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ESTIMATION OF GENETIC PARAMETERS AND SIRE RANKINGS FOR HOLSTEIN LINEAR TYPE SCORES AND MILK PRODUCTION BY MULTIPLE TRAIT ANALYSIS

By

Bobby Dennis Banks

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ABSTRACT

ESTIMATION OF GENETIC PARAMETERS AND SIRE RANKINGS FOR HOLSTEIN LINEAR TYPE SCORES AND MILK PRODUCTION BY MULTIPLE TRAIT ANALYSIS

By

Bobby Dennis Banks

Linear scores of 15 primary type traits on Holstein cattle in Michigan and Wisconsin were analyzed by a mixed model containing fixed effects of herd, group of sires and a random sire effect. The intra-herd heritability estimates using sire and residual variance components for the type traits ranged from .10 to .39.

The phenotypic correlations between the type traits were all positive and generally large, while genetic correlations were generally smaller than the corresponding phenotypic correlations. These correlation estimates suggest a strong positive environmental correlation exists among type traits.

The same single trait mixed model and a multiple trait mixed model containing the same factors were then used to examine the relationships between milk and type. The differences between the estimates obtained by the single trait method and those by the multiple trait method were examined in order to ascertain if selection would introduce significant bias in the estimates of genetic parameters involving linear type data.

Five data sets of 150 sires each were independently sampled at random from a data set containing 475,855 daughter records from 1,495 sires. Each sire had at least one daughter measured for both milk and type traits, and 20 daughters in 10 herds. A triangular transformation algorithm was implemented in the expectation maximization of restricted maximum likelihood estimation procedure to estimate genetic parameters and sire rankings from each data set. Over the data sets, mean and sampling variances for each parameter were computed.

Heritability estimates of type traits from the multiple trait analysis ranged between .05 and .38. Genetic correlations were negative between milk and linear type traits except those involving angularity, rump angle, rear leg side view and foot angle. Phenotypic correlations were positive except between milk and strength, foot angle, fore udder attachment or udder depth. Standard deviations for genetic correlations exceeded mean estimates in most cases, while those for heritabilities and phenotypic correlations were consistently smaller than mean estimates. Sire rankings and estimates of heritability between single and multiple trait methods did not differ greatly.

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I. Introduction

The primary goal of dairy cattle breeding is to develop more profitable cows. The selection for increased milk yield has been the major means of attaining this goal. However, other traits, such as type have been recognized as a factor affecting profitability. Sound functional type traits may extend a cow's productive life.

Type traits are jointly selected with other traits. These selection pressures have been accomplished by either voluntary or involuntary culling. The voluntary selection is the result of mating systems such as independent culling levels or tandem selection. Other criteria used for selection of type characteristics have been based on a mixture of common sense, physical attributes, beliefs and rumors.

Theoretically, the best approach is the use of a selection index which pools different traits by genetic parameters and desired relative weights. However, many such applications were done in a manner which pools the breeding values of different traits estimated by different procedures (e.g. Total Performance Index, Holstein-Friesian Association of America, 1985). The accuracy and precision of such indices are questionable due to the lack of knowledge of the statistical properties of some of the procedures. The ultimate solution is to use the best linear unbiased prediction (BLUP) procedure and mixed model methodology.

The genetic parameters of type traits have been estimated for various populations numerous times. However, only a fraction of the total milk recorded population is measured for type. This population may not represent a random sample of the total population. The implementation of the new linear scoring system may additionally restrict the subpopulation of cows with recorded type scores while it is becoming established as a scoring procedure.

If the subpopulation of individuals scored for type is a non-random sample, the estimated genetic parameters and ranking of sires may be inaccurate for the total population.

A recently developed statistical procedure, multiple trait analysis, can remove such possible inaccuracies by jointly analyzing type traits and milk production. The type data is from a selected subpopulation and the more abundant production data is more representative of the entire population.

The objectives of this study are:

1) Estimate the heritabilities for the new type traits, and the phenotypic and genetic correlations between type and production, for the entire population in which selection for both type and milk production are of interest;
2) For the same population, rank the breeding values of Holstein bulls for type traits;
3) Establish the differences, if any, in the genetic parameters and bull ranking between the subpopulation which provides the linear type scores and the total population.

II. Literature Review

II.1 Body conformation systems

Systems to evaluate the body conformation of dairy cattle have evolved from the assignment of a single score of the cow to a complex system that consists of a final score of the cow, and the scorecard divisions for general appearance, dairy character, body capacity and mammary systems.

The Holstein-Friesian Association of America (HFAA) introduced the classification of body conformation traits to the United States in 1929 (White, 1974). The early systems compared the cow's body conformation to that of the prototype of the breed. This system did not allow for specific identification of strengths or weaknesses of the individual.

Another undesirable property of the descriptive system was that the traits were scored from one to six and did not lend themselves to statistical methods assuming a continuous scale of measurement. The scoring from one to six also reduced the potential measurable variation within a body conformation trait.

The HFAA implemented a linear system of scoring type traits on January of 1983. This new system allowed classifiers to separate many biological traits that were included in the scorecard divisions. The scoring system consists of 29 linear type traits each scored on a scale of one to 50. The wide range of scores produced more biologically meaningful scores and are more desirable for statistical methods.

Fifteen of the linear type traits have been designated as primary traits. They are considered by the HFAA to be important economically. The other 14 traits are secondary traits. The secondary traits have been included to gather additional information for research and development.

The new system also includes the traditional scorecard traits of general appearance, dairy character, body and mammary and the final score of the cow.

The linear scoring system adopted by HFAA should provide the information necessary to estimate the genetic parameters and breeding values of animals in many different biological areas. The retention of the traditional scorecard traits and final score provide comparison to the prototype of the breed and provide an excellent merchandising tool for the purebred breeder.

The Holstein Association Linear Classification Program is included in Appendix A.

II.2 Environmental effects on body conformation traits

II.2.1 Herd

Legates (1971) estimated the variance component of herd effect on 130,000 Holstein cows for final score and the four scorecard traits (general appearance, dairy character, body capacity and mammary system). As percentages of the total variation, they varied from 13% to 25%. These results are based on discretely measured data. The results will be assumed to come from discrete data if not indicated as linear. Carter et al. (1965) used Canadian Holsteins and reported herd effect to account for 8% of the total variation in final score.

Norman and Van Vleck (1972b) estimated the variance components of the herd effect for body, udder and management traits. The estimates were all less than 25% of the total variation.

The portion of total variation accounted for by the herd effect ranged from 14% for final score to 1% for udder support in a study by Vinson et al. (1976). These were data collected on 78,151 Holstein cows distributed across 2,117 herds.

Thompson et al. (1983) reported a significant herd-classifier subclass effect when investigating sources of variation of 11,240 appraisals of Holsteins scored linearly (50 point scale).

Norman et al. (1983a) analyzed data collected on Ayrshires, Guernseys, Jerseys and Milking Shorthorns. These cattle were scored linearly from 50 to 99. Herd variances by trait and breed ranged from 2% to 23%. Herd effects were largest for stature and rear udder width of Ayrshires and udder depth in Milking Shorthorn.

II.2.2 Year

Norman et al. (1978) reported that the effects of year accounted for only 1% to 4% of the total variation. These data were collected on Jerseys from 1968 through 1976. The model contained the additional effects of herd and herd by year interaction. Norman and Van Vleck (1972b) analyzed 16,000 appraisals that were performed every two years from 1961 to 1968 through the New York type appraisal program. They found the variance components for year almost nonexistent as they ranged from 2% to 3% for udder halving and mastitis, respectively.

II.2.3 Herd by year interaction

Norman et al. (1983b) reported that the herd by year interaction effect explained a high of 23% of the total variation in final score to a low of only 9% in suspensory ligament. Moreno et al. (1979) observed the fraction of variance due to herd-year subclass to range from 8% for mammary system to 17% for body capacity. These proportions were generally below 10% for the descriptive traits. However, these data were not adjusted for stage nor age at classification effects.

Hay et al. (1983) found that the effect of the herd-year subclass needed to be removed when estimating the components of genetic variation for descriptive type traits in Holsteins. Norman et al. (1979) followed the same strategy in a sire evaluation model developed for Jersey type data. Norman et al. (1978) observed that herd-year subclass effects accounted for 21% of the variation in final score and 14% to 18% in the component traits. Herd-year explained a substantial amount of variation above that explained by years or herds. They postulated that this could have indicated a change in type confo mation within herds over time or could have been caused by classifiers.

II.2.4 Age at classification

Hyatt and Tyler (1948) remarked that as cows advanced in age there was a tendency for the inspectors to raise their ratings. On a scale of one to five, with five preferred, the average score increased from 2.27 for a 2-year-old to 4.06 for an eleven-year-old. They commented that this factor was not all age effect as selection had to be considered in the interpretation of the results. They later analyzed multiple classifications within the same cow. Results indicated the change in type rating due to age was not large but was significant in the case of 30 animals classified as four and five-year-olds.

Hansen *et al.* (1969) found age at classification to be a significant source of variation among classification scores of Holstein cows, in final score as well as for the four major descriptive categories. Norman and Van Vleck (1972a) showed age differences were large for about one-third of 35 traits studied, especially for mastitis, body weight and depth of udder. Older cows tended to be coded as longer in the rear udder, weaker in the fore and rear attachments and deeper in the udder than younger cows. The linear effect of age accounted for 93% to 100% of age sum of squares.

Cassell *et al.* (1973b) concluded age to be a significant effect for all traits in the analysis of 336,253 Holstein records scored for final score, five descriptive traits as well as twelve scorecard traits. Multiplicative age adjustment factors for final score and five descriptively scored traits were developed. A significant age effect was reported for all traits by Norman *et al.* (1978). They concluded the greatest effect was on body capacity and dairy character, changing the multiple correlation coefficient squared by 10.1% and 7.6%, respectively. Mammary score and feet and legs were least affected by age.

Thompson *et al.* (1983), in evaluating scores on 19,152 Holstein cows under the Mating Appraisal for Profit (M A P) program, found age to be significant ($P<.01$) for all traits except rear legs and heel depth.

II.2.5 Parity

Thompson *et al.* (1980) showed parity to affect all traits with the exception of basic form and legs ($P<.05$). Constants for the four udder traits, legs and feet were negative for first and second parities and positive for fourth and fifth plus parities. Since a score of one was superior, they suggested a deterioration of these traits as a cow aged. All other traits had a positive constant for first and negative for fifth parities. Barton et al. (1982) found similar results as they stated that in general, younger cows had lower scores for most traits. However, udder depth and foot shape had higher scores for younger cows.

Hayes et al. (1985), using the same data base as this study, reported a parity by age interaction. First and second parity interactions were evident in form and rump traits and in teat placement.

II.2.6 Stage of lactation

Differences in type scores due to stage of lactation effects were highly significant ($P<.01$) for final score and the four type components in a study by Hansen et al. (1969). The first and seventh months of lactation were significantly different from the average of other months. Cows averaged .82 points above the mean in the first month and .42 points below in the seventh month. Dairy character scores improved until the third month of lactation while body capacity showed the reverse trend. Mammary system scored lowest at the seventh month and lower than any other type trait.

Norman and Van Vleck (1972a) observed small differences were accounted for by stage of lactation among 44 type traits. Norman et al. (1978) concluded that stage of lactation had little effect on type traits except on body capacity and dairy character. The effect of stage of lactation was nonsignificant for feet, and accounted for only 1.7% and 1.6% of the variability in dairy character and chest and barrel, respectively.

Thompson et al. (1980) found all traits except frame were affected by a quadratic term of days milked and all traits by the linear term of days milked. A significant stage of lactation effect was reported by Thompson et al. (1983). They reported that the traits that might be most affected by body weight (strength, dairy character) or edema and udder condition (fore udder attachment, udder depth) were most affected by stage of lactation. Rear leg side view was least affected by stage of lactation.

II.2.7 Age by stage of lactation

Hansen et al. (1969) reported the interaction of age by stage of lactation was significant (P<.01) only for dairy character. At older ages the effect of stage was to lower the score for dairy character more drastically than younger cows.

Norman and Van Vleck (1972a) found the interaction between age and stage of lactation to be relatively small. They concluded that such interaction could be ignored if corrections were made for age and stage separately. Norman et al. (1978) showed a nonsignificant interaction for all but four traits studied. The inclusion of the interaction term in the model explained only .2% to .5% additional variation.

II.2.8 Season of classification

Mao et al. (1977) noticed an increase in Guernsey type scores for cows classified during the month of August and February. They hypothesized the August increase was due to a preparation of cattle for showing. Carter et al. (1965) used Canadian Holsteins and reported month of classification to have a small effect on final type score. Walter and Mao (1983) reported many type traits of Guernseys appeared to exhibit seasonal trends, but no consistent pattern was apparent across traits. Norman et al. (1983b) suggested the month of classification was a trivial source of environmental variation. Their month constants also showed August to have the greatest effect while November had the smallest constant. The difference between the August and November constants was only 1.5. They noted the sire evaluation within herd-year was invariant to the effect of season regardless of the size of constants.

Bensen et al. (1951) concluded season to be insignificant in its effect upon classification scores of Ayrshire cows. Wilcox et al. (1958) observed type scores were lower for cows scored in the fall in comparison to those scored in the spring. Traits most affected were feet and legs, body capacity and rear udder. However, they offered no reason for the origins of these differences.

II.2.9 Classifier

Tyler and Hyatt (1948) found a significant ($P<.01$) component of variance for classifiers when they studied the scoring of 3,738 Ayrshire cows by 10 classifiers. McGilliard and Lush (1956) found the differences between judges were negligible. They further commented that in all kinds of subjective measurements the knowledge of the range may unconsciously cause the observer to offset high ratings with low ones. The difference in judges' scores was moderately affected by years. They suggested a change in the appearance of the animal may be an environmental effect of the animal or a different intangible optimistic or pessimistic frame of mind possessed by the judge that day. However, a more precise measure was obtained for old cows than for younger and judges agreed more closely with each other on the same date than with themselves on different dates.

Vinson _et_ _al._ (1976) reported differences in the emphasis placed on specific descriptive traits in arriving at final score. Classifiers tended to disagree more on less specifically and clearly defined traits (e.g. udder quality, feet and front end) than on more clearly defined attributes (e.g. stature, back, rump and udder support). However, the percent of variance due to classifier was small for all traits (0.7% to 5.0%).

Thompson _et_ _al._ (1980) observed that differences between evaluators among all traits were small. Norman _et_ _al._ (1983b) observed, however, a significant classifier effect across all traits. Final score, general appearance and mammary system were most affected by classifier differences which explained 18.6%, 17.8% and 16.9% of the total variation, respectively.

II.2.10 Interactions involving classifier

McGilliard and Lush (1956) observed a cow by judge interaction, which could be a measure of disagreement among judges concerning the ideal they have established. This is to say that classifiers may prioritize traits differently. However, this interaction effect explained only 3% to 11% of the total variation. The effect of a cow by year interaction on the scores accounted for 12% to 31% of the total variation. They stated that this factor may have been partly due to a stage of lactation effect unaccounted for in the model. This study indicated nonsignificant judge by year interaction.

Thompson et al. (1983) reported a significant classifier by age effect for all traits except for final score and stature. A model including classifier, herd within classifier, age at classification, the interaction of classifier by age and stage of lactation was used to partition the total sum of squares. Two classifiers were found to be the greatest contributors to this interaction. They were also the two who had the least experience.

Vinson et al. (1976) found herd by classifier interaction effect to be of more importance than classifier effect for all traits, and more important than herd effect for all descriptive traits. However, only 16% of the subclasses were filled and the effects of stage of lactation, herd by year and classifier by year were not included in the model. The effect of evaluator was reported by Thompson et al. (1980) to interact with the parity effect in the study of 42,539 cows involved in the Mating Appraisal Program.

II.3 Phenotypic and genetic parameters

The literature review of milk and type traits has covered not only a large number of traits but also many different models and estimators of parameters. No estimator clearly surfaces as the most desirable for all data collection schemes. Therefore, some time should be spent reviewing these estimators.

II.3.1 Heritability estimators

Lush (1940) defined heritability in the narrow sense as the proportion of the total variance in a trait that is attributable to the average or additive effects of genes. Shelby et al. (1963)

noted the phenotypic and genetic relationships existing between and within various traits used as criteria for selection must be known to maximize the rate of progress in selection programs.

Dickerson (1958) discussed the advantages and disadvantages of various estimates of heritability. He suggested the regression of offspring on midparent is the most nearly unbiased estimate of heritability. This estimate is, however, subject to bias from environmental correlations between parent and offspring by selection of parents. Other estimates included double regression of offspring on dam and twice the regression of offspring on sire. The prior tends to overestimate heritability while the latter produces an underestimation. Three additional methods were presented by Dickerson: 1) from the sire component, 2) from the dam component and 3) from the full-sib correlation. The estimate from the sire component or the paternal half-sib correlation lends itself more readily to sire evaluation models and the data collection scheme currently intact in today's dairy cattle populations. Heritability estimates from the sire component may be obtained as follows:

$$\hat{h}^2 = \frac{4\hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_e^2}$$

where $\hat{h}^2$ = estimated heritability;

$\hat{\sigma}_s^2$ = estimated sire variance component; and

$\hat{\sigma}_e^2$ = estimated error variance component.

The denominator is the phenotypic variance adjusted per se for fixed effects which were included in the model. Two sources of bias are inherent to this estimator: 1) epistatic bias (Dickerson, 1969) and 2) ratio bias (Kendal and Stuart, 1969). The expectation of the estimator is then:

$$E[h^2] = (h^2 + \text{epistatic bias})(1 + \text{ratio bias}).$$

II.3.2 Genetic correlation estimators

Warwick and Legates (1979) defined genetic correlation as the correlation between the additive breeding values for two traits or between the sum of additive effects of the genes influencing these two traits. Falconer (1960) identified the need to distinguish the two causes of correlation between characters, genetic and environmental. The genetic cause of correlation is chiefly pleiotropy. Pleiotropy is the property of a gene affecting two or more characters. The genetic correlation between traits can be affected if selection is placed on the parents. Van Vleck (1968) reported large biases in estimates of the genetic correlation when selection was intense.

II.3.3 Phenotypic correlation estimators

The phenotypic correlations are the gross correlations that include both the environmental and genetic portions of the covariances. The phenotypic correlations calculated by means of estimated components of sire and residual variance are dependent upon the specified model with many relevant fixed effects not considered.

II.4 Genetic parameters of body conformation traits

II.4.1 Descriptively scored type traits

Wilcox et al. (1955) analyzed semi-annual official type classification scores from the Holstein-Friesian herd of the New Jersey Agricultural Experiment Station. They reported repeatabilities of .41, .43, .32, .56, .26, .19, .33, .36, and .29 for overall type, general appearance, feet and legs, rump, dairy character, body capacity, mammary system, fore udder and rear udder, respectively. These data were coded as 1 through 6 with the latter being the superior score.

The Mating Appraisal for Profit (M A P) database was used by Thompson et al. (1980) in studying the sources of variation in type data. Cows were scored on 12 components of type on a scale of 1 to 5 with 1 being the most desirable. The model included effects of evaluator, evaluator by herd, parity, evaluator by parity and days in milk which was classified as both a linear and quadratic effect.

Heritabilities ranged from .55 (scale) to .13 (back, rump, rear udder and center support) for cows in milk. The heritability of basic form was .95. The authors suggested that this large heritability was partially caused by the knowledge of parentage while scoring, thus producing a correlation between paternal half sisters. Heritability of basic form was recalculated by the method of regression of daughter on dam and produced an estimate of .14. Analysis of subtrait heritability adjusted for discontinuity, ranged from .52 (wide front teats) to .00 (teats too far back on the udder). Other traits with heritability above .20 were low front end, wing shoulders, weak crops, too much set to the legs, stance, toes out in front, teats too large, fore udder too shallow-tilted, rear udder too deep-tilted, high tailhead, narrow rump and toes spread.

Genetic and phenotypic correlations between type traits from Thompson et al. (1980) are presented in Table 1. Genetic correlations are higher in absolute value in general than phenotypic correlations. Feet and legs exhibited the largest genetic correlation (.89) and the third largest phenotypic correlation (.41).

Norman and Van Vleck (1972c) analyzed 49 body, udder and management traits of over 16,000 daughters sired by Holstein artificial insemination sires. Henderson's Method 1 estimates of variance components from a model consisting of year, herd, sire, herd by sire and error were used to estimate heritabilities over all lactations. The highest heritabilities were for measures related to body size. Heritability of upstandingness was estimated to be .43 for first lactation records and .38 for later lactation data.

Rump characteristics ranged in heritability from .16 to .19. The remaining body traits were more lowly heritable. Fifteen of the 21 heritabilities for the udder traits were equal to or less than .10. Strength of rear udder attachment, rear teat spacing, depth of udder, height of rear udder, slope of udder and udder quartering had estimates between .11 to .16. Most of these type traits were threshold characters and eighteen of the 49 were scored binomially; thus some underestimation may have occurred.

Cassell et al. (1973) analyzed 336,253 first scores at classification of records supplied by the Holstein-Friesian Association of America. The data set consisted of 12 descriptive traits, scored 1 through 6 with 1 being superior, in addition to final score (60 to 100) and four descriptive measures. Heritability and genetic and phenotypic correlations are shown in Table 2. Heritabilities were

Table 1. Phenotypic and genetic correlations of descriptively scored type[a,b]

Trait	Basic Form	Scale	Front	Body	Back	Legs	Feet	Rump	Rear Udder	Fore Udder	Center Support	Teats
Basic Form	-	-.08	-.29	-.18	-.01	-.08	-.01	-.06	-.09	-.08	.04	.05
Scale	-.05	-	.26	.07	.16	.06	.08	.01	.03	.03	.02	.02
Front	-.70	.32	-	.26	.16	.13	.09	.13	.09	.07	.04	.02
Body	-.56	-.09	.56	-	.26	.14	.10	.14	.06	.08	.06	.02
Back	-.20	.38	.50	.51	-	.08	.05	.19	.03	.03	.04	.04
Legs	-.35	.03	.41	.58	.35	-	.41	.14	.15	.11	.10	.06
Feet	.32	.12	.45	.52	.32	.89	-	.12	.12	.08	.08	.05
Rump	-.33	-.36	.10	.42	-.03	.14	.10	-	.15	.13	.09	.08
Rear Udder	-.12	-.09	.06	.02	-.28	.08	-.01	.24	-	.42	.33	.30
Fore Udder	-.26	-.10	-.01	.01	-.29	.04	-.05	.31	.72	-	.31	.38
Center Support	.04	.10	.16	.02	.19	.24	.23	.02	.28	.38	-	.46
Teats	.18	.18	-.15	-.32	-.07	-.09	-.17	.02	.23	.50	.67	-

[a] Thompson _et al._ (1980)

[b] Phenotypic correlations are above the diagonal while the genetic correlations are below the diagonal

Table 2. Heritability, phenotypic and genetic correlations among descriptively scored type traits[a,b,c,d]

Trait	Final[e] Score	Final Classification	General Appearance	Dairy Character	Body Capacity	Mammary System	Stature	Head	Front End	Back	Rump	Hind Legs	Feet	Fore Udder	Rear Udder	Udder Support	Udder Quality	Teat Placement
Final Score	(.31)	1.01	.93	.64	.81	.82	.70	.43	.79	.44	.58	.48	.40	.56	.62	.44	.52	.48
Final Classification	.91	(.25)	.94	.61	.82	.82	.70	.46	.79	.47	.50	.69	.42	.60	.61	.44	.64	.49
General Appearance	.79	.77	(.26)	.57	.84	.60	.74	.43	.82	.51	.66	.49	.47	.35	.43	.27	.42	.30
Dairy Character	.47	.45	.34	(.15)	.49	.36	.55	.23	.45	.27	.34	.23	.03	.10	.34	.11	.46	.24
Body Capacity	.56	.53	.55	.23	(.23)	.42	.77	.41	.95	.44	.42	.46	.44	.26	.20	.16	.14	.14
Mammary System	.74	.72	.45	.27	.23	(.20)	.31	.36	.45	.22	.37	.39	.32	.84	.80	.59	.74	.27
Stature	.46	.44	.50	.28	.51	.18	(.38)	.20	.62	.29	.25	.24	.32	.13	.13	.05	.27	.12
Head	.29	.28	.30	.17	.23	.18	.16	(.11)	.49	.24	.30	.10	.23	.24	.31	.12	.02	.07
Front End	.42	.39	.44	.21	.54	.19	.34	.29	(.11)	.47	.51	.39	.32	.20	.32	.11	.02	.08
Back	.30	.29	.38	.11	.26	.14	.20	.16	.25	(.14)	.34	.16	.11	.10	.10	.09	.09	.12
Rump	.41	.40	.47	.14	.26	.25	.19	.19	.25	.26	(.21)	.48	.19	.16	.31	.13	.08	.20
Hind Legs	.28	.27	.33	.11	.20	.16	.12	.16	.19	.10	.20	(.07)	.11	.22	.07	.13	.19	.21
Feet	.25	.24	.28	.08	.18	.15	.13	.12	.16	.08	.13	.24	(.18)	.30	.18	.18	.16	.22
Fore Udder	.45	.44	.27	.08	.14	.60	.11	.13	.14	.11	.18	.09	.10	(.16)	.50	.42	.56	.53
Rear Udder	.50	.48	.33	.22	.18	.57	.14	.14	.18	.11	.22	.15	.12	.25	(.17)	.38	.58	.36
Udder Support	.38	.36	.19	.10	.08	.46	.04	.05	.06	.04	.09	.05	.05	.25	.25	(.13)	.62	.42
Udder Quality	.31	.29	.16	.17	.04	.38	.09	.09	.05	.06	.10	.05	.03	.29	.20	.24	(.04)	.54
Teat Placement	.35	.34	.19	.11	.07	.48	.05	.10	.07	.08	.12	.08	.06	.34	.19	.23	.23	(.17)

[a] Cassell _et al._ (1973)
[b] Genetic correlations above and phenotypic correlations below the diagonal
[c] Heritability on the diagonal, standard error approximately .10
[d] All phenotypic correlations significant (P<.01)
[e] Scored 60-100

determined by an intraherd analysis of daughter-dam type scores. Age effects were removed by adjustment factors. Stature was the most highly heritable trait (.38), while udder quality, hind leg, feet, head and front end were low.

The correlations between final score with all type traits indicated selection on final score alone would produce significant improvement in the other traits. Genetic correlations were generally larger than the phenotypic. Among the scorecard traits, general appearance was most genetically related to final score (.93) and descriptive traits including stature (.46), front end (.42), rump (.41), fore udder (.45) and rear udder (.50).

The components of genetic variation in various type traits were investigated by Hay <u>et</u> <u>al.</u> (1983). Within herd heritability estimates are presented in Table 3. Heritability estimates from daughter-dam regressions were slightly higher than those from paternal half-sib correlations for all traits, indicating the possibility of common environmental effects and maternal effects. Covariances among maternal half sisters ranged from 3 to 8 times as large as those for paternal half sisters. These differences could have been caused by either maternal genetic or common environment effects.

Dominance components ranged from 1.3 to 7 times as great as the additive components. Hind legs and udder support were greatly influenced by dominant genic effects. Additive maternal components were similar to additive direct effects in most traits. All traits showed negative components of covariance between additive direct and additive maternal effects. This would seem to indicate a generally small but consistently negative relationship between additive effects of genes directly affecting the trait in the offspring and

Table 3. Heritabilities of linearly scored type traits[a]

Trait	Heritabilities from daughter-dam regression	S.E.	Heritabilities from paternal half sib correlation	S.E.
Final Score	.482	.003	.393	.08
Stature	.380	.004	.390	.08
Head	.148	.004	.128	.03
Front end	.189	.004	.185	.04
Back	.184	.003	.158	.04
Rump	.246	.004	.237	.05
Hind legs	.099	.004	.056	.02
Feet	.127	.004	.110	.03
Fore udder	.189	.003	.180	.04
Rear udder	.225	.004	.196	.04
Udder support	.135	.003	.113	.03
Teats	.189	.003	.186	.04

[a] Hay *et al.* (1983)

additive effects of genes for maternal performance. The authors suggested that the large effects of nonadditive genetic effects may be used to maximize the frequency of desirable genes in the progeny through the use of corrective mating.

II.4.2 Linearly scored type traits

Thompson et al. (1981) analyzed 18 traits in the linearized type appraisal program at Midwest Breeders Cooperative. Traits were scored on a scale of one to 50.

Heritability estimates from their study of linear type traits are shown in Table 4. Heritability estimates ranged from .11 (legs, rear view) to .68 (basic form) and were all greater than the heritability estimates for the descriptive traits.

Heritability of legs viewed from the rear (.11) was slightly less than heritability for a single appraisal of legs (.14) in the descriptive program. Heritability for legs viewed from the side (.24) was larger than the single appraisal.

Heritability estimates for linearly scored fore udder, rear udder height and rear udder width were larger than the heritability estimates of the fore udder and rear udder (both .21) from the Holstein-Friesian classification program (White and Vinson, 1976).

Their estimates of phenotypic and genetic correlations among linear type traits are in Table 5. Most phenotypic correlations were less than .30. Phenotypic correlations were negative between linearly scored traits in contrast to few, if any, negative phenotypic correlations in the descriptive program (Aitchison et al., 1972 and Thompson et al., 1980).

Large phenotypic correlations in the data indicated that cows

Table 4. Heritability estimates of linear type traits from Midwest Breeders' mating appraisal program[a]

Trait	heritability	S.E.[g]	Deviation[b]
Basic form	.68	.08	-.28
Strength	.39	.05	---[c]
Dairy character	.28	.04	---
Stature	.59	.07	.04
Body depth	.48	.06	.06
Rump (side)	.27	.04	.14[d]
Legs (side view)	.24	.03	.10[e]
Foot angle	.19	.03	.03
Fore udder	.28	.04	.14
Udder depth	.27	.04	---
Rump width	.25	.04	.12[d]
Legs (rear view)	.11	.02	-.03[e]
Rear udder height	.27	.04	.14[f]
Rear udder width	.28	.04	.15[f]
Center support	.20	.03	.07
Teat placement	.19	.03	.00
Disposition	.07	.02	---
Milkout	.10	.02	---

[a] Thompson *et al.* (1981)

[b] Heritability of linear trait minus heritability from descriptive program of Midwest Breeders' Cooperative

[c] No simnilar trait in descriptive trait program

[d] Single appraisal for rump in descriptive program

[e] Single appraisal for legs in descriptive program

[f] Single appraisal for rear udder in descriptive program

[g] Approximate standard error

Table 5. Phenotypic and genetic correlations for Midwest Breeders linear conformation appraisal program[a,b,c]

Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1 Basic form		.75	-.48	.18	.08	-.16	-.22	.15	.07	-.02	.22	.12	-.05	.05	-.11	-.11	-.06	-.09
2 Strength	.94		-.22	.22	.22	-.16	-.21	.17	.10	-.05	.24	.14	.02	.10	-.08	-.08	-.06	-.07
3 Dairy character	-.79	-.62		.11	.26	-.01	.05	-.08	-.01	-.13	-.04	-.06	.11	.07	.08	.08	.01	.03
4 Stature	.06	.07	.20		.02	.07	-.06	.06	.01	.11	.16	-.02	-.03	-.02	-.04	-.02	.00	-.02
5 Body depth	.10	.18	.12	-.22		-.10	-.02	-.02	-.02	-.28	.14	-.01	.06	.06	-.01	.00	-.02	-.04
6 Rump (side)	-.30	-.26	.33	.40	-.31		.03	-.12	-.13	-.10	-.18	-.15	-.18	-.18	-.10	-.09	-.03	-.06
7 Leg (side)	-.45	-.55	.27	.21	.05	.26		-.23	-.11	-.12	-.09	-.30	-.11	-.11	-.01	.00	-.04	-.03
8 Foot angle	.37	.49	-.16	.09	-.25	.12	-.57		.11	.04	.06	.27	.06	.06	-.01	-.01	-.03	-.02
9 Fore udder	.05	.19	.25	-.08	.05	-.10	-.52	.30		.43	.03	.10	.30	.28	.26	.26	-.01	.06
10 Udder depth	-.15	-.06	.34	.41	-.37	.30	-.22	.16	.61		-.07	.05	.12	.04	.26	.25	-.04	.07
11 Rump width	.36	.40	-.32	-.20	.95	-.42	-.25	.18	.09	-.12		.07	.07	.14	-.02	-.05	.01	-.03
12 Legs (rear)	.49	.63	-.30	-.10	-.05	-.05	-.48	.55	.12	.07	.63		.15	.16	.04	-.02	-.02	-.01
13 Rear udder height	-.08	.05	.23	-.20	.06	-.17	-.44	.30	.57	.39	.34	.35		.72	.24	.20	.00	.01
14 Rear udderd width	.10	.23	.02	-.27	.07	-.32	-.52	.26	.50	.24	.59	.47	.93		.14	.14	-.01	-.01
15 Center support	-.02	.11	.31	.07	-.11	-.05	-.23	.22	.62	.54	-.17	.08	.26	.11		.67	-.01	.04
16 Teats	-.13	-.09	.33	.15	-.16	-.07	-.14	.05	.51	.42	-.24	-.14	.13	.00	.92		.00	.05
17 Disposition	-.16	-.23	.02	.01	-.01	.16	.30	-.39	-.23	-.10	-.38	-.43	-.35	-.38	-.09	.06		.11[d]
18 Milkout	-.33	-.33	.39	.12	-.18	.19	.01	-.02	.42	.48	-.39	-.29	.05	-.11	.42	.54	.51[d]	

[a] Thompson *et al.* (1981)

[b] Phenotypic above the diagonal and genetic below

[c] Phenotypic correlations (with absolute value) > .08 are significant (P<.01)

[d] These correlations computed by model including herd, sire, parity and error

with wide rear udders also have higher rear udders and cows scored as thick in basic forms were stronger but less dairy. Stronger fore udder attachment was related to shallow udder depth and strong suspensory ligaments were associated with close teat placement.

Correlations among udder characteristics were greater than .20 and were more highly correlated among themselves.

Genetic correlations were generally greater than corresponding phenotypic correlations. Dairy character had large negative genetic correlations with basic form (-.79) and strength (-.62). Thus, selecting for animals with favorable dairy character also would result in a more angular female. Selection for dairy character would also result in taller animals, stronger in all udder traits, narrower and slightly sloping in rump and more sickled in rear legs.

Thompson et al. (1983) analyzed 19,152 cows scored from 50 to 99 with a model including classifier, herd, herd by classifier, age, classifier by age, stage of lactations, sire and error. Heritability estimates of the traits in the Linear Scoring System (Table 6) were very similar to those in the Uniform Functional Type Trait Appraisal Program. Stature was the most highly heritable trait (.50) followed by rump width, udder depth, final score and body. Phenotypic and genetic correlations are in Table 7. Genetic correlations were again generally greater than phenotypic. Phenotypic correlations ranged from -.29 (rear legs, rear view with rear legs, side view) to .76 (rear udder height with rear udder width). Udder traits yielded the highest correlations.

Table 6. Heritabilities of type traits scored linearly[a,b]

Trait	Heritability	Standard Error
Stature	.32	.04
Strength of body	.22	.03
Dairy character	.16	.02
Rump	.17	.03
Rump width	.26	.03
Rear leg, side view	.15	.02
Rear leg, rear view	.12	.02
Heel depth	.15	.02
Fore udder attachment	.15	.02
Rear udder height	.22	.03
Rear udder depth	.15	.02
Udder depth	.26	.03
Suspensory ligament	.12	.02
Teat placement	.23	.03
Final score[c]	.28	.03
Stature[c]	.25	.03
General appearance[c]	.24	.03
Body[c]	.26	.03
Dairy character[c]	.24	.03
Mammary system[c]	.23	.03

[a] Thompson _et_ _al._ (1983)
[b] Variance components estimated by Henderson's Method III
[c] Classification traits scored 1 through 5

Table 7. Phenotypic and genetic correlations among type traits scored linearly[a,b,c]

Trait	Stature	Strength of Body	Dairy Character	Rump	Rump Width	Rear Leg Side View	Rear Leg Rear View	Heel Depth	Fore Udder Attachment	Rear Udder Height	Rear Udder Width	Udder Depth	Suspensory Ligament	Teat Placement
Stature	-	.49	.12	.04	.30	-.06	.12	.17	.14	.15	.19	.16	.08	.08
Strength of Body	.65	-	-.06	.01	.31	-.12	.17	.23	.17	.20	.24	.09	.06	.07
Dairy Character	-.04	-.28	-	.00	.12	.11	.06	.02	.07	.15	.16	.03	.13	.11
Rump	-.02	-.18	.11	-	-.01	-.01	-.05	-.05	-.09	-.10	-.08	-.07	-.08	-.06
Rump Width	.28	.35	-.16	.00	-	-.01	.15	.16	.14	.19	.24	.11	.08	.10
Rear Leg, Side View	-.17	-.41	.36	.27	.12	-	-.29	-.18	-.06	-.10	-.09	-.08	-.03	-.03
Rear Leg, Rear View	.24	.44	-.02	-.29	.09	-.57	-	.35	.15	.20	.22	.14	.12	.11
Heel Depth	.38	.62	-.11	-.19	.21	-.59	.80	-	.19	.23	.23	.17	.12	.12
Fore Udder Attachment	.34	.40	-.06	-.33	.23	-.32	.41	.44	-	.45	.41	.53	.39	.41
Rear Udder Height	.22	.41	.04	-.35	-.03	-.38	.49	.48	.73	-	.76	.38	.34	.32
Rear Udder Width	.22	.44	.11	-.31	.05	-.32	.50	.49	.72	.95	-	.35	.32	.31
Udder Depth	.36	.21	-.14	-.14	.10	-.29	.41	.30	.79	.53	.47	-	.54	.43
Suspensory Ligament	.18	.19	-.04	-.22	.03	-.24	.51	.30	.68	.51	.50	.75	-	.57
Teat Placement	.17	.12	.15	-.14	.19	-.16	.49	.30	.65	.42	.48	.63	.82	-

[a] Thompson *et al.* (1983)

[b] Phenotypic above the diagonal and genetic below

[c] Henderson's Method III estimates

II.5 Phenotypic and genetic correlations between type traits

Touchberry (1951) used data from Iowa State College Holstein herd to investigate the genetic and phenotypic correlations between five body measurements and a single type rating, scored 0 to 17, with milk yield. Results are shown in Table 8. The three phenotypic correlation estimates between body length and heart girth, body length and paunch girth, paunch girth and weight show evidence of a high environmental correlation, or physiological correlation or both.

Table 8. Heritability, genetic and phenotypic correlations for body measurements and milk production[a,b,c]

Trait	WH	CD	BL	HG	PG	W	T	MP
Wither height (WH)	.73	.81	.80	.05	.31	.70	0	-.08
Chest depth (CD)	.74	.80	.75	.84	.51	.72	0	-.14
Body length (BL)	.67	.71	.58	.56	.18	.83	0	-.32
Heart girth (HG)	.63	.81	.58	.61	.79	.88	0	-.35
Paunch girth (PG)	.27	.43	.40	.61	.27	.69	0	-.58
Weight (W)	.53	.67	.70	.81	.84	.37	0	-.53
Type (T)	.14	.18	.15	.21	.20	.23	.25	0
Milk Production[d] (MP)	.02	.02	.02	-.08	-.00	-.04	.18	.35

[a] Touchberry, 1951

[a] Genetic correlations above diagonal, phenotypic below and heritability on the diagonal

[c] Phenotypic correlations are intra-sire

[d] 2X,243-day mature equivalent

Genetic correlation estimates are high among body measurements. However, milk seems to be genetically independent of the body measurements and weight.

Blackmore *et al.* (1958) also used the data from the Iowa State College herd to observe negative genetic associations between milk production and all measures of size except wither height. They reported genetic correlations of 0.23, -0.23, -0.12, -0.34, -0.13 and -0.02 between milk yield and wither height, chest depth, chest girth, paunch girth and weight, respectively. They concluded that selection for milk production alone would eventually lead to animals with some decrease in chest depth, body length and paunch girth and with even more drastic reduction in chest girth. They further stated that selection on milk would result in an increase in height at the withers with no weight change.

O'Bleness et al. (1960) investigated the phenotypic and genetic relationships between type traits and milk yield using data from the New York Type Appraisal Program (Table 9). The majority of genetic correlation estimates were positive but small with the exception of that between milk yield and dairy character. Three traits were found to have an antagonistic relationship with milk production, namely hind leg, rear leg movement and udder quartering.

Phenotypic correlation estimates were small with many of them approaching zero. They observed that head, depth of barrel and depth of udder were positively correlated with dairy character and attributed this to the influence of these traits on the rating of dairy character.

Intra-sire and intra-herd variances and covariances of daughters and dams were used by Mitchel et al. (1961) to estimate the phenotypic and genetic correlations between type ratings and milk production in Holstein-Friesian cattle. Type ratings were scored as 1 through 5 with 5 being superior. Milk yield was adjusted to a twice a day, 305-day lactation and a mature equivalent base. Three milk production levels were used to stratify the cows into produc-

Table 9. Heritability estimates of type and production traits[a,b,c]

Trait	h^2	S.E.	Correlation with Milk Production[d] Phenotypic	Correlation with Milk Production[d] Genetic
Production and body traits				
Dairy character	.10	.080	.209	.98
Head	.15	.092	.080	.24
Shoulder	.10	.062	-.077	.20
Withers	.16	.118	.150	.22
Hind leg (side)	.08	.078	.021	-.05
Hind leg (rear)	.04	.077	.004	.14
Pasterns	.12	.075	-.033	.32
Rear leg movement	.07	.057	-.033	-.10
Depth of barrel	.33	.115	.158	.24
Pin bone width	.05	.096	.054	.30
Milk yield	.40	.077	---	--
Udder characteristics				
Udder shape (rear)	.04	.109	.177	.29
Udder shape (fore)	-.05	.094	.093	--
Udder texture	.28	.069	-.026	.14
Depth	.22	.096	.191	.14
Levelness	.09	.072	-.017	.14
Strength of:				
rear attachment	.30	.065	-.044	.02
fore attachment	.16	.060	-.088	.12
Udder quartering	.18	.078	.003	-.02
Teat length (rear)	-.09	.090	---	--
Teat length (fore)	.05	.088	-.022	.66

[a] O'Bleness _et al._ (1960)
[b] Within herd-year analysis
[c] Twice the daughter-dam regression
[d] Correlations > .08 are different from zero ($P<.05$)

tion groups. This was done to examine the possibility of a production level by rating interaction.

Phenotypic and genetic correlation estimates for the three production levels are presented in Table 10. The most highly correlated, both phenotypically and genetically, trait with milk production was dairy character in all three groups. Phenotypic correlations were approximately the same in all production levels. However, the genetic correlations varied greatly both in signs and magnitudes.

The inconsistency in genetic correlations in different production groups, as compared to the consistency in phenotypic correlations, could be attributed to the environmental correlation.

McDaniel and Legates (1965) stated that the role of body size is very influential in the showring and in the official breed type classification programs. Generally larger animals are chosen over smaller. Environmental conditions that favor higher milk yields are also conducive to heavier body weights. In their study, larger cows in all four age classes showed slight but significant linear increases in both 90-day and 305-day milk yield. A change of 181 pounds of milk per 100 pounds of weight in first lactation cows was observed. Heritability estimates of body weight ranged from .44 to

and length of productive life and stated than an opportunity exists to increase milk yield without materially increasing body size. Atkeson _et al._ (1969) investigated the phenotypic relationships between type traits, scored on a five point scale, with milk yield. The correlations between milk yield and dairy character (.36) was the strongest. The next largest correlation was between body capa-

Table 10. Phenotypic and genetic correlations between type rating and milk yield stratified into (L)ow:<11,960, (M)edium:11,960-13,230 and (H)igh:>13,230 lbs. milk production groups[a,b,c]

Type Trait		Genetic			Phenotypic		
		L	M	H	L	M	H
Final Score	L	.08			.13		
	M		.28			.16	
	H			-.04			.14
General Appearance	L	.01			.09		
	M		.02			.12	
	H			-.02			.09
Dairy Character	L	.61			.23		
	M		.82			.25	
	H			.61			.24
Breed Character	L	-.06			.08		
	M		.33			.10	
	H			.12			.06
Mammary System	L	.11			.11		
	M		.23			.13	
	H			-.13			.11
Feet & Legs	L	-.17			.02		
	M		.26			.06	
	H			.07			.03
Rump	L	-.05			.04		
	M		.12			.04	
	H			-.01			.04

Correlation with milk yield (spans Genetic and Phenotypic columns)

[a] O'Bleness *et al.* (1960)

[b] Standard error of phenotypic correlations range from .01 to .02

[c] Approximate standard error of genetic correlations was .10

city and milk yield (.09). The relationship of milk to fore udder score was negative (-.02) and was the only negative relationship obtained.

Miller et al. (1971) observed descriptive type traits to have a weak association with progeny merit for production (Table 11). Udder support was highly but negatively associated with predicted difference (PD) milk (-.18). The highest correlation was between fore udder and rear udder (.55).

Their multiple regression analysis revealed that udder support, rear udder and fore udder were statistically significant in explaining the variation in predicted difference milk. However, the negative coefficient indicated that high transmitting ability for milk was associated with poor udder support and floor.

Norman and Van Vleck (1972c) estimated the genetic and phenotypic correlations between type traits and milk production (Tables 12 and 13). Most phenotypic correlations among these type traits were near zero. Depth of udder was the appraisal trait having the highest correlation with first lactation milk.

Genetic correlations were again generally larger than phenotypic in absolute value and varied greatly in the sign of the estimates. The traits strength and high carriage of the udder were negatively correlated with production: strength of fore udder (-.71), rear udder attachment (-.27) and height of udder (-.15). The magnitude of the estimates would indicate a very large sampling variance of the estimates.

Grantham et al. (1974) investigated 336,253 Holstein daughters of 27,907 sires. Daughters were scored with an assigned value (range 1 to 5) for each of twelve type traits, as well as a miscel-

Table 11. Phenotypic correlations between type traits and predicted difference (PD) milk[a]

Trait	Stature	Head	Front End	Back	Rump	Hind Legs	Feet	Fore Udder	Rear Udder	Udder Support	Udder Quality	Teats
PD Milk	.00	.07	.02	-.01	-.04	.04	.04	-.12	.04	-.18	-.09	-.09
Stature		.33	.42	.31	.29	.28	.23	.27	.24	.20	.21	.07
Head			.41	.21	.44	.34	.25	.36	.36	.18	.17	.29
Front End				.25	.40	.34	.26	.42	.35	.28	.16	.12
Back					.42	.15	.08	.22	.10	.06	.10	.08
Rump						.41	.22	.46	.45	.26	.14	.20
Hind Legs							.49	.36	.36	.21	.14	.18
Feet								.28	.24	.19	.16	.09
Fore Udder									.55	.50	.32	.47
Rear Udder										.43	.22	.31
Udder Support											.36	.34
Udder Quality												

[a] Miller *et al.* (1971)

Table 12. Phenotypic correlations between milk production and type traits[a,b]

Trait	Herdmate Deviation Milk	Lifetime Milk	Number of Lactations
Body traits			
Body weight	.08	.01	.00
Sharpness	.15	.16	.13
Tightness of shoulder	-.05	-.01	.00
Depth of body	.10	.02	.00
Levelness of rump	.00	.03	.03
Smoothness of pelvic arch	-.04	-.02	-.01
Height of tail setting	.00	.03	.03
Upstandingness	.05	.04	.02
Udder traits			
Rear udder length	.14	.06	.03
Fore udder length	.07	.08	.08
Fore udder bulginess	.09	.01	.01
Fore udder funnelness	.03	-.03	-.03
Udder quality	-.07	.06	.06
Depth of udder	.27	.03	-.01
Forward slope to udder	.08	-.03	-.05
Height of rear udder	.10	.09	.07
Strength rear udder attach.	-.06	.02	.04
Strength fore udder attach.	-.10	.00	.02
Fore teats forward	.04	.00	.01
Fore teats spacing	.01	-.05	-.05
Rear to fore teat spacing	.03	-.01	-.01
Production traits			
Milk, herdmate deviation	1.00	.34	.20
Lifetime milk	-	1.00	.95
Number of lactations	-	-	1.00

[a] Norman and Van Vleck, 1972c

[b] Henderson's Method I variance component estimator from a model including year, herd, sire, sire by herd and error

Table 13. Genetic correlations between milk production and type traits[a,b]

Trait	Herdmate Deviation Milk	Lifetime Milk	Number of Lactations
Body traits			
Body weight	.15	.56	.60
Sharpness	.34	1.88	1.34
Tightness of shoulder	-.47	-.49	-.22
Depth of body	.16	-.02	.00
Levelness of rump	-.33	.06	.25
Smoothness of pelvic arch	-.18	-.28	-.43
Height of tail setting	-.37	.04	.28
Upstandingness	.02	.71	.55
Udder traits			
Rear udder length	.21	.48	.14
Fore udder length	-.54	.31	.66
Fore udder bulginess	-.01	-2.57	-2.23
Fore udder funnelness	.47	.49	.34
Udder quality	-.50	.99	1.58
Depth of udder	.36	-1.08	-1.36
Forward slope to udder	1.48	.07	-.54
Height of rear udder	-.15	.25	.10
Strength rear udder attach.	-.27	-.02	.26
Strength fore udder attach.	-.71	2.23	2.36
Fore teats forward	-.13	.10	.23
Fore teats spacing	.00	-.22	-.30
Rear to fore teat spacing	.15	1.88	1.43
Production traits			
Milk, herdmate deviation	1.00	1.14	.90
Lifetime milk	-	1.00	.98
Number of lactations	-	-	1.00

[a] Norman and Van Vleck, 1972c

[b] Henderson's Method I variance component estimator from a model including year, herd, sire, sire by herd and error

laneous category, along with scorecard traits (general appearance, dairy character, body capacity and mammary system) and final score.

Genetic correlations between predicted difference milk and type are presented in Table 14. All correlations between type and milk production, with the exception of dairy character were negative. Traits were scored as percent desirable. They, therefore, suggest a strong negative relationship exists genetically between type and milk production.

Everett et al. (1976) analyzed 558,654 Holstein cows for the relationships between type, production and stayability. Predicted difference for type (PDT) was obtained from the Holstein Association and 305-day, ME milk and stayability were computed by the Northeast AI Sire Comparison with the relationship matrix included. The correlation between PDT and milk proofs was -.28 while the phenotypic correlation was -.32. Schaeffer and Burnside (1974) reported a correlation of -.05 between type and milk proofs.

II.6 Sire evaluation

The true genetic values of bulls are never known. Therefore, prediction results cannot be compared with true values to confirm the accuracy of the methodology. Henderson (1973, 1974) described, nonetheless, various criteria desirable in sire evaluations:

1. The predictor has the same expectation as the unknown variable that is to be predicted.
2. Minimization of the variance of the error of prediction in the class of linear unbiased predictors.
3. Maximization of the correlation between the predictor and the predictand in the class of linear unbiased predictors.
4. When the distribution is multinomial normal:
    a. yields the maximum likelihood and the best linear unbiased estimator of the conditional mean of the predictand.

Table 14. Genetic correlations between type and milk[a]

Trait	Predicted Difference Milk[b,d,f]	Predicted Difference Milk[c,e]
Final score	-.14	-.23
General appearance	-.16	-.24
Dairy character	.38	.41
Body capacity	-.14	-.22
Mammary system	-.15	-.24
Stature	-.07	-.11
Head	-.09	-.10
Front end	-.11	-.19
Back	-.11	-.16
Rump	-.20	-.23
Hind legs	-.10	-.15
Feet	-.06	-.16
Fore udder	-.22	-.36
Rear udder	-.07	-.14
Udder support	-.14	-.08
Udder quality	-.02	-.13
Teats	-.06	-.09

[a] Grantham _et al._ (1974)

[b] Sires restricted to at least 20 daughters in 10 herds, 1,095 bulls.

[c] Sires restricted to at least 100 daughters in 10 herds, 455 bulls.

[d] All correlations are significant with absolute value greater than .06 ($P<.03$) and .08 ($P<.01$).

[e] All correlations are significant with absolute value greater than .09 ($P<.05$) and .12 ($P<.01$).

[f] USDA Predicted Difference Sire summaries

b. in the class of linear, unbiased predictors, maximizes the probability of a correct pairwise ranking.

Many methods have been used over time to predict the performance of a sire's progeny. However, the development of Best Linear Unbiased Prediction (BLUP) (Henderson, 1950) has quickly proven its superiority for such purposes.

Henderson (1975) examined the consequences of modeling errors in the application of BLUP. The consequences of ignoring relevant fixed effects led to biased estimators. The inclusion of irrelevant factors increased the sampling variance. If random factors were excluded, whether relevant or not, the estimator and predictor remained unbiased but the sampling variance would increase.

The HFAA introduced predicted difference type (PDT) in January, 1971 to provide a method of evaluating the transmitting ability of dairy bulls for final classification score. This method is not a BLUP method and does not have known statistical properties. The current method of estimating PDT is (Kliewer, 1973):

$$PDT = b[(P - B) - .15(D - B)]$$

where b is the repeatability of the PDT and is the regression of future on past daughters;

P is the daughter average for final score adjusted for type;

B is the breed average adjusted for age;

.15 is the correlation ($.5h^2$) between classification scores of daughters and dams; and

D is the mean type score of classified dams adjusted for age.

This method has been applied to final score only and does not use the linearly scored traits.

II.7 Maximum likelihood and restricted maximum likelihood estimators of variance and covariance components

The use of maximum likelihood (ML) and restricted maximum likelihood (REML) (Thompson, 1962 and Patterson and Thompson, 1971) for the estimation of variance components has been the preferred estimator in recent years. The initial use of ML and REML can be traced back to Crump (1947) and Anderson and Bancroft (1952).

Harville (1977) described many desirable properties of the maximum likelihood approach. The ML estimators are functions of every sufficient statistic, consistent, asymptotically normal and efficient. In addition, the ML approach is always well-defined in that estimates, although biased, remain consistently within the parameter space.

Undesirable properties are also inherent to ML. Maximum likelihood estimators of variance components take no account of the loss in degrees of freedom resulting from the estimation of the model's fixed effects. An additional constraint of ML is that a particular estimator is distribution dependent and the desirable properties are contingent on the assumed distribution to which the estimator was derived. The first problem is rectified by the use of REML. The second, as is suggested by Harville (1977), may be unnecessary as ML estimators derived under normality may be suitable even when the form of the distribution is unspecified.

Banks *et al.* (1983) report that variance components estimated by REML assuming normality were not greatly affected if the underlying data were skewed. However, the sampling variances tended to increase as the degree of skewness became more pronounced.

Henderson (1984) stated that REML estimated by an algorithm described by Dempster et al. (1977) guarantees a positive definite estimated matrix. The expectation maximization (EM) algorithm takes the expectations of each round of iteration under the pretense that $\hat{G} = G$ and $\hat{R} = R$.

II.8 Multiple trait analysis

Multiple trait analysis is merely an extension of single trait MME and Henderson's Best Linear Unbiased Prediction. Mao (1982) stated that multiple trait analysis is most advantageous when the absolute value of the correlation between traits are high. This allows the information on each trait to contribute to the accuracy of estimation and prediction of the other. Selection pressures within the population would bias ranking and variance component estimation if estimated by single trait methods. This selection could possibly be in the form of a nonrandom sample of the population for which inferences are to be applied, such as those animals within the milk recorded population which have type scores. Selection on correlated traits could also introduce selection bias within the data. An example of this would be the estimation of genetic parameters and rankings of bulls from second lactation daughters after selection had occurred on the first lactation records. Multiple trait analysis allows the data for which selection decisions were made to be included in the analyses thus reducing selection bias.

II.8.1 Selection bias

Selection bias in the estimation of variance components was researched by Song and Schaeffer (1978). Four levels of selection were imposed: 100, 90, 75 and 60%. When the two traits were uncorrelated either single trait or multiple trait restricted maximum likelihood would generate the same estimate of genetic correlation. When the genetic correlation was .5 or .9 the effects of selection were pronounced. They concluded that if selection was apparent in the data, single trait restricted maximum likelihood estimators would lead to biased estimates. Multi-trait estimators tended to compensate for the selection and should have been used in situations where selection was involved. It should be noted that the residual covariance was assumed to be zero throughout the study.

Pollack _et_ _al._ (1984) examined selection bias and multiple trait evaluation. For single trait methods the analysis of a second trait, correlated with another, may not include the data on which the selection decisions were made. In a single trait analysis of yearling and weaning weights they reported a tendency to overpredict the worst bulls and underpredict the best bulls. This simulation study revealed that bulls with less than or equal to 6 progeny remaining after selection were overevaluated by an average of 17 kg and those with greater than or equal to 14 progeny were under evaluated by approximately 14 kg. This result indicates that the use of single trait analysis on selected data could result in misranking the bulls. The use of multiple trait analysis and the inclusion of records from which selection decisions were made removed the bias.

A simulation study by Walter and Mao (1985) indicated that with no selection, a single trait restricted maximum likelihood (REML) estimator and a multitrait REML with nonzero residual covariance yielded similar results. With selection, the use of the single trait estimators resulted in significant bias in the estimated components of variance as well as estimates of genetic and phenotypic correlations. The use of multi-trait REML assuming residual covariances of zero produced marginal improvement over that of single trait REML. Multi-trait analysis with a full variance and covariance structure was unaffected by selection. The estimated genetic and residual correlations are presented in Tables 15 and 16, respectively.

Rothschild et al. (1979) noted that estimates of variance components via Henderson's Method I were biased with 50% selection. This is due to the fact that expectations of estimators are not parameters of the unselected population. Maximum likelihood estimates were obtained and exhibited only slight differences between the simulation parameters and the estimates. It was neither implied or proved the maximum likelihood or restricted maximum likelihood removed selection bias; however, selection within fixed classes did not affect estimates of variance and covariance.

The impact of culling on sire evaluation was researched by Cassell et al. (1983). Three models were investigated: (1) Separate single trait evaluations of first and second lactations; (2) Single trait analysis combining first and second lactations but added a random cow component in the model; and (3) a multi-trait procedure where first and second lactation evaluations were calculated simultaneously. Culling was simulated at 10, 20 and 30% and relationships of sires were included in all models. Model one was most affected by culling with the least variability due to selection

Table 15. Comparison of genetic correlations for traits 1 and 2 computed from single trait (ST), multiple trait with residual covariance assumed zero (MT-0), and multiple trait (MT) restricted maximum likelihood approaches.[a]

Simulated correlation of residuals	Simulated genetic correlation .15 ST	.15 MT-0	.15 MT	.45 ST	.45 MT-0	.45 MT	.75 ST	.75 MT-0	.75 MT	Culling (%)
.15	.140	.158	.140	.436	.453	.436	.736	.753	.736	0
	.076	.084	.132	.378	.387	.427	.699	.709	.728	20
	.055	.052	.121	.359	.359	.419	.692	.691	.724	40
	.040	.041	.129	.330	.346	.424	.651	.672	.723	60
.35	.144	.185	.144	.439	.481	.439	.738	.779	.738	0
	-.001	.020	.136	.306	.331	.431	.653	.682	.731	20
	-.052	-.047	.125	.255	.266	.423	.619	.637	.727	60
	-.078	-.081	.133	.211	.230	.428	.563	.605	.727	60
.55	.147	.213	.147	.442	.508	.442	.741	.806	.741	0
	.078	-.045	.140	.230	.270	.435	.600	.647	.735	20
	-.156	-.143	.130	.144	.165	.428	.531	.563	.732	40
	-.189	-.197	.138	.008	.102	.423	.457	.505	.732	60

[a] Walter and Mao (1985)

Table 16. Comparison of residual correlations for trait 2 computed from single trait (ST) and multiple trait (MT) restricted maximum likelihood approaches[a]

Residual correlation simulated	Genetic correlation simulated .15 ST	.15 MT	.45 ST	.45 MT	.75 ST	.75 MT	Culling
							(%)
.15	.148	.148	.148	.149	.148	.149	0
	.112	.143	.112	.144	.112	.144	20
	.091	.136	.091	.138	.091	.139	40
	.084	.143	.084	.144	.084	.145	60
.35	.348	.348	.348	.348	.348	.349	0
	.274	.343	.274.	.344	.274	.345	20
	.233	.338	.233	.339	.233	.340	40
	.207	.343	.208	.344	.208	.346	60
.55	.549	.548	.549	.548	.549	.549	0
	.452	.545	.452	.545	.452	.546	20
	.395	.541	.395	.542	.395	.543	40
	.352	.541	.353	.545	.353	.547	60

[a] Walter and Mao (1985)

occuring in model 2. Model 3, the multi-trait model, was not affected by the differential selection; however, the variability was dependent on the genetic correlation.

II.8.2 Sire evaluation and variance and covariance estimation

Schaeffer (1984) suggested that multiple trait analysis improved the accuracy of evaluations as compared to single trait analysis. A multiple trait analysis should, theoretically, improve the accuracy of ranking animals for genetic merit of each trait. Table 17 shows the percentage reduction in prediction error variance over single trait analysis (Schaeffer, 1984). The greater the absolute difference in the correlations, the greater the reduction in prediction error variance for both traits. When the error correlation was less (greater) than the genetic correlation, in absolute terms, then the trait with the lower (higher) heritability achieved the greatest percentage reduction of prediction error variance. The effect of additional numbers of animals in the evaluation was minimal compared to the influence of the correlations.

Schaeffer (1984) also noted that the type of multiple trait model had an effect on the influence of the correlations on the solutions. An individual animal model may be affected more by error and genetic correlations than a sire model. Accuracy also may be improved more in the animal model as compared to a sire evaluation model.

The sensitivity of multiple trait analysis to erroneous assumptions was investigated by Schaeffer (1984). Although dependent on the model, the increase in prediction error variance was directly related to the differences between true and estimated correlations.

Table 17. Percentage reduction of variances of prediction error variance for a multiple trait analysis versus single trait analysis[a,b,c]

Correlation Between Traits		Number of Animals Evaluated[d]							
		10		20		30		40	
Error	Genetic	Trait 1	Trait 2	Trait 1	Trait 2	Trait 1	Trait 2	Trait 1	Trait 2
.1	.3	.92	.13	.97	.14	.99	.14	1.00	.14
.1	-.3	2.15	1.35	2.28	1.45	2.33	1.48	2.35	1.49
.1	.7	6.77	1.92	7.19	2.06	7.32	2.10	7.39	2.12
.1	-.7	9.46	4.72	10.03	5.05	10.23	5.16	10.32	5.21
.5	.3	.01	1.96	.01	2.09	.01	2.14	.01	2.16
.5	-.3	7.22	8.91	7.66	9.52	7.81	9.73	7.88	9.84
.5	.7	3.28	.07	3.48	.08	3.54	.08	3.58	.08
.5	-.7	18.79	15.93	19.93	17.02	20.32	17.39	20.51	17.58

[a] Schaeffer, 1984

[b] Heritability of Trait 1 = .1

[c] Heritability of Trait 2 = .25

[d] Animals measured on all traits

The trait with the smaller heritability usually showed the greater increase in prediction error variance from incorrect estimates, unless the estimated error correlation was greater than the estimated genetic correlation. The absolute difference was defined as:

$$AD = |(r_e - r_e') - (r_g - r_g')|$$

where r_e = estimated correlation residual;
r_e' = parameter residual;
r_g = estimated genetic correlation; and
r_g' = parameter genetic.

The average percentage increase in the prediction error variance for various deviations of estimated correlations from the true correlations are shown in Table 18. The largest percentage increase in prediction error variance was 35.45%. This resulted from $AD = |(.5 - .1) - (-.7 - .7)|$. However, small errors in estimated correlations compared to true correlations should result in less than a 5% increase of the prediction error variance.

Two types of error may exist in assumed a priori values. One error is nonpositive definiteness of the variance-covariance matrix. If this is the case, the eigenvalue, which by definition must be positive, must be modified such that all eigenvalues are greater than zero. The second and most frequent error is that the a priori estimates of variances and covariances may be greatly different than the underlying true values.

Henderson (1975) showed that solutions to mixed model equations were not biased by an incorrect variance-covariance structure. However, he noted this did result in increased prediction error variances.

Table 18. Average percentage increase of variances of prediction for various absolute differences of estimated correlations from true correlations[a]

Absolute Deviation	Percentage errors in Prediction Error Variance	
	Trait 1	Trait 2
0	1.36	1.09
.1	.87	.76
.3	1.61	3.35
.4	4.62	1.39
.5	4.45	2.51
.6	6.20	5.11
.7	6.96	6.44
.8	11.55	4.95
.9	12.85	5.05
1.0	14.39	10.87
1.1	15.59	13.03
1.2	21.05	12.04
1.3	24.20	9.35
1.4	24.66	17.08
1.8	35.45	24.18

[a] Schaeffer, 1984

III. MATERIALS AND METHODS

III.1 Genetic parameters of linear type traits

III.1.1 Data

Linear type scores of 64,875 cows distributed across 2,168 herds were supplied by the Holstein-Friesian Association of America (HFAA). These data were recorded from cows in Michigan and Wisconsin that were classified between January one and November 31, 1983. Grade and registered daughters represented a total of 64,875 records. Each cow had 29 linear type scores each on a scale ranging from one to 50, four classification scores each on a scale from one through five and final score with a range of 50 to 100. The Dairy Herd Improvement Association (DHIA) herd number and the identification of the cow, sire, dam and maternal grandsire were provided for each cow as well as dates of birth, classification and calving, classifier, lactation number and stage of lactation at classification. The linear type scores were given by twenty-five HFAA classifiers. The average number of cows scored by a given classifier was 2,595 and ranged from one to 9,871 cows scored.

The linear type traits were subdivided by the HFAA into 15 primary and 14 secondary traits (Table 19). The primary traits are considered economically important and sufficiently variable to merit recognition in a selection program. A complete description of the linear type scoring system is presented in Appendix A.

This data base of type scores represents a highly selected population, since it is a subpopulation of cows from Michigan and Wisconsin that were scored for type. A further restriction, which is necessary for any genetic study involving a paternal half-sib

Table 19. Primary and secondary linear type traits[a]

Primary	Secondary
Stature	Relative Height Front End
Strength	Shoulders
Body Depth	Back
Angularity	Tailhead
Rump Angle	Vulva Angle
Rump Length	Rear Leg Position
Rump Width	Rear Leg Rear View
Rear Leg Side View	Mobility
Foot Angle	Pasterns
Fore Udder Attachment	Toes
Rear Udder Height	Fore Udder Length
Rear Udder Width	Udder Balance
Udder Support	Teat Placement Side View
Udder Depth	Teat Size
Teat Placement Rear View	

[a] Holstein-Friesian Association of America, 1985

analysis, is that daughters must be identified by sire.

Crude averages, ranges and standard deviations of the data are shown in Table 20. And, additional data characteristics are shown in Appendix B.

The criteria used to edit the HFAA type data are shown in Table 21.

To enhance connectedness of the data structure, sires were required to have at least 20 daughters distributed in at least 10 herds. A total of 15,070 records were deleted leaving a data set of 299 sires with 41,834 daughters distributed in 1,945 herds.

III.1.2 *A priori* adjustments

Individual scores of 15 primary type traits were adjusted separately for differences due to stage of lactation and age within lactation number. The multiplicative adjustment factors were supplied by the HFAA. The origin of the derivation of these factors was not known, but it is evident that these factors were not derived from solutions of a simultaneous model. It was assumed that the adjustments were perfect such that stage of lactation and within lactation age effects were considered simultaneously and only these effects were adjusted.

Hayes et al. (1985) reported no interaction between stage of lactation and age within lactation number. These results would justify the use of a two stage adjustment for stage and age within lactation.

The structure of the data set for type was such that all the data were collected within one year, 1-1-83 to 11-31-83. The administration of the linear scoring system at the time of the procure-

Table 20. Crude averages, ranges and standard deviations from the original linear type data base[a]

Variable	Mean	Range	Standard Deviation
Date of Birth	6-15-78	1-1-66 to 12-31-84	N/A
Date of Classification	6-15-83	1-1-83 to 11-31-83	N/A
Last Date of Calving	6-15-80	0-0-00 to 12-31-83	N/A
Lactation Number	2.07	0 to 22	1.41
Stature	28.43	1 to 50	7.52
Strength	26.08	1 to 50	7.30
Body Depth	28.03	1 to 50	7.26
Angularity	28.47	1 to 50	7.79
Rump Angle	25.24	1 to 50	5.70
Rump Length	28.29	5 to 50	5.63
Rump Width	24.78	1 to 50	6.73
Rear Leg Side View	26.59	1 to 50	6.68
Foot Angle	23.44	1 to 50	6.76
Fore Udder Attachment	24.83	1 to 50	7.76
Rear Udder Height	25.36	1 to 50	7.68
Rear Udder Width	24.82	1 to 50	7.56
Udder Support	26.71	1 to 50	6.91
Udder Depth	25.53	1 to 50	6.72
Teat Placement Rear View	24.59	1 to 50	6.46

[a] Primary traits with 64,875 observations

Table 21. Data editing criteria and number of records deleted from linearly scored type data

Editing Criteria	Number of Records Deleted
No DHIA Herd Code	4031
No Lactation Code	3450
No Calving Date	359
Lactation ≥ 10	34
Lactation = 1 and 21 < Age[a] < 67	11
Lactation = 2 and 27 < Age[a] < 77	5
Lactation = 3 and 40 < Age[a] < 89	6
Lactation = 4 and 49 < Age[a] < 98	17
Lactation = 5 and 65 < Age[a] < 120	10
Lactation = 6 and 75 < Age[a] < 124	19
Lactation = 7 and 98 < Age[a] < 136	15
Lactation ≥ 8 and ≤ 10 and 111 < Age[a] < 167	17

[a] Age at classification in months

ment of the data allowed only one classification within a years time. Thus, the effect of year is nonexistent in our model.

III.1.3 Model

The model used to estimate the genetic parameters of each linear type trait and relationships between those traits was:

$$y = \mu 1 + Hh + Gg + Ss + e \qquad \text{III.1}$$

where:

y is the observation vector of 41,834 observations on one of 15 primary type traits. Observations were individually adjusted for stage of lactation and within lactation number age effects;

μ is the overall constant;

1 is a column vector of ones;

h is a vector of length 1,945 containing unknown constants of the fixed effect of herds;

H is an incidence matrix for the number of cows and herds, respectively, corresponding to h with size 41,834 by 1,945;

g is a vector of length seven containing unknown constants of the fixed effects of sire groups;

G is an incidence matrix corresponding to g with size 41,834 by seven;

s is a vector of length 299 containing unknown random effects of sire;

S is an incidence matrix corresponding to s of size 41,834 by 299; and

e is a vector of nonobservable random residuals corresponding to y.

The expectations are:

$$E[y] = \mu 1 + Hh + Gg$$

$$E[e] = 0$$

$$E[s] = 0$$

The variance-covariance matrix of the random factors is:

$$\mathrm{Var}\begin{bmatrix} y \\ s \\ e \end{bmatrix} = \begin{bmatrix} V_n & S\sigma_s^2 & I_n\sigma_e^2 \\ \sigma_s^2 S' & I_p\sigma_s^2 & 0 \\ I_n\sigma_e^2 & 0 & I_n\sigma_e^2 \end{bmatrix}$$

where $V_n = SS'\sigma_s^2 + I_n\sigma_e^2$.

Further assumptions implicit to the given model are:

Since each herd was scored only once and by only one classifier in our sample of data, the herd and classifier effects were completely confounded. For the same reason, the season at classification and season by classifier effect were also confounded with herd.

Henderson (1975) pointed out that ignoring groups, if bulls come from differing genetic populations, could lead to biased estimators. Additionally, if groups are included and not significant, the result would be an increase in the prediction error. Jensen (1979) suggested using the registration number of the bull as a convenient method of grouping by sire's age. The 299 bulls in this study were assigned to seven groups by their registration numbers. The mixed model equations (MME) are:

$$\begin{bmatrix} 1'1 & 1'H & 1'G & 1'S \\ H'1 & H'H & H'G & H'S \\ G'1 & G'H & G'G & G'S \\ S'1 & S'H & S'G & S'S + Ik \end{bmatrix} \begin{bmatrix} \mu \\ h \\ g \\ s \end{bmatrix} = \begin{bmatrix} 1'y \\ H'y \\ G'y \\ S'y \end{bmatrix}$$

where $k = \sigma_e^2/\sigma_s^2$.

III.1.4 Absorption of herds

The total number of mixed model equations (MME), if constructed as above, would be 2,254. Therefore, the 1,495 herd equations were absorbed by loop absorption, one herd at a time, while constructing equations for μ, group and sire. After absorption the total number of equations was 307.

The variance ratio, k, is assumed to be constant. This allows k to be added after absorption. The process of absorption reduces the number of equations but does not change the total sum of squares or the rank of the matrix. Therefore, the sum of squares of absorbed factors must be accounted for in the process of variance component estimation. Consider the original equations without the variance ratio:

$$\begin{bmatrix} 1'1 & 1'G & 1'S & 1'H \\ G'1 & G'G & G'S & G'H \\ S'1 & S'G & S'S & S'H \\ H'1 & H'G & S'H & H'H \end{bmatrix} \begin{bmatrix} \mu \\ g \\ s \\ h \end{bmatrix} = \begin{bmatrix} 1'y \\ G'y \\ S'y \\ H'y \end{bmatrix}$$

The equation for herd can be written as

$$(H'1)\mu + (H'G)g + (S'H)s + (H'H)h = H'y$$

and subsequently the herd solutions are:

$$h = (H'H)^{-1}(H'y - (H'1)\mu - (H'G)g - (H'S)s)$$

The total sum of squares for the model is defined as the transposed solutions postmultiplied by their right hand sides.

$$
\begin{aligned}
\text{Total Sum of Squares} &= \mu'(1'y) + g'(G'y) + s'(S'y) + h'(H'y) \\
&= \mu'(1'y) + g'(G'y) + s'(S'y) + (H'y - (H'1)\mu - (H'G)g \\
&\quad - (H'S)s)'(H'H)^{-1}(H'y) \\
&= \mu'(1'y) + g'(G'y) + s'(S'y) + (y'H(H'H)^{-1}(H'y) - \\
&\quad \mu'(1'H)(H'H)^{-1}(H'y) - g'(G'H)(H'H)^{-1}(H'y) - \\
&\quad s'(S'H)(H'H)^{-1}(H'y) \\
&= \mu'(1'y) - \mu'(1'H)(H'H)^{-1}(H'y) + g'(G'y) - \\
&\quad g'(G'H)(H'H)^{-1}(H'y) + s'(S'y) - s'(S'H)(H'H)^{-1}(H'y) + \\
&\quad (y'H)(H'H)^{-1}(H'y) \\
&= \mu'(1'y - 1'H(H'H)^{-1}H'y) + g'(G'H(H'H)^{-1}H'y) + s'(S'y \\
&\quad - S'H(H'H)^{-1}H'y) + (y'H)(H'H)^{-1}(H'y)
\end{aligned}
$$

where

$\mu'(1'y - 1'H(H'H)^{-1}H'y)$	is the overall constant multiplied by the total sum, adjusted for herds;
$g'(G'y - G'H(H'H)^{-1}H'y)$	is the solution for groups multiplied by the group right hand sides, adjusted for herds;
$s'(S'y - S'H(H'H)^{-1}H'y)$	is the solution for sires multiplied by the sire right hand sides, adjusted for herds;
$y'H(H'H)^{-1}H'y$	is the uncorrected total sum of squares for herds;

The process of loop absorption was performed to reduce the number of MME. This method allows the effect of herd to be absorbed into other factors in the model while reading the data. This process also allows for the accumulation of the herd sums of squares, $y'H(H'H)^{-1}H'y$, for the variance component estimation. Absorption was performed as follows:

1. Data were first sorted by herd and sire within herd.
2. Absorbing herd right hand sides into the right hand sides of factor j = the sum of the observations for factor j in a herd - (number of daughters in factor j for that herd * the herd sum/ the number of daughters in that herd).

   where j = μ, group, sire
3. Absorbing the incidence matrix for herds into the diagonal matrices of factor j = number of daughters in factor j - (number of daughters in factor j $)^2$/number of daughters in the herd.

   where j = μ, group, sire
4. Absorbing the incidence matrix for herds into the off-diagonal matrices of factor j = number of daughters in factor j - (number of daughters in factor j * the number of daughters in factor j')/number of daughters in the herd.

   where j = μ, group, sire and j $\neq$ j'

After the absorption of one herd the storage vectors for herd were zeroed and absorption of the next herd began. This procedure requires only one pass of the data to complete the absorption process and set up the normal equations. The MME are then constructed by the addition of the variance ratio, k, to the diagonal of the random portion, S'S, of the normal equation and are shown below:

$$\begin{bmatrix} 1'A1 & 1'AG & 1'AS \\ G'A1 & G'AG & G'AS \\ S'A1 & S'AG & S'AS + Ik \end{bmatrix} \begin{bmatrix} \mu \\ g \\ s \end{bmatrix} = \begin{bmatrix} 1'Ay \\ G'Ay \\ S'Ay \end{bmatrix} \qquad \text{III.2}$$

where $A = I - H(H'H)^{-1}H'$.

The reduced equations were then solved by direct inverse of the coefficient matrix.

III.1.5 Variance component estimation

An iterative restricted maximum likelihood estimator (REML) (Patterson and Thompson, 1971) using an expectation maximization (EM) algorithm (Dempster et al, 1977) was utilized for variance and covariance component estimation. Each iteration of the EM algorithm involved two steps. The first step is that the expectation is taken under the pretense that $\hat{G} = G$ and $\hat{R} = R$. The second is the maximization of the log-likelihood function of the data vector.

Henderson (1983) pointed out that solutions and estimates obtained by the use of the EM algorithm are guaranteed to converge within the parameter space. The EM algorithm for variance component estimation is obtained as a by-product of the solution to the ordinary mixed model equations. Let C be the generalized inverse of the MME.

$$\begin{matrix} G'AG & G'AS \\ S'AG & S'AS + Ik \end{matrix}^{-} = \begin{matrix} C_{g'g} & C_{g's} \\ C_{s'g} & C_{s's} \end{matrix}$$

The EM REML estimator for the residual variance component is

$$\hat{\sigma}_e^2 = (y'y - \tilde{g}'G'Ay - \hat{s}'Z'Ay - y'H(H'H)^{-1}H'y)/(n - r(G) - r(H)) \qquad \text{III.3}$$

where

$y'y$	is the total unadjusted sum of squares of one of 15 type traits.
$\tilde{g}'G'Ay$	are the solutions to the fixed effects of 7 groups in the MME multiplied by their respective right hand sides adjusted for herds.
$\hat{s}'S'Ay$	are the solutions to the random effects of the 299 sires in the MME multiplied by their respective

	right hand sides adjusted for herds.
$y'H(H'H)^{-1}H'y$	is the sum of squares due to herd which was accumulated during the process of loop absorption.
n	is the number of observations.
$r(G)$	is the rank of the coefficient matrix pertaining to group fixed effects.
$r(H)$	is the rank of the coefficient matrix pertaining to herd fixed effects.

The estimator for the sire component of variance is

$$\hat{\sigma}^2_s = (\hat{s}'\hat{s} + \hat{\sigma}^2_e(tr(C_{s's})))/q_s \qquad \text{III.4}$$

where

$\hat{s}'\hat{s}$	is the sum of squares of sire solutions.
$tr\ (C_{s's})$	is the trace of the random portion of the inverse of the coefficient matrix.
q_s	is the number of sires.

Iterations were continued until the absolute change in the ratio of $_e/_s$ was less than .1 or after 20 rounds of iteration.

The a priori variance ratio may be computed for a given heritability since $\hat{h}^2 = 4 / [\hat{\sigma}^2_e/\hat{\sigma}^2_s + 1]$. Thus, $\hat{\sigma}^2_e/\hat{\sigma}^2_s = 4/\hat{h}^2 - 1$.

For all analyses involving the relationships among type traits the a priori variance used was 25.0 which corresponds to a heritability of 0.15. If A and B represent two linear type traits, the covariance between the two type traits was estimated by the following method:

First, a new trait, A+B, was generated by summing A and B. Then, variance components were estimated for A, B and A+B. The relationship below was then used to estimate the covariance between the two type traits.

$$\mathrm{Var}(A+B) = \mathrm{Var}(A) + \mathrm{Var}(B) + 2\mathrm{Cov}(AB) \text{ and}$$

$$\mathrm{Cov}(AB) = (\mathrm{Var}(A+B) - \mathrm{Var}(A) - \mathrm{Var}(B))/2$$

III.1.6 Heritability and genotypic and phenotypic correlations

The heritability estimates were calculated using the paternal half-sib correlation method with the EM REML estimates of ${}_s$ and ${}_e$:

$$\hat{h}^2 = 4\hat{\sigma}_s^2/(\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$$

The approximate standard errors of the estimated heritabilities were calculated according to Gill (1978).

$$\begin{aligned}\mathrm{Var}[Y_1/Y_2] &\approx [(E[Y_1])^2\mathrm{Var}[Y_2] + (E[Y_2])^2\mathrm{Var}(Y_1) - \\ &\qquad 2E[Y_1]E[Y_2]\mathrm{Cov}[Y_1Y_2]]/(E[Y_2])^4 \\ &\approx (\mu_1^2\sigma_2^2 + \mu_2^2\sigma_1^2 - 2\mu_1\mu_2\sigma_{12})/\mu_2^4\end{aligned}$$

Now let:

$$\begin{aligned}Y_1 &= 4\hat{\sigma}_s^2 = \mu_1 \\ Y_2 &= \hat{\sigma}_s^2 + \hat{\sigma}_e^2 = \mu_2 \\ \sigma_1 &= 16\mathrm{Var}[\hat{\sigma}_s^2] \\ \sigma_2 &= \mathrm{Var}[\hat{\sigma}_s^2] + [(r_o + 2)/r_o]\mathrm{Var}[\hat{\sigma}_e^2] \\ \sigma_{12} &= 4[(\mathrm{Var}[\hat{\sigma}_s^2] - \mathrm{Var}[\hat{\sigma}_e]/r_o] \\ \text{and } r_o &= [n - (\sum_{i=1}^{s} r_i/n)]/(s-1)\end{aligned}$$

The genetic correlation between type traits for sires may be estimated by:

$$\hat{r}_G = \hat{\sigma}_{s_i s_{i'}} / (\hat{\sigma}^2_{s_i} \hat{\sigma}^2_{s_{i'}})^{.5},$$

where $\sigma_{s\ s}$ = the estimate of the sire component of covariance between traits i and i';

$\sigma^2_{s_i}$ = the estimate of the sire variance for trait i; and

$\sigma^2_{s_{i'}}$ = the estimate of the sire variance for trait i'.

Estimates of phenotypic correlations were obtained similarly by adding together the components of variance for sire and error:

$$\hat{r}_p = \frac{\hat{\sigma}_{s\ s} + \hat{\sigma}_{e\ e}}{[(\hat{\sigma}^2_s + \hat{\sigma}^2_e) * (\hat{\sigma}^2_s + \hat{\sigma}^2_e)]^{.5}}$$

where:

$\hat{\sigma}_{e_i e_{i'}}$ is the estimate of the residual component of covariance between trait i and i';

$\hat{\sigma}_{e_i}$ is the estimate of the component of variance for trait i;

$\hat{\sigma}_{e_{i'}}$ is the estimate of the component of variance for trait i'.

The approximate standard errors were obtained by methods described by Gill (1978).

III.2 Genetic parameters of milk production and linearly scored type traits

Computation of a relationship between two characteristics requires the records to be paired. This restriction often limits the sample of data from which the estimates of the population are to be obtained. Cows that are scored for type are a small subset of the total milk recorded population. This type of data structure lends itself to multiple trait analysis very well. Mao (1982) stated that multiple trait analysis was most advantageous when 1) the absolute value of the correlations between traits are high so that information on each trait would contribute to the estimation of the other trait, 2) some traits are measured on a limited number of individuals and 3) some animals lack records as a result of selection on one or more other traits.

III.2.1 Data

A total of 1,574,718 completed lactation records were supplied by the Michigan Dairy Herd Improvement Association (DHIA) and Wisconsin DHIA. These lactations were completed between 1-1-82 and 12-31-84. The Michigan DHIA contributed 595,038 records and the Wisconsin DHIA 979,680 observations. All records were standardized 305 day, twice a day, and mature equivalent (ME) milk production records (Norman et al, 1974).

III.2.1.1 Linear type data

Linear type data were edited as in the investigation among type traits with the exception of the restriction requiring that sires have at least 20 daughters in a herd. Therefore, 56,804 type records were available for consideration of the merger with production records.

III.2.1.2 Milk production data

The data files contained numerous records that had either an alpha-numeric character in a supposedly numeric field or had a state code other than Michigan or Wisconsin. Any of these problems resulted in the deletion of the entire record from the research file. Additional data editing criteria and the number of records deleted are presented in Table 22. Note that approximately 50% of the Michigan records were eliminated due to the lack of sire identification.

III.2.1.3 Merger of milk production and linear type data

The type scores from HFAA and milk production records from DHIA were merged and additional editing was done during the process of merging. Merging was accomplished by the following steps:

1. The milk production data were sorted by herd, cow within herd and calving date within cow.
2. The linear type data were sorted by herd and cow within herd.
3. If the DHIA herd codes of milk and type data matched, as well as, the sire identification and calving date, the milk yield and type scores were written to tape. Any remaining records for that particular cow were discarded.
4. If a cow had milk production recorded with no corresponding type scores, her earliest lactation was written to tape. This was done to reduce selection pressure that may be inherent to later records.

The merged data consisted of 48,190 cows with both milk records and corresponding type scores (paired) and 581,364 cows with only milk records (unpaired). The 629,554 records represented 29,246 sires. Table 23 shows the distribution of sires classified by the number of daughters across the number of herds.

III. 2.1.4 Sampling procedures

A decision to solve the MME by using a direct inverse of the coefficient matrix limited the number of equations to approximately

Table 22. Data editing criteria and number of records deleted from milk production data

Editing Criteria	Number Records Deleted	
	Michigan	Wisconsin
No Sire Identification	323,795	0
No Cow Identifcation	8	0
305-day, 2X, ME Milk ≤ 1 or $\geq 60{,}500$	2,882	119
$21 < \text{Age} < 167$	599	-
No Calving Date	0	0
No DHIA Herd Code	0	0
Lactation ≥ 10	-	1,677
Lactation = 1 and 21 < Age[a] < 67	-	1,501
Lactation = 2 and 27 < Age[a] < 77	-	14
Lactation = 3 and 40 < Age[a] < 89	-	366
Lactation = 4 and 49 < Age[a] < 98	-	239
Lactation = 5 and 65 < Age[a] < 120	-	694
Lactation = 6 and 75 < Age[a] < 124	-	443
Lactation = 7 and 98 < Age[a] < 136	-	3,584
Lactation ≥ 8 and ≤ 10 and 111 < Age[a] < 167	-	2,544

[a] Age at last calving in months

Table 23. Distribution of sires by number of daughters and herds

	Number of Herds																								
	1	2	3	4 - 5	6 - 7	8 - 10	11 - 15	16 - 20	21 - 25	26 - 30	31 - 40	41 - 50	51 - 60	61 - 70	71 - 80	81 - 90	91 - 100	101 - 200	201 - 300	301 - 400	401 - 500	501 - 650	651 - 800	801 - 9999	Total Sires
Code	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	
1	11,129																								
2	2,066	2,255																							
N 3	975	463	979																						
U 4	1,081	322	494	1,059																					
M 5	869	151	177	486	755																				
B 6	303	41	79	106	255	259																			
E 7	416	28	96	127	172	174	507																		
R 8	195	12	45	45	63	37	152	284																	
9	89	5	20	21	15	18	41	82	167																
O 10	60	3	8	10	7	9	9	17	47	148															
F 11	52	1	7	6	8	4	17	14	10	57	246														
12	17	1	1	4	2	0	4	6	5	7	49	175													
D 13	6	1	2	2	0	2	1	0	0	1	4	27	88												
A 14	6	0	1	1	0	1	0	0	0	0	1	1	21	70											
U 15	1	0	0	0	0	0	0	0	1	2	0	2	0	20	59										
G 16	0	0	0	0	0	0	0	0	0	0	0	0	0	1	10	32									
H 17	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	10	42								
T 18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	231							
E 19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	115						
R 20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	67					
S 21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	46				
22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	42			
23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	29		
24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	153	
Total Sires	17,265	3,283	1,909	1,867	1,277	504	731	403	230	215	301	205	109	91	70	42	51	236	117	69	46	43	29	153	29,246

300. Therefore, a random sample of 150 sires without replacement was selected from the 1,495 sires in the merged data set. These 150 sires represented 10% of the total number of sires. Daughter records of these sires then were pulled from the 475,855 in the edited research file for all analyses outlined in the next section. The sampling was repeated five times independent of each other using different randomly sampled seeds. A description of the data sets are shown in Table 24. The distribution of sires by number of herds and number of daughters for each sample are included in Appendix D.

Table 24. Descriptions of Sampled Data Sets

Data Set	Sires	Total Herds	Herds with Paired Data	Total Records	Paired Records	Percent Paired
1	150	9,441	1,433	60,008	4,882	8.14
2	150	9,147	1,268	51,651	3,749	7.26
3	150	9,532	1,547	65,264	6,416	9.83
4	150	8,975	1,332	50,472	3,960	7.85
5	150	9,688	1,466	69,087	5,550	8.03

The same data base of 64,875 Holstein cows described earlier was used in the investigation of genetic parameters while jointly considering milk production and the linear type score. Each lactation record was identified by DHIA herd number and dam, sire and cow numbers. Cow's age, parity number and the date of calving which initiated the lactation were also recorded.

III.2.2 A *priori* adjustments and assumptions

The scores of the 15 linearly scored type traits for each cow were adjusted for differences due to stage of lactation and age within lactation number using adjustment factors supplied by the association.

The milk production records supplied by the Wisconsin and Michigan DHIA were adjusted for lactation length, times per day milking and age and season at calving (Norman et al, 1980 and Wiggins and Powell, 1980). Age and season at calving differences were adjusted on a within lactation basis assuming that the parity by age effect is negligible. Records were standardized to a twice a day milking. Incomplete records that were less than 305 days in length and not coded a normal termination were extended to 305 days. The production data covered 3 years, 1982 through 1984, but an assumption was made that the effects of year were negligible. The assumption that all adjustment factors are perfect and any interaction of factors in the model with those of *a priori* adjustment are nil is also necessary.

III.2.2.1 Single trait model

The equation is

$$y_i = \mu_i 1 + H_i h_i + G_i g_i + S_i s_i + e_i \qquad \text{III.5}$$

where, y_i is the observation vector of the ith trait; the trait is one of the 15 primary type traits or milk production;

μ_i is the overall constant;

1 is a column vector of ones;

h_i is a vector of length m_i containing the unknown fixed constants pertaining to herd;

H_i is an $n_i x m_i$ incidence matrix pertaining to herds, where n_i and m_i depend on the data set sampled;

g_i is a vector of length 10 containing the unknown fixed constants pertaining to sire groups;

G_i is an $n_i x k$ incidence matrix pertaining to sire groups, where $k=10$;

s_i is a vector of length 150 containing the unknown random effects of sires;

S_i is an $n_i x P$ incidence matrix pertaining to sires, where $P=150$; and

e_i is an $n_i x 1$ vector of nonobservable random residuals corresponding to y_i.

The expectations are:

$$E[y_i] = \mu_i 1 + H_i h_i + G_i g_i$$

$$E[e_i] = 0$$

$$E[s_i] = 0$$

The corresponding variance-covariance structure is:

$$\mathrm{Var} \begin{array}{c} y_i \\ s_i \\ e_i \end{array} = \begin{array}{ccc} V_n & S_i \sigma^2_{s_i} & I_n \sigma^2_{e_i} \\ \sigma^2_{s_i} S' & I_p \sigma^2_{s_i} & 0 \\ I_n \sigma^2_{e_i} & 0 & I_n \sigma^2_{e_i} \end{array}$$

where $V_n = S_i S_i \sigma^2_{s_i} + I_n \sigma^2_{e_i}$

The *a priori* variance ratios used in these analysis were derived from estimates of heritability obtained from the single trait analysis among type traits in Section III.1 and are shown in Table

25. The milk estimate of .25 was obtained from literature. The effect of herds was absorbed into the sire and group equations. The solutions to the MTMME were iterated until the change in the variance ratios between successive iterations was less than .1 in absolute value. Variance components were estimated using the expectation maximization algorithm of the restricted maximum likelihood estimator described earlier (Equations III.3 and III.4).

The analysis was repeated five times, each with a different random data set. The sampling variance of a genetic parameter estimate was computed from the five estimates. Estimates of heritability and phenotypic and genetic correlations were obtained using the methodology described in the analysis of the relationships among type traits.

III.2.2.2 Multiple trait model

The linear model for the multiple trait analysis is outlined below. Note that (1) milk production and one of the 15 primary linear type traits were considered in each analysis; (2) some individuals missed records on type traits; (3) fixed and random factors are the same for both traits; and (4) non-zero residual covariances were assumed.

The general form of the model can be written:

$$y = Xb + Zu + e$$

Table 25. Heritability values and variance ratios used as initial values in the single trait analyses of milk production and linearly scored type traits

Trait	Heritability (h^2)	Variance Ratio[a]
Stature	.39	9.31
Strength	.22	17.61
Body Depth	.28	13.22
Angularity	.18	20.70
Rump Angle	.23	16.03
Rump Length	.22	17.03
Rump Width	.27	13.89
Rear Leg Side View	.17	22.26
Foot Angle	.27	13.53
Fore Udder Attachment	.20	18.79
Rear Udder Height	.22	16.74
Rear Udder Width	.17	22.26
Udder Support	.10	39.04
Udder Depth	.27	14.03
Teat Placement Rear View	.20	19.38
305 Day ME Milk Production	.25	15.00

[a] Variance ratio is estimated as $(4-h^2)/h^2$

The structure of the data allows the equations to be expanded to:

$$\begin{bmatrix} y_{10} \\ y_{12} \\ y_{21} \end{bmatrix} = \begin{bmatrix} X_{10} & 0 \\ X_{12} & 0 \\ 0 & X_{21} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_{10} & 0 \\ Z_{12} & 0 \\ 0 & Z_{21} \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_{10} \\ e_{12} \\ e_{21} \end{bmatrix} \qquad \text{III.6}$$

where

y_{10}	is a vector of length n containing milk records that have no corresponding type score;
y_{12}	is a vector of length n containing milk records that have a corresponding type score;
y_{21}	is a vector of length n containing type scores that have a corresponding milk record;
b_1	is a vector of length q containing unknown fixed constants of , herds and sire groups pertaining to milk;
X_{10}	is an n x p design matrix corresponding to b_1 for unpaired milk records;
X_{12}	is an n x q design matrix corresponding to b_1 for milk records that have corresponding type scores;
b_2	is a vector of length q containing unknown fixed contants of , herds and sire groups pertaining to type;
X_{21}	is an n x q design matrix corresponding to b_2 for type scores that have corresponding milk records;
u_1	is a vector of length 150 of unknown random effects of sires for milk;
Z_{10}	is an n x 150 design matrix corresponding to u_1 for unpaired milk records;
Z_{12}	is an n x 150 design matrix corresponding to u_1 for milk records that have a corresponding type score;
u_2	is a vector of length 150 of unknown random effects of sire for type;
Z_{21}	is an n x 150 design matrix corresponding to u_2 for type scores that have corresponding milk records;
e_{10}	is a vector of length n of nonobservable random residuals corresponding to y_{10};

e_{12} is a vector of length n of nonobservable random residuals corresponding to y_{12}; and

e_{21} is a vector of length n of nonobservable random residuals corresponding to y_{21}.

The 150 sires involved in each of the five sampled data sets were arbitrarily divided into 10 groups. This was done in hopes of capturing any differences among the genetic groups of the sires.

Each pair of milk and type traits was analyzed using five data sets, therefore, the dimension parameters, p and q, and n, were different from set to set. However, the number of sires, 150, in each application of the model stayed constant.

The expectations (E) and variance-covariance structure (Var) of the random vectors in the model were:

$$E\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} (\Sigma^{+}X_i)b \\ 0 \\ 0 \end{bmatrix}$$

where Σ^{+} denotes direct summation.

$$\mathrm{Var}\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} V & ZG & R \\ GZ' & G & 0 \\ R & 0 & R \end{bmatrix}$$

and

$$\mathrm{Var}(u) = G = \mathrm{Var}\begin{bmatrix} u_1 \\ u_2 \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} \\ G_{21} & G_{22} \end{bmatrix},$$

where G_{11} is the sire variance and covariance matrix for milk;

G_{12} is the sire covariance matrix between milk and one of 15 linear type traits; and

G_{22} is the sire variance and covariance matrix for one of 15 linear type traits.

$$\mathrm{Var}(e) = R = \mathrm{Var}\begin{bmatrix} e_{10} \\ e_{12} \\ e_{21} \end{bmatrix} = \begin{bmatrix} R_{10,10} & 0 & 0 \\ 0 & R_{12,12} & R_{12,21} \\ 0 & R_{21,12} & R_{21,21} \end{bmatrix}$$

where $R_{10,10}$ is the residual variance and covariance matrix for unpaired milk;

$R_{12,12}$ is the residual variance and covariance matrix for paired milk;

$R_{12,21}$ is the residual covariance matrix for paired milk and one of 15 linear type traits;

$R_{21,21}$ is the residual variance and covariance matrix for one of 15 linear type traits.

The variance-covariance matrix of y can now be written as a linear function of G and R:

$$\mathrm{Var}(y) = V = ZGZ' + R$$
$$= (\Sigma^{+}Z_i)G(\Sigma^{+}Z'_i) + R$$

The multiple trait mixed model equations for solving the unknown **b** and u vectors can now be written in familiar form:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$

Exact knowledge of R and G is assumed initially. Since sire is the only random factor and no genetic covariance is assumed within traits, G^{-1} may be expressed as a matrix of scalars, the sire variances, and identity matrices of order 150, where

$$G = \begin{bmatrix} w_{11}I_{150} w_{12}I_{150} \\ w_{21}I_{150} w_{22}I_{150} \end{bmatrix}$$

and w_{11} is the sire variance for milk;

w_{12} is the sire covariance between milk and one of 15 linear type traits; and

w_{21} is the sire variance for type.

Now G^{-1} may be written as:

$$G^{-1} = I_{150} * W^{-1} = \begin{bmatrix} w^{11}I_{150} & w^{12}I_{150} \\ w^{21}I_{150} & w^{22}I_{150} \end{bmatrix}$$

where * denotes a direct product operator, and

w^{ij} is the portion of the inverse of the sire variance or covariance of traits i and j.

The matrix G is nonsingular and positive definite as $w_{ij} \leq w_{ii}w_{jj}$.

If a homogeneous residual variance is assumed within traits, R may be expressed as:

$$R = \begin{bmatrix} q_{10,10}I & 0 & 0 \\ 0 & q_{12,12}I & q_{12,21}I \\ 0 & q_{21,12}I & q_{21,21}I \end{bmatrix}$$

where $q_{10,10}$ is the residual variance for unpaired milk records;

$q_{12,12}$	is the residual variance for paired milk records;
$q_{12,21}$	is the residual covariance for milk and one of 15 linear type traits; and
$q_{21,21}$	is the residual variance for one of 15 linear type traits.

Now R^{-1} may be written as:

$$R^{-1} = I_n * Q^{-1} = \begin{bmatrix} q^{-1}_{10,10}I & 0 & 0 \\ 0 & q^{12,12}I & q^{12,21}I \\ 0 & q^{21,12}I & q^{21,21}I \end{bmatrix}$$

where q^{ij} is the inverse portion of the error variance and covariance for traits i and j.

The matrix R is also nonsingular and therefore $q_{ij} \leq q_{ii}q_{jj}$. The MTMME, given R and G as defined above for the two trait case, are:

$$\left[\begin{array}{cc|cc} X'_{12}X_{12}*Q^{12,12} + I*Q^{-1}_{10,10}X'_{10}X_{10} & X'_{12}X_{21}*Q^{12,21} & X'_{12}Z_{12}*Q^{12,12} + I*Q^{-1}_{10,10}X'_{10}Z_{10} & X'_{12}Z_{21}*Q^{12,21} \\ X'_{21}X_{12}*Q^{21,12} & X'_{21}X_{21}*Q^{21,21} & X'_{21}X_{12}*Q^{21,12} & X'_{21}Z_{21}*Q^{21,21} \\ \hline Z'_{12}X_{12}*Q^{12,12} + I*Q^{-1}_{10,10}Z'_{10}X_{10} & Z'_{12}X_{12}*Q^{12,21} & Z'_{12}Z_{12}*Q^{12,12} + I*Q^{-1}_{10,10}Z'_{10}Z_{10} + Iw^{11} & Z'_{12}Z_{21}*Q^{12,21} + Iw^{12} \\ Z'_{21}X_{12}*Q^{21,12} & Z'_{21}X_{21}*Q^{21,21} & Z'_{21}Z_{12}*Q^{21,12} + Iw^{21} & Z'_{21}Z_{21}*Q^{21,21} + Iw^{21} \end{array}\right] \left[\begin{array}{c} b_1 \\ b_2 \\ \hline u_1 \\ u_2 \end{array}\right]$$

$$= \left[\begin{array}{c} (X'_{12}*Q^{12,12})y_{12} + (X'_{21}*Q^{12,21})y_{21} + (I*Q^{-1}_{10,10}X_{10})y_{10} \\ (X'_{21}*Q^{21,21})y_{21} + (X'_{21}*Q^{21,12})y_{12} \\ \hline (Z'_{12}*Q^{12,12})y_{12} + (Z'_{21}*Q^{12,21})y_{21} + (I*Q^{-1}_{10,10}X_{10})y_{10} \\ (Z'_{21}*Q^{21,21})y_{12} + (Z'_{21}*Q^{21,12})y_{12} \end{array}\right] \qquad \text{III.7}$$

The *a priori* values used for the genetic and residual variance-covariance matrices were obtained by the single trait estimates from the same sample of data. These values can be found in the discussion of single trait estimates of milk and type (Section III.2.2.1).

Estimates of the residual covariance, q_{ij}, were obtained assuming a residual correlation of .01 and the formula:

$$q_{ij} = \sigma_{ij}/\sigma_i\sigma_j$$

Estimates of the genetic covariance, w_{ij}, between traits i and j, where i=j, was assumed to be 0.0 which corresponds to a genetic correlation of 0.0 between milk and type.

The arrangement of factors within traits forms nondiagonal block matrices for fixed and random effects. This complicates the process of absorption of fixed effects. The complication is due to the assumption of nonzero residual covariances. This characteristic makes loop absorption one trait at a time impossible. Thus, a transformation of the data to possess zero residual covariance was performed.

III.2.2.2.1 Triangular transformation of MTMME

The method of triangularization is described by Schaeffer (1985) and Pollack and Quass (1982) as cited by Van Den Werf (1983). This method requires a specific data structure and model:

1. The random effects must be the same for all traits;
2. Fixed effects may be different for different traits;
3. Data may be missing on some traits, but with restrictions on the missing traits as follows: If y_k contains t traits and trait j is missing then,

a. traits 1 to j-1 must be present
b. traits j to t must all be missing

These data and model meet all of the above criteria. We wish to find a transformation matrix P such that Var(Pe) = I. To obtain this assume

$$\mathrm{Var}(Pe) = P\mathrm{Var}(e)P' = PRP'.$$

It is known that R is symmetric and may be broken down into QQ' where Q is a lower triangular matrix formed by a Cholesky decomposition:

$$Q = \begin{bmatrix} Q_{11} & 0 & 0 \\ 0 & Q_{11} & 0 \\ 0 & Q_{12} & Q_{22} \end{bmatrix}$$

PQQ'P' is equal to I if $P = Q^{-1}$. Assume that

$$P = \begin{bmatrix} It^{11} & 0 & 0 \\ 0 & It^{11} & 0 \\ 0 & It^{12} & It^{22} \end{bmatrix}$$

$$\text{where} \quad T = \begin{bmatrix} t_{11} & 0 \\ t_{12} & t_{22} \end{bmatrix} \quad \text{and} \quad T^{-1} = \begin{bmatrix} t^{11} & 0 \\ t^{12} & t^{22} \end{bmatrix}.$$

Furthermore,

$$TT' = \begin{bmatrix} R_{11} & R_{12} \\ R_{21} & R_{22} \end{bmatrix} \quad \text{and} \qquad \text{III.8}$$

$$T^{-1\prime}T^{-1} = \begin{bmatrix} R^{11} & R^{12} \\ R^{21} & R^{22} \end{bmatrix}.$$

where $PQQ'P' = \begin{bmatrix} IT^{11} & 0 & 0 \\ 0 & IT^{11} & 0 \\ 0 & IT^{12} & IT^{22} \end{bmatrix}$

and $PQQ'P' = I$ if $P = Q^{-1}$.

Also noted is the fact that $PX = XT^{-1}$ and $PZ = ZT^{-1}$. The transformation of y is:

$$y^* = \begin{bmatrix} y_{10}^* \\ y_{12}^* \\ y_{21}^* \end{bmatrix} = \begin{bmatrix} y_{10}T^{11} \\ y_{12}T^{11} \\ y_{12}T^{12} + y_{21}T^{22} \end{bmatrix}$$

The equation can now be expressed as:

$$\begin{aligned} Py = y^* &= PXb + PZu + Pe \\ &= XT^{-1}b + ZT^{-1}u + Pe \\ &= Xb^* + Zu^* + Pe \end{aligned}$$

where

$$\begin{aligned} \mathrm{Var}(Py) &= P(ZGZ' + R)P' \\ &= PZGZ'P' + PRP' \\ &= ZT^{-1}GT^{-1\prime}Z' + PRP' \\ &= ZG^*Z' + I \end{aligned}$$

The transformation is complete with the new variance-covariance matrix of random factors expressed as G^* and a residual variance-covariance matrix expressed as I. The advantage of the transformed equations is that in the case where the residual covariance is assumed to be nonzero, the transformed equation may have factors absorbed one trait at a time by loop absorption processes due to the nature of the transformed residual variance-covariance structure. The transfomed MTMME are:

$$\left[\begin{array}{cc|cc} X_{12}'X_{12} + X_{10}'X_{10} & 0 & X_{12}'Z_{12} + X_{10}'Z_{10} & 0 \\ 0 & X_{21}'X_{21} & 0 & X_{21}'Z_{21} \\ \hline Z_{12}'X_{12} + Z_{10}'X_{10} & 0 & Z_{12}'Z_{12} + Z_{10}'Z_{10} + Ig^{*11} & Ig^{*12} \\ 0 & Z_{21}'X_{21} & Ig^{*21} & Z_{21}'Z_{21} + Ig^{*22} \end{array}\right] \left[\begin{array}{c} b_1^* \\ b_2^* \\ \hline u_1^* \\ u_2^* \end{array}\right] = \left[\begin{array}{c} X_{10}'y_{10}^* + X_{12}'y_{12}^* \\ X_{21}y_{21}^* \\ \hline Z_{10}'y_{10}^* + Z_{12}'y_{12}^* \\ Z_{21}'y_{21}^* \end{array}\right] \qquad \text{III.9}$$

III.2.2.2.2 Absorption of herds

The herd equations were absorbed one trait at a time into group and sire equations for both milk and type by a loop absorption procedure. The data were first sorted by herd and a transformed by the P matrix. The transformed sum of squares, crossproducts and a herd counter for each herd were stored. This process continued until all herds were absorbed.

The loop absorption, as described in the section on single trait analysis (Section III.4.1), was carried out for each trait before they were combined to form the reduced MTMME shown below:

$$\begin{bmatrix} X_{12}'A_1X_{12}+X_{10}'A_2X_{10} & 0 & X_{12}'A_1Z_{12}+X_{10}'A_2Z_{10} & 0 \\ 0 & X_{21}'A_3X_{21} & 0 & X_{21}'A_3Z_{21} \\ Z_{12}'A_1X_{12}+Z_{10}'A_2X_{10} & 0 & Z_{12}'A_1Z_{12}+Z_{10}'A_2Z_{10}+Ig^{*11} & Ig^{*12} \\ 0 & Z_{21}'A_3X_{21} & Ig^{*12} & Z_{21}'A_3Z_{21}+Ig^{*22} \end{bmatrix} \begin{bmatrix} b_1^* \\ b_2^* \\ u_1^* \\ u_2^* \end{bmatrix} = \begin{bmatrix} X_{10}'A_2y_{10}^*+X_{12}'A_1y_{12}^* \\ X_{21}'A_3y_{21}^* \\ Z_{10}'A_2y_{10}^*+Z_{12}'A_1y_{12}^* \\ Z_{21}'A_3y_{21}^* \end{bmatrix}$$

$$\begin{aligned} \text{where } A_1 &= I - X_{12H}(X_{12H}'X_{12H})^{-}X_{12H}' \\ A_2 &= I - X_{10H}(X_{10H}'X_{10H})^{-}X_{10H}' \\ A_3 &= I - X_{21H}(X_{21H}'X_{21H})^{-}X_{21H}' \end{aligned} \qquad \text{III.10}$$

and X_{12H}, X_{10H} and X_{21} represent the herd portion of the fixed effects of paired milk, unpaired milk and type respectively.

III.2.2.2.3 Variance component estimation

Restricted maximum likelihood (REML) by the expectation maximization (EM) algorithm (Dempster et al., 1977) was chosen for estimation of variance components since convergence of estimates to nonnegative from positive priors is guaranteed (Henderson, 1985 and Taylor et al., 1985). Additionally, all the properties of single trait REML will also hold true for multiple trait analysis. The REML estimators are shown below (Mao,1982).

$$g_{ij} = (\hat{u}_i'\hat{u}_j + tr(C^{ij}))/q$$

where $i \leq j = 1$ to 2.

g_{ij}	is the estimated variance or covariance component for sire for trait $i \leq j$;
u_i and u_j	are sire solutions for traits i and j;
C^{ij}	is the random portion of the inverse of the coefficient matrix for $i \leq j = 1,2$; and
q	is the number of sires.

$$r_{ij} = (\hat{e}_i'\hat{e}_j + tr(C^{ij}Z_i'Z_j))/((n_i - r(X_i))(n_j - r(X_j)))^{0.5}$$

where r_{ij}	is the estimated variance or covariance component for residual of trait $i \leq j$;
$\hat{e}_i'\hat{e}_j$	is the residual sum of squares or crossproductions for trait $i \leq j = 1,2$;
C^{ij}	is the random portion of the inverse of the coefficient matrix for $i \leq j = 1,2$;
Z_iZ_j	is the incidence matrix from the MTMME;
n_i	is the number of observations for trait i;

n_j is the number of observations for trait j; and

$r(X_i)$ and $r(X_j)$ are the ranks of X_i and X_j which are incidence matrices of the fixed effects for traits i and j.

The only factor not directly obtainable from the MTMME is $\hat{e}_i'\hat{e}_j$. The common practice is to calculate residuals by backsolving for the absorbed factors and deviating each observation from the estimates obtained by the MTMME. This is required since the absorbed factor is represented in the total variability of the trait. This method requires the entire data to be processed again.

An alternative method of calculating residuals without backsolving for herds was used (Walter, 1986). The residual sum of squares and crossproducts,

$$\begin{bmatrix} \hat{e}_{12}^{*\prime}\hat{e}_{12}^{*} + \hat{e}_{10}^{*\prime}\hat{e}_{10}^{*} & \hat{e}_{12}^{*\prime}\hat{e}_{21}^{*} \\ \hat{e}_{21}^{*\prime}\hat{e}_{12}^{*} & \hat{e}_{21}^{*\prime}\hat{e}_{21}^{*} \end{bmatrix}$$

can be estimated by:

$$\begin{bmatrix} \hat{e}_{10}^{*} \\ \hat{e}_{12}^{*} \\ \hat{e}_{21}^{*} \end{bmatrix} = \begin{bmatrix} y_{10}^{*} - X_{10}\tilde{b}_1^{*} - Z_{10}\hat{u}_1^{*} \\ y_{12}^{*} - X_{12}\tilde{b}_1^{*} - Z_{12}\hat{u}_1^{*} \\ y_{21}^{*} - X_{21}\tilde{b}_2^{*} - Z_{21}\hat{u}_2^{*} \end{bmatrix}$$

where $y^* = Py$

$b^* = T^{-1}b$

$u^* = T^{-1}u$

and although not noted, the effects of b^* and u^* are adjusted by the absorption of herd effects. The vector y^*, however, retains herd effects which must be removed. Let

$$\hat{e}^{*\prime}_{21} A_3 \hat{e}^{*}_{21} = (y^*_{21} - X_{21}\tilde{b}^*_2 - Z_{21}\hat{u}^*_2)' A_3 (y^*_{21} - X_{21}\tilde{b}^*_2 - Z_{21}\hat{u}^*_2)$$

$$= y^{*\prime}_{21} A_3 y_{21} - [\tilde{b}^{*\prime}_2 \quad \hat{u}^{*\prime}_2] \begin{bmatrix} X'_{21}A_3y^*_{21} \\ Z'_{21}A_3y^*_{21} \end{bmatrix} - [\tilde{b}^{*\prime}_2 \quad \hat{u}^{*\prime}_2] \begin{bmatrix} X'_{21}A_3y^*_{21} \\ Z'_{21}A_3y^*_{21} \end{bmatrix} +$$

$$[\tilde{b}^{*\prime}_2 \quad \hat{u}^{*\prime}_2] \begin{bmatrix} X'_{21}A_3X_{21} & X'_{21}A_3Z_{21} \\ Z'_{21}A_3X_{21} & Z'_{21}A_3Z_{21} \end{bmatrix} \begin{bmatrix} \tilde{b}^*_2 \\ \hat{u}^*_2 \end{bmatrix}$$

where: A_3 is $I - X'_{21H}(X_{21H}X_{21H})^{-}X'_{21H}$.

The herd effects of linear type scores that also have recorded milk production data were absorbed while reading the data. The coefficient matrix, not including the assumed variances and covariances, multiplied by the solutions for the fixed and random factors may be expanded to:

$$\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & X'_{21}A_3X_{21} & 0 & X'_{21}A_3Z_{21} \\ 0 & 0 & 0 & 0 \\ 0 & Z'_{21}A_3X_{21} & 0 & Z'_{21}A_3Z_{21} \end{bmatrix} \begin{bmatrix} \tilde{b}^*_1 \\ \tilde{b}^*_2 \\ \tilde{u}^*_1 \\ \hat{u}^*_2 \end{bmatrix}$$

The transformed type variance and the covariance between milk production and type can be added to the coefficient matrix and then subtracted post-multiplication. This maintains the properties of the original expression and is denoted as:

$$\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & X_{21}'A_3X_{21} & 0 & X_{21}'A_3Z_{21} \\ 0 & 0 & 0 & 0 \\ 0 & Z_{21}'A_3X_{21} & Ig^{*21} & Z_{21}'A_3Z_{21}+Ig^{*22} \end{bmatrix} \begin{bmatrix} \tilde{b}_1^* \\ \tilde{b}_2^* \\ \hat{u}_1^* \\ \hat{u}_2^* \end{bmatrix} - \begin{bmatrix} 0 \\ 0 \\ 0 \\ \hat{u}_1^*g^{*21} + \hat{u}_2^*g^{*22} \end{bmatrix}$$

The addition of the transformed variance and covariance structure pertaining to sire to the coefficient matrix makes its postmultiplication be the vector of solutions equal to the right hand sides adjusted for herds. The simplified expression may now be written:

$$\begin{bmatrix} X_{21}'A_3y_{21}^* \\ Z_{21}'A_3y_{21}^* \end{bmatrix} - \begin{bmatrix} 0 \\ g^{*12}\hat{u}_1^*+g^{*22}\hat{u}_2^* \end{bmatrix}$$

The estimate of $\hat{e}_{21}^{*\prime}\hat{e}_{21}^*$ becomes (Walter 1986):

$$\hat{e}_{21}^{*\prime}A_3\hat{e}_{21}^* = y_{21}^{*\prime}A_3y_{21}^* - 2[\tilde{b}_2^{*\prime} \quad \hat{u}_2^{*\prime}] \begin{bmatrix} X_{21}'A_3y_{21}^* \\ Z_{21}'A_3y_{21}^* \end{bmatrix} +$$

$$[\tilde{b}_2^{*\prime} \quad \hat{u}_2^{*\prime}] \begin{bmatrix} X_{21}'A_3y_{21}^* \\ Z_{21}'A_3y_{21}^* \end{bmatrix} - [\tilde{b}_2^{*\prime} \quad \hat{u}_2^{*\prime}] \begin{bmatrix} 0 \\ g^{*12}\hat{u}_1^*+g^{*22}\hat{u}_2^* \end{bmatrix}$$

$$= y_{21}^{*\prime}A_3y_{21}^* - [\tilde{b}_2^{*\prime} \quad \hat{u}_2^{*\prime}] \begin{bmatrix} X_{21}'A_3y_{21}^* \\ Z_{21}'A_3y_{21}^* \end{bmatrix} - \hat{u}_2^{*\prime}\hat{u}_1^*g^{*12} - \hat{u}_2^{*\prime}\hat{u}_2^*g^{*22}$$

The estimator of the residual sum of squares for milk contains paired as well as unpaired records. This estimator is in the form of:

$$\hat{e}^{*\prime}_{10}A_2\hat{e}^{*}_{10} + \hat{e}^{*\prime}_{12}A_1\hat{e}^{*}_{12} = y^{*\prime}_{10}A_2y^{*}_{10} + y^{*\prime}_{12}A_1y^{*}_{23} -$$

$$2[\tilde{b}^{*\prime}_1 \quad \hat{u}^{*\prime}_1]\begin{bmatrix} X'_{10}A_2y^{*}_{10} + X'_{12}A_1y^{*}_{12} \\ Z'_{10}A_2y^{*}_{10} + Z'_{12}A_1y^{*}_{12} \end{bmatrix} +$$

$$\begin{bmatrix} \tilde{b}^{*\prime}_1 & \hat{u}^{*\prime}_1 \end{bmatrix} \begin{bmatrix} X'_{10}A_2X_{10}+X'_{12}A_1X_{12} \\ Z'_{10}A_2X_{10}+Z'_{12}A_1X_{12} \end{bmatrix} \begin{bmatrix} X'_{10}A_2Z_{10}+X'_{12}A_1Z_{10} \\ Z'_{10}A_2Z_{10}+Z'_{12}A_1Z_{12} \end{bmatrix} \begin{bmatrix} \tilde{b}^{*}_1 \\ \hat{u}^{*}_1 \end{bmatrix}$$

where $A_1 = I - X_{12H}(X'_{12H}X_{12H})^{-}X'_{12H}$

$A_2 = I - X_{10H}(X'_{10H}X_{10H})^{-}X'_{10H}$.

The addition of the sire variance-covariance structure to the coefficient matrix allows it to be equated to the right hand sides for paired and unpaired milk production records as is shown below:

$$\begin{bmatrix} X'_{10}A_2X_{10}+X'_{12}A_1X_{12} & 0 & X'_{10}A_2Z_{10}+X'_{12}A_1Z_{10} & 0 \\ 0 & 0 & 0 & 0 \\ Z'_{10}A_2X_{10}+Z'_{12}A_1X_{12} & 0 & Z'_{10}A_2Z_{10}+Z'_{12}A_1Z_{12}+Ig^{*12} & Ig^{*12} \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \tilde{b}^{*}_1 \\ \tilde{b}^{*}_2 \\ \hat{u}^{*}_1 \\ \hat{u}^{*}_2 \end{bmatrix}$$

$$\begin{bmatrix} 0 \\ 0 \\ \hat{u}^{*}_1Ig^{*11}+\hat{u}^{*}_2Ig^{*12} \\ 0 \end{bmatrix} = \begin{bmatrix} X'_{10}A_2y^{*}_{10}+X'_{12}A_1y^{*}_{12} \\ 0 \\ Z'_{10}A_2y^{*}_{10}+Z'_{12}A_1y^{*}_{12} \\ 0 \end{bmatrix}$$

The estimator of the residual milk sum of squares becomes

$$\hat{e}_{10}^{*}{}'A_2\hat{e}_{10}^{*} + \hat{e}_{12}^{*}{}'A_1\hat{e}_{12}^{*} = y_{10}^{*}{}'A_2y_{12}^{*} + y_{12}^{*}{}'A_1y_{12}^{*} -$$

$$\begin{bmatrix} \tilde{b}_1^{*}{}' & \hat{u}_1^{*}{}' \end{bmatrix} \begin{bmatrix} X_{10}'A_2y_{10}^{*} + X_{12}'A_1y_{10}^{*} \\ Z_{10}'A_2y_{10}^{*} + Z_{12}'A_1y_{12}^{*} \end{bmatrix} - \hat{u}_1^{*}\hat{u}_1^{*}g^{*11} - \hat{u}_1^{*}\hat{u}_2^{*}g^{*12}$$

The estimator of residual crossproducts is defined as:

$$\hat{e}_{12}^{*}{}'A_4\hat{e}_{21}^{*} = (y_{12}^{*} - X_{12}\tilde{b}_1^{*} - Z_{12}\hat{u}_1^{*})'A_4(y_{21}^{*} - X_{21}\tilde{b}_2^{*} - Z_{21}\hat{u}_2^{*})$$

where $A_4 = I - X_{12H}(X_{12H}'X_{21H})^{-}X_{21H}'$.

The coefficient matrix post-multiplied by the solutions of type are again equated to the right hand sides by the expansion:

$$\begin{bmatrix} 0 & X_{12}'A_4X_{21} & 0 & X_{12}'A_4Z_{21} \\ 0 & 0 & 0 & 0 \\ 0 & Z_{21}'A_4X_{12} & Ig^{*11} & Z_{12}'A_4Z_{21} + Ig^{*12} \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \tilde{b}_1^{*} \\ \tilde{b}_2^{*} \\ \hat{u}_1^{*} \\ \hat{u}_2^{*} \end{bmatrix} -$$

$$\begin{bmatrix} 0 \\ 0 \\ \hat{u}_1^{*}g^{*11} + \hat{u}_2^{*}g^{*12} \\ 0 \end{bmatrix} = \begin{bmatrix} X_{21}'A_4y_{21}^{*} \\ 0 \\ Z_{21}'A_4y_{21}^{*} \\ 0 \end{bmatrix}$$

This expression is an equality since X_{12} and X_{21H} consider only paired records. Thus, X_{12} is equivalent to X_{21} and $A_4 = A_2 = A_3$.

The estimator of the residual crossproducts is:

$$\hat{e}^{*\prime}_{12}A_4\hat{e}^*_{21} = y^*_{12}{}'A_4y^*_{21} - \begin{bmatrix} \tilde{b}^{*\prime}_2 & \hat{u}^{*\prime}_2 \end{bmatrix} \begin{bmatrix} X'_{12}A_4y^*_{12} \\ Z'_{12}A_4y^*_{12} \end{bmatrix} - \hat{u}^{*\prime}_1\hat{u}^*_1 g^{*11} - \hat{u}^{*\prime}_1\hat{u}^*_2 g^{*12}$$

The transformed MTMME (Equation III.9) were solved by direct inverse. The transformed estimates of sire, g_{ij}, and residual, r_{ij}, variance and covariances were back-transformed to the original scale by:

$$G = TG^*T'$$

$$\text{and } R = TR^*T'$$

where T is described in Equation III.8. The new estimate of R was used to obtain a new T and T^{-1}.

The equations were iterated for 20 rounds or until the absolute change between the consecutive estimates of heritabilities or genetic and phenotypic correlations was less than .001.

III.2.3 Heritabilities and genetic and phenotypic correlations

Heritability estimates were calculated using the paternal half-sib correlation method. Solutions from MTMME and REML variance component estimates obtained by the EM algorithm.

$$\hat{h}_i = 4\hat{\sigma}^2_s / \hat{\sigma}^2_s + \hat{\sigma}^2_e$$

where $\hat{\sigma}^2_s$ is the estimate of the sire component of variance for trait i, and

$\hat{\sigma}^2_e$ is the estimate of the error component of variance for trait i.

The genetic correlation, r_G , between milk and type was calculated as:

$$\hat{r}_G = \hat{\sigma}_{s_i s_{i'}}/(\hat{\sigma}^2_{s_i}\ \hat{\sigma}^2_{s_{i'}})^{1/2}$$

where $\hat{\sigma}_{s_i s_{i'}}$	is the estimate of the sire component of covariance between trait i and i'.
$\hat{\sigma}^2_{s_i}$	is the estimate of the sire component of variance for trait i.
$\hat{\sigma}^2_{s_{i'}}$	is the estimate of the sire component of variance for trait i'.

The estimate of phenotypic correlation will be computed by adding the error component to the sire component as shown below:

$$\hat{r}_p = \frac{\hat{\sigma}_{s_i s_{i'}} + \hat{\sigma}_{e_i e_{i'}}}{(\hat{\sigma}^2_{s_i} + \hat{\sigma}^2_{e_i}) * (\hat{\sigma}^2_{s_{i'}} + \hat{\sigma}^2_{e_{i'}})}$$

where:

$\hat{\sigma}_{e_i e_{i'}}$	is the estimate of the residual component of covariance between trait i and i';
$\hat{\sigma}^2_{e_i}$	is the estimate of the component of variance for trait i;
$\hat{\sigma}^2_{e_{i'}}$	is the estimate of the component of variance for trait i'.

Estimates of the empirical sampling variances of genetic parameters were computed by using the estimates of the five randomly sampled data sets for each combination of milk and type.

III.2.4 Comparison of sire BLUPS from single and multiple trait analysis

If selection effects play an important role in population estimates of type traits, the rankings of sires may differ between single and multiple trait analyses. The Spearman's rank and simple product-moment correlations were computed between the BLUPS for sires analyzed by single and multiple trait models for each of the five data sets for each trait. If the rank of sire i for trait j in data set k resulting from the single trait model is u_{ijk1} and from the multiple trait model is u_{ijk2} the correlation between the ranks of 150 bulls determined from the two models is:

$$r_{jk} = 1 - (6 \quad (u_{ijk1} - u_{ijk2})^2/(150^3 - 150))$$

and the simple product-moment correlation becomes:

$$r_{jk} = \frac{u_{ijk1}u_{ijk2} - ((\ u_{ijk1})(\ u_{ijk2})/150)}{((\ u_{ijk1} - ((\ u_{ijk1})^2/150))*(\ u_{ijk2} - ((\ u_{ijk2})^2/150)))^{0.5}}.$$

IV. Results and Discussion

IV.1 Heritability and genetic and phenotypic correlations of linearly scored type traits

IV.1.1 Heritability estimates

The estimated sire and error components of variance and heritability values are presented in Table 26 for the 15 primary linear type traits. The most highly heritable trait was stature (.39). This is in agreement with Thompson _et_ _al._ (1983) and Hay _et_ _al._ (1983) who also reported stature as the most highly heritable type trait.

The most lowly heritable trait was udder support (.10). This estimate agrees closely with Thompson _et_ _al._ (1983) also, as they reported a heritability of .12 for suspensory ligament. Hay _et_ _al._ (1983) found that the variance component estimate of dominance was greater than that of additive in affecting udder support. This relationship would confirm the observed low heritability as large nonadditive effects would lower heritability in the narrow sense.

The heritability of rear leg side view was also small (.17) and agrees with research by Thompson _et_ _al._ (1983) and Thompson _et_ _al._ (1980).

In general, traits that are linear scores of the entire body such as stature, strength, body depth and the rump traits were more highly heritable than those of udder or feet and legs. These findings are supported by the work of Thompson _et_ _al._ (1981) using linear scores from the Mating Appraisal for Profit program.

The general magnitude of the heritability estimates are similar to corresponding estimates obtained from type data measured on a

Table 26. Estimated sire and error variance components and heritability values for primary linear type scores

Trait	Sire Variance	Error Variance	Heritability	Standard Error of Heritability
Stature	4.7513	44.2602	.3878	.0031
Strength	2.2710	39.9747	.2150	.0019
Body depth	2.7382	36.2065	.2812	.0235
Angularity	2.2364	46.2997	.1843	.0017
Rump angle	1.6127	25.8492	.2349	.0020
Rump length	1.3550	23.0810	.2218	.0017
Rump width	2.5437	35.3424	.2686	.0023
Rear leg side veiw	1.7810	39.6683	.1719	.0016
Foot angle	2.7284	36.9082	.2753	.0023
Fore udder attachment	2.5516	47.9603	.2021	.0324
Rear udder height	2.5749	43.0926	.2255	.0019
Rear udder width	2.0166	44.8741	.1720	.0016
Udder support	1.4395	40.0301	.0999	.0013
Udder depth	1.6139	22.6335	.2662	.0022
Teat placement rear view	1.8846	36.5244	.1963	.0017

descriptive scale of one through six (Cassell et al., 1973 and Hay et al., 1983). Thus, the scoring of type traits on a 50-point scale appears to have little effect on the heritability values when compared to estimates of type traits scored one through six.

IV.1.2 Phenotypic correlations

Estimates of phenotypic correlations between the 15 primary linear type traits are presented in Table 27. All correlations are positive and greater than .30 with the exception of correlations between angularity and udder depth, rear leg side view and foot angle, rear leg side view and udder depth and rear udder height and rear udder width. All correlations are significant ($P<.05$). These results disagree with the work of Thompson et al. (1981) which showed mostly small and negative phenotypic correlations between linear type scores.

Udder traits were more highly correlated among themselves than with other type traits. In the present study, the phenotypic relationships between the udder traits were greater than .50 with the exception of that between rear udder width and rear udder height (.09) and between udder depth and rear udder width (.47). Thompson et al. (1981) reported the similar tendency and that 11 out of the 15 phenotypic correlations among udder traits were greater than .20.

The rear udder height of Holstein cattle appears to be relatively independent of the rear udder width. This could additionally be explained by the fact that a highly attached udder may visually appear more narrow than an udder more lowly attached.

Teat placement rear view was highly correlated with udder support (.94) as expected since the support of the suspensory liga-

Table 27. Phenotypic correlations among the fifteen linear type traits

Trait	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)
(1) Stature														
(2) Strength	.50													
(3) Body depth	.61	.74												
(4) Angularity	.59	.34	.56											
(5) Rump angle	.41	.36	.39	.33										
(6) Rump length	.86	.76	.83	.41	.46									
(7) Rump Width	.76	.84	.86	.40	.46	1.00								
(8) Rear leg side view	.34	.32	.39	.57	.51	.57	.44							
(9) Foot angle	.50	.58	.57	.35	.44	.63	.57	.23						
(10) Fore udder att.	.57	.62	.63	.49	.48	.75	.62	.43	.63					
(11) Rear udder hgt.	.53	.60	.62	.53	.43	.72	.63	.38	.60	.88				
(12) Rear udder wth.	.58	.69	.70	.56	.50	.53	.73	.39	.63	.87	.09			
(13) Udder support	.47	.49	.52	.56	.48	.65	.53	.48	.54	.76	.73	.75		
(14) Udder depth	.46	.34	.32	.24	.33	.50	.39	.29	.89	.76	.53	.47	.67	
(15) Teat placement rear view	.44	.47	.49	.49	.46	.61	.49	.45	.50	.82	.67	.67	.94	.90

ment would influence the placement of the teats.

The correlation between rump width and rump length was 1.00. The measurements among those traits influenced by size and scale should change proportionately. Rump length and width were highly correlated with stature, strength and body depth. The correlations between these traits exceeded .75.

Cattle that were stronger and deeper bodied tended to have udders that were stronger in the fore attachment, more highly attached and wider in the rear udder.

Phenotypic correlations between rear leg side view and foot angle indicated that cattle with more set to the hock tended to be deeper heeled. This relationship, however, is illogical since additional angularity in the set of the rear leg should place more weight and wear on the heel.

Additionally, cattle which were taller tended to have more set to the rear leg. The height of a cow may be altered by a change in either the length of the bone or angle of the attachment. This phenotypic relationship suggests that the skeletal structure is elongated while the angle of the hock becomes more acute.

IV.1.3 Genetic correlations

Genetic correlations between the 15 primary linear type traits are presented in Table 28 and all are significant ($P<.05$). The genetic correlation estimates are generally smaller than the corresponding phenotypic correlation values. This contradicts the work of Thompson <u>et</u> <u>al.</u> (1981) and Thompson <u>et</u> <u>al.</u> (1980).

The genetic associations between stature, strength and body depth are high. The estimated correlation between stature and

Table 28. Genetic correlations among the fifteen linear type traits

Trait	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)
(1) Stature														
(2) Strength	.68													
(3) Body depth	.76	.93												
(4) Angularity	.13	-.24	.03											
(5) Rump angle	.11	.03	.01	.11										
(6) Rump length	.88	.62	.72	.20	.02									
(7) Rump Width	.54	.55	.58	.01	-.01	.68								
(8) Rear leg side view	-.20	-.34	-.24	.38	-.00	-.07	-.11							
(9) Foot angle	.13	.04	-.01	-.34	-.35	-.10	-.05	-.57						
(10) Fore udder att.	.29	.14	.15	-.02	-.27	.25	.10	-.17	-.08					
(11) Rear udder hgt.	.12	.10	.12	-.01	-.35	.11	.07	-.35	-.11	.58				
(12) Rear udder wth.	.15	.21	.23	.03	-.32	.17	.20	-.33	-.12	.54	.93			
(13) Udder support	.13	.15	.17	.14	-.25	.18	.05	-.07	-.13	.53	.37	.41		
(14) Udder depth	.36	.02	.02	-.09	-.14	.30	.07	-.15	-.10	.83	.35	.26	.47	
(15) Teat placement rear view	.13	.02	.02	.18	-.13	.21	.06	.03	-.19	.63	.28	.35	.77	.52

strength (.68) is very similar to that reported by Thompson et al. (1981).

The daughters of bulls which are stronger, taller and deeper bodied tend to have less set to the rear leg, have longer and wider rumps and have deeper udders. These relationships also suggest that selection for taller cows would lead to elongation of the skeletal structure and additional height due to more posty rear legs and deeper heels.

The genetic correlations between udder traits were positive and ranged from .26 to .93. Thompson et al. (1981) also reported positive genetic correlations between udder traits. Therefore, selection for any udder trait would tend to enhance other udder scores.

Rear udder height and width had the highest genetic correlation (.93) which agrees with the results by Thompson et al. (1981).

Udder traits did appear to be negatively associated genetically with feet and leg traits. Therefore, cattle selected for desirable udder characteristics would generally be straighter in the rear leg and more shallow heeled. However, daughters of bulls which are taller, stronger and deeper bodied tend to have more desirable udders.

The negative genetic correlations between feet and leg traits and the majority of other linear type traits agree with the work by Thompson et al. (1981) on Hosteins and Norman et al. (1983) on Ayrshire, Guernsey, Jersey and Milking Shorthorn cattle. Selection programs designed to improve the average udder traits would result in a more posty rear leg and more shallow heel.

IV.1.4 Environmental correlations

Searle (1961) reported that the phenotypic correlation may be expressed as:

$$r_p = r_g(h_1h_2)^{.5} + r_e[(1-h_1)(1-h_2)]^{.5}$$

where r_p is the phenotypic correlation.

r_g is the genetic correlation.

r_e is the environmental correlation.

h_1 is the heritability of trait one.

h_2 is the heritability of trait two.

Thus, the phenotypic correlation is a function of the joint genetic and environmental variation between two traits. Additionally he notes that the phenotypic correlation between two traits exceeds the genetic correlation if the ratio of the environmental correlation to the genetic correlation exceeds the value $[1-(h_1h_2)^{.5}]/[(1-h_1)(1-h_2)]^{.5}$.

Hence, if the genetic and phenotypic correlations are opposite in signs, the environmental correlation has the sign of the phenotypic correlation. If the phenotypic and genetic correlations share the same sign, the environmental correlation is positive if the ratio of phenotypic to genetic correlation is greater than the geometric mean of the heritabilities of the two traits.

Therefore, the genetic and phenotypic correlations in this study seem to suggest a large positive environmental correlation.

The factors contributing to this environmental influence were not investigated in this research.

IV.2 Heritability and genetic and phenotypic correlations of milk production and linearly scored type traits

The estimation of genetic parameters of type characteristics of Holstein dairy cattle has progressed over many years and many classification systems. Yet, it has been hypothesized that the animals scored for type may represent a superior population since few dairy cows are scored for type. Selection pressure for milk production may additionally lower the probability that an animal receives a type score by culling animals for low production.

Henderson (1975) reports that under normality, with selection decisions invariant to the fixed effects and with data upon which the selection decisions were made included in the analysis, that Best Linear Unbiased Prediction (BLUP) with selection is computed as BLUP with selection. Thus, the inclusion of milk records in the model with type may reduce the effects of selection.

Walter and Mao (1985) reported that under selection, a multiple trait algorithm was superior to single trait estimates in improving the accuracy of estimated sire and error variance components.

The milk record population is less selected than those cows scored for type. The simultaneous consideration of milk with type traits may reduce any selection bias inherent to the population scored for type. This simultaneous consideration is accomplished by the variance and covariance structure of the random factors in the multiple trait mixed model equations.

The 15 primary linear type traits and milk yield were first analyzed by a single trait mixed model (Equation III.1), which is henceforth referred to as single trait analysis (ST). The resulting variance estimates were then used as the *a priori* values in a multiple trait (MT) analysis of milk with each of the type traits. The milk yield and one of the 15 primary linear type traits were analyzed in each of the MT analysis.

IV.2.1 Single trait MME methods

IV.2.1.1 Heritability

The estimates of sire and error variance components obtained by ST REML are presented in Table 29 and Table 30. The heritability values estimated from the variance components are in Table 31 and are significant ($P<.05$). The mean estimates of the heritability values of linear type traits, averaged over the five data sets, correspond closely to the estimates obtained in the analysis of type traits alone. The ST estimates of heritability for rump length and rump width appear to be the most variable, while strength and rear udder width were the least variable across data sets.

Stature was the most highly heritable type trait (.35) and rear leg side view the least (.15). The greatest difference between single and multiple trait estimated heritabilities was the larger estimate by MT for udder support. The estimate increased from .09 with a single estimate on a relatively large data set (41,834 observations pertaining to 299 sires) to .14 across five data sets of 150 sires each. However, the average heritability was different from zero ($P<.05$) for all linear traits studied.

IV.2.2 Multiple trait

IV.2.2.1 Heritability

Estimates of heritability and phenotypic and genetic correlations for milk production and linear type traits from MTMME method

Table 29. Estimated sire variance components of milk and linear type traits obtained through single trait methodology

Trait	Data Set 1	2	3	4	5	Mean	Standard Deviation
Milk	324154.06	362598.27	462100.35	379459.17	329796.48	371621.67	55524.23
Stature	4.75	4.38	3.17	4.33	4.08	4.14	.59
Strength	2.00	2.57	2.28	2.61	1.85	2.26	.34
Body depth	2.69	2.56	1.83	3.67	2.16	2.58	.70
Angularity	2.22	.62	3.00	3.13	1.85	2.17	1.01
Rump angle	.68	2.51	1.95	1.46	2.08	1.73	.70
Rump length	2.03	.31	1.49	.77	1.28	1.18	.66
Rump width	3.50	2.52	4.57	1.04	2.49	2.82	1.31
Rear leg side view	1.93	1.87	1.63	1.11	1.42	1.59	.34
Foot angle	1.93	1.30	.53	.77	1.30	1.17	.54
Fore udder attachment	3.03	3.22	2.63	3.08	2.13	2.82	.44
Rear udder height	2.98	2.55	1.92	1.36	1.14	1.99	.78
Rear udder width	2.10	2.77	2.22	2.02	1.86	2.19	.35
Udder support	1.78	2.69	.65	.78	1.77	1.53	.84
Udder depth	1.57	1.61	2.06	.75	1.00	1.40	.52
Teat placement rear view	2.21	2.39	1.60	1.72	1.47	1.88	.40

Table 30. Estimated error variance components of milk and linear type traits obtained through single trait methodology

Trait	Data Set 1	2	3	4	5	Mean	Standard Deviation
Milk	9,517,680.12	9,924,236.07	9,588,083.17	9,682,940.55	9,465,815.24	9,635,751.03	180,652.71
Stature	45.17	44.65	40.60	43.47	44.36	43.69	1.81
Strength	39.32	37.21	38.59	41.32	39.72	39.23	1.51
Body depth	35.14	33.27	34.53	37.05	36.86	35.37	1.60
Angularity	50.81	45.29	45.16	47.05	46.23	46.90	2.31
Rump angle	25.89	26.53	28.12	24.53	26.99	26.36	1.43
Rump length	22.50	23.29	21.86	23.13	22.66	22.69	.57
Rump width	36.53	34.13	35.77	36.77	35.71	35.78	1.03
Rear leg side view	44.31	38.59	37.43	43.81	41.63	41.15	3.07
Foot angle	38.52	35.42	37.94	36.72	40.18	37.76	1.81
Fore udder attachment	46.33	47.75	50.17	44.24	49.00	47.50	2.32
Rear udder height	40.80	40.84	45.89	42.34	43.80	42.74	2.16
Rear udder width	42.94	43.36	47.16	44.44	45.93	44.77	1.77
Udder support	42.67	40.94	41.85	37.69	41.65	40.96	1.93
Udder depth	23.09	22.53	23.61	21.66	23.91	22.96	.90
Teat placement rear view	37.78	34.36	38.45	33.53	38.75	36.57	2.44

Table 31. Estimated heritabilities for milk and linear type traits obtained through single trait methodology

	Data Set						
Trait	1	2	3	4	5	Mean	Standard Deviation
Milk	.13	.14	.18	.15	.13	.15	.02
Stature	.38	.36	.29	.36	.34	.35	.04
Strength	.19	.26	.22	.24	.18	.22	.03
Body depth	.29	.29	.20	.36	.22	.27	.06
Angularity	.17	.05	.25	.25	.15	.18	.08
Rump angle	.10	.35	.26	.23	.28	.24	.09
Rump length	.33	.05	.26	.13	.21	.20	.11
Rump width	.35	.27	.45	.11	.26	.29	.13
Rear leg side view	.17	.19	.17	.10	.13	.15	.04
Foot angle	.19	.14	.06	.08	.12	.12	.05
Fore udder attachment	.25	.25	.20	.26	.17	.22	.04
Rear udder height	.27	.23	.16	.12	.10	.18	.07
Rear udder width	.19	.24	.18	.17	.16	.19	.03
Udder support	.16	.25	.06	.08	.16	.14	.07
Udder depth	.25	.27	.32	.13	.16	.23	.08
Teat placement rear view	.22	.26	.16	.19	.15	.20	.05

are shown in Table 32 through Table 46.

The heritability of milk yield increased slightly from .15 by ST methodology to .16 by MT methods. This difference is not statistically significant since the standard deviations overlap considerably. However, the standard deviations of the heritability estimates from both ST and MT analyses are approximately the same. The additional information on type had little effect on the estimates of heritability for milk yield.

The estimated heritabilities of linear type traits obtained via MT analysis were marginally less than or equal to the corresponding ST estimates. The exception to this was udder support and angularity which had a .PN116 .OP slightly larger average estimate by MT analysis. The traits most affected by method of analysis were stature and foot angle as the MT estimate was 4 points smaller than the corresponding ST estimate. Multiple trait analysis seems to offer no great advantage for improving the precision of heritability estimates since the standard deviations of the estimates are similar to those obtained from ST analysis.

Schaeffer (1984) stated that the correlation between error effects for different traits has a direct effect on the interchanging contributions that one trait will have upon another. He also notes that as the number of observations on trait i increases the contribution of trait j would tend to have no influence.

Therefore, if the relationships between milk yield and type characteristics are small and the number of progeny large, the contribution of milk yield information to improve genetic estimates of type would be expected to be small. This could possibly explain the small or negligible changes in genetic parameters for type when

Table 32. Estimated genetic parameters between milk and stature

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Stature	Phenotypic	Genetic
1	60,008	4,882	.15	.31	.03	-.41
2	51,651	3,749	.14	.38	.02	-.18
3	65,264	6,416	.19	.26	.02	-.16
4	50,472	3,960	.16	.32	.01	-.19
5	69,078	5,550	.14	.31	.06	.06
Average			.16	.31	.03[a]	-.16
Std. deviation			.02	.04	.02	.17

[a] Estimates are significant (P<.05)

Table 33. Estimated genetic parameters between milk and strength

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Strength	Phenotypic	Genetic
1	60,008	4,882	.19	.22	-.00	.03
2	51,651	3,749	.14	.17	-.04	-.36
3	65,264	6,416	.15	.26	-.00	-.14
4	50,472	3,960	.16	.24	-.03	-.17
5	69,078	5,550	.14	.17	-.02	-.01
Average			.16	.21	-.02	-.13
Std. deviation			.02	.04	.02	.16

Table 34. Estimated genetic parameters between milk and body depth

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Body Depth	Phenotypic	Genetic
1	60,008	4,882	.15	.26	.07	-.22
2	51,651	3,749	.14	.26	.02	-.30
3	65,264	6,416	.19	.19	.04	.02
4	50,472	3,960	.16	.36	.01	-.09
5	69,078	5,550	.14	.20	.04	-.21
Average			.16	.25	.04[a]	-.16
Std. deviation			.02	.07	.02	.13

[a] Estimates are significant ($P<.05$)

Table 35. Estimated genetic parameters between milk and angularity

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Angularity	Phenotypic	Genetic
1	60,008	4,882	.14	.19	.36	.20
2	51,651	3,749	.15	.05	.35	-.11
3	65,264	6,416	.19	.22	.30	.15
4	50,472	3,960	.16	.31	.34	.56
5	69,078	5,550	.14	.23	.34	.07
Average			.15	.20	.34[a]	.17
Std. deviation			.02	.09	.02	.24

[a] Estimates are significant (P<.05)

Table 36. Estimated genetic parameters between milk and rump angle

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Rump Angle	Phenotypic	Genetic
1	60,008	4,882	.16	.19	.06	.23
2	51,651	3,749	.14	.10	.01	.22
3	65,264	6,416	.15	.33	.01	.28
4	50,472	3,960	.19	.26	.01	.17
5	69,078	5,550	.14	.29	.04	.05
Average			.16	.23	.03[a]	.19[a]
Std. deviation			.02	.09	.02	.09

[a] Estimates are significant ($P<.05$)

Table 37. Estimated genetic parameters between milk and rump length

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Rump Length	Phenotypic	Genetic
1	60,008	4,882	.14	.20	.05	.05
2	51,651	3,749	.14	.32	.00	-.26
3	65,264	6,416	.15	.05	.05	-.23
4	50,472	3,960	.19	.26	.00	-.33
5	69,078	5,550	.16	.13	.01	-.55
Average			.16	.19	.02	-.26
Std. deviation			.02	.11	.03	.21

Table 38. Estimated genetic parameters between milk and rump width

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Rump Width	Phenotypic	Genetic
1	60,008	4,882	.15	.27	-.00	-.22
2	51,651	3,749	.14	.35	.02	-.32
3	65,264	6,416	.19	.46	.01	-.33
4	50,472	3,960	.16	.11	.01	-.40
5	69,078	5,550	.14	.25	.03	.03
Average			.15	.29	.01	-.25[a]
Std. deviation			.02	.13	.01	.17

[a] Estimates are significant ($P<.05$)

Table 39. Estimated genetic parameters between milk and rear leg side view

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Rear leg side view	Phenotypic	Genetic
1	60,008	4,882	.14	.17	.04	.19
2	51,651	3,749	.15	.18	.05	-.02
3	65,264	6,416	.19	.16	.02	.13
4	50,472	3,960	.16	.09	.04	-.18
5	69,078	5,550	.14	.12	.01	-.13
Average			.16	.15	.03[a]	.05
Std. deviation			.02	.04	.02	.15

[a] Estimates are significant (P<.05)

Table 40. Estimated genetic parameters between milk and foot angle

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Foot Angle	Phenotypic	Genetic
1	60,008	4,882	.14	.12	.01	-.19
2	51,651	3,749	.14	.18	-.02	-.14
3	65,264	6,416	.15	.13	-.01	.45
4	50,472	3,960	.16	.07	.01	.12
5	69,078	5,550	.19	.06	.01	.10
Average			.16	.11	.01	.07
Std. deviation			.02	.05	.01	.25

Table 41. Estimated genetic parameters between milk and fore udder attachment

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Fore udder attachment	Phenotypic	Genetic
1	60,008	4,882	.14	.24	-.04	-.36
2	51,651	3,749	.15	.25	-.02	.08
3	65,264	6,416	.19	.19	-.04	-.34
4	50,472	3,960	.16	.28	-.06	-.57
5	69,078	5,550	.14	.15	-.05	-.26
Average			.16	.22	-.04[a]	-.29
Std. deviation			.02	.05	.01	.24

[a] Estimates are significant (P<.05)

Table 42. Estimated genetic parameters between milk and rear udder height

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Rear udder height	Phenotypic	Genetic
1	60,008	4,882	.19	.15	.08	-.33
2	51,651	3,749	.14	.29	.08	.07
3	65,264	6,416	.15	.22	.09	-.30
4	50,472	3,960	.16	.12	.08	-.17
5	69,078	5,550	.14	.10	.07	.01
Average			.16	.18	.08[a]	-.14
Std. deviation			.02	.08	.01	.18

[a] Estimates are significant (P<.05)

Table 43. Estimated genetic parameters between milk and rear udder width

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Rear udder width	Phenotypic	Genetic
1	60,008	4,882	.14	.22	.09	-.51
2	51,651	3,749	.15	.23	.12	.13
3	65,264	6,416	.19	.18	.11	-.10
4	50,472	3,960	.16	.18	.12	-.14
5	69,078	5,550	.14	.14	.10	-.05
Average			.16	.19	.11[a]	-.01
Std. deviation			.02	.04	.01	.20

[a] Estimates are significant (P<.05)

Table 44. Estimated genetic parameters between milk and udder support

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Udder support	Phenotypic	Genetic
1	60,008	4,882	.14	.17	.08	-.15
2	51,651	3,749	.15	.26	.10	-.21
3	65,264	6,416	.19	.06	.08	.42
4	50,472	3,960	.16	.08	.07	.02
5	69,078	5,550	.14	.16	.05	-.39
Average			.16	.15	.08[a]	-.06
Std. deviation			.02	.08	.02	.31

[a] Estimates are significant ($P<.05$)

Table 45. Estimated genetic parameters between milk and udder depth

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Udder depth	Phenotypic	Genetic
1	60,008	4,882	.14	.23	-.15	-.42
2	51,651	3,749	.15	.25	-.11	.16
3	65,264	6,416	.19	.33	-.14	-.13
4	50,472	3,960	.16	.14	-.16	-.45
5	69,078	5,550	.14	.21	-.17	-.00
Average			.16	.23	-.15[a]	-.17
Std. deviation			.02	.07	.02	.26

[a] Estimates are significant ($P<.05$)

Table 46. Estimated genetic parameters between milk and teat placement rear view

Data set	Total number of records	Number of paired records	Heritability		Correlation	
			Milk	Teat placement rear view	Phenotypic	Genetic
1	60,008	4,882	.16	.18	.01	-.18
2	51,651	3,749	.14	.22	.05	-.25
3	65,264	6,416	.15	.26	.03	-.06
4	50,472	3,960	.19	.15	.02	-.36
5	69,078	5,550	.14	.13	.00	-.28
Average			.16	.19	.02	-.22[a]
Std. deviation			.02	.05	.02	.11

[a] Estimates are significant (P<.05)

MT analysis was applied.

IV.2.2.2 Phenotypic correlations

Phenotypic correlations between milk yield and linear type traits estimated from MTMME methodology are also presented in Table 32 through Table 46. In general, phenotypic correlations were small and positive. This relationship indicates that cattle which were more desirable in type had a tendency to also produce more milk. Norman and Van Vleck (1972c), using Holstein data collected in the New York Type Appraisal Program, reported that most of the phenotypic correlations between milk yield and type score were positive.

The phenotypic correlations between milk yield and type traits which measure the overall physical characteristics of the body such as stature, strength, body depth and angularity were generally positive and small. The exceptions were strength, which was negatively related to milk yield, and angularity which exhibited the largest positive phenotypic relationship with milk yield. The correlations between milk yield and overall body measurements were significant ($P<.05$), with the exception of the correlation between milk yield and strength. This suggests that taller, deeper bodied cows that were more angular in their physical attributes have a tendency to produce more milk.

Carter et al. (1965) using descriptively scored Holsteins, compared to the ideal breed type, suggested that the phenotypic relationship between dairy character and milk production was the highest (.29) among all type traits studied.

Although angularity and dairy character differ in the choice of scale (linear versus ordinal), the same characteristics should prove to be desirable in both traits.

Traits describing the rump structure of a cow such as rump angle, rump length and rump width were essentially independent of the cow's milk yield. Although the correlation between milk yield with rump angle was significant ($P<.05$) the estimated value was only .03.

The phenotypic correlations between rear leg side view and foot angle with milk yield were also practically zero. Thus, any phenotypic association between milk yield and the desirability of the rear leg from the side view and the angle of the foot would be minimal.

The udder traits were generally correlated positively with milk yield and were significantly different from zero ($P<.05$) with the exception of teat placement rear view. The width of the rear udder exhibited the highest positive correlation with milk yield (.11). Other udder traits that correlate positively with milk yield are rear udder height (.08) and udder support (.08). The depth of the udder was negatively associated with milk yield (-.15) as was the fore udder attachment (-.04).

The two type traits most highly related phenotypically to milk yield were the depth of the udder and angularity. Norman and Van Vleck (1972) reported the depth of the udder and sharpness to be the best predictor of first lactation production. Burnside _et_ _al._ (1963) also reports a positive relationship between the depth of the udder and milk yield.

Dairy cattle which gave more milk tended to be deeper and wider in the udder and were more angular in their appearance. Cows with a higher milk yield on the average would be taller, deeper bodied and be looser in the fore udder, more highly attached in the rear udder and have more udder support.

IV.2.2.3 Genetic correlations

Genetic correlations between milk yield and type traits obtained by MT analysis are also presented in Table 32 through Table 46. The genetic relationships between the majority of type traits with milk yield was negative. The only positive correlations with milk were recorded for angularity, rump angle, rear leg side view and foot angle.

The variability of estimates of genetic correlations among data sets was much greater than those of the corresponding phenotypic correlation estimates. The coefficients of variation of the mean estimates ranged from 47% to 517% for rump angle and udder support, respectively.

Grantham et al. (1974) and White (1974) reported all descriptively measured type traits except dairy character were negatively genetically associated with milk yield. The antagonistic relationships would result in poorer milk yield if selection were placed on type characteristics in the dairy cattle population.

In this study, the estimated genetic correlations between milk yield and the traits which measure the entire body, stature, strength, body depth and angularity, were not different from zero ($P>.05$). None the less, the estimates obtained were negative for the correlation between milk yield and stature, strength and body depth. A great deal of variation was exhibited across sample data sets with a majority of estimates being negative. The average genetic correlation between angularity and milk yield was positive and moderate in magnitude (.17). However, estimates ranged from -.11 to .56 and thus the estimate was not different from zero (P>.05). The linearly scored type trait of angularity measures the similar attributes as the old descriptive trait dairy character. This suggests that sires which produce more angular daughters also have daughters which, on the average, produce more pounds of milk.

The traits describing the rump structure of the dairy cow were mixed in their genetic relationship with milk yield. The correlation between milk yield and rump angle was positive. Selection programs developed for milk yield would also produce progeny which would be lower at the pins.

Rump length and rump width were moderately, but negatively correlated with milk yield as the estimates were -.26 and -.25, respectively. The estimate between milk yield and rump width was significant (P<.05). These traits were among the greatest in their average genetic association with milk yield.

It would seem logical that if the correlations between milk yield and stature, strength or body depth are negative, rump length and rump width would correlate with milk in a similar manner. This is expected since taller and deeper bodied animals should also be longer rumped and wider rumped.

The genetic relationship between milk and rear leg side view or foot angle appeared to be small, as the estiamtes were .05 and .12, respectively. However, the standard error among estimates across data sets was large. The estimated genetic correlations ranged from -.19 to .45 for foot angle and milk.

All udder traits were negatively correlated genetically with milk yield. The two largest correlations were between milk and fore udder attachment (-.29) and between milk and teat placement rear view (-.22). However, teat placement rear view was the only significant correlation ($P<.05$) among the udder traits. It appears that selection for milk yield would eventually change the population to be more broken in the fore udder attachment and have teats that are more widely spaced and not parallel in their structure.

The estimated genetic correlations between udder traits and milk yield varied from data set to data set more than other estimated correlations. The variation in estimates was the greatest for estimates involving udder support and udder depth. The implication of negative genetic correlations between milk yield and udder traits is that a sire that produces daughters that excel in milk yield would also sire daughters that are more broken in fore udder, narrower in the width of the rear udder and lower at the rear udder attachment. Furthermore, these daughters would have less udder support, more udder depth and have a wider teat placement.

Genetic correlation estimates indicated that the traits which measure the angles of the body are most likely to be positively related to milk yield genetically. These traits such as angularity, rump angle, rear leg side view and foot angle may reflect the general dairyness of the cow.

IV.2.3 Correlations of sire solutions from single and multiple trait methodology

Multiple trait mixed model methods can improve the accuracy of sire ranking for type traits by incorporating large milk yield data bases. This improvement would be available if only selected subpopulations contribute type information.

If MT methodology is successful in increasing the accuracy of sire ranking for type, the BLUP results from ST may be different from those from MT methodology. The rank correlations between ST sire solutions from (Equation III.5) and MT sire solutions (Equation III.6) were computed and presented in Table 47 and Table 48, respectively.

The average rank correlations range from .955 for strength to .675 for angularity. Product moment correlations between ST and MT methodologies follow similar patterns for all traits but are marginally higher in magnitude.

The ranking of the sire solutions for stature, strength, body depth, rear leg side view and rump angle changed little from analysis by ST or by MT methods, as the average rank and product moment correlations were all above .90. These results seem to suggest little additional accuracy is gained by MT analysis over a more simple ST method.

Rump length, rump width, foot angle and all traits associated with the udder had rank correlations greater than .80 but less than .90. The sire solutions of these traits are more influenced by the method of analysis. However, no noticeable trend in the estimated genetic or phenotypic correlations was discovered between the traits that had sire solutions correlated above .90 and those correlated between .81 and .89.

Angularity was most affected by the method of analysis. The rank and product moment correlations between ST and MT methodology were .675 and .710, respectively. The rank correlation for data set two was .246. The removal of this estimate raises the average to .782 which is still slightly below other traits.

Table 47. Rank correlations between sire solutions for single and multiple trait analysis

Trait	Data set 1	2	3	4	5	Average	Std. Dev.
Stature	.97	.85	.96	.96	.99	.95	.06
Strength	.86	.97	.99	.96	.99	.96	.06
Body depth	.88	.86	.99	.98	.88	.92	.07
Angularity	.76	.25	.81	.80	.78	.67	.24
Rump angle	.88	.92	.96	.93	.99	.94	.04
Rump length	.94	.60	.88	.64	.99	.81	.18
Rump width	.89	.93	.93	.66	.99	.88	.13
Rear leg side view	.95	.98	.96	.79	.94	.92	.08
Foot angle	.94	.96	.58	.95	.98	.89	.17
Fore udder attachment	.88	.97	.86	.77	.93	.88	.08
Rear udder height	.82	.99	.74	.80	.97	.86	.11
Rear udder width	.69	.98	.85	.87	.90	.86	.11
Udder support	.90	.86	.72	.92	.72	.82	.10
Udder depth	.94	.87	.96	.81	.90	.90	.06
Teat placement rear view	.93	.88	.98	.76	.84	.88	.09

Table 48. Product moment correlations between sire solutions for single and multiple trait analysis

Trait	Data set					Average	Std. Dev.
	1	2	3	4	5		
Stature	.98	.86	.98	.96	.99	.97	.05
Strength	.91	.98	.99	.98	.99	.96	.03
Body depth	.93	.92	.99	.99	.94	.95	.04
Angularity	.77	.29	.83	.88	.78	.71	.24
Rump angle	.94	.95	.98	.96	.99	.96	.02
Rump length	.96	.73	.91	.70	.99	.86	.14
Rump width	.94	.96	.93	.74	.99	.91	.10
Rear leg side view	.98	.99	.98	.89	.97	.96	.04
Foot angle	.98	.98	.66	.97	.99	.91	.15
Fore udder attachment	.93	.99	.90	.79	.96	.91	.08
Rear udder height	.89	.99	.81	.86	.98	.91	.08
Rear udder width	.77	.99	.91	.89	.94	.90	.08
Udder support	.93	.91	.81	.96	.83	.89	.07
Udder depth	.94	.91	.98	.88	.92	.92	.03
Teat placement rear view	.95	.93	.99	.83	.91	.92	.06

Low correlations were also found in one of the five data sets for foot angle, rump length and rump angle. Coincidentally, the estimated sire variance components from single trait analysis were relatively small for these traits. Thus, sampling error would probably be relatively great for these traits.

The standard deviations of sire solutions of linear type scores obtained by single and by multiple trait analysis are shown in Table 49. The estimates from MT methodology were generally more variable within data set across all samples. It seems that MT analysis would result in greater relative differences between sires.

The standard deviations of sire solutions from the five data sets show that results from MT analysis tend to be more variable. However, data set five had only five of the 15 traits more variable in the MT estimates than ST estimates.

Udder support and udder depth were the only traits consistent in variability among solutions. Multiple trait analysis separated more of the sire differences across all five randomly sampled data sets.

Table 49. Mean standard deviation of sire estimates for type traits analyzed by single and multiple trait methodology

	Data Set													
	1		2		3		4		5		Avg.		Std.	
Trait	ST	MT	ST	MT	ST	MT	ST	MT	ST	MT	ST	MT	ST	MT
Stature	1.246	1.272	1.010	1.138	.859	.830	1.006	.947	1.100	1.053	1.044	1.480	.142	.170
Strength	.665	.666	.793	.802	.686	.685	.701	.723	.623	.615	.694	.698	.063	.070
Body depth	.860	.877	.806	.829	.585	.571	.942	.947	.714	.709	.781	.787	.138	.148
Angularity	.673	.790	.231	.521	.816	.784	.780	.892	.597	.923	.619	.782	.234	.158
Rump angle	.323	.326	.848	.853	.666	.692	.505	.453	.762	.765	.621	.618	.210	.221
Rump length	.786	.794	.161	.200	.579	.655	.308	.474	.543	.532	.475	.531	.244	.222
Rump width	1.044	1.111	.797	.812	1.195	1.304	.339	.453	.801	.777	.835	.891	.325	.328
Rear leg side view	.637	.647	.614	.604	.528	.530	.339	.375	.499	.495	.523	.530	.118	.106
Foot angle	.652	.653	.462	.454	.212	.333	.266	.259	.469	.462	.412	.432	.176	.150
Fore udder attach.	.888	.934	.881	.880	.700	.759	.784	1.029	.654	.642	.781	.664	.105	.333
Rear udder height	.904	1.079	.758	.728	.560	.690	.404	.480	.413	.407	.608	.677	.219	.263
Rear udder width	.684	1.023	.804	.777	.635	.700	.561	.667	.599	.577	.657	.749	.094	.169
Udder support	.603	.671	.799	.925	.240	.272	.266	.267	.601	.722	.502	.571	.241	.291
Udder depth	.634	.610	.628	.653	.726	.752	.307	.336	.444	.582	.548	.587	.169	.154
Teat placement rear view	.736	.785	.764	.828	.512	.488	.523	.583	.524	.533	.612	.643	.127	.153

V. Summary and Conclusions

Genetic selection for some body conformation characteristics, with various degrees of relative emphasis and accuracy, has been practiced by Holstein dairymen. Only a subpopulation of Holstein cows have contributed information for the genetic evaluation of bulls and for estimation of genetic parameters involving type traits. This subpopulation may not represent a random sample of the total milk recorded population in which genetic selection for type has been of interest. If not, the bull ranking for type and the relationship estimates between type and production from this subpopulation may be inaccurate for the total population.

A new linear scoring system was implemented by the HFAA in January of 1983. The infancy of this new system may further restrict the subpopulation which provides the database.

A recently developed statistical procedure, multiple trait analysis, can be used to remove such possible inaccuracies by a joint analysis of type and milk production. Type data is from a subpopulation which may not be random, while the more abundant production data is more likely to randomly represent the entire population.

The purposes of this study were to estimate heritabilities and genetic and phenotypic correlations among the linear type traits, and the phenotypic and genetic correlations between type and production for the entire population in which genetic selection for both milk and type is of interest. The goal was to establish the differences, if any, in the genetic parameters and bull ranking between the small population which provides the linear type scores and the larger population.

The 305-day 2X-ME lactation records were provided by Michigan and Wisconsin DHIA and the first linear scores were provided by HFAA.

The most highly heritable type trait in the subpopulation was stature, while the least heritable was udder support. The scores encompassing the entire body such as stature, strength, body depth and the rump traits were more highly heritable than those of the udder or the feet and leg traits.

The phenotypic correlations among the 15 primary type traits were generally large and all were positive. Phenotypic correlations greater than .90 were: rump length and rump width; udder support and teat placement rear view; and udder depth and teat placement rear view. The traits that were least associated with each other phenotypically were: udder depth and angularity, rear leg side view and foot angle, udder depth and rear leg side view, and rear udder height and rear udder width.

Genetic correlations among the 15 linear type traits were generally smaller than their corresponding phenotypic correlations. Rump angle, foot angle and rear leg side view were negatively associated genetically with most of the other type traits.

The largest genetic correlations were between stature, strength and body depth. The udder traits were also highly genetically associated among themselves.

Selection programs designed to improve the udder characteristics would also tend to produce taller, stronger, deeper bodied cattle that were lower at the pins and more posty in the rear leg.

Heritability estimates from the subpopulation using single trait (ST) methodology and for the larger population using multiple trait (MT) methodology were similar. The trait exhibiting the largest heritability was stature, regardless of methodology. The traits with the greatest change in estimated heritability between methods were stature and foot angle as both were smaller from MT methods than those from ST. In general, MT methodology seems to offer no great change in estimating heritability of linear type traits.

The phenotypic correlations between milk yield and linear type traits from MT for the larger population were generally small and positive. Milk yield was significantly ($P<.05$) correlated with stature, body depth, angularity, rump angle, rear leg side view, fore udder attachment, rear udder height, rear udder width, udder support and udder depth. The strongest phenotypic correlations were between milk yield and angularity (.34) and milk yield and udder depth (-.15).

Dairy cattle which gave more milk tended to be deeper and wider in the udder and more angular in their appearance. Cows with a higher milk yield, on the average, would be taller, deeper bodied and looser in the fore udder, more highly attached in the rear udder and have more udder support.

The genetic correlations between milk yield and the 15 linear type traits were generally negative from MT for the larger population. The only traits positively correlated with milk yield were angularity, rump angle, rear leg side view and foot angle.

The variances of genetic correlation estimates were much greater than those of the corresponding phenotypic correlation estimates. In fact, the genetic correlations between milk and 12 of the

15 type traits were not signficantly different from zero. Only those between milk and rump angle, rump width and teat placement rear view were significantly different from zero ($P<.05$).

Traits which measure body angles are most likely to be positively related to milk yield, while milk production seems to have little genetic association or is negatively related with the remaining type traits.

Walter and Mao (1985), using simulated data, found the differences between single and multiple trait analysis with zero residual covariance and full multiple trait analysis to be influenced by the amount of selection and the magnitude of the genetic and residual covariances. Full multiple trait analysis removed the effects of selection regardless of either the level of selection or the magnitude of the correlations.

The results of the present study would suggest that the cattle scored for type do randomly represent the total milk recorded population. This conclusion is based on the fact that single and multiple trait results differ very little.

The rank and product moment correlations between best linear unbiased prediction (BLUP) results from ST and those from MT methods revealed little difference between the ranking of sires based on the subpopulation and from the larger population. The average rank correlations ranged from .955 for strength to .675 for angularity.

The standard deviations of sire solutions of the linear type scores from MT methodology were generally greater than those from ST, suggesting that MT analysis produces greater relative differences between sires.

For MT analysis, the entire data set available was not used.

Rather, five samples of 150 sires and their daughters' data sets were randomly sampled with replacement. Possibly, a stratified sampling strategy which divides the sires into classes by the number of daughters would aid in the prevention of selection of sires which have an enormous number of daughters with milk records and very sparse type information. This would prevent the saturation of the data set with milk records.

A sampling procedure which chooses the 150 sires with the highest percent of paired records may indicate the need of quality data structure. This would prove to be interesting work particularly in the evaluation of milk and type since heritabilities and genetic and phenotypic correlations between the traits can be low.

The general framework in the application of the triangular transformation to achieve zero residual covariances in MT has been described in the literature. However, the methods which were used to calculate residuals and the algorithms used to estimate the variance components have not been used in simulation to confirm their efficiency or convergence characteristics. Such comparisons among alternative algorithms should be most useful in practice and probably can be done most effectively by the simulation approach.

VI. APPENDICES

Table A.1 The Holstein Association Linear Classification Program

Table B.1 Description of the linear type data

Item	Number of Observations
Michigan	14,587
Wisconsin	50,288
Grade cows	2,899
Registered cows	61,976
Canadian sires	1,378
United States sires	63,497
Stage of lactation	
dry	3,286
springing	274
milking	61,515
Number of classifiers	25

Table B.2 Distribution of cows by parity

Parity	Counts
0	3,715
1	23,743
2	17,017
3	11,482
4	5,619
5	1,782
6	781
7	368
8	183
9	92
10	57
≥11	36

Table C.1 Lactation number distribution

Lactation Number	Count	
	Michigan	Wisconsin
1	193665	324771
2	142998	226589
3	100317	159553
4	66966	109048
5	42054	70794
6	24445	42825
7	13030	23479
8	6454	12148
9	3026	5969
10	1249	2708
≥11	835	1796

Table C.2 Distribution of month of last calf

Month	Count Michigan	 Wisconsin
January	45877	82283
February	40971	80852
March	49937	96519
April	45460	81399
May	46177	81058
June	48818	46031
July	54984	73971
August	55772	74620
September	52608	82672
October	51167	83264
November	51633	83444
December	50638	83444

Table D.1 Distribution of sires by number of daughters and herds: Data set 1

		Number of Herds																		
Class		11 - 15	16 - 20	21 - 25	26 - 30	31 - 40	41 - 50	51 - 60	61 - 70	71 - 80	81 - 90	91 - 100	101 - 200	201 - 300	301 - 400	401 - 500	501 - 650	651 - 800	801 - 9999	Total Sires
Code		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
NUMBER OF DAUGHTERS	3	3	2	8																
	4	0	1	4	8															
	5	0	0	2	1	14														
	6	1	0	0	0	3	2													
	7	0	0	0	0	0	1	11												
	8	0	0	0	0	0	0	0	4											
	9	0	0	0	0	0	0	0	2	4										
	10	0	0	0	0	0	0	0	0	0	3									
	11	0	0	0	0	1	0	0	0	0	0	4								
	12	0	0	0	0	0	0	0	0	0	0	0	16							
	13	0	0	0	0	0	0	0	0	0	0	0	1	11						
	14	0	0	0	0	0	0	0	0	0	0	0	0	0	6					
	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6				
	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3			
	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3		
	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25	
	Total Sires	4	3	14	9	18	3	11	6	4	3	4	17	11	6	6	3	3	25	150

Table D.2 Distribution of sires by number of daughters and herds: Data set 2

		Number of Herds																		
Class		11 - 15	16 - 20	21 - 25	26 - 30	31 - 40	41 - 50	51 - 60	61 - 70	71 - 80	81 - 90	91 - 100	101 - 200	201 - 300	301 - 400	401 - 500	501 - 650	651 - 800	801 - 9999	Total Sires
Code		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
NUMBER OF DAUGHTERS	3	2	2	11																
	4	1	2	0	9															
	5	2	0	2	0	15														
	6	0	0	0	0	3	10													
	7	0	0	0	0	0	2	6												
	8	0	0	0	0	0	0	1	3											
	9	0	0	0	0	0	0	0	0	4										
	10	0	0	0	0	0	0	0	0	0	1									
	*11	0	0	0	0	0	0	0	0	0	1	3								
	12	0	0	0	0	0	0	0	0	0	0	0	19							
	13	0	0	0	0	0	0	0	0	0	0	0	2	8						
	14	0	0	0	0	0	0	0	0	0	0	0	0	0	5					
	15	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4				
	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8			
	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6		
	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	
	Total Sires	5	4	13	9	18	12	7	3	4	2	3	21	8	6	4	8	6	17	150

Table D.3 Distribution of sires by number, of daughters and herds: Data set 3

Class		11 – 15	16 – 20	21 – 25	26 – 30	31 – 40	41 – 50	51 – 60	61 – 70	71 – 80	81 – 90	91 – 100	101 – 200	201 – 300	301 – 400	401 – 500	501 – 650	651 – 800	801 – 9999	Total Sires
		Number of Herds																		
Code		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
NUMBER OF DAUGHTERS	3	2	3	10																
	4	0	2	4	13															
	5	0	1	1	5	10														
	6	0	0	0	0	1	19													
	7	0	0	0	0	0	1	6												
	8	0	0	0	0	0	0	2	5											
	9	0	0	0	1	0	0	0	1	5										
	10	0	0	0	0	0	0	0	0	1	2									
	11	0	0	0	0	0	0	0	0	0	1	2								
	12	0	0	0	0	0	0	0	0	0	0	0	13							
	13	0	0	0	0	0	0	0	0	0	0	0	0	7						
	14	0	0	0	0	0	0	0	0	0	0	0	0	0	8					
	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2				
	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2			
	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3		
	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	
	Total Sires	2	6	15	19	11	20	8	6	6	3	2	13	7	8	2	2	3	17	150

Table B.4 Distribution of sires by number of daughters and herds: Data set 4

		Number of Herds																		
Class		11 – 15	16 – 20	21 – 25	26 – 30	31 – 40	41 – 50	51 – 60	61 – 70	71 – 80	81 – 90	91 – 100	101 – 200	201 – 300	301 – 400	401 – 500	501 – 650	651 – 800	801 – 9999	Total Sires
Code		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
NUMBER OF DAUGHTERS	3	7	4	10																
	4	1	1	2	8															
	5	2	0	3	3	9														
	6	0	1	1	1	3	10													
	7	0	0	0	0	1	1	3												
	8	0	0	0	0	0	0	1	4											
	9	0	0	0	0	0	0	0	1	4										
	10	0	0	0	0	0	0	0	0	2	2									
	11	0	0	0	0	1	0	0	0	0	0	1								
	12	0	0	0	0	0	0	0	0	0	0	0	21							
	13	0	0	0	0	0	0	0	0	0	0	0	0	11						
	14	0	0	0	0	0	0	0	0	0	0	0	0	0	3					
	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3				
	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6			
	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3		
	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	
	Total Sires	10	6	16	12	14	11	4	5	6	2	1	21	11	3	3	6	3	16	150

Table D.5 Distribution of sires by number of daughters and herds: Data set 5

Class		11 - 15	16 - 20	21 - 25	26 - 30	31 - 40	41 - 50	51 - 60	61 - 70	71 - 80	81 - 90	91 - 100	101 - 200	201 - 300	301 - 400	401 - 500	501 - 650	651 - 800	801 - 9999	Total Sires
Code		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
NUMBER OF DAUGHTERS	3	3	6	7																
	4	0	1	1	6															
	5	1	0	2	2	4														
	6	0	0	0	0	6	13													
	7	0	0	0	0	1	1	6												
	8	0	0	0	0	0	0	0	9											
	9	0	0	0	0	0	0	0	0	5										
	10	0	0	0	0	0	0	0	0	0	1									
	11	0	0	0	0	0	0	0	0	0	0	4								
	12	0	0	0	0	0	0	0	0	0	0	0	16							
	13	0	0	0	0	0	0	0	0	0	0	0	0	10						
	14	0	0	0	0	0	0	0	0	0	0	0	0	0	11					
	15	0	0	0	0	0	0	0	0	0	0	0	0	0	1	5				
	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5			
	17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3		
	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	
	Total	4	7	10	8	11	14	6	9	5	1	4	16	10	12	5	5	3	20	150

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