 to D4 were slightly larger than with the model including linear regressions only (Table 11) for all traits except dairy character, which was much larger. All linear regressions differed significantly from zero except for foot angle for D1 and D2, and rear legs for D1, similar to results in Table 11.

Quadratic coefficients for sires were significant ($P < .05$) for most models for nearly all traits. Exceptions were for rear legs, fore udder, suspensory ligament, and teat placement across all models, and for foot angle for D3 and D4 and for rump angle for D4. All significant quadratic coefficients for sires were negative except for foot angle and udder depth, traits with intermediate optima. The largest (absolute value) quadratic coefficients were for strength, dairy character, foot angle, and rear udder height, ranging from -.24 to .16.

Quadratic coefficients for D1 to D3 (i.e., those including the dam's own score) generally were significant ($P < .05$) and positive for the udder traits, excluding teat placement, and for rump width, and significant and negative for foot angle. Results for D4 were quite different, being significant for all body traits except stature and rump width, and nonsignificant for all udder traits except suspensory ligament. The significant quadratic coefficients were negative except for foot angle.

Herd average for final score effects were similar to results in Table 10. All traits were significantly ($P < .05$) affected in at least

Table 12. Linear and quadratic regession coefficients, multiple squared correlations (R^2) and significance of herd average final score (FS) for regession of offspring score on predicted differences of sires (S) and measures of dam's merit (D1 – D4)[a].

Trait	S	D1	FS	R2	S	D2	FS	R^2	S	D3	FS	R^2	S	D4	FS	R^2
Stature	1.14[b]	.68		.09	1.16	.81		.10	1.15	.68		.11	1.14	.55		.08
	-.05[c]	.04[d]			-.06	.01[d]			-.05	.02[d]			-.06	.04[d]		
Strength	1.40	.92		.07	1.41	.56		.07	1.40	.66		.08	1.40	.59		.07
	-.23	-.09[d]			-.24	-.20[d]			-.22	-.06[d]			-.23	- .37		
Dairy Character	1.31	.81	d	.05	1.33	.99		.05	1.30	.71		.05	1.31	.60		.05
	-.19	.12[d]			-.19	.06[d]			-.19	.02[d]			-.19	- .40		
Foot Angle	1.02	.07[d]	d	.02	1.02	.04[d]	d	.02	1.03	.72	d	.02	1.03	.99	d	.02
	.15	-.97			.15	-.96			.15[d]	-.39			.15[d]	.72		
Rear Legs	1.22	-.06[d]		.03	1.22	.34		.03	1.22	.59		.04	1.22	.74		.03
	-.03[d]	-.36[d]			-.03[d]	.09[d]			-.02[d]	.08[d]			-.02[d]	-1.06		
Rump Angle	1.08	.48		.07	1.09	.63		.07	1.09	.72		.07	1.09	.58		.06
	-.06	.01[d]			-.06	.01[d]			-.06	-.02[d]			-.05[d]	- .19		
Rump Width	1.18	.33		.05	1.18	.49		.05	1.18	.74		.05	1.18	.68		.05
	-.10	.29			-.10	.27			-.10	.16			-.10	.13[d]		
Fore Udder	1.09	.66	d	.04	1.10	.93	d	.04	1.08	.68	d	.05	1.10	.69	d	.04
	.03[d]	.20			.03[d]	.31			.03[d]	.09			.03[d]	.19[d]		
Rear Udder Height	1.25	.54	d	.04	1.25	.92		.05	1.24	.63	d	.05	1.25	.69	d	.04
	-.15	.35			-.15	.67			-.15	.16			-.15	.12[d]		
Rear Udder Width	1.27	.44	d	.04	1.27	.79	d	.04	1.27	.56	d	.04	1.28	.62	d	.04
	-.13	.60			-.13	.77			-.13	.23			-.13	.30[d]		
Udder Depth	.90	.46	d	.05	.91	.58	d	.05	.89	.71	d	.05	.89	.70	d	.05
	.16	.14			.16	.21			.16	.19			.16	.06[d]		
Suspensory Ligament	1.02	.70		.04	1.02	.83		.04	1.02	.60		.04	1.03	.56		.04
	-.04[d]	.31			-.04[d]	.39			-.04[d]	.06[d]			-.04[d]	- .21		
Teat Placement	1.34	.71		.04	1.34	.74		.04	1.34	1.01		.05	1.34	.87		.04
	.02[d]	.12[d]			.02[d]	.17[d]			.03[d]	.17[d]			.03[d]	.37[d]		

[a]$D1 = .5h^2(y-\mu)$; $D2 = .5h^2(y-\overline{H})$; D3 = dams's cow index; D4 = .5 maternal grandsire predicted difference; y = dam's score; μ = overall mean; $\overline{H}$ = herd mean.

[b]Linear regression coefficient on first line for trait.

[c]Quadratic regression coefficent on second line for trait.

[d]Not significant; others significant ($P < .05$).

one model, except for foot angle, fore udder, rear udder width, and udder depth. Also, R^2's did not show an increase over the linear only model (Table 11).

Negative quadratic coefficients indicate a tendency for a decrease in slope at higher scores while positive coefficients indicate the opposite. However for most traits, quadratic effects will have relatively little effect on predictions. For example, -.24 for strength was the largest quadratic coefficient observed. For extreme PD_S of ± 2 points, contribution to the predicted offspring score will be less than one point. The largest quadratic coefficient for dam measures was -1.06 for D4 and rear legs. With an extreme of ± .5 points (twice the standard deviation of .27 in Table 8), approximately ± .25 points is contributed to predicted offspring score.

These results were consistent with those from Table 11 in that least squares regression indicated improved prediction by allowing for curvilinear relationships and accounting for herd level for final score, but the improvement was not reflected in higher R^2's.

Analysis of Offspring Scores by Categorical Performance Levels of Parents

Results from this section represent an alternative method of quantitating relationships between offspring scores and measures of parental merit. Due to similarity of results in regression analysis for D1 to D4, categorical levels of dam's performance were defined and evaluated for dam's score (equivalent to D1) and dam's cow index (D3) only. Mean squares for analyses of variance are in Table 13 for

Table 13. Means squares for effects on offspring scores of categorical levels of predicted differences for sires (S), scores (D1) and cow indexes (D3) for dams, interaction of sire and dam, and herd averages for final score (FS).

Trait	S	D1	SxD1	FS	S	D3	SxD3	FS
Stature	7103.7	1177.7	39.8[a]	166.4	5347.9	2559.7	46.2[a]	174.8
Strength	4770.0	509.3	26.8[a]	188.1	4842.0	854.3	40.1[a]	224.4
Dairy Character	4046.8	247.2	37.1[a]	58.7[a]	3008.6	852.3	22.6[a]	96.9
Foot Angle	1004.8	48.1[a]	15.5[a]	41.8[a]	956.3	403.9	28.2[a]	29.3[a]
Rear Legs	1847.3	7.5[a]	32.8[a]	51.9[a]	2124.1	302.9	37.3	49.7[a]
Rump Angle	3774.3	362.4	26.3[a]	78.3	3173.0	782.0	19.3[a]	83.7
Rump Width	3281.2	165.0	28.6[a]	133.6	3300.1	692.0	20.2[a]	141.7
Fore Udder	3489.3	233.2	30.5[a]	21.9[a]	3257.6	854.8	28.3[a]	15.4[a]
Rear Udder Height	2743.4	90.4	19.6[a]	53.5	2274.8	564.5	36.4[a]	48.9[a]
Rear Udder Width	2207.0	153.1	25.8[a]	44.8[a]	2683.5	518.5	24.4[a]	48.7[a]
Udder Depth	1318.8	175.9	13.2[a]	4.7[a]	1387.8	470.8	15.2[a]	5.2[a]
Suspensory Ligament	3267.1	349.2	50.3	108.5	2445.2	683.2	43.8[a]	102.2
Teat Placement	2662.4	212.1	16.9[a]	93.9	2944.2	667.2	32.9[a]	104.0

[a]Not significant; others significant ($P < .05$).

effects on linear scores of categorical levels of predicted differences for sires (PD_S), scores (D1) and cow indexes (D3) for dams, the interaction of sire and dam measures, and herd average final score (HAFS) class. Categorical levels of PD_S, D1, and D3 significantly ($P < .05$) affected differences in offspring score for all traits except for D1 with foot angle and rear legs, which is in agreement with the small regression coefficients for these traits in Tables 11 and 12.

Effects of HAFS categories generally agreed with results in the regression models. Exceptions included a nonsignificant ($P < .05$) effect of HAFS with D1 and D3 for rear legs, which was significant in regression models, and for D1, a significant ($P < .05$) effect of HAFS on rear udder height, which was nonsignificant in the regression models.

Sire by D1 interactions were significant ($P < .05$) only for suspensory ligament, and for rear legs for the sire by D3 interactions. The lack of significant interaction between sire and dam indicates that we can assume additivity for most traits, without significant loss of accuracy.

Least squares means of offspring scores for five categorical levels of HAFS, adjusted for effects of categorical levels of PD_S, D1 or D3, and interaction of sire and dam measure are in Tables 14 (model includes D1) and 15 (model includes D3). Least squares means should be interpreted relative to average deviated offspring scores in Table 8, since the latter were not zero.

Table 14. Least squares means of deviated offspring scores for categorical levels of herd average for final score adjusted for effects of categorical levels of predicted differences for sires, scores for dams, and interaction of sire and dam.

	Herd averages for final score				
Trait	60 to 72	73 to 75	76 to 77	78 to 80	81 to 90
Stature	- .46	.25	.04	.12	-.38
Strength	- .56	-.06	-.05	.21	-.48
Dairy Character	- .06	.18	.37	.18	.41
Foot Angle	.34	.32	.56	.53	.57
Rear Legs	- .02	-.40	-.44	-.51	-.31
Rump Angle	-1.04	-.77	-.71	-.48	-.78
Rump Width	- .20	.39	.37	.31	-.12
Fore Udder	.13	-.15	-.02	.01	-.08
Rear Udder Height	- .14	-.07	.10	.22	-.03
Rear Udder Width	.77	1.11	1.07	1.22	.99
Udder Depth	- .06	-.11	-.06	-.12	-.17
Suspensory Ligament	- .20	-.53	-.10	-.15	-.35
Teat Placement	1.12	1.11	1.36	1.37	1.67

Table 15. Least squares means of deviated offspring scores for categorical levels of herd average for final score adjusted for effects of categorical levels of predicted differences for sires, cow indexes for dams, and interaction of sire and dam.

	Herd Averages for Final Score				
Trait	60 to 72	73 to 75	76 to 77	78 to 80	81 to 90
Stature	-.61	.09	-.08	.14	-.40
Strength	-.81	-.26	-.25	.11	-.55
Dairy Character	-.13	.20	.42	.26	.55
Foot Angle	.39	.40	.61	.56	.58
Rear Legs	.04	-.36	-.37	-.43	-.22
Rump Angle	-1.11	-.84	-.79	-.53	-.79
Rump Width	-.37	.28	.22	.19	-.22
Fore Udder	.11	-.09	.02	.05	-.08
Rear Udder Height	-.13	-.01	.14	.25	.02
Rear Udder Width	.81	1.16	1.11	1.28	1.04
Udder Depth	.06	-.00	.01	-.04	-.10
Suspensory Ligament	-.25	-.49	-.07	-.10	-.24
Teat Placement	1.02	1.02	1.29	1.29	1.60

For traits significantly ($P < .05$) effected by HAFS (Table 13) in the model with D1 (stature, strength, rump angle, rump width, rear udder height, suspensory ligament, and teat placement), all traits except teat placement tended to be scored slightly lower in herds with lowest and highest averages for final score. For teat placement, the tendency was for teats to be scored more closely placed in herds with higher levels of final score. For the model with D3, stature, strength, dairy character, rump angle, rump width, suspensory ligament and teat placement were significantly ($P < .05$) effected by HAFS (Table 15). The pattern of least squares means was similar to the model containing D1, except for dairy character, where herds with highest average final score had cattle scored highest in dairy character.

Differences in average offspring scores by HAFS were not large. The largest difference was for stature in the two lowest levels of HAFS (-.46 versus .25) which was less than one point.

Least squares means in Tables 16 and 17 show average offspring scores for categories of sires, dams, and sire by dam combinations, adjusted for effects of HAFS levels (categories are for D1 in Table 16 and D3 in Table 17). Least squares means for sires adjusted for D1 and HAFS, increased consistently with PD_S for all traits. That is, the rank of the least squares mean for offspring score was always identical to the rank of the PD_S category. There was no such consistency for categories of D1, adjusted for PD_S and HAFS. Highest offspring scores did occur at highest levels of D1 for all traits except foot angle. However, considerable variation in rank of offspring scores occurred

Table 16. Least squares means of offspring scores for categorical levels of predicted differences for sires and scores of dams adjusted for effects of categorical levels of herd average for final score.

Dam Score	Predicted Differences of Sires					
Stature	-5.50 < to < -2.00	-2.00 < to < -.75	-.75 < to < 1.00	1.00 < to < 2.00	2.00 < to < 4.80	ALL
50 to 59	-3.78	-1.77	- .37	1.33	1.95	- .53
60 to 69	-3.21	-2.78	-1.17	.81	1.04	-1.06
70 to 77	-3 98	-2.04	- .30	1.22	2.27	- .56
78 to 83	-2.79	-1.31	.80	2.51	3.11	.47
84 to 99	-1.10	- .46	1.46	3.08	3.32	1.26
ALL	-2.97	-1.67	.09	1.79	2.34	
Strength	-3.90 < to < -1.00	-1.00 < to < -.25	-.25 < to < .50	.50 < to < 1.38	1.38 < to < 2.70	ALL
50 to 59	-2.46	- .85	- .14	1.20	2.00	- .05
60 to 75	-3.28	-1.54	-1.26	- .48	1.10	-1.09
76 to 83	-2.76	-1.20	- .32	.67	1.61	- .40
84 to 86	-2.65	- .47	.32	1.04	2.04	.06
87 to 99	-2.50	.36	.61	1.68	2.61	.55
ALL	-2.73	- .74	- .16	.82	1.87	
Dairy Character	-3.10 < to < -.75	-.75 < to < -.10	-.10 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
50 to 59	-1.78	- .38	.35	1.05	1.88	.22
60 to 79	-2.82	- .93	.17	.34	1.77	-.29
80 to 84	-1.54	- .67	.29	.64	2.01	.15
85 to 87	-1.18	- .27	.38	.83	1.81	.31
88 to 99	-1.64	.42	1.13	1.18	2.36	.69
ALL	-1.79	- .37	.46	.81	1.96	

Table 16. (Continued)

Dam Score	Predicted Differences of Sires					
Foot Angle	-1.60 < to < -.96	-.96 < to < -.32	-.32 < to < .32	.32 < to < .96	.96 < to < 1.60	ALL
50 to 59	- .67	- .08	.29	1.09	1.52	.43
60 to 65	- .53	.25	.42	1.51	1.71	.67
66 to 68	- .21	.15	.42	1.30	1.33	.60
69 to 75	- .60	- .09	.38	1.31	1.74	.55
76 to 99	-1.21	- .86	- .04	1.73	.69	.06
ALL	- .64	- .12	.29	1.39	1.40	
Rear Legs	-2.10 < to < -.85	-.85 < to < -.25	-.25 < to < .30	.30 < to < 1.10	1.10 < to < 1.90	ALL
50 to 59	-1.68	- .81	- .52	.36	.89	- .35
60 to 75	-2.14	- .92	- .78	.68	1.66	- .30
76 to 82	-1.82	-1.19	- .51	.79	.88	- .37
83 to 85	-1.49	-1.34	- .69	.31	.99	- .44
86 to 99	- .83	-1.57	- .32	.76	.82	- .23
ALL	-1.59	-1.17	- .56	.58	1.05	
Rump Angle	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .28	.28 < to < 1.44	1.44 < to < 2.60	ALL
50 to 59	-2.28	-2.08	- .90	.30	.57	- .88
60 to 75	-3.24	-2.35	-1.01	- .17	- .18	-1.39
76 to 79	-2.37	-1.83	- .68	.39	.76	- .75
80 to 84	-2.46	-1.79	- .56	.23	1.18	- .68
85 to 99	-2.12	-1.52	- .13	1.66	1.70	- .08
ALL	-2.50	-1.91	- .65	.48	.80	

Table 16. (Continued)

Dam Score	Predicted Differences of Sires					
Rump Width	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .22	.22 < to < 1.36	1.36 < to < 2.50	ALL
50 to 59	-1.52	-1.79	.23	.94	2.47	.07
60 to 69	-2.48	-1.23	.12	1.02	2.29	- .06
70 to 79	-1.93	-1.17	.16	.89	1.76	- .06
80 to 84	-1.94	-1.14	.10	1.16	1.90	.02
85 to 99	-1.36	.35	.95	1.71	2.32	.79
ALL	-1.84	-1.00	.31	1.14	2.15	
Fore Udder	-2.90 < to < -1.25	-1.25 < to < -.54	-.54 < to < .64	.64 < to < 1.25	1.25 < to < 3.00	ALL
50 to 59	-1.61	- .46	.10	.46	2.51	.20
60 to 73	-2.90	-1.11	- .52	.65	.90	- .60
74 to 79	-2.29	-1.00	- .19	.71	1.86	- .18
80 to 84	-2.10	- .57	- .06	1.09	1.92	.06
85 to 99	-1.43	- .72	.46	1.54	2.13	.40
ALL	-2.06	- .77	- .04	.89	1.86	
Rear Udder Height	-2.80 < to < -.90	-.90 < to < -.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.10	ALL
50 to 59	-1.77	-1.12	.35	.81	1.65	- .02
60 to 75	-1.93	-1.02	.03	.59	.73	- .32
76 to 82	-1.70	- .80	- .02	1.07	1.50	.01
83 to 86	-1.76	- .94	.22	.96	1.73	.04
87 to 99	-1.26	- .30	.46	1.45	1.46	.36
ALL	-1.69	- .84	.21	.98	1.41	

Table 16. (Continued)

Dam Score	Predicted Differences of Sires					
Rear Udder Width	-3.80 < to < -.75	-.75 < to <-.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
50 to 59	- .26	.14	.77	1.74	2.45	.97
60 to 69	- .09	.20	1.32	1.73	3.17	1.27
70 to 79	-1.43	.08	.59	1.80	2.71	.75
80 to 84	- .96	.08	.86	1.63	2.49	.82
85 to 99	- .36	.72	1.33	2.19	2.88	1.35
ALL	- .62	.24	.97	1.82	2.74	
Udder Depth	-3.50 < to < -.75	-.75 < to < -.25	-.25 < to < .50	.50 < to < 1.14	1.14 < to < 2.30	ALL
50 to 59	-1.05	- .82	- .63	.46	1.12	- .18
60 to 75	-1.51	- .99	- .50	- .07	.94	- .43
76 to 79	-1.58	- .97	- .59	.03	1.49	- .32
80 to 84	- .89	- .67	- .42	.46	1.40	- .02
85 to 99	- .80	- .30	.34	1.02	1.90	.43
ALL	-1.16	- .75	- .36	.38	1.37	
Suspensory Ligament	-3.30 < to < -1.00	-1.00 < to < -.25	-.25 < to < .60	.60 < to < 1.00	1.00 < to < 3.20	ALL
50 to 59	-2.45	-1.32	- .00	1.14	.82	- .36
60 to 72	-3.82	-1.05	- .16	.53	.66	- .77
73 to 79	-2.31	-1.27	.19	.40	.95	- .41
80 to 84	-1.66	- .63	.33	.34	1.17	- .09
85 to 99	-1.35	- .46	.46	1.25	1.57	.30
ALL	-2.32	- .95	.16	.73	1.04	

Table 16. (Continued)

Dam Score	Predicted Differences of Sires					
Teat Placement	-1.90 < to < -.50	-.50 < to < -.14	-.14 < to < .74	.74 < to < 1.25	1.25 < to < 2.50	ALL
50 to 59	- .28	.03	.93	2.13	3.01	1.16
60 to 65	- .59	- .37	.65	1.88	3.43	1.00
66 to 69	- .47	- .02	1.02	1.71	2.87	1.02
70 to 73	.51	.62	1.89	2.25	3.53	1.76
74 to 99	.20	.70	1.60	2.85	3.10	1.69
ALL	- .13	.19	1.22	2.16	3.19	

Table 17. Least squares means of offspring scores for categorical levels of predicted differences for sires and cow indexes of dams adjusted for effects of categorical levels of herd average for final score.

Cow Index	Predicted Differences of Sires					
Stature	-5.50 < to < -2.00	-2.00 < to < -.75	-.75 < to < 1.00	1.00 < to < 2.00	2.00 < to < 4.80	ALL
-6.50 < to < -2.00	-5.04	-3.56	-1.79	- .33	- .25	-2.20
-2.00 < to < -1.06	-3.60	-2.80	-1.10	.37	1.27	-1.17
-1.06 < to < 1.25	-3.62	-1.91	- .11	1.52	2.80	- .26
1.25 < to < 2.50	-2.16	- .81	.84	3.05	2.34	.65
2.50 < to < 7.10	- .63	.51	2.59	3.89	4.20	2.11
ALL	-3.01	-1.71	.09	1.70	2.07	
Strength	-3.90 < to < -1.00	-1.00 < to < -.25	-.25 < to < .50	.50 < to < 1.38	1.38 < to < 2.70	ALL
-4.30 < to < -1.00	-3.85	-1.93	-1.26	- .52	.40	-1.43
-1.00 < to < - .50	-2.86	-1.66	- .46	- .14	1.56	- .71
- .50 < to < .32	-2.68	- .98	- .34	1.00	1.83	- .23
.32 < to < 1.00	-2.30	- .66	.35	1.01	2.07	.09
1.00 < to < 3.40	-2.41	.48	.38	1.82	2.40	.53
ALL	-2.82	- .95	- .27	.63	1.65	
Dairy Character	-3.10 < to < -.75	-.75 < to < -.10	-.10 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
-5.10 < to < - .75	-3.10	-1.34	- .27	- .02	.76	- .79
- .75 < to < .10	-1.92	- .83	.21	.49	1.67	- .08
.10 < to < .50	-1.28	- .11	.56	.86	2.50	.51
.50 < to < .98	-1.39	.09	.68	1.44	2.24	.61
.98 < to < 2.50	- .81	.82	1.39	1.42	2.51	1.06
ALL	-1.70	- .27	.51	.84	1.93	

Table 17. (Continued)

Cow Index	Predicted Differences of Sires					
Foot Angle	-1.60 < to < -.96	-.96 < to < -.32	-.32 < to < .32	.32 < to < .96	.96 < to < 1.60	ALL
-2.20 < to < - .50	- .89	- .94	- .32	.33	1.47	- .07
- .50 < to < - .28	-1.21	- .44	.08	.93	1.06	.08
- .28 < to < .40	- .45	.02	.34	1.42	1.52	.57
.40 < to < .70	.17	.65	.86	2.47	2.54	1.34
.70 < to < 2.60	- .85	.31	1.09	1.20	1.35	.62
ALL	- .65	- .08	.41	1.27	1.59	

Rear Legs	-2.10 < to < -.85	-.85 < to < -.25	-.25 < to < .30	.30 < to < 1.10	1.10 < to < 1.90	ALL
-2.90 < to < - .50	-2.45	-1.08	-1.23	.19	.71	- .77
- .50 < to < .10	-1.84	-1.39	- .70	.45	.30	- .64
.10 < to < .22	- .74	- .86	- .33	.71	1.35	.03
.22 < to < .50	-1.91	- .96	- .31	.72	1.69	- .16
.50 < to < 2.30	-1.49	- .98	- .00	1.27	2.11	.18
ALL	-1.69	-1.06	- .52	.67	1.23	

Rump Angle	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .28	.28 < to < 1.44	1.44 < to < 2.60	ALL
-3.30 < to < -1.00	-3.99	-2.44	-1.88	- .96	- .51	-1.96
-1.00 < to < - .10	-2.70	-2.24	-1.02	- .05	.36	-1.13
- .10 < to < .48	-2.58	-1.83	- .61	.24	.89	- .78
.48 < to < 1.00	-2.15	-1.65	- .31	1.06	1.21	- .37
1.00 < to < 3.00	-1.66	-1.46	.24	1.53	2.20	.17
ALL	-2.62	-1.92	- .72	.36	.83	

Table 17. (Continued)

Cow Index	Predicted Differences of Sires					
Rump Width	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .22	.22 < to < 1.36	1.36 < to < 2.50	ALL
-3.60 < to < -1.00	-2.69	-1.57	- .60	.18	1.90	- .56
-1.00 < to < -0.50	-2.35	-1.96	- .43	.72	1.48	- .51
- .50 < to < .06	-2.09	-1.31	.06	.86	1.55	- .19
.06 < to < .75	-1.66	-1.07	.54	1.17	2.23	.24
.75 < to < 2.50	-1.00	.44	1.06	2.03	3.00	1.11
ALL	-1.96	-1.09	.13	.99	2.03	

Cow Index	Predicted Differences of Sires					
Fore Udder	-2.90 < to < -1.25	-1.25 < to < -.54	-.54 < to < .64	.64 < to < 1.25	1.25 < to < 3.00	ALL
-4.20 < to < -1.00	-2.96	-1.77	- .96	- .39	1.08	-1.00
-1.00 < to < - .10	-2.60	-1.19	- .38	.52	1.49	- .43
- .10 < to < .50	-1.60	- .60	- .10	.99	1.87	.11
.50 < to < 1.00	-2.38	- .29	.32	.96	2.40	.20
1.00 < to < 2.60	- .39	- .13	1.14	2.33	2.71	1.13
ALL	-1.99	- .80	.00	.88	1.91	

Cow Index	Predicted Differences of Sires					
Rear Udder Height	-2.80 < to < -.90	-.90 < to < -.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.10	ALL
-3.70 < to < -1.00	-2.24	-1.03	- .46	- .43	.57	- .72
-1.00 < to < - .10	-2.14	-1.15	- .09	.94	1.06	- .28
- .10 < to < .40	-2.04	- .83	.33	.91	1.72	.02
.40 < to < .75	-1.17	- .83	.37	1.20	1.62	.24
.75 < to < 2.20	- .20	.07	.82	2.09	2.27	1.01
ALL	-1.56	- .75	.19	.94	1.45	

Table 17. (Continued)

Cow Index	Predicted Differences of Sires					
Rear Udder Width	-3.80 < to < -.75	-.75 < to < -.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
-3.60 < to < - .75	-1.24	- .23	.53	1.35	2.93	0.67
- .75 < to < - .10	-1.37	- .15	.44	1.78	1.86	0.51
- .10 < to < .50	-1.02	.14	.88	1.73	2.84	0.91
.50 < to < 1.00	- .30	.65	1.23	2.17	3.08	1.37
1.00 < to < 2.70	.68	1.32	1.77	2.57	3.32	1.93
ALL	- .65	.34	.97	1.92	2.81	
Udder Depth	-3.50 < to < -0.75	-.75 < to < -.25	-.25 < to < .50	.50 < to < 1.14	1.14 < to < 2.30	ALL
-4.40 < to < - .25	-1.52	-1.03	- .78	- .05	.99	- .48
- .25 < to < .10	-1.48	- .78	- .70	.23	.95	- .36
.10 < to < .30	-1.14	- .56	- .35	.57	1.82	.07
.30 < to < .50	- .44	- .85	.03	.57	1.22	.10
.50 < to < 2.20	- .28	- .22	.25	1.07	2.17	.60
ALL	- .97	- .69	- .31	.48	1.43	
Suspensory Ligament	-3.30 < to < -1.00	-1.00 < to < -.25	-.25 < to < .60	.60 < to < 1.00	1.00 < to < 3.20	ALL
-4.10 < to < -1.25	-3.62	-2.08	- .50	.49	.47	-1.05
-1.25 < to < - .25	-2.89	-1.22	- .01	- .13	.44	- .76
- .25 < to < .04	-1.70	- .49	.07	.75	1.10	- .05
.04 < to < 1.00	-1.79	- .70	.30	1.17	1.54	.11
1.00 < to < 2.80	- .91	- .30	1.31	1.29	1.68	.61
ALL	-2.18	- .96	.23	.72	1.05	

Table 17. (Continued)

Cow Index	Predicted Differences of Sires					
Teat Placement	-1.90 < to < -.50	-.50 < to < -.14	-.14 < to < .74	.74 < to < 1.25	1.25 < to < 2.50	ALL
-2.50 < to < - .50	-1.11	- .65	.52	1.51	2.18	.49
- .50 < to < - .20	- .80	- .58	.74	.95	2.87	.64
- .20 < to < .30	- .17	.05	1.05	2.25	3.10	1.26
.30 < to < .50	- .15	.59	1.80	2.70	4.19	1.83
.50 < to < 2.70	.93	1.18	1.81	2.60	3.59	2.02
ALL	- .26	.12	1.18	2.00	3.19	

for other D1 categories. For example, offspring scores for stature for the lowest category of D1 (50-59) exceeded offspring scores for dam categories 60 to 69 and 70 to 77. Similar results occurred for other traits.

Least squares means for sires adjusted for D3 and HAFS (Table 17), increased consistently with PD_S for all traits, similar to results with D1 (Table 16). However, unlike least squares means for categories of D1 (Table 16), those for D3, adjusted for PD_S and HAFS (Table 17), increased consistently with increasing performance of dams, except for foot angle and rear legs, traits with intermediate optima. These results suggest that average results of specific matings can be predicted more accurately using D3 than D1. This conclusion is not contradictory to results of regression models in which use of D3 failed to increase R^2's, since regression models are relevant to prediction of individual offspring. That is, for predicting scores of individual offspring relative to herd average, there is no evidence to support the use of D3 as opposed to D1. However, D3 does appear more accurate for predicting average offspring performance. Since the latter is relevant to average results of corrective mating programs (e.g., for large groups of offspring or over time), it seems reasonable to recommend the use of cow indexes rather than cow score for corrective mating purposes.

Analysis of Errors of Predicting Offspring Scores

Means, standard deviations, and ranges for errors of predicted offspring score (predicted minus actual score), using PD_S with each of D1 to D4 are in Table 18.

Table 18. Means, standard deviations and ranges for error of predicted offspring score, using predicted differences of sires with four measures of dam's merit (D1-D4)[a], deviated from the actual score.

Trait	D1 $\bar{X}$	D1 σ	D1 MIN	D1 MAX	D2 $\bar{X}$	D2 σ	D2 MIN	D2 MAX	D3 $\bar{X}$	D3 σ	D3 MIN	D3 MAX	D4 $\bar{X}$	D4 σ	D4 MIN	D4 MAX
Stature	.27	5.99	-25.8	24.8	.24	5.97	-26.2	24.4	.25	5.96	-26.6	25.1	.21	6.03	-25.6	25.2
Strength	.35	5.50	-19.0	24.2	.33	5.52	-19.3	24.0	.32	5.50	-20.1	24.2	.30	5.52	-19.3	25.0
Dairy Character	.08	5.17	-19.2	29.8	.05	5.17	-19.1	29.8	.03	5.16	-18.3	29.7	.02	5.18	-19.1	29.3
Foot Angle	-.51	5.07	-31.4	21.9	-.51	5.07	-31.3	21.7	-.49	5.06	-31.4	21.7	-.50	5.06	-31.6	21.7
Rear Legs	.48	4.80	-20.0	27.7	.48	4.79	-19.9	27.8	.41	4.79	-19.3	27.8	.42	4.79	-19.9	27.3
Rump Angle	.79	4.42	-19.5	25.7	.77	4.40	-19.5	25.6	.66	4.39	-20.6	25.0	.64	4.41	-21.1	25.0
Rump Width	-.35	5.34	-20.6	22.9	-.35	5.32	-20.3	23.0	-.33	5.30	-20.5	22.2	-.31	5.31	-20.2	22.5
Fore Udder	.02	5.50	-18.5	29.0	.01	5.49	-18.5	29.0	.01	5.49	-19.5	28.9	-.02	5.50	-18.1	29.0
Rear Udder Height	.05	4.76	-14.1	30.8	.04	4.75	-13.8	30.5	.02	4.75	-14.0	30.3	-.00	4.75	-13.6	30.5
Rear Udder Width	-.86	5.26	-27.2	26.4	-.86	5.25	-26.9	26.3	-.82	5.25	-27.9	26.9	-.81	5.25	-26.6	26.9
Udder Depth	.35	3.43	-16.0	31.1	.36	3.42	-15.7	30.7	.25	3.41	-15.7	31.4	.27	3.41	-16.5	33.1
Suspensory Ligament	.20	5.40	-17.5	31.3	.20	5.39	-17.5	31.3	.15	5.39	-17.9	31.6	.14	5.39	-18.3	31.8
Teat Placement	-.91	5.12	-26.3	20.0	-.89	5.12	-26.3	19.9	-.80	5.11	-26.2	20.3	-.83	5.12	-25.6	19.9

[a] D1 = $.5h^2(y-\mu)$; D2 = $.5h^2(y-\bar{H})$; D3 = dam's cow index; D4 = .5 maternal grandsire predicted difference; y = dam's score; μ = overall mean; $\bar{H}$ = herd mean.

Average errors were similar across dam measures. However, average deviations from actual scores were smallest for 8 of the 13 traits with the prediction equation consisting of PD_S and D4.

Standard deviations of errors were similar across dam measures, and were largest for traits with largest within herd variation. That is, the range of errors (and therefore the accuracy of predicting individual offspring phenotypes) did not differ appreciably for alternative measures of dam's merit. Variation in errors was related much more closely to phenotypic variation of each trait. For example, standard deviations consistently were largest for stature, the most variable trait, and smallest for udder depth, the least variable trait. Standard deviations ranged from approximately 3.5 to 6.0, indicating substantial errors in predicting scores of individual offspring.

Frequencies of errors of given sizes are in Tables 19 through 22 for models predicting offspring scores from PD_S and D1 to D4. Frequencies of errors in the four tables are nearly identical, again indicating little difference among measures of dam's performance in accuracy of predicting scores of individual offspring.

Frequencies in Tables 19-22 can be used to quantitate the efficacy of corrective mating in terms of additive prediction of scores for individual offspring. These results reflect partly the phenotypic variability of each trait since ranges of errors are in actual points rather than standard deviations. For example, 28% of predicted scores for stature (the most variable trait) were within ± 2 points of the actual score, while 47% of predicted scores for udder depth (the least

Table 19. Frequency of errors of predicted offspring score, using predicted differences of sires with a measure of dam's merit (D1), deviated from the actual score.[a]

Trait	<-8	-8< to <-6	-6< to <-4	-4< to <-2	-2< to <0	0< to <2	2< to <4	4< to <6	6< to <8	> 8
Stature	.08	.06	.09	.12	.14	.14	.12	.10	.07	.09
Strength	.05	.06	.10	.14	.15	.14	.11	.09	.06	.09
Dairy Character	.03	.06	.11	.16	.17	.15	.11	.08	.05	.07
Foot Angle	.08	.05	.08	.12	.17	.19	.16	.08	.04	.03
Rear Legs	.02	.04	.09	.15	.18	.17	.14	.08	.05	.07
Rump Angle	.02	.03	.07	.12	.18	.20	.17	.10	.05	.05
Rump Width	.06	.07	.11	.15	.17	.14	.11	.07	.05	.07
Fore Udder	.05	.07	.11	.15	.16	.14	.12	.08	.05	.08
Rear Udder Height	.02	.05	.12	.17	.18	.15	.11	.09	.05	.06
Rear Udder Width	.07	.09	.13	.16	.15	.13	.10	.07	.04	.06
Udder Depth	.01	.02	.06	.15	.24	.23	.16	.08	.03	.02
Suspensory Ligament	.04	.06	.11	.16	.17	.14	.11	.08	.05	.08
Teat Placement	.10	.06	.08	.12	.18	.20	.14	.07	.03	.03

[a] $D1 = .5h^2(y-\mu)$; y = dam's score; μ = overall mean.

Table 20. Frequency of errors of predicted offspring score, using predicted differences of sires with a measure of dam's merit (D2), deviated from the actual score.[a]

Trait	<-8	-8< to <-6	-6< to <-4	-4< to <-2	-2< to <0	0< to <2	2< to <4	4< to <6	6< to <8	> 8
Stature	.08	.06	.09	.12	.14	.14	.12	.10	.07	.09
Strength	.05	.06	.10	.14	.15	.14	.11	.09	.06	.09
Dairy Character	.03	.06	.12	.17	.17	.15	.11	.08	.05	.07
Foot Angle	.08	.05	.08	.12	.17	.20	.16	.08	.04	.03
Rear Legs	.02	.04	.09	.16	.18	.17	.14	.08	.05	.07
Rump Angle	.02	.03	.07	.12	.18	.20	.17	.10	.05	.06
Rump Width	.06	.07	.11	.15	.17	.14	.11	.07	.05	.07
Fore Udder	.05	.07	.12	.15	.16	.14	.11	.08	.05	.08
Rear Udder Height	.02	.05	.12	.18	.18	.15	.12	.09	.05	.06
Rear Udder Width	.06	.09	.14	.16	.15	.13	.10	.07	.04	.06
Udder Depth	.01	.02	.06	.16	.25	.23	.16	.08	.03	.02
Suspensory Ligament	.04	.06	.11	.16	.17	.14	.11	.08	.05	.07
Teat Placement	.10	.06	.07	.12	.18	.20	.14	.07	.03	.03

[a] $D2 = .5h^2(y-\overline{H})$; y = dam's score; $\overline{H}$ = herd mean.

Table 21. Frequency of errors of predicted offspring score, using predicted differences of sires with a measure of dam's merit (D3), deviated from the actual score.[a]

Trait	<-8	-8< to <-6	-6< to <-4	-4< to <-2	-2< to <0	0< to <2	2< to <4	4< to <6	6< to <8	> 8
Stature	.08	.06	.09	.12	.14	.14	.12	.09	.07	.10
Strength	.05	.06	.10	.14	.15	.14	.11	.09	.06	.09
Dairy Character	.03	.06	.11	.17	.17	.15	.11	.08	.05	.07
Foot Angle	.08	.05	.08	.12	.17	.20	.16	.08	.04	.03
Rear Legs	.02	.04	.09	.16	.19	.17	.14	.08	.05	.07
Rump Angle	.02	.03	.08	.12	.18	.21	.16	.09	.05	.05
Rump Width	.06	.07	.11	.15	.17	.15	.11	.07	.05	.07
Fore Udder	.05	.07	.11	.15	.16	.14	.11	.08	.05	.08
Rear Udder Height	.02	.05	.12	.17	.18	.15	.12	.08	.05	.06
Rear Udder Width	.06	.09	.14	.16	.15	.13	.10	.07	.04	.06
Udder Depth	.01	.02	.06	.16	.25	.23	.16	.07	.03	.02
Suspensory Ligament	.04	.06	.12	.15	.16	.14	.11	.08	.05	.07
Teat Placement	.09	.06	.07	.12	.18	.20	.14	.07	.04	.03

[a]D3 = dam's cow index.

Table 22. Frequency of errors of predicted offspring score, using predicted differences of sires with a measure of dam's merit (D4), deviated from the actual score.[a]

Trait	<-8	-8< to <-6	-6< to <-4	-4< to <-2	-2< to <0	0< to <2	2< to <4	4< to <6	6< to <8	> 8
Stature	.08	.06	.09	.12	.14	.14	.12	.10	.06	.10
Strength	.05	.06	.10	.14	.15	.14	.11	.09	.06	.09
Dairy Character	.03	.06	.12	.17	.17	.15	.11	.08	.05	.07
Foot Angle	.08	.05	.08	.12	.17	.20	.16	.08	.04	.03
Rear Legs	.02	.04	.09	.15	.19	.17	.14	.08	.05	.07
Rump Angle	.02	.04	.08	.12	.18	.20	.16	.09	.05	.05
Rump Width	.06	.07	.11	.15	.17	.14	.11	.07	.05	.07
Fore Udder	.05	.07	.12	.15	.16	.14	.11	.08	.05	.08
Rear Udder Height	.02	.05	.12	.17	.18	.15	.11	.08	.05	.06
Rear Udder Width	.06	.09	.14	.16	.15	.13	.10	.07	.04	.06
Udder Depth	.01	.02	.06	.16	.25	.23	.16	.07	.03	.02
Suspensory Ligament	.04	.06	.12	.16	.17	.14	.11	.08	.05	.07
Teat Placement	.09	.06	.07	.12	.18	.20	.14	.07	.03	.03

[a]D4 = .5 maternal grandsire predicted difference.

variable trait) were within ± 2 points of actual offspring score. Likewise, precentages of predicted scores within ± 4 points of actual score ranged from 78% for udder depth to 52% for stature.

Mean squares from analyses of variance for effects on errors of categorical levels of PD_S, D1, D3, the interaction between sire and dam measure, and HAFS were computed (Table 23). For this and subsequent tables, errors are for predicted offspring score using PD_S and D3. Categorical levels of PD_S and D1 or D3 significantly ($P < .05$) affected differences in errors of predicted offspring scores for all traits except fore udder and rear udder width in the first model for levels of PD_S, and in the second model, fore udder and foot angle for PD_S, and teat placement for levels of D3.

Sire predicted difference by D3 interactions were significant only for rear legs and rear udder height. No interactions between PD_S and D1 were significant.

Effects of final score categories were identical for the two models. Errors of prediction were associated with final score level of the herd for all traits except foot angle, rear legs, fore udder, rear udder height, rear udder width, and udder depth.

Least squares means for errors of prediction for five categorical levels of HAFS, similar to those computed earlier for offspring scores, are in Tables 24 (for the model with D1) and 25 (for the model with D3). For traits significantly ($P < .05$) affected by HAFS in models with D1 and D3 (stature, strength, dairy character, rump angle, rump width, suspensory ligament, and teat placement) there was a slight

Table 23. Mean squares for effects on errors of predicted offspring scores (using predicted differences for sires and cow indexes for dams) of categorical levels of predicted differences for sires (S), scores (D1) and cow indexes (D3) for dams, interaction of sire and dam, and herd averages for final score (FS).

Trait	S	D1	S × D1	FS	S	D3	S × D3	FS
Stature	134.8	916.2	46.4[a]	150.0	123.0	785.3	49.5[a]	155.4
Strength	497.1	105.1	29.7[a]	256.2	449.1	276.5	38.7[a]	221.6
Dairy Character	365.6	118.1	37.3[a]	107.1	282.9	101.1	23.1[a]	79.8
Foot Angle	84.6	372.9	14.8[a]	37.0[a]	22.9[a]	207.2	27.7[a]	29.3[a]
Rear Legs	208.8	258.8	28.4[a]	45.1[a]	217.1	124.1	37.4	51.9[a]
Rump Angle	227.6	111.4	25.5[a]	80.8	154.4	127.3	20.8[a]	84.7
Rump Width	134.4	296.8	27.8[a]	127.6	112.9	204.0	21.0[a]	142.3
Fore Udder	37.1[a]	294.8	28.9[a]	11.7[a]	35.2[a]	257.2	29.9[a]	15.5[a]
Rear Udder Height	201.1	330.6	18.2[a]	42.3[a]	107.6	245.0	39.1	41.8[a]
Rear Udder Width	51.8[a]	636.0	25.2[a]	54.2[a]	72.7	482.9	22.3[a]	44.4[a]
Udder Depth	104.4	161.3	10.0[a]	8.3[a]	144.8	146.0	15.4[a]	11.7[a]
Suspensory Ligament	169.2	99.7	45.7[a]	108.8	134.2	297.9	43.0[a]	109.4
Teat Placement	193.1	76.3	16.3[a]	108.8	233.2	41.2[a]	33.7[a]	111.2

[a]Not significant; others significant ($P < .05$).

Table 24. Least squares means of errors on predicted offspring scores[a] for categorical levels of herd average for final score adjusted for effects of categorical levels of predicted differences for sires, scores for dams, and interaction of sire and dam.

	Herd Averages for Final Score				
Trait	60 to 72	73 to 75	76 to 77	78 to 80	81 to 90
Stature	.89	.29	.41	.13	.63
Strength	.92	.37	.34	-.06	.64
Dairy Character	.56	.17	-.04	.12	-.18
Foot Angle	-.28	-.29	-.52	-.49	-.50
Rear Legs	.08	.47	.47	.54	.36
Rump Angle	1.12	.88	.83	.56	.77
Rump Width	.18	-.46	-.38	-.35	.03
Fore Udder	-.10	.02	-.07	-.10	.05
Rear Udder Height	.23	.10	-.04	-.14	.05
Rear Udder Width	-.61	-.95	-.96	-1.12	-.91
Udder Depth	.00	.08	.06	.14	.19
Suspensory Ligament	.21	.44	.01	.02	.14
Teat Placement	-.67	-.67	-.94	-.96	-1.26

[a]Using predicted differences for sires and cow indexes for dams, deviated from the actual score.

Table 25. Least squares means of errors on predicted offspring scores[a] for categorical levels of herd average for final score adjusted for effects of categorical levels of predicted differences for sires, cow index for dams, and interaction of sire and dam.

	Herd Averages for Final Score				
Trait	60 to 72	73 to 75	76 to 77	78 to 80	81 to 90
Stature	.79	.15	.31	.11	.65
Strength	.86	.36	.34	-.03	.66
Dairy Character	.50	.18	-.01	.16	-.11
Foot Angle	-.38	-.38	-.59	-.55	-.54
Rear Legs	.01	.42	.45	.49	.31
Rump Angle	1.12	.86	.80	.54	.80
Rump Width	.10	-.54	-.47	-.41	.00
Fore Udder	-.13	.05	-.05	-.07	.09
Rear Udder Height	.19	.09	-.06	-.15	.10
Rear Udder Width	-.50	-.82	-.79	-.95	-.71
Udder Depth	.14	.23	.20	.29	.36
Suspensory Ligament	.12	.39	-.05	-.02	.12
Teat Placement	-.69	-.70	-.97	-.99	-1.29

[a]Using predicted differences for sires and cow indexes for dams, deviated from the actual score.

tendency for largest errors (greatest overprediction) to occur in herds with lowest and highest averages for final score, except for teat placement where a continual decrease in the magnitude of errors was observed as HAFS increased. Results were similar to least squares means for offspring scores where differences by HAFS class were not large. Differences in errors of prediction for levels of HAFS were all less than one point. Results were very similar for models including D1 and D3, with differences among least squares means for levels of HAFS being slightly less for the model with D3.

Least squares means of prediction errors for categorical levels of PD_S, D1, and their combination (Table 26) were similar to those for PD_S, D3, and their combination (Table 27). For both measures of dam's performance, largest errors (greatest relative overprediction) tended to occur at the lowest category of PD_S and highest category of dam's performance. This suggests sires with lowest predicted differences and dams with highest scores or cow indexes are over-evaluated slightly. However, the magnitude of differences among least squares means was not large. For example, the largest difference among least squares means for categories of PD_S was 1.34 points among extreme means for strength (Table 26). Similiarly, largest differences among least squares means for categories of dam's performance were 2.17 and 1.83 points among extreme means for stature in models using D1 (Table 26) and D3 (Table 27), respectively.

Table 26. Least squares means of errors on predicted offspring scores[a] for categorical levels of predicted differences for sires and scores for dams adjusted for effects of categorical levels of herd average for final score.

Dam Score	Predicted Differences of Sires					
Stature	-5.50 < to < -2.00	-2.00 < to < -.75	-.75 < to < 1.00	1.00 < to < 2.00	2.00 < to < 4.80	ALL
50 to 59	1.45	.57	.42	.54	.40	.67
60 to 69	-1.38	- .44	- .73	-1.11	- .55	- .84
70 to 77	1.26	.48	.13	.19	.01	.41
78 to 83	1.46	1.15	.39	.24	.55	.76
84 to 99	1.06	1.60	1.15	1.00	1.86	1.33
ALL	.77	.67	.27	.17	.45	
Strength	-3.90 < to < -1.00	-1.00 < to < -.25	-.25 < to < .50	.50 < to < 1.38	1.38 < to < 2.70	ALL
50 to 59	1.21	.52	.48	- .29	.30	.44
60 to 75	.54	- .27	.11	- .06	- .43	- .02
76 to 83	1.13	.50	.28	- .03	.31	.44
84 to 86	1.71	.47	.31	.26	.50	.65
87 to 99	2.14	.11	.56	.18	.49	.70
ALL	1.35	.27	.35	.01	.23	
Dairy Character	-3.10 < to < -.75	-.75 < to < -.10	-.10 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
50 to 59	.83	.03	- .12	- .15	.31	.18
60 to 79	.90	- .36	- .91	- .35	- .55	- .26
80 to 84	.36	.16	- .23	.08	- .03	.07
85 to 87	.46	.17	.10	.29	.51	.30
88 to 99	1.29	- .13	- .29	.36	.42	.33
ALL	.77	- .03	- .29	.05	.13	

Table 26. (Continued)

Dam Score	Predicted Differences of Sires					
Foot Angle	-1.60 < to < -.96	-.96 < to < -.32	-.32 < to < .32	.32 < to < .96	.96 < to < 1.60	ALL
50 to 59	- .73	- .62	- .41	- .69	- .65	- .62
60 to 65	-1.04	-1.18	- .78	-1.30	-1.05	-1.07
66 to 68	-1.03	- .81	- .49	- .81	- .34	- .70
69 to 75	- .46	- .33	- .23	- .58	- .51	- .42
76 to 99	.81	1.14	.85	- .33	1.17	.73
ALL	- .49	- .36	- .21	- .74	- .28	
Rear Legs	-2.10 < to < -.85	-.85 < to < -.25	-.25 < to < .30	.30 < to < 1.10	1.10 < to < 1.90	ALL
50 to 59	.46	.43	.65	.29	.68	.50
60 to 75	.08	- .32	.05	- .84	- .88	- .38
76 to 82	.41	.60	.44	- .27	.52	.34
83 to 85	.44	1.05	.90	.44	.66	.70
86 to 99	.17	1.56	.79	.26	1.03	.76
ALL	.31	.66	.56	- .02	.40	
Rump Angle	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .28	.28 < to < 1.44	1.44 < to < 2.60	ALL
50 to 59	.71	1.33	.83	.53	1.12	.91
60 to 75	.80	.74	.16	.17	1.03	.58
76 to 79	.63	.92	.49	.24	.77	.61
80 to 84	1.11	1.32	.81	.88	.77	.98
85 to 99	1.57	1.72	1.01	.13	1.02	1.09
ALL	.97	1.21	.66	.39	.94	

Table 26. (Continued)

Dam Score	Predicted Differences of Sires					
Rump Width	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .22	.22 < to < 1.36	1.36 < to < 2.50	ALL
50 to 59	- .05	.93	- .27	- .16	- .69	- .05
60 to 69	- .20	- .73	-1.17	-1.27	-1.50	- .97
70 to 79	.00	.04	- .48	- .43	- .25	- .22
80 to 84	.62	.54	.08	- .13	.15	.25
85 to 99	.48	- .41	- .17	- .18	.35	.01
ALL	.17	.08	- .40	- .43	- .39	
Fore Udder	-2.90 < to < -1.25	-1.25 < to < -.54	-.54 < to < .64	.64 < to < 1.25	1.25 < to < 3.00	ALL
50 to 59	- .34	- .38	- .13	.41	- .88	- .26
60 to 73	- .17	- .79	- .64	- .88	- .45	- .59
74 to 79	.20	- .01	- .03	- .09	- .42	- .07
80 to 84	.64	.06	.34	.11	.01	.23
85 to 99	.48	.79	.42	.29	.40	.48
ALL	.16	- .07	- .01	- .03	- .27	
Rear Udder Height	-2.80 < to < -.90	-.90 < to < -.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.10	ALL
50 to 59	.51	.69	- .20	.08	.21	.26
60 to 75	- .60	- .64	-1.10	-1.03	- .15	- .70
76 to 82	.03	- .02	- .21	- .57	- .08	- .17
83 to 86	.65	.66	.06	.06	.27	.34
87 to 99	.64	.49	.29	- .01	.93	.47
ALL	.25	.24	- .23	- .29	.24	

Table 26. (Continued)

Dam Score	Predicted Differences of Sires					
Rear Udder Width	-3.80 < to < -.75	-.75 < to < -.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
50 to 59	- .84	- .58	- .65	- .77	- .44	- .66
60 to 69	-2.27	-1.83	-2.48	-2.16	-2.62	-2.27
70 to 79	- .11	- .91	- .91	-1.27	-1.27	- .89
80 to 84	.07	- .27	- .53	- .56	- .36	- .33
85 to 99	- .06	- .45	- .51	- .65	- .34	- .40
ALL	- .64	- .81	-1.02	-1.08	-1.01	
Udder Depth	-3.50 < to < -.75	-.75 < to < -.25	-.25 < to < .50	.50 < to < 1.14	1.14 < to < 2.30	ALL
50 to 59	- .22	.34	.69	.30	.31	.29
60 to 75	- .92	- .58	- .46	- .28	- .46	- .54
76 to 79	.05	.14	.38	.37	- .24	.14
80 to 84	- .21	.33	.65	.43	.22	.29
85 to 99	.07	.41	.40	.34	.22	.29
ALL	- .24	.13	.33	.23	.01	
Suspensory Ligament	-3.30 < to < -1.00	-1.00 < to < -.25	-.25 < to < .60	.60 < to < 1.00	1.00 < to < 3.20	ALL
50 to 59	.60	.43	- .04	- .38	.50	.22
60 to 72	1.10	- .63	- .73	- .76	- .26	- .26
73 to 79	.47	.40	- .30	.09	.19	.17
80 to 84	.28	.20	.01	.64	.42	.31
85 to 99	.33	.48	.35	.18	.53	.37
ALL	.56	.18	- .14	- .05	.28	

Table 26. (Continued)

Dam Score	Predicted Differences of Sires					
Teat Placement	-1.90 < to < -.50	-.50 < to <-.14	-.14 < to < .74	.74 < to < 1.25	1.25 < to < 2.50	ALL
50 to 59	- .68	- .54	- .83	-1.33	-1.54	- .98
60 to 65	- .59	- .35	- .75	-1.29	-2.11	-1.02
66 to 69	- .38	- .35	- .78	- .80	-1.34	- .73
70 to 73	-1.05	- .71	-1.36	-1.01	-1.65	-1.15
74 to 99	- .29	- .32	- .61	-1.15	- .66	- .60
ALL	- .60	- .46	- .86	-1.11	-1.46	

[a]Using predicted differences for sires and cow indexes for dams, deviated from the actual score.

Table 27. Least squares means of errors on predicted offspring scores[a] for categorical levels of predicted differences for sires and cow indexes for dams adjusted for effects of categorical levels of herd average for final score.

Cow Index	Predicted Differences of Sires					
Stature	-5.50 < to < -2.00	-2.00 < to < -.75	-.75 < to < 1.00	1.00 < to < 2.00	2.00 < to < 4.80	ALL
-6.50 < to < -2.00	- .42	- .62	-1.04	- .97	- .03	- .61
-2.00 < to < -1.06	- .41	- .03	- .33	- .18	- .28	- .25
-1.06 < to < 1.25	1.29	.68	.26	.21	- .16	.46
1.25 < to < 2.50	1.45	1.24	.97	.41	2.04	1.22
2.50 < to < 7.10	1.36	1.34	.72	.93	1.65	1.20
ALL	.65	.52	.12	.08	.64	
Strength	-3.90 < to < -1.00	-1.00 < to < -.25	-.25 < to < .50	.50 < to < 1.38	1.38 < to < 2.70	ALL
-4.30 < to < -1.00	.83	- .15	- .16	- .23	- .01	.05
-1.00 < to < - .50	.60	.33	- .21	.11	- .31	.10
- .50 < to < .32	1.14	.35	.34	- .31	.15	.33
.32 < to < 1.00	1.47	.72	.33	.37	.61	.70
1.00 < to < 3.40	2.29	.33	1.06	.32	.91	.98
ALL	1.27	.32	.27	.05	.27	
Dairy Character	-3.10 < to < -.75	-.75 < to < -.10	- .10 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
-5.10 < to < - .75	.82	- .34	- .84	- .44	.00	- .16
- .75 < to < .10	.57	.09	- .39	- .00	.05	.06
.10 < to < .50	.45	- .08	- .18	.17	- .25	.02
.50 < to < .98	1.01	.17	.15	.03	.41	.35
.98 < to < 2.50	1.01	- .03	- .05	.61	.66	.44
ALL	.77	- .04	- .26	.07	.17	

Table 27. (Continued)

Cow Index	Predicted Differences of Sires					
Foot Angle	-1.60 < to < -.96	-.96 < to < -.32	-.32 < to < .32	.32 < to < .96	.96 < to < 1.60	ALL
-2.20 < to < - .50	-1.13	- .48	- .51	- .57	-1.27	- .79
- .50 < to < - .28	- .39	- .51	- .44	- .71	- .39	- .49
- .28 < to < .40	- .75	- .58	- .30	- .80	- .42	- .57
.40 < to < .70	- .93	- .76	- .37	-1.38	-1.02	- .89
.70 < to < 2.60	.56	.08	- .11	.36	.62	.30
ALL	- .53	- .45	- .35	- .62	- .49	
Rear Legs	-2.10 < to < -.85	-.85 < to < -.25	-.25 < to < .30	.30 < to < 1.10	1.10 < to < 1.90	ALL
-2.90 < to < - .50	.20	- .31	.34	- .52	- .15	- .09
- .50 < to < .10	.32	.67	.50	- .08	.98	.48
.10 < to < .22	- .41	.49	.48	.01	.27	.17
.22 < to < .50	.91	.79	.65	.19	.10	.53
.50 < to < 2.30	.96	1.21	.74	.01	.08	.60
ALL	.40	.57	.54	- .08	.26	
Rump Angle	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .28	.28 < to < 1.44	1.44 < to < 2.60	ALL
-3.30 < to < -1.00	.93	.20	.35	.30	.75	.51
-1.00 < to < - .10	.50	.89	.40	.30	.82	.58
- .10 < to < .48	1.01	1.15	.66	.68	.91	.88
.48 < to < 1.00	1.13	1.47	.87	.34	1.16	.99
1.00 < to < 3.00	1.35	2.02	.97	.54	.84	1.14
ALL	.98	1.15	.65	.43	.90	

Table 27. (Continued)

Cow Index	Predicted Differences of Sires					
Rump Width	-3.20 < to < -1.25	-1.25 < to < -.50	-.50 < to < .22	.22 < to < 1.36	1.36 < to < 2.50	ALL
-3.60 < to < -1.00	- .49	- .84	- .95	- .92	-1.60	- .96
-1.00 < to < - .50	- .09	.26	- .42	- .79	- .51	- .31
- .50 < to < .06	.20	.17	- .38	- .38	- .02	- .08
.06 < to < .75	.35	.52	- .25	- .10	- .09	.08
.75 < to < 2.50	.49	- .29	- .05	- .27	- .10	- .05
ALL	.09	- .04	- .41	- .49	- .46	
Fore Udder	-2.90 < to < -1.25	-1.25 < to < -.54	-.54 < to < .64	.64 < to < 1.25	1.25 < to < 3.00	ALL
-4.20 < to < -1.00	- .55	- .66	- .70	- .36	-1.11	- .68
-1.00 < to < - .10	.28	- .14	- .14	- .15	- .36	- .10
- .10 < to < .50	- .05	- .05	.26	.05	- .08	.03
.50 < to < 1.00	1.26	.16	.38	.61	- .09	.47
1.00 < to < 2.60	- .13	.65	.17	- .11	.30	.18
ALL	.16	- .01	- .00	.01	- .26	
Rear Udder Height	-2.80 < to < -.90	-.90 < to < -.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.10	ALL
-3.70 < to < -1.00	- .66	-1.05	-1.01	- .30	- .33	- .67
-1.00 < to < - .10	.26	.14	- .34	- .65	.16	- .09
- .10 < to < .40	.87	.44	- .13	- .01	.10	.26
.40 < to < .75	.43	.89	.28	.11	.65	.47
.75 < to < 2.20	- .07	.50	.34	- .26	.52	.21
ALL	.16	.18	- .17	- .22	.22	

Table 27. (Continued)

Cow Index	Predicted Differences of Sires					
Rear Udder Width	-3.80 < to < -.75	-.75 < to < -.25	-.25 < to < .50	.50 < to < 1.50	1.50 < to < 2.40	ALL
-3.60 < to < - .75	-1.10	-1.45	-1.68	-1.67	-2.30	-1.64
- .75 < to < - .10	- .21	- .75	- .80	-1.29	- .48	- .71
- .10 < to < .50	.01	- .48	- .68	- .71	- .83	- .54
.50 < to < 1.00	- .11	- .44	- .49	- .63	- .55	- .45
1.00 < to < 2.70	- .55	- .52	- .47	- .42	- .22	- .44
ALL	- .39	- .73	- .83	- .94	- .88	
Udder Depth	-3.50 < to < -.75	-.75 < to < -.25	-.25 < to < .50	.50 < to < 1.14	1.14 < to < 2.30	ALL
-4.40 < to < - .25	- .45	- .22	.13	.05	- .23	- .14
- .25 < to < .10	.23	.23	.74	.44	.49	.43
.10 < to < .30	.09	.25	.63	.36	- .14	.24
.30 < to < .50	- .41	.74	.47	.55	.60	.39
.50 < to < 2.20	- .19	.52	.63	.43	.12	.30
ALL	- .15	.30	.52	.36	.17	
Suspensory Ligament	-3.30 < to < -1.00	-1.00 < to < -.25	-.25 < to < .60	.60 < to < 1.00	1.00 < to < 3.20	ALL
-4.10 < to < -1.25	.23	- .36	-1.14	-1.43	- .76	- .69
-1.25 < to < - .25	.66	- .02	- .47	.28	.40	.17
- .25 < to < .04	- .03	- .17	.01	- .04	.30	.02
.04 < to < 1.00	.57	.55	.33	.10	.39	.39
1.00 < to < 2.80	.55	.95	.15	.77	1.00	.68
ALL	.40	.19	- .23	- .06	.27	

Table 27. (Continued)

Cow Index			Predicted Differences of Sires			
Teat Placement	-1.90 < to < -.50	-.50 < to < -.14	-.14 < to < .74	.74 < to < 1.25	1.25 < to < 2.50	ALL
-2.50 < to < - .50	- .52	- .54	-1.07	-1.42	-1.31	- .97
- .50 < to < - .20	- .42	- .16	- .86	- .39	-1.59	- .68
- .20 < to < .30	- .64	- .41	- .78	-1.30	-1.46	- .92
.30 < to < .50	- .32	- .61	-1.18	-1.39	-2.21	-1.14
.50 < to < 2.70	- .98	- .79	- .78	- .85	-1.19	- .92
ALL	- .58	- .50	- .93	-1.07	-1.55	

[a]Using predicted differences for sires and cow indexes for dams, deviated from the actual score.

Extent of Assortative Mating

Correlations were caculated between PD_s and D1 to D4 (Table 28) as a measure of the extent and direction (positive or negative of corrective mating. It was suggested by Lush (15) that if assortative mating is to be practiced simultaneously for several traits, it becomes difficult to find individuals which are exactly opposite each other, or exactly like each other for all the traits of interest. This is why it is difficult or impossible to achieve high phenotypic correlations between mates for each of several different traits at once.

Our results are in agreement with this statement, and, in fact, do not indicate a meaningful degree of assortative mating for any of the traits examined. In general, correlations were very small, indicating that mating among selected individuals was nearly at random. This may be partly due to the recent adoption of linear evaluation and the lack of sufficient time for corrective mating to have been practiced. For the data as a whole, PD_s was not considered when the dam was mated. However, corrective mating may have occurred in specific subsets of the data not examined.

In a study by Burnside et. al. (6), the extend of corrective mating in Canadian Holsteins was determined by correlating sire progeny tests for conformation at the time of mating, with their mates' classification score for major score card components of type. Correlations were positive for all traits suggesting Canadian Holstein breeders tended to practice positive assortative mating. Results in this study differ dramatically, possible due to the difference in

Table 28. Correlations between predicted differences of sires and four measures of dam's merit (D1-D4)[a].

Trait	D1	D2	D3	D4
Stature	.003	-.033[b]	-.016[b]	.005
Strength	.012	-.023[b]	-.003	-.014
Dairy Character	.019[b]	-.020[b]	.029[b]	.031[b]
Foot Angle	-.009	-.019[b]	-.029[b]	-.034[b]
Rear Legs	.032[b]	.005	.002	-.006
Rump Angle	.023[b]	-.005	-.011	-.018[b]
Rump Width	.026[b]	-.007	.007	.009
Fore Udder	.037[b]	.007	.033[b]	.012
Rear Udder Height	.020[b]	.001	.025[b]	.008
Rear Udder Width	.045[b]	.003	.018[b]	-.001
Udder Depth	-.011	-.030[b]	.013	-.001
Suspensory Ligament	.023[b]	.010	.009	-.016[b]
Teat Placement	.011	-.009	-.009	-.019[b]

[a]D1 = $.5h^2(y-\mu)$; D2 = $.5h^2(y-\bar{H})$; D3 = dam's cow index; D4 = .5 maternal grandsire predicted difference; y = dam's score; μ = overall mean;

$\bar{H}$ = herd mean.

[b]$P < .05$.

populations (breed and country) examined, or the comparatively short term use of linear evaluation in U. S. Jerseys.

SUMMARY AND CONCLUSIONS

Age and stage adjusted scores and genetic evaluations of sires and cows for 13 linear type traits appraised by the AJCC were used in this study to estimate genetic parameters and to evaluate procedures of corrective mating. First available appraisals on 67644 cows scored between January 1980 and December 1983 made up one data set, while 14721 cows required to have a dam with cow indexes for type, and a sire and maternal grandsire with predicted differences for type were represented in a second data set.

Covariances among four types of relatives were used to estimate components of genetic variance and covariance for each of the 13 traits. Direct additive, direct dominance, and additive maternal genetic variances, and the direct-maternal additive genetic covariances, were estimated using covariances among paternal half-sibs, full-sibs, daughters and dams, and maternal half-sibs.

Heritabilities of the type traits, ranging from .11 for foot angle to .36 for stature, indicated that additive effects, which were approximately ten times their standard errors, were moderate for stature, strength, rump angle, rump width, and udder depth. Dominance effects were large for dairy character, rump width, and most udder traits, but were small for over half of the traits. Maternal effects were essentially nonexistent, as were the components of covariance between direct additive and additive maternal effects. Dominance variance was a large proportion (more than 50%) of the total phenotypic variation for dairy character, fore udder, rear udder height, and rear udder width. These estimates were unexpectedly large, suggesting some source of bias. However, the possibility that estimates of dominance genetic variance were inflated by common environmental components of full-sibs seemed unlikely based on the magnitude of covariances among maternal half-sibs. Since selection will be less effective in improving linear type traits controlled largely by nonadditive gene action, these results suggest that we could maximize genetic improvement for several type traits by forming and crossing specific sire lines.

Linear type appraisals provide the opportunity to predict outcomes of specific matings with respect to each trait using the assumption of completely additive inheritance. Sire predicted differences and four measures of dam's merit were used to predict offspring scores, deviated from herd average. Dam's phenotypic score, this score relative to herd average, dam's cow index, and half the maternal grandsire predicted difference were the four measures of dam's merit. Four models were used to regress offspring score for each trait on measures of parental performance. Whether sire and dam measures were weighted equally, or offspring score was regressed separately on the measures of parental performance, did not affect accuracy (R^2) of predicting individual offspring scores. However, sire regression coefficients were much larger than those for dam's measures, suggesting that sire evaluations should receive more weight than dam measures in a corrective mating context. Quadratic regressions included to detect nonlinear relationships between measures of parents and offspring, and herd average for final score, were significant for several traits. However, these added very little to accuracy (R^2) of prediction. Although R^2's for predicting scores of individual offspring were small, they consistently were highest for predictions involving the dam's cow index.

Analysis of variance was used as an alternative to regression analysis for quantitating relationships between measures of parental performance and scores for linear traits of offspring. Mean squares for effects on offspring scores of interactions between categorical levels of sire predicted differences and dam measures generally were nonsignificant, indicating that additively combining measures is appropriate for predicting offspring performance. Least squares means of offspring scores across categorical levels of sire predicted differences increased consistantly, which was also true for dam's cow indexes, but not dam's phenotypic score. This suggests that dam's cow index is superior to dam's score for predicting mean performance of offspring groups (e.g., for large groups of offspring or over time) and is therefore preferred for corrective mating decisions. A tendency was observed for least squares means of offspring scores for herd average final score class, (adjusted for categorical levels of sire predicted difference, dam's score or cow index, and their interaction) to be smallest in low and high scoring herds, but these effects were small.

Frequencies of errors in predicting offspring scores, were nearly identical for the four measures of dam's performance. Errors of prediction were associated with categorical levels of parental performance for nearly all traits, with overpredictions at lowest sire predicted differences and highest dam measures. Additionally, errors were associated with herd average final score for over half of the traits with overpredictions at lowest and highest herd final score. However, effects on errors of both parental performance and herd average final score were relatively small in magnitude for most traits.

The largest correlation between any combination of sire predicted difference and four measures of dam's performance was .045, indicating that little, if any, assortative mating was practiced for the individual linear traits.

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