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CONSIDERATION OF MATES' SCORES IN THE RANKING OF GUERNSEY SIRES FOR GENETIC ABILITY IN BODY CONFORMATION

By

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ABSTRACT

CONSIDERATION OF MATES' SCORES IN THE RANKING OF GUERNSEY SIRES FOR GENETIC ABILITY IN BODY CONFORMATION

By

John Paul Walter

Body conformation scores of 192,640 Guernsey cows for 1956-1977 were matched to their dams' scores to investigate the effect of mates' scores on sire rankings based on progeny records. A chi-square goodness of fit test indicated that many Guernsey sires had mates that were non-representative samples of the population. Mates' effect on sire rankings, therefore, was examined for each of twelve type traits. Sire rankings from two models were compared using two data sets, one containing all progeny of the sires and the other containing only each sire's first twenty daughters. Both models include a random sire factor and fixed age, month, and herd-year factors. One model contained an additional covariate of dam's score. Eighty sires having a total of 33,634 daughter first scores were used in the analysis. Results indicate that the addition of mate's score as a covariate did not appreciably change sire rankings when all progeny were included. When only the initial daughters were used, rankings were changed somewhat more, but with no improvement in accuracy.

DEDICATION

In gratitude,

to my Dad and Mom

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1. INTRODUCTION

Sire evaluation has been an essential tool for dairy cattle selection since 1936, when the United States Department of Agriculture (USDA) released its first sire summary for milk production. This first ranking was based mainly on a survey reporting the percentage of daughters who exceeded their dams' production, and the percent by which a sire's daughters' average exceeded their dams' average, making use of only primitive corrections for herd differences. Since then, gradual improvements in statistical methods have enabled, and refutations of certain distribution assumptions have necessitated, changes in the methods by which sires are evaluated. Also, sires have been evaluated for other traits, such as body conformation and dollar returns from milk and its fat percentage.

The advent of artificial insemination (AI) enabled breeders to use much more intense selection than previously possible. However, to make optimum use of AI, genetically superior bulls must be identified at an early age, thereby decreasing the generation interval and increasing the rate of progress. For sex-limited traits, such as milk yield, this is accomplished by using available information on female relatives, in particular daughters. The purpose of statistical procedures is to eliminate variation not caused by differences among sires, and thus to rank the bulls according to their breeding values.

The evolution of sire evaluation procedure is a history of recognizing, and adjusting for, simplifying assumptions such as no herd differences, no selection among sires, no genetic progress, and others. One recent consideration which may not hold true is that mates are a random sample from a static population. Therefore, some researchers have looked into the inclusion of daughter's maternal grandsire as a factor contributing to phenotypic expression of a characteristic. Incorporation of daughters' maternal relatives in sire evaluation should have the advantage of reducing the potential source of bias due to a sire being bred to mates not truly representative of the population. This bias is more likely to occur in the evaluation of young sires, because they have few progeny and the inclusion of a disproportion of superior or inferior mates can result in an unreasonably high or low progeny test. Additionally, inclusion of relatives on the daughter's maternal side could somewhat increase the information available on phenotypically poor daughters, who might have disproportionately few records.

Bias caused by non-representative selection of mates may be of greater concern when evaluating a bull's genetic ability for body conformation than for milk production. Because sale of milk is the primary source of revenue for most herds, bulls might be chosen for their conformational ability only when it is necessary to correct a type trait within a herd. Mates for these bulls would generally be phenotypically poorer than if they were a random sample of cows.

Body conformation records of Guernsey cows were used to examine three objectives in this study:

1. to determine the extent of non-random mating for body conformation within the Guernsey breed;
2. to determine the effect of mates' conformation scores on sire evaluations and rankings; and
3. to determine whether the inclusion of mate's score can improve the ranking of sires based on a small number of daughters.

2. REVIEW OF LITERATURE

The body conformation of dairy cows long has been of interest to dairymen as well as dairy breeders. In addition to the economic value of type classification in the promotion and sale of cattle, its relationship to milk and fat production, herdlife, health, and total merit, to name a few, make it imperative that cows be logically and consistently scored and that sires be accurately evaluated and ranked for genetic merit of type traits.

2.1 Type Classification of Dairy Cows

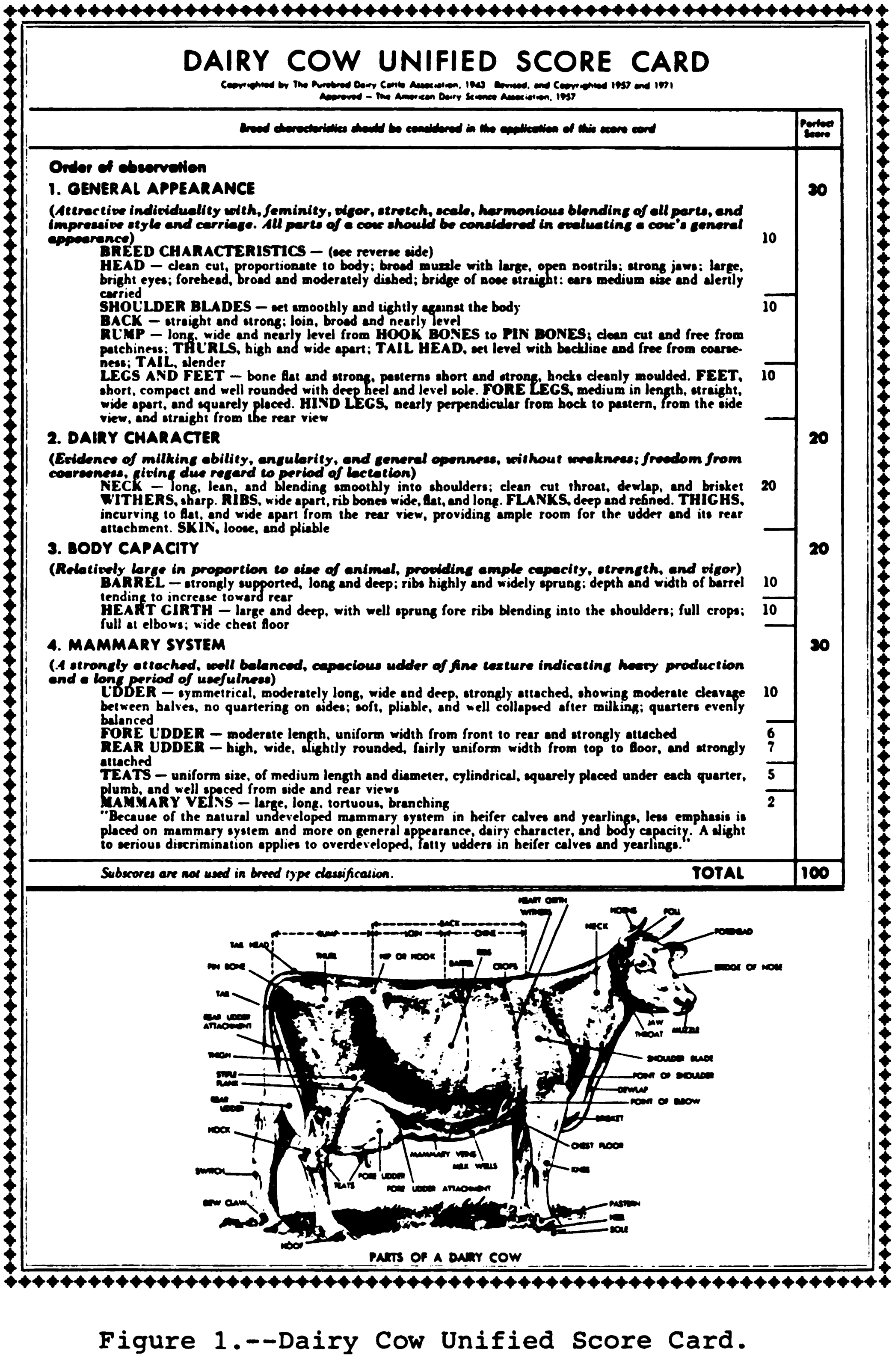
Over the years, various methods have been proposed to classify cows in the most objective and descriptive way possible. Many methods share several common features, necessary for widespread acceptance:

1. Simplicity. To be readily understood, a classification system must include only a small number of the almost limitless body characteristics of a dairy cow. Each trait should have some economic value to a dairyman and be at least moderately heritable, so that selection can occur.
2. Objectivity. If cows are to be measured consistently, the same set of objective guidelines must be applied, which enable a trait to be accurately evaluated. This also implies that traits be sufficiently variable to ensure that differences are distinguishable.

3. Logic. If a scoring method is to be accepted, it must be easily understood. Most currently employed methods have an ordinal system of grading, with a limited range of classification scores for the inferior through the most favorable animals.

Whereas many different systems of classification exist today, two of the most common will be described as examples typical of all. One of the first widespread methods used to classify cattle was through use of the Purebred Dairy Cattle Association's (PDCA) Dairy Cow Score Card (Figure 1). Being so widespread, the PDCA scorecard could be applied across all breeds, and today is the basis for many classification systems, such as those for the Guernsey and Jersey breeds. As outlined by the scorecard, cows are evaluated for traits within four major categories (general appearance, dairy character, body capacity, and mammary system), each having a maximum number of points awarded. The sum of the points for all traits determines an animal's final score, which in an ideal cow is 100.

The Holstein-Friesian Association of America (HFAA) makes use of a descriptive method of type classification. The HFAA does not define ideals of conformation traits in general terms, as in the PDCA Score Card. Rather, traits are judged categorically, from 1 through 5 for most traits. Lower scores indicate more favorable conformation than higher scores, except for miscellaneous



DAIRY COW UNIFIED SCORE CARD

Copyrighted by The Purebred Dairy Cattle Association, 1943 Revised, and Copyrighted 1957 and 1971
Approved – The American Dairy Science Association, 1957

Breed characteristics should be considered in the application of this score card		**Perfect Score**
Order of observation		
1. GENERAL APPEARANCE		**30**
(Attractive individuality with, feminity, vigor, stretch, scale, harmonious blending of all parts, and impressive style and carriage. All parts of a cow should be considered in evaluating a cow's general appearance) **BREED CHARACTERISTICS** — (see reverse side) **HEAD** — clean cut, proportionate to body; broad muzzle with large, open nostrils; strong jaws; large, bright eyes; forehead, broad and moderately dished; bridge of nose straight; ears medium size and alertly carried	10	
SHOULDER BLADES — set smoothly and tightly against the body **BACK** — straight and strong; loin, broad and nearly level **RUMP** — long, wide and nearly level from **HOOK BONES** to **PIN BONES**; clean cut and free from patchiness; **THURLS**, high and wide apart; **TAIL HEAD**, set level with backline and free from coarseness; **TAIL**, slender	10	
LEGS AND FEET — bone flat and strong, pasterns short and strong, hocks cleanly moulded. **FEET**, short, compact and well rounded with deep heel and level sole. **FORE LEGS**, medium in length, straight, wide apart, and squarely placed. **HIND LEGS**, nearly perpendicular from hock to pastern, from the side view, and straight from the rear view	10	
2. DAIRY CHARACTER		**20**
(Evidence of milking ability, angularity, and general openness, without weakness; freedom from coarseness, giving due regard to period of lactation) **NECK** — long, lean, and blending smoothly into shoulders; clean cut throat, dewlap, and brisket **WITHERS**, sharp. **RIBS**, wide apart, rib bones wide, flat, and long. **FLANKS**, deep and refined. **THIGHS**, incurving to flat, and wide apart from the rear view, providing ample room for the udder and its rear attachment. **SKIN**, loose, and pliable	20	
3. BODY CAPACITY		**20**
(Relatively large in proportion to size of animal, providing ample capacity, strength, and vigor) **BARREL** — strongly supported, long and deep; ribs highly and widely sprung; depth and width of barrel tending to increase toward rear	10	
HEART GIRTH — large and deep, with well sprung fore ribs blending into the shoulders; full crops; full at elbows; wide chest floor	10	
4. MAMMARY SYSTEM		**30**
(A strongly attached, well balanced, capacious udder of fine texture indicating heavy production and a long period of usefulness) **UDDER** — symmetrical, moderately long, wide and deep, strongly attached, showing moderate cleavage between halves, no quartering on sides; soft, pliable, and well collapsed after milking; quarters evenly balanced	10	
FORE UDDER — moderate length, uniform width from front to rear and strongly attached	6	
REAR UDDER — high, wide, slightly rounded, fairly uniform width from top to floor, and strongly attached	7	
TEATS — uniform size, of medium length and diameter, cylindrical, squarely placed under each quarter, plumb, and well spaced from side and rear views	5	
MAMMARY VEINS — large, long, tortuous, branching "Because of the natural undeveloped mammary system in heifer calves and yearlings, less emphasis is placed on mammary system and more on general appearance, dairy character, and body capacity. A slight to serious discrimination applies to overdeveloped, fatty udders in heifer calves and yearlings."	2	
Subscores are not used in breed type classification. **TOTAL**		**100**

PARTS OF A DAIRY COW

Figure 1.--Dairy Cow Unified Score Card.

traits (Figure 2). The advantage of this method is that for all traits except final score, no ideal need be used by each judge against which to compare each cow. Classifiers merely designate the category for each trait which most aptly describes a cow.

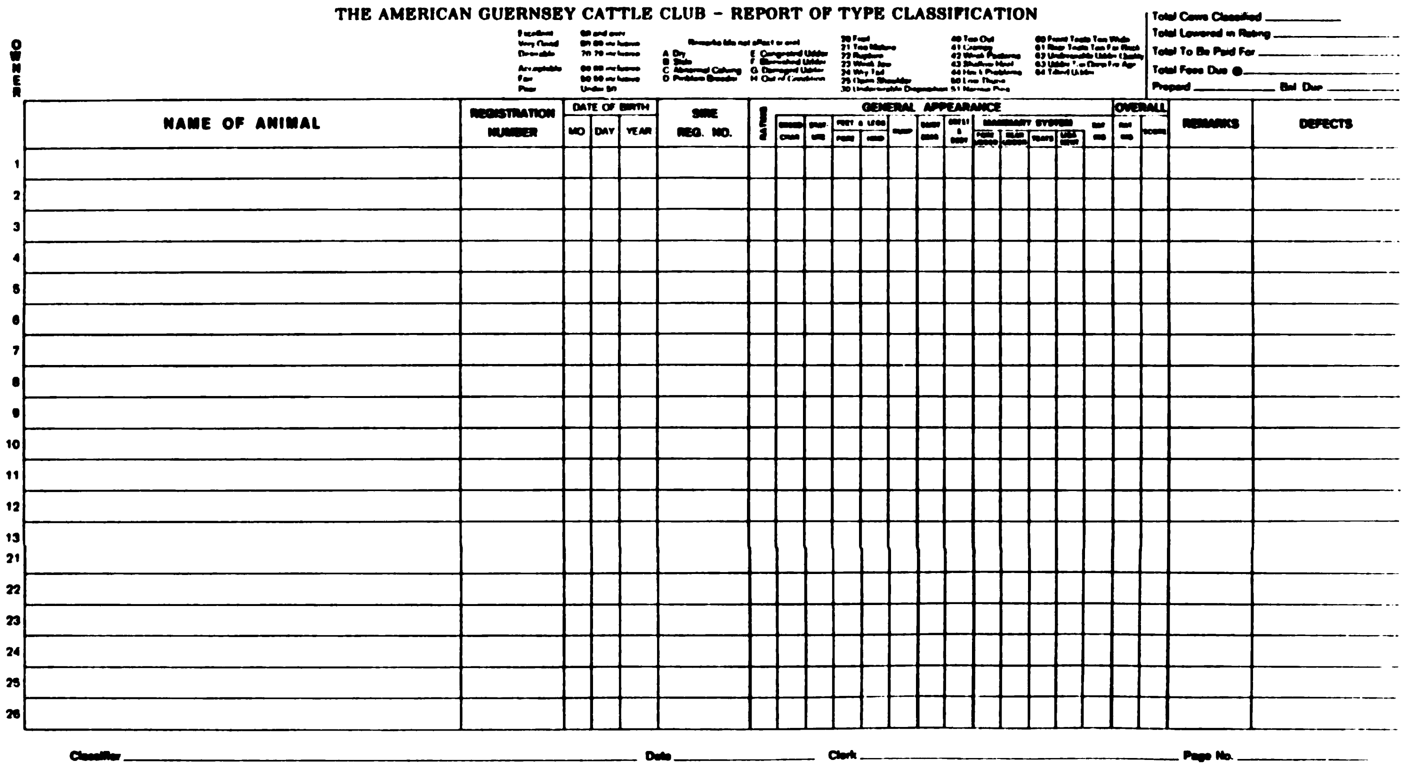
Currently, the American Guernsey Cattle Club (AGCC) employs in its classification system the scorecard found in Figure 3. The AGCC Type Committee rates in six different categories (excellent, very good, desirable, acceptable, fair, and poor) the thirteen different characteristics of type shown. Final score and rating are arrived at by balancing the strengths and weaknesses of each trait, those that indicate a long useful life against those that impair an animal's usefulness. Descriptions of desirable properties of the thirteen traits can be found in Sowerby (1978).

2.2 Sources of Variation in Body Conformation Scores: Environmental

When sires are compared, it is essential to eliminate as nearly as possible all sources of variation which can affect the evaluation. At the same time, the inclusion in models of factors which have no effect on a characteristic is of no use to an investigator, wastes computing time and core memory, and may actually decrease the accuracy of comparisons. Of the many factors which have

Trait	Code	Abbreviated Description
Stature	1	Upstanding
	2	Intermediate
	3	Low set
Head	1	Clean-cut, well proportioned
	2	Strong, lacks style
	3	Short
	4	Plain or coarse
	5	Weak
Front End	1	Smooth shoulder, wide chest
	2	Medium strength and width
	3	Coarse shoulder and neck
	4	Narrow and weak
Back	1	Straight, strong, wide loin
	2	Medium strength and width
	3	Low front end
	4	Weak loin and/or back
Rump	1	Long and wide, nearly level
	2	Medium width, length, levelness
	3	Pins higher than hips
	4	Narrow, especially at pins
	5	Sloping
Hind Legs	1	Strong, clean, squarely placed
	2	Acceptable
	3	Sickled and/or close at hock
	4	Bone too light
	5	Too straight
Feet	1	Strong, well formed
	2	Acceptable
	3	Spread toes
	4	Shallow heel
Fore Udder	1	Moderate length, firmly attached
	2	Moderate length, slightly bulgy
	3	Short
	4	Bulgy or loose
	5	Broken
Rear Udder	1	Firmly attached, high, wide
	2	Intermediate in height and width
	3	Low
	4	Narrow and pinched
	5	Loose or broken
Udder Support	1	Strong suspensory, clean halving
	2	Lack of defined halving
	3	Floor too low
	4	Tilted
	5	Broken, suspensory ligament
Teats	1	Plumb, desirable length, size, and placement
	2	Acceptable
	3	Rear teats too far back
	4	Wide front teats
	5	Undesirable shape
Miscellaneous	1	Winged shoulders
	2	Front legs toe out
	3	Weak pasterns
	4	Crampy
	5	Too small for age

Figure 2.--Holstein Descriptive Type Traits.



THE AMERICAN GUERNSEY CATTLE CLUB - REPORT OF TYPE CLASSIFICATION

Total Cows Classified
Total Lowered in Rating
Total To Be Paid For
Total Fees Due @
Prepaid — Bal Due

OWNER

	NAME OF ANIMAL	REGISTRATION NUMBER	DATE OF BIRTH MO	DATE OF BIRTH DAY	DATE OF BIRTH YEAR	SIRE REG. NO.	RATING	GENERAL APPEARANCE	OVERALL	REMARKS	DEFECTS
1											
2											
3											
4											
5											
6											
7											
8											
9											
10											
11											
12											
13 21											
22											
23											
24											
25											
26											

Classifier — Date — Clerk — Page No.

Figure 3.--Portion of American Guernsey Cattle Club Scorecard.

been studied, some of the more significant are reported below.

2.2.1 Herd

In an examination of nearly 23,000 appraisals of all breeds, Van Vleck (1964) performed an analysis of variance components which demonstrated that herd effects comprise less than 10% of the total variance for most traits. Legates (1971) used single evaluations of over 130,000 Holstein cows to obtain herd components of variance of between 13% and 25% for final score and the four major categories of traits (general appearance, dairy character, body capacity, and mammary system). For descriptive traits estimates of proportion of variance caused by differences among herds were 6% to 14%. Carter et al. (1965), analyzing the sources of variation of type scores within Canadian Holsteins, gave a comparable figure for proportion of total variance caused by herds (8%). Norman and Van Vleck (1972b) also reported that variation among herds accounted for less than 10% of total variance in most body conformation traits. They used more than 16,000 appraisals of Holsteins obtained through the New York type appraisal program. However, for milk production, as well as some health-related traits (such as incidence of edema) the herd component approached 25%. Hanson et al. (1969) obtained 4,656 appraisals of 2,518

Holstein cows in 41 Wisconsin herds. They found that for final score and each descriptive trait, herd accounted for not more than 10% of the variance. In analyses of Brown Swiss classification data, Moreno et al. (1979) found that herd-year variation accounted for 8% to 17% of total variance. In the Jersey breed the same factors accounted for 14% to 21% of the variation, as reported by Norman and Cassell (1978). In a recent study of Holsteins, Vinson et al. (1976) determined that, for 78,151 cows in 2,117 herds, herd component of variance was less than 14% for all body conformation traits.

2.2.2 Age at Classification

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 categories. Rennie et al. (1971) accounted for age in their analysis of environmental and genetic parameters for 51,044 Holstein first calf heifers. He found age at classification to be a significant factor for most traits. Norman and Van Vleck (1972a) uncovered large age differences in about a third of the classification and management traits they considered, especially incidence of mastitis, body weight, and depth of udder. A significant effect of age of classification score was found in New Jersey Holsteins by Wilcox et al. (1958), and in North

Carolina institutional herds of Holsteins by White et al. (1967). Based on these reports, Cassell et al (1973) computed age correction factors for conformation similar to those already in existence for milk production. These factors were derived from first available classification scores of 336,253 registered Holstein cows, classified between 1967 and 1971. Within the Jersey breed, Norman (1978) found age effects significant for all traits, especially on body capacity and dairy character. Mao et al. (1977) also found significant age differences in the Guernsey breed, and calculated age-season adjustment factors to compensate for these differences.

2.2.3 Stage of Lactation

The effect of stage of lactation is considered in analyses of classification scores in several studies. Hansen et al. (1969) found stage of lactation highly significant in accounting for some of the variance of Holstein scores. Classification scores appeared to be somewhat higher if a cow were scored near the beginning or end of her lactation than during the middle. An interaction of stage of lactation with age in the same study was insignificant. Norman and Van Vleck (1972a) reported that differences caused by stage of lactation in Holsteins were smaller than those caused by age, and they uncovered no age by stage interaction. Udder quality appeared most affected by stage of lactation in their study. Analyses by Wilcox et al. (1958) and White et al. (1967) reported similar significant effects of stage of lactation. Purohit et al. (1973) found stage of lactation to be significant for all traits in a population of 12,030 Canadian Holstein daughters of 200 AI sires. When evaluating the sires, records were adjusted for effects of stage. Norman and Cassell (1978) found that effects of stage and interaction of age with stage of lactation were small in the Jersey breed.

2.2.4 Season of Classification

Month of classification effect was examined by Carter et al. (1965) and determined to have a small effect on final type score of Canadian Holsteins. For United States Holstein cows, White et al. (1967) reported that date of appraisal had a significant effect on type classification scores for many traits. Wilcox et al. (1958) published evidence of seasonal variation among type ratings of Holstein cows, although only two seasons, spring and fall, were included in their analysis. In the Guernsey breed, Mao et al. (1977) noted definite rises in classification scores in several months, notably August and February. It was speculated that the August increases were the result of preparation of cows for showing activities; no explanation was offered for the rise in February scores.

2.2.5 Year of Classification

Evidence of trend in classification scores over time has been moderate in most previous studies. Carter et al. (1965) found that, for Canadian Holsteins, rounds (or groups of years) accounted for less than 1% of total variation between 1961 and 1963. In a later investigation of Canadian Holsteins by Schaeffer et al. (1978), annual changes in genetic ability varied from .13% for final score to 1.28% for general appearance. Their research used records collected from 1971 through 1975. In United States populations, Norman and Van Vleck (1972b) reported that up to 3% of variation in type scores could be explained by year differences, though for most traits this figure was below 1%. Studying the Guernsey population, Mao et al. (1977) discovered a small but definite upward trend in final score between 1959 and 1971. While working with Jerseys, Norman and Cassell (1978) found 1% to 4% of variation in type traits explained by differences among years.

2.2.6 Classifier

Differences among classifiers are an unavoidable source of variation in analyzing conformation scores. As early as 1942, Johnson and Lush (1942) demonstrated a repeatability of type scores of only .34, which varied little with interval between classifications. Though this is small, undoubtedly partly because of changes in the animal, the subjectivity of the judges cannot be discounted. Touchberry and Tabler (1951) investigated the changes in type ratings of Holstein and Guernsey cows when rated by the same judge at two different times. They found that differences among classifiers contributed significantly to total variance only for general appearance and body capacity. The effect of time on variability of conformation score, though statistically significant in several traits, was small. Investigating appraiser effect on classification scores of the Iowa State Holstein herd, McGilliard and Lush (1956) stated that, except when appraising heifers, the effect of classifier was negligible. Wilcox et al. (1959), using records of 233 cows scored by 13 judges, found rather large variation between judges. An analysis of variance was not done, however, because all effects were treated as fixed. Vinson et al. (1976) reported that the proportion of variation caused by differences among classifiers was small (from 0.7% to 5%) for the first-available Holstein appraisals. However, herd by classifier interaction appeared to account for twice the variation of classifier alone in most traits, perhaps indicating some variation in classifiers' standards from herd to herd.

2.3 Sources of Variation in Body Conformation Scores: Genetic

Variation among phenotypic characteristics is of use to dairy breeders only if sufficient genetic variation exists. Because of the widespread use of AI, the sire is the main vehicle by which most genetic improvement is passed from generation to generation. The fundamental relationship in the study of dairy populations is that of parent-offspring, between a sire and his daughters. Therefore, in analysis of variation among half-sibs, measures of proportion of sire variance and estimates of heritability are associated and will be discussed together.

2.3.1 Sire

In studying the role of sire in contributing to total variation, genetic theory holds that, in a half-sib population, differences among sires account for one-fourth of the additive genetic variance, along with small fractions of variances caused by various inter-locus interactions of additive effects. Because heritability (h^2) can be expressed as the ratio of additive to total variance ($\frac{\sigma_A^2}{\sigma_T^2}$), the proportion of variance caused by sires in half-sib populations usually is assumed to be one-fourth of the heritability. Heritabilities estimated by many researchers for various breeds and traits are shown in Table 1. The research will be reviewed by breeds.

TABLE 1.--Summary of Heritabilities for Conformation Traits in Five Dairy Breeds.

	Ayrshire		Jersey			Brown Swiss		Guernsey		Holstein					
Trait	Freeman and Dunbar (1955)	Butcher et al. (1963)	Harvey and Lush (1952)	Tabler and Touchberry (1956)	Norman et al. (1978)	Johnson and Fourt (1960)	Moreno et al. (1980)	Berousek et al. (1959)	Mao et al. (1977)	Legates (1971)	Cassell et al. (1973)	Hansen et al. (1969)	Wilcox et al. (1962)	Mitchell et al. (1961)	Schaeffer et al. (1977)
Final Score	.31	.18	.14	.28	.23	.35	.43	.28	.27	.58	.31	.26	.24	.20	.31
Head and Neck	.30	.27													
Shoulders and Chest	.15	.16													
Middle and Loin	.31	.16													
Rump and Thighs	.32	.22													
Udder Shape and Size	.08	.06													
Udder Attachments	.06	.05													
Teats, Veins, Quality	.27	.07													
General Quality	.13	.13													
Breed Character	.32	.22			.12				.22						
General Appearance					.19	.33	.39	.24	.24	.54	.29	.21	.29	.19	.26
Dairy Character					.20	.30	.26	.16	.16	.25	.19	.20	.50	.09	.28
Body Capacity					.14	.23	.36	.28	.25	.46	.27	.24	.66	.12	.25
Rump					.15	.36	.41	.28	.31	.20	.25				.34
Feet and Legs	.18	.16			.26	.19	.24								.11
Mammary System					.22	.23	.29	.24	.23	.37	.22	.27	.22	.18	.21
Fore Udder					.21	.28	.30	.22	.21	.19	.21				.17
Rear Udder					.19	.35	.29	.26	.19	.19	.21				.19
Teats								.30	.24	.23	.31				
Shoulders								.20	.24						

Ayrshire

Freeman and Dunbar (1955) used 1,180 daughter-dam pairs to estimate heritabilities of Ayrshire body conformation traits. They obtained an h^2 for final score of .31 ± .15, while the heritabilities of other traits varied between .06 for udder attachments to .32 for breed character and rump and thighs. Several years later, Butcher et al. (1963) used a larger sample Ayrshire daughter-dam pairs (8,165), and obtained an h^2 of .18 ± .05 for final score. The range of heritabilities was from .05 (udder attachments) to .27 (head and neck). In that study, the authors adjusted each record for age, but ignored differences among years and classifiers. Because of the small numbers in the Ayrshire breed and the limited use of AI in the time periods of these studies, an estimate of the sire component of variance as $\frac{h^2}{4}$ may not be accurate; there may be too many full-sib relationships among daughters of natural service sires. A confounding effect between natural service sire and herd also may occur.

Jersey

In an early study, Harvey and Lush (1952) reported an h^2 of .14 for final score. Tabler and Touchberry (1956) used 2,810 daughter-dam pairs of Jersey cows to obtain twice the former estimate, or .28. Recently, Norman et al. (1978) calculated heritabilities from 4,539 pairs, appraised between 1968 and 1976. These records were adjusted by age and stage of lactation, and provided a heritability figure of .23 ± .03 for final score, with other h^2 ranging from .12 to .26. The latter heritabilities corresponded to a proportion of sire variance of 3% to 6.5%.

Brown Swiss

In two major studies, estimates of genetic parameters for body conformation in the Brown Swiss breed were reported. The first, by Johnson and Fourt (1960), included type records from 3,161 daughter-dam pairs, appraised between 1950 and 1953. Their estimates among traits varied from .19 for feet and legs to .36 for rump, with an h^2 of .35 for final score. Standard errors of these figures were .05 to .07. The second study was completed by Moreno et al. (1979), using 12,838 records in an analysis of variance. Heritabilities of .24 (feet and legs) to .43 (final classification) were reported. These investigations indicate that generally between 5% and 10% of the variation of classification data is attributable to sire effect.

Guernsey

A report by Berousek et al. (1959), based on daughter-dam regression within sire and herd of 1,981 pairs of Guernsey cows attributes to final score a heritability of .28. Dairy character was found to be the least heritable trait, while teat placement had the highest h^2 of .30. Mao et al. (1977) reported heritabilities calculated from results of an analysis of variance on more than 200,000 Guernsey appraisals. They found a similar heritability of final score, .27, and heritabilities for each trait similar to those reported by Berousek et al. (1959). These h^2 evince proportions of variance caused by variability among sires of 4% to 8%.

Holstein

More reports of heritabilities of conformation in Holsteins have been published than for any other dairy breed. Mitchell et al. (1961) used 14,727 daughter-dam pairs from Wisconsin herds to estimate heritabilities. Dairy character had the lowest h^2, .09, whereas final score had the highest, .20. Hanson et al. (1969) also used animals from Wisconsin herds to estimate heritabilities. From 4,656 records on 2,518 cows, they obtained a heritability of final score of .26, with extremes of .20 for dairy character and .27 for mammary system. Least squares procedures were used to obtain variance components in this investigation. Sire differences accounted for up to 7% of the variance.

Wilcox et al. (1962) analyzed the conformation records of 233 daughters of 51 bulls in one herd, as appraised over a period of 13 years. A heritability of .24 was computed for final score, comparable to previous estimates. Heritabilities of .50 and .66 were reported for dairy character and body capacity, respectively, figures which were well above any estimates reported previously for any breed. These high estimates may have been caused by sampling errors resulting from the small amount of data considered. Legates (1971) calculated variance components on single records of 44,030 three year old Holsteins. He reported a wide range of h^2, from .58 for final score to .19 for fore udder and rear udder.

Cassell et al. (1973) reported heritabilities between .19 (for dairy character) and .31 (for final score). These were computed by daughter-dam regression of 30,714 pairs of Holstein cows. From Canadian Holstein type data, Schaeffer et al. (1978) analyzed 182,608 classification records of daughters of 10,360 sires. The highest heritability calculated from variance components was .34 for rump; the lowest was .11 for feet and legs. An h^2 of .31 was published for final score.

Using records from all breeds, Van Vleck (1964) found that the fraction of variance caused by variation among sires was less than 10% for most of 34 traits. This agrees with results previously cited, in which very few heritabilities exceed .40.

2.3.2 Group of Sire

By nesting effects, sires within genetic group in a model, additional variation can be eliminated. However, to date no studies have been reported in which this reduction has been quantified using conformation records. Using milk production data, Rothschild et al. (1976) found that consideration of genetic groups of sires can remove a substantial portion of bias favoring older sires as well as natural service sires. Using simulated populations, Tong et al. (1980) have shown that ignoring genetic groups of sires can increase the variance of a sire's predicted breeding value by 9% to 12%.

2.3.3 Relationships Among Sires

When sires are evaluated using mixed model techniques developed by Henderson (1974), provisions exist for the inclusion of variance-covariance (VCV) matrices for random effects. If sire is the only random factor in the model, represented by a sample of $\underline{n}$ sires, the dimension of its VCV matrix is $\underline{n} \times \underline{n}$. The VCV matrix can be expressed as $\underline{k}\ \underset{\sim}{A}\ \sigma^2$, where $\underline{k}$ is a scalar and $\underset{\sim}{A}$ is a matrix of genetic relationships among sires. Residual variance is deonted by σ^2.

To incorporate the VCV matrix for sire, the relationship matrix A must be inverted, which can be unwieldly and expensive. Henderson (1975a, 1975b) introduced a

method of directly computing the desired inverse of the relationship matrix. He also pointed out some of the potential advantages of incorporating these relationships:

1. improvement in the accuracy of prediction, particularly for sires with few progeny;
2. need for fewer groups to account for genetic differences among sires; and
3. earlier evaluation of sires due to the use of additional information not previously included in the evaluation (Henderson, 1975c).

In a comparison of evaluations of bulls grouped by year of entry-into-service and bulls related by a VCV matrix, Kennedy and Moxley (1975) found correlations of .88 to .93 for evaluating Predicted Differences (PD's) of milk, fat, and protein production. They also showed the variance of prediction error to be 18% larger when considering genetic groups than when considering sires' relationships, all other factors remaining the same.

2.3.4 Cow

No investigations have been found examining the effect of cows' multiple classification records on sire evaluation for type. There are several, however, which use milk production to examine that effect. The flexibility of mixed model equations (MME's) allows as many lactations to be included as are desirable, but there may be some question whether inclusion of several or all of a cow's records in her sire's evaluation is necessary or eve

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even beneficial to accurate results. Ufford et al. (1979), using records from the Ayrshire, Jersey, Guernsey, and Brown Swiss breeds, found the variance of estimated effects of sire reduced 7% to 14% by including all lactations over using only first records, with AI sires. The difference was much greater (20%-24%) for sires used in natural service. These reductions enable a decrease of 40% in the number of daughters needed to prove a sire at a given accuracy if all lactations are used rather than only the first. They indicated that, because of the improved accuracy of evaluation, potential genetic progress in the selection of bulls could be 10%-15% greater when all lactations are included.

However, caution is also advised when using more than the first lactation. Computational difficulties may offset the theoretical advantage of including all records. Further, Wickham and Henderson (1977), comparing sires' evaluations based on their daughters' second lactation and the same daughters' first lactations, found a rank correlation of only .77; this could indicate the presence of some selection bias from including second lactation daughters.

2.4 Relationship of Body Conformation to Production

It has long been of interest to breeders whether selection of dairy cattle for production traits influences the body conformation of future progeny. Many studies have been conducted to determine the genetic relationships of conformation traits to milk production in the Jersey, Guernsey, Brown Swiss, and Holstein breeds. In the Ayrshire breed, butterfat production's relationship to conformation has been emphasized in studies. These investigations will be reviewed by breeds. Table 2 summarizes the work discussed in the following sections.

2.4.1 Ayrshire

Studies of the butterfat production-type score relationship within the Ayrshire breed have been inconsistent. Tyler and Hyatt (1948) found a genetic correlation between butterfat production and final type score of .16, using intrasire regression of daughter on dam for 5,177 pairs. Using the same method, Freeman and Dunbar (1955) obtained a correlation of -.52. They made use of only 729 daughter-dam pairs in 165 herds, and although a standard error was not reported, it may have been larger than those found in comparable studies, due to the fewer pairs studied. This would make their high negative estimate somewhat more unreliable than other estimates within the breed. Butcher et al. (1963) reported a correlation

TABLE 2.--Genetic Correlation of Official Final Score to Production in Five Dairy Breeds.[a]

Breed	Researchers	Year	Correlation
AYRSHIRE	Tyler and Hyatt	1948	.16
	Freeman and Bunbar	1955	-.52
	Butcher et al.	1963	.02
JERSEY	Harvey and Lush	1952	.18
	Tabler and Touchberry	1956	.07
	Liang and Fosgate	1967	.25 (phenotypic)
BROWN SWISS	Johnson and Fourt	1960	.24
	Van Vleck et al.	1980	.27
HOLSTEIN	Touchberry	1951	.00
	Carter et al.	1965	.12
	Mitchell et al.	1961	-.04 -.28
	Wilcox et al.	1962	.08
	Everett et al.	1976	-.32
	Grantham et al.	1974	-.23
GUERNSEY	Mao	1977	.52

[a] For all breeds except Ayrshire, final score is correlated to milk production. For the Ayrshire, correlations are to fat production.

of .02 from 8,165 daughter-dam pairs in 2,924 sire-herd groups. Other type traits varied in their relationship to butterfat production, having correlations ranging from -.15 to .16.

2.4.2 Jersey

Harvey and Lush (1952), using daughter-dam regression techniques, obtained a genetic correlation between final type score and milk yield of .18 in Jersey cows. Tabler and Touchberry (1956), with 2,810 pairs of Jersey daughters and dams, estimated the same correlation at .07. More recently, Liang and Fosgate (1967) used a multiple regression technique on a herd of 382 Jerseys to obtain a phenotypic correlation of .25. They computed other phenotypic correlations to milk production, which ranged from .12 for fore udder to .32 for dairy character.

2.4.3 Brown Swiss

Using 3,161 daughter-dam paired records supplied by the Brown Swiss Cattle Breeders Association, Johnson and Fourt (1960) obtained a milk-final score genetic correlation of .24. The lowest genetic correlation to milk production they reported was .21 for rump; correlations ranged as high as .48 (for rear udder). Van Vleck et al. (1980) analyzed nearly six thousand Brown Swiss records with a two-way, cross-classified model (herd-year and sire factors). They reported a genetic correlation of .27 for final score and milk production. The lowest genetic correlation reported was .03 for milk production with feet and legs, while the highest was .29 for milk production with rump.

2.4.4 Guernsey

In work with Guernsey cattle, Mao et al. (1977) analyzed 54,638 type-production records. They found the genetic correlation between final score and milk production to be quite high, .46 to .63, depending on the year of classification. Similar high correlations with milk production range from .83 for dairy character to .25 for mammary system. All the cows were scored on only one classifier, and it was speculated that his philosophy of a desired positive relationship between conformation and production may have subjectively affected type evaluations in favor of higher producing cows and thus led to high correlation values.

2.4.5 Holstein

Records of 187 daughter-dam pairs in the Iowa State University Holstein herd provided data for a study by Touchberry (1951). He reported zero correlation between final score and milk production, although he warned that with the relatively small number of records, sampling errors could mask any correlations. Using 8,287 Canadian Holstein type and production records, Carter et al. (1965)

found genetic correlations with milk production of from -.06 for body capacity to .49 for dairy character. Final score and milk production were correlated at .12. Mitchell et al. (1961) divided cows into three levels of milk production, then calculated correlations of various type traits to production of cows at each level. By far the highest correlations were for dairy character with production, at .61 to .82. Dairy character was correlated with fat production at .34 to .84. They stated that progress in level of milk production would be one-third to one-half as fast if selecting for dairy character alone than if selecting for milk production, based on their analysis of the records of 14,727 Holstein cows.

With 671 lactation records and 2,272 type classification records of 233 Holsteins from one herd, Wilcox et al. (1962) found a correlation of .08 between final score and milk production. This was the lowest correlation they found of any type trait with milk production. The highest was .16, for mammary system. More recently, Everett et al. (1976) evaluated 2,390 sires used in artificial insemination in the northeastern United States using the milk and fat production records of their 558,654 daughters. Solutions obtained were correlated to Predicted Difference Type (PDT) of the same sires, obtained from the Holstein-Friesian Association of America. Genetic correlations were measured by a formula developed by Calo et al. (1973). Predicted Difference Type was found to be negatively correlated to sire solutions for both milk and fat production. Schaeffer and Burnside (1974) examined PDT and Predicted Difference Milk (PDM) computed from Canadian Holstein data and found a much smaller negative correlation between the two of -.05.

In an often cited study, Grantham et al. (1974) obtained genetic correlations between PDM, as computed by USDA and included in the USDA sire summaries, and final score as calculated by daughter averages. More than 750,000 official Holstein cow appraisals were used to obtain the daughter average for body conformation traits. Genetic correlation of PDM with final score was -.23 for sires having at least 20 daughters in 10 herds. Correlations of PDM with scorecard traits ranged from -.22 to -.24, except for .41 for dairy character.

2.5 Effects of Body Conformation on Herd Management Traits

Though undeniably a major consideration, the relationship between conformation and production is not the only important correlation studied when evaluating the effect of breeding for body conformation. Its relationship to traits of herd management, such as herdlife or total merit, has also been investigated.

In a study of six institutional herds, Berger et al. (1973) found that type score ranged between one-third and nearly twice as important as milk yield in determining herdlife. This illustrates the significant role of type in influencing management decisions. They also reported that, if one were to construct an index of type and production designed to predict herdlife, the efficienty of selection for lifetime production on that index rather than production alone would be 31% to 52%. O'Bleness and Van Vleck (1962) investigated the reasons for disposal of dairy cows from New York herds and discovered that two to four percent of disposals were for undesirable dairy type. This figure may be somewhat misleading, however. Udder trouble and mastitis, grouped together in the survey as a reason for disposal, accounted for 14% to 20% of the disposals within a herd. Unfortunately, the proportion of these animals without mastitis but having poorly conforming or severely broken-down udders is not known. In a later study, Van Vleck and Norman (1972) found udder (22%), inabilities or disease (8%), and type (3%) all to be significant reasons for disposal of a cow from a herd. The survey fails to distinguish, however, whether the cause of an udder problem or an inability or disease, is originally due to some shortcoming in the animal's conformation. This may underestimate the proportion of disposals attributable to faulty type. Subsequent analysis of these data indicated that few traits measured before 49 months of age have any significant value in predicting the eventual reason for a cow's disposal. These results, when coupled with the medium to low heritability of many type traits, indicate that selection for longevity based on an index of conformation scores in first lactation would have only limited effectiveness.

Studying the daughters of AI sires, Schaeffer and Burnside (1974) reported significant correlations of sire's PDT to survival rate of two year old daughters to year three (.34) and year four (.31), among Canadian Holsteins. These figures are only slightly lower than those for PDM (.39 and .44).

Honnette et al. (1980), studying the records of 34,675 Holsteins, concluded that selection for conformational improvement in udder traits was consistent with objectives of increasing herdlife and lifetime milk. They found udder traits, as well as miscellaneous traits such as winged shoulders, to exceed other traits by far in predictive value for lifetime milk yield and herdlife. A correlation between first type score and herdlife of .20 was determined by Specht et al. (1967), although as a source of variation the effect of first score was rather minor.

In close relationship to longevity is the value of type in reducing labor or health costs. Blake and McDaniel (1979), working with 522 Holstein and Jersey cows, found significant positive correlation between the conformation scores of mammary traits and decreased cost of milk harvest in Holsteins. A similar correlation of Jersey cows, however, did not exist, perhaps owing to the somewhat smaller scale of the Jersey mammary system. The predictive value of these correlations, which range as high as .35 for the correlation of volume of rear teats to average flow rate, is rather low.

Gilmore and McDaniel (1977a) developed an annualized income model including such factors as values of calves, milk revenue, health costs and feed costs. They also calculated the relationships between several factors and annualized income, including milk revenue, mastitis cost, dairy character, and other variables. A correlation of .25 was found between dairy character and annualized income. In addition, dairy character was found to be nearly half as important as milk production in first lactation for predicting annualized income, and about 40% as important as fat in first lactation. In their study, other type traits did not significantly affect annualized income. Gilmore and McDaniel (1977b) also studied the association between milk yield, type score, and health costs. A correlation of -.14 was reported between first mammary system score and overall health cost. These results suggest that costs of treatment of mastitis or other health problems can be decreased by improving mammary conformation.

It can be seen, on review, that many studies have shown a positive value for conformation by improving production and herdlife and decreasing costs associated with dairy production. A consideration for type score improvement through breeding, therefore, would be of benefit to producers of dairy cattle in increasing production and income, and decreasing some related expenses.

2.6 Prior Consideration of Mates in Evaluation of Bulls

As early as 1944, Lush (1944) determined the expected optimum emphasis on sires' mates' records in their proofs. However, this was prior to the advent of widespread AI, and most sires were bred to relatively few mates. Inclusion of any additional information to a sire's proof was of great benefit to more accurate evaluation, and Lush (1944) reports an expected genetic improvement from sire selection of 12%-20%.

As AI became widespread, little additional benefit was seen from including a sire's mates in his evaluation. In one of two studies reported in 1965, Bereskin and Freeman (1965) conclude that, if deviations from contemporary herdmates are used to evaluate bulls, little additional information is gained by including the records of mates in bull proofs. Miller and Corley (1965) found that rank correlation between PDMs calculated with and without mates' records was .998. Sires in this study had an average of more than a hundred daughters each, and both daughter and mate records were weighted as a function of their respective number of herdmates. They also concluded that inclusion of production data of sires' mates' does not alter the relative standing of individual bulls.

Hillers and Freeman (1966) investigated sources of genetic error in sire proofs for production traits. They found significant differences among sires in their mates' level of milk and fat production when ten mates were considered, but not when considering twenty or forty mates. They asserted that this bias is relatively unimportant in the selection of sires, but in certain situations it could cause inaccurate selections.

Bodoh and Shook (1972) computed mean bias of 13.2 kg milk in sires' PDMs due to non-random selection of mates. Rank correlations between PDMs corrected and uncorrected for this bias were .996, for 126 Holstein bulls with published proofs. Also, they concluded that bias due to non-random mating of sires for milk production was too small to consider at that time.

Everett et al. (1979) designed a model wherein the effect of non-random mate selection was not directly measured, but was determined through the genetic value of mates' sires. The sire solutions from two models were compared, one including maternal grandsire (MGS) effect and one excluding it, using 808,796 production records from all five dairy breeds. Rank correlations ranged from .91 for both the Ayrshire and Guernsey breeds when all sires are evaluated, to .99 when only sires having more than a hundred daughters in the Holstein, Guernsey, or Jersey breeds were evaluated. They conclude that including MGS in the sire evaluation model is of benefit both in decreasing prediction error variance and reducing bias in young sire proofs caused by non-random mate distribution of young sires. They also point out a 25% increase in computing time if the model includes MGS.

2.7 Sire Evaluation for Type

Many methods have been devised to evaluate sires for genetic ability for body conformation traits. The simplest may be the average score of a sire's progeny, or Daughter Average. Daughter Average takes into account no herd differences nor environmental or genetic differences over time, and assumes a random distribution of sires' mates. It is also subject to sampling error by failing to account for the number of daughters of a sire. Obviously, the evaluation of sires by this method is subject to many inaccuracies when any of its necessary conditions is violated.

A second method has been used by the Holstein-Friesian Association of America to determine Predicted Difference Type (PDT). Predicted Difference is the expected difference between the performance of a sire's daughters and the daughters of sires of breed average at some base period, under similar herd management conditions (Vinson, 1981). The method uses the formula: $PDT = b[\bar{P}-\bar{B} - .15(\bar{D}-\bar{B})]$ where $\underline{b}$ is the repeatability of the PDT (regression of future on past daughters), $\bar{P}$ is the daughter average for final score adjusted for age, $\bar{B}$ is the breed average adjusted for age, .15 is the correlation between the classification scores of daughters and dams, and $\bar{D}$ is the average dam score, adjusted for age. While this method accounts for a sire's mates and his number of daughters, it cannot adjust for herd differences nor variation in scores over time due to environmental and genetic changes.

2.7.1 BLUP Approach

The shortcomings of both of these methods can be overcome using a method developed by Henderson (1950, 1966). Originally called Maximum Likelihood technique, this method was later termed Best Linear Unbiased Prediction (BLUP). However, it was almost two decades before the development of improved computers made his method cost-efficient for large dairy populations (Henderson, 1974).

Using this procedure, as many fixed and random effects can be included in a model as are desired or computationally feasible. Mixed model equations (MME's) are constructed, and adjustments are made within the random effects for their variance-covariance structure. Solution of the MME's yields constants for every level of each fixed effect in the MME's, as well as estimates for the random factors. Three investigations will be reviewed which use BLUP techniques to evaluate sires for type traits.

Norman et al. (1979) evaluated 726 Jersey bulls for conformation and then examined various Production - Type Indices (PTIs) for recommendation to the American Jersey Cattle Club. Their model contained fixed effect for herd-year sub-classes and genetic groups for sires, and random sire, herd by sire, and cow effects. Although they did not state, they assumed that categorical type scores have an underlying continuous relationship to the cow's conformation. The sire estimates obtained, when added to group constants calculated, were PDTs, which were correlated to prior estimates of the bulls' genetic ability based on Daughter Averages. These correlations ranged among traits from .48 to .76, with most between .6 and .7.

Predicted Difference Milk (PDM) and Predicted Difference for Fat Percentage (PD%) were obtained for all sires, and used to calculate a Predicted Difference in

Dollar Income (PD$). Various PTIs were computed using combinations of PD$ and PDT. They investigated the effect of the PTIs on expected genetic improvement for milk production, and noted very small differences between expected PDMs for weights of 3:1 and 1:0 (PD$:PDT). Desiring to improve milk production as well as maintain adequate conformation within the breed, they recommended relative weights of 3:1 in calculating PTIs for Jersey sires.

A study of Brown Swiss cattle by Karner and Van Vleck (1980) presented several differences from the aforementioned study. The most striking is their treatment of categorical data without assuming continuity. The results are predicted categorical frequencies on every trait for each sire, rather than PD's for each sire. The researchers evaluated 712 Brown Swiss bulls for conformation in twelve descriptive traits with a model having random herd by year subclass and sire effects, and fixed sire by category subclasses. The data consisted of the official classification scores of 12,838 Brown Swiss cows, younger than 47 months of age when classified between 1971 and 1976. Each sire was required to have daughters in more than one herd. No relationships were considered between sires, and herd by sire covariances also were assumed zero. One major difficulty was the inclusion of categories with very low frequencies, causing computing difficulties due to core storage limitations. Therefore, categories occasionally were merged together to yield a new combined category with greater frequency of occurrence. It was recommended that a comparison be made between the effectiveness of this system and that of linearized systems of scoring in predicting sire genetic values for conformation.

Schaeffer et al. (1978) evaluated more than 14,000 Canadian Holstein sires based on the records of 230,000 cows and records on 180,000 of their dams. Fixed factors in the model included age at classification, year, classification of the dam, and genetic group of sires. The only random factor in the model was sire effect. Though most studies have found herd effect to be a significant source of variation, herd effect was not included in this study. This may result in somewhat greater variance of prediction error than if it were included.

Classification of the dam was included as a categorical variable in the model. The dam's classification for final class was used for the analysis of final score and final class, and for all other traits the corresponding classification of the dam for the same trait was used. The inclusion of this factor would adjust resulting sire proofs for any differential mating which might exist.

3. METHODS AND PROCEDURES

3.1 Data

3.1.1 Data Source and Preparation

The data, as supplied by the American Guernsey Cattle Club, consisted of 301,321 records of body conformation scores. The appraisals were made on purebred Guernsey cows in United States herds by ten classifiers, between 1956 and 1977. In addition to conformation data, each record contained identification numbers of the appraised cow, her sire and dam, the herd in which she was classified (several cows were classified in more than one herd at different times) and the appraiser. Also included in each record were the cow's date of birth and the date of the appraisal.

All cows were appraised for twelve conformation traits, as listed in Figure 4. The evaluation of three other traits was either discontinued or begun within the period covered by the data. These were shoulder (discontinued in 1977), suspensary ligament (begun in 1973), and stature (begun in 1972). For each trait, every cow was assigned one of six classifications: excellent, very good, desirable, acceptable, fair, or poor. A numerical final score between 40 and 99 was assigned each animal, based on the evaluations of its component traits. This numerical final score determined a cow's final classification. If its score was at least 90, a cow received a final classification of excellent; if at least 80 but not more than 89, very good; and so on.

Final Classification
Breed Character
Dairy Character
General Appearance
Mammary System
Chest and Body
Fore Feet and Legs
Rear Feet and Legs
Rump
Fore Udder
Rear Udder
Teats

Figure 4.--Traits Evaluated for All Animals

3.1.2 Merger of Data

To incorporate the relationship between a cow's body conformation with that of her dam, the records of both animals were paired. This merging was enabled by sorting the data into two separate files. The first was sorted by dam identification number, while the second was sorted by cow number and, within cow number, by date of classification. Often a cow in this second file was appraised more than once; when merging a record of such a cow to those of its daughters, the appraisal was used whose date was closest to the date of the breeding which produced each daughter. Use of this criterion for pairing maximized the resultant number of daughter-dam records, and resulted in 192,640 paired records from 132,318 daughters of 14,310 sires.

3.2 Examination of Randomness of Sires' Mates

Before studying mates' effect on sire evaluation, the extent of non-random mating for type was examined. To determine the degree of non-random mating, the distributions for final classification of sires' mates and that of the dam population were compared, using a Chi-square goodness of fit test. If few sires were bred to biased groups of mates, consideration of mates in sire evaluation for final class might be unnecessary. Distributions in this test were specified by frequencies of animals' final classifications into each of the six categories previously described. A tabulation of the paired data file was made for dams' final classification, and the frequencies for each category are shown in Table 3. Similarly, the frequencies of each sire's daughters' classifications were tabulated, as well as the number of his progeny in the paired data.

Broffitt and Randles (1977) published formulae to determine the minimum sample size necessary to obtain a

TABLE 3.--Tabulation of Frequencies for Final Classification of Guernsey Dams.

Code	Category	Frequency
1	Excellent	.0319
2	Very good	.4831
3	Desirable	.3664
4	Acceptable	.1069
5	Fair	.0114
6	Poor	.0003

valid goodness-of-fit test, for given expected frequencies. This would be interpreted as the minimum number of a sire's daughter appraisals needed, given the parameters of the dam population. For all six categories, solution of the Broffitt-Randles equations indicated that only sires with more than a thousand daughter appraisals could be included in the test; there were only five such sires in the paired data. However, when the fair and poor categories were combined, yielding five categories, the necessary number of daughter appraisals was reduced to 40. Because more than 300 sires each had at least 40 daughters, addition of the two least favorable categories was performed for the daughters of these sires. Daughter records for all sires having fewer than 40 progeny were eliminated from the data.

3.2.1 Goodness-of-Fit Procedure

For the remaining data, the Chi-square goodness-of-fit test was performed for each sire; a test statistic, q, was obtained:

$$q = n \sum_{i=1}^{5} \frac{(O_i - E_i)^2}{E_i},$$

where n is the number of the sire's daughter appraisals, O_i is the observed frequency of a sire's daughters being classified in category i, and E_i is the frequency of the dam population in category i. Only five categories were used, as a result of combining the fair and poor classes.

A level of confidence was determined by locating q in a Chi-square table, with 4 degrees of freedom. For each of the 306 sires having at least 40 daughters, α indicated the probability of Type I error when stating that a sire's distribution of daughter appraisals for final class differs from the dam population distribution.

3.3 Mates' Influence on Sire Ranking Using All Sire's Progeny

3.3.1 Models

Two models were used to study the effect of a sire's mates on his evaluation for each of the twelve body conformation traits.

The first model can be expressed as:

$$Y_{ijklmn} = \mu + S_i + A_j + M_k + HY_{lm} + e_{ijklmn}.$$

In this equation, Y_{ijklmn} is a discrete classification score for a cow on one of the traits. These scores varied from 6 (excellent) through 1 (poor), and were assumed to represent an underlying continuous distribution of phenotypes within each trait.

The factors included in the model to explain variation in Y_{ijklmn} were:

1. μ, the population mean;
2. S_i, the effect of the i^{th} sire. It is considered a random effect with mean zero and homogenous variance, σ^2_s. Covariances between sires were assumed zero.
3. A_j, the effect of the j^{th} age group at classification. It is considered a fixed effect, with eight classes. The upper limits for these categories, in years, were: 3,4,5, 6,7,8,10, and 20. Each cow was included in exactly one of these classes;
4. M_k, the fixed effect of the K^{th} month of classification, with k ranging from 1 for January through 12 for December;

5. HY_{lm}, the fixed effects of the $l^{\underline{th}}$ herd, $m^{\underline{th}}$ year group of classification, and the interaction between the two. Years from 1956 through 1973 were grouped into six sets of three, while the final four years formed the seventh group. These groupings were used to account for any trends in scores over time, while resulting in fewer empty subclasses than if single years had been used to form 22 year groups; and

6. e_{ijklmn}, the random residual effect unique to each observation. This factor was assumed to have mean of zero and homogenous variance of σ_e^2, with zero covariance between residuals of any two observations.

This model will be referred to as NOCOV.

The second model used in this study was:

$$Y_{ijklmn} = \mu + S_i + A_j + M_k + HY_{lm} + bD_{ijklmn} + e_{ijlkmn}$$

Each factor represented in NOCOV was included in this model, which will be termed WITHCOV. All definitions of these factors and assumptions pertaining to them are unchanged. In addition, consideration was given to a covariate of each cow's dam score, D_{ijklmn}, for the trait being considered. This factor was described in the same method, and subject to the same assumptions, as Y_{ijklmn}, discussed above in this section. The covariate is incorporated into WITHCOV as a product of D_{ijklmn} and a regression coefficient, b.

3.3.2 Editing the Data

Before analyses by these two models, the paired daughter-dam data file was edited. Because body conformation records made by animals less than thirty months of age are not likely to accurately reflect genetic ability for mature conformation, these appraisals were eliminated. Because use of only first records would reduce permanent environmental effects and eliminate the need for a cow factor in the model, all second and later appraisals were removed from the data.

From the remaining records, 80 sires having the largest number of appraised daughters were tabulated. The progeny of these sires were selected to make up the new set of data, called ALL. In this file were 33,534 daughter records, comprising 3,454 herd-year groups. Each sire had at least 140 daughters in the data. Limiting the records to progeny of these 80 sires served two purposes: it restricted the number of equations to be solved to a reasonable size while maximizing the amount of information per sire, and the need was foreseen to use small, equal-sized subsets of progeny from each sire in the later evaluations. Use of daughters of sires with the most progeny would produce meaningful contrasts between results of the current evaluation and evaluations to be described later.

3.3.3 Absorption of Herd-Year Groups

Obtaining solutions using these data for every level of all factors would necessitate solving a system of 3,553 equations for NOCOV model and 3,554 equations using the WITHCOV model. To reduce the number of equations to a more manageable size, the nuisance factor of herd-year group was absorbed into the remaining terms as follows: after sorting the data by herd and year within herd, the mixed model equations (MME's) were constructed using the records of one herd-year group at a time. After all of its records were read, the nuisance factor was immediately absorbed into the rest of the equations. In this way, it was never necessary to store more than one herd-year group at a time in computer core memory, nor was execution time spent to obtain solutions for 3,453 levels of a nuisance factor.

3.3.4 Adjustments to Random Portion of Mixed Model Equations

In solving mixed model equations, the inverse of a random factor's variance-covariance (VCV) matrix must be added to the portion of the MME's corresponding to that factor. After some manipulations of MME formulae using matrix algebra, it can be shown that this addition is somewhat simplified when all random factors are assumed to have homogeneous variance and no covariance, as in this investigation. Because sire is the only random factor in MME, only diagonal terms of the sire portion of MME need to be adjusted by the addition of a variance ratio,

$$\frac{\sigma^2_{\text{error}}}{\sigma^2_{\text{sire}}}$$

Mao et al. (1977) determined the heritabilities (h^2) of each trait, based on a subset of the same Guernsey population.

In half-sibs from randomly mated populations, genetic theory indicates that σ^2_{sire} is equal to one-quarter of the additive genetic variance (assuming zero epistatic variance), and $\sigma^2_{\text{sire}} + \sigma^2_{\text{error}}$ expresses the total phenotypic variance. Because the ratio of additive genetic variance to total phenotypic variance is the definition of heritability in the narrow sense, and assuming any existing relationship between cows in this Guernsey population to be half-sib, the heritability therefore can be expressed as

$$\frac{4\ \sigma^2_{\text{sire}}}{\sigma^2_{\text{sire}} + \sigma^2_{\text{error}}}.$$

The desired variance ratio to be added to the diagonal of the sire portion of the MME can be calculated as

$$\frac{4}{h^2} - 1,$$

given the heritability for each trait. Heritabilities as calculated by Mao et al. (1977) and the resultant variance ratios are shown in Table 4.

3.3.5 Solutions of Mixed Model Equations

Mixed model equations were constructed using the set of data ALL, and in the process, herd-year group factor was absorbed into the remaining effects. After the diagonal of the sire portion of the MME matrix was adjusted by the variance ratio for the trait being evaluated, four rows and columns corresponding to levels of fixed effects were deleted to eliminate linear dependencies within the MME's. This was because a singular matrix, that is, one which contained linear dependencies, could not be solved as efficiently as a non-singular matrix. However, the deletion of dependent rows and columns had no effect on the sire solutions.

Solutions were found within all traits using each model. Sire estimates as well as age group and month constants were determined; results of using WITHCOV model included a regression coefficient for dam covariate. Age group and month were considered nuisance variables and their solutions were not of interest in this study.

The International Mathematical and Statistical Library (IMSL) of Fortran subroutines was used in part to solve the MME's. All computations were performed on a CDC

TABLE 4.--Heritabilities of Guernsey Type Traits[a] and Resultant Variance Ratios.

Trait	Heritability	$\frac{\sigma^2_{error}}{\sigma^2_{sire}}$
General appearance	.24	15.67
Breed character	.22	17.18
Fore feet and legs	.18	21.22
Rear feet and legs	.06	65.67
Rump	.31	11.90
Dairy character	.16	24.00
Chest and body	.25	15.00
Fore udder	.21	18.05
Rear udder	.19	10.05
Teats	.24	15.67
Mammary system	.23	16.39
Final score	.24	15.67

[a] MAO, 1977.

Cyber series computer at Michigan State University. Because the order of the matrix was nearly 100 for each evaluation, the cost of obtaining an inverse would have been many times higher than the cost of obtaining only solutions, and for this reason no inverses were calculated.

The VCV matrix for solutions of fixed effects can be calculated as $\underset{\sim}{P}\,\sigma^2_{error}$, where $\underset{\sim}{P}$ is the fixed portion of the inverse of the MME coefficient matrix. Also, the VCV matrix of sire prediction error would be $\underset{\sim}{S}\,\sigma^2_{error}$, where $\underset{\sim}{S}$ is the random portion of the inverse of the MME coefficient matrix. Without an inverse of the coefficient matrix, neither of these sets of variances and covariances could be computed.

3.3.6 Disconnectedness

Disconnectedness among groups of sires must be considered if sire solutions are compared. For one group of sires to be disconnected from another group in this study, all of the progeny of sires in the first group must be appraised in different herd-year groups, and/or different age groups, and/or different months than all of the daughters of the second group of sires. If this condition is not true, the two groups of sires are actually one connected group.

For example, suppose all of the daughters of one sire were classified in December, while no other cows were classified in that month. It would be impossible to separate the effect of that month from the sire effect, and hence that sire could not be compared to other sires. In this study, there were only eight age groups and twelve months, so disconnectedness by month or age group would be extremely unlikely. Because there were so many herd-year groups, however, it was possible that a sire or group of sires was disconnected through that factor.

A program written by the author was used to search for disconnected groups of sires. All sires were completely connected within the herd-year group factor.

3.3.7 Comparison of Sire Rankings

For each trait, bulls were ranked twice, based on sire estimates obtained using both models, NOCOV and WITHCOV. Spearman's rank correlation was calculated for each trait to determine correspondence between the two sets of rankings. If the rank of sire i resulting from the NOCOV model is t_{i1} and from the WITHCOV model is t_{i2}, then correlation between the ranks of the 80 bulls determined from two models is:

$$r = 1 - \frac{6 \sum_{i-1}^{80} (t_{i1} - t_{i2})^2}{80^3 - 80}.$$

3.4 Mates' Influence on Sire Ranking Using Initial Daughter Samples

The influence of a sire's mates on his evaluation for body conformation was studied when a much smaller number of progeny was available. The models used to investigate this effect are identical to those described in section 3.3.1.

3.4.1 Editing the Data

From the set of data ALL, the first 20 daughters of each sire were included in the data file termed FIRST. There were 1,600 appraisals within this file, comprising 557 herd-year groups.

Absorption of herd-year group, addition of variance ratios to the diagonal of sire portion of the MME, and solution of mixed model equations were performed as described in sections 3.3.3 through 3.3.5, respectively, for each trait.

3.4.2 Disconnectedness Among Sires Having Few Progeny

One of the effects of reducing the number of progeny per sire to 20 is the occurrence of disconnected groups. Using the program described in section 3.3.6, it was determined that 35 groups of sires in the FIRST data file were disconnected by herd-year group. Single disconnected sires made up 28 of these disconnected groups; solutions for these sires cannot be separated from constants of herd-year groups in which their daughters were appraised, and therefore are not meaningful. Of the remaining seven disconnected groups, only three contain more than three sires.

Comparisons should not be made between sires in disconnected groups, although within connected groups comparisons are valid. Therefore to obtain rank correlations between two sets of sire solutions, at least one of which was calculated from the set of data FIRST, a weighted average is used. Rank correlations are calculated as described in section 3.3.7, except that instead of including all 80 sires, the calculations employ only the number of sires within a connected group. The three major connected groups consist of 9, 11, and 23 sires. If the rank correlations obtained within these groups are denoted r_1, r_2, and r_3, then the weighted rank correlation as described by Donner and Rosner (1980) is:

$$r = \frac{9r_1 + 11r_2 + 23r_3}{9 + 11 + 23}.$$

3.4.3 Comparisons Made Using Results of Evaluations Based on Few Progeny

Weighted correlations as described in the previous section were used to make three comparisons. First, weighted correlations were calculated between results of using both models, NOCOV (without covariate) and WITHCOV

(with a covariate), with only the sires' first 20 daughters. Then, the same two sets of sire estimates were correlated, one at a time, to estimates obtained using all the data (ALL data set) with the NOCOV model. This was in an attempt to determine the accuracy with which either model using few progeny records could predict a sire's evaluation when more records on daughters are available.

In calculating the latter two weighted correlations, sire estimates resulting from using the ALL file were considered within the connected groups of the smaller FIRST file. This is because connected sires, if split into groups, would maintain their relative ranks within groups. On the other hand, if disconnected sires are combined into one group, there is no assurance that a ranking based on their estimates would be correct.

4. RESULTS AND DISCUSSION

4.1 Extent of Non-Random Mating for Final Class

A Chi-square goodness-of-fit test was performed on each of 306 sires having at least 40 daughters. Results, reported in Table 5, indicate the proportion of sires whose mates are not representative of the population at three levels of confidence.

TABLE 5. Proportion of Sires Having Mates Distributed Differently from the Population at Various Confidence Levels.

Level of Confidence	Proportion of Sires
90%	45.4%
95%	37.2%
99%	28.1%

This procedure does not quantify the amount nor direction of mates' bias. For example, the three distributions shown in Figure 5 might be judged significantly different. However, this procedure will not indicate

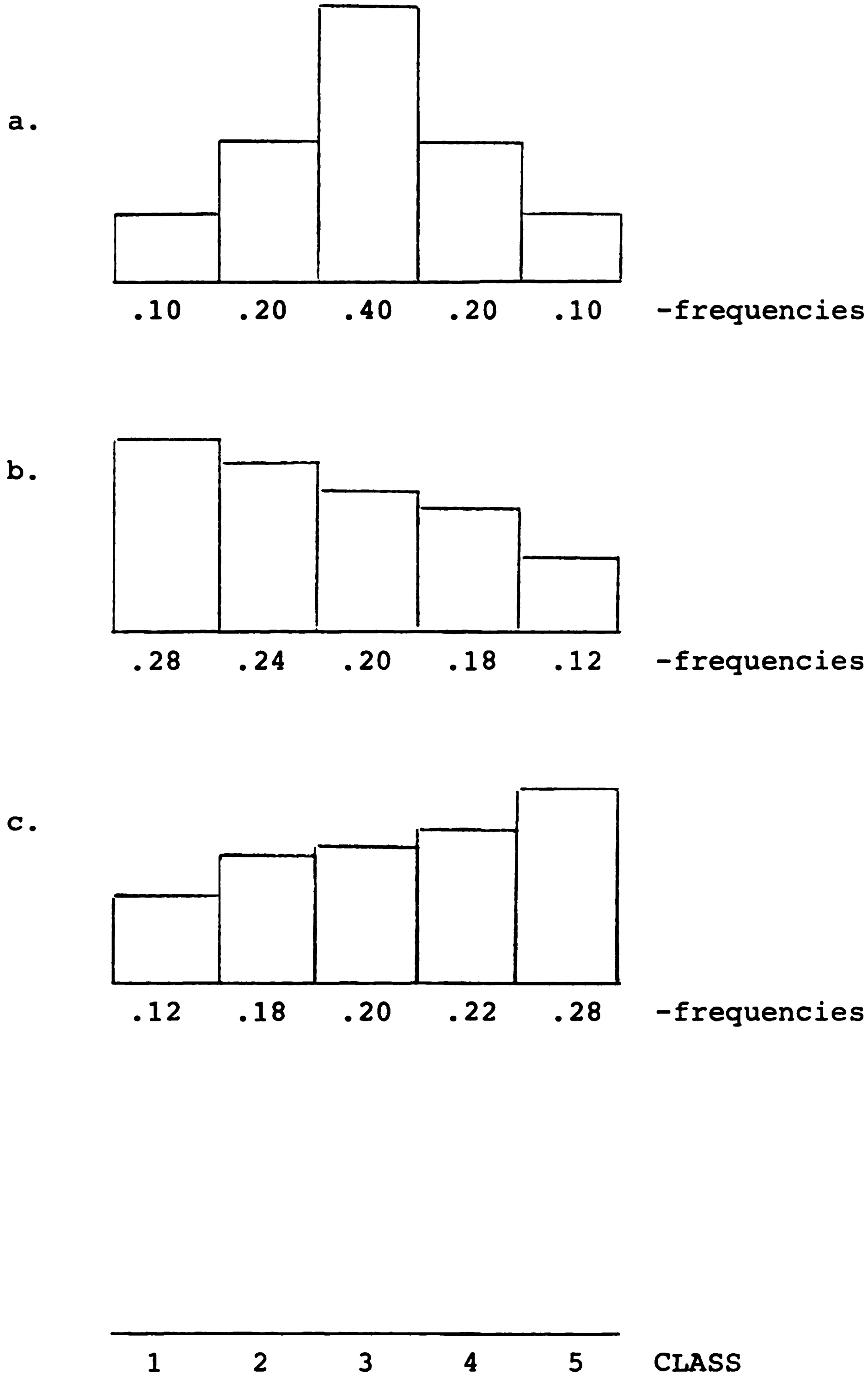

Figure 5.--Examples of Differing Descriptions

whether a distribution is biased up (figure c) or down (figure b) or to what degree it differs, from figure a.

From these results, then, it seems that many sires may have been bred to samples of mates which were not representative of the population. This could be the result of deliberate non-random mating, such as corrective mating for type, practiced by Guernsey breeders. It also could be the incidental result of any preferential mating for other traits which may be positively correlated to body conformation traits.

If left unadjusted for mates' scores, provided that mates were a selected non-random sample from the population, bulls' rankings based on daughters' scores could be biased.

4.2 Effect of Mates' Scores on Sire Rankings Based on Many Progeny

Sire solutions were obtained for each of the twelve traits using both models (NOCOV, without covariate, and WITHCOV, with covariate) and all of the sires' progeny (ALL). The expected values of all means of sire estimates and the observed means of those estimates were zero. The standard deviations of estimates are shown in Table 6. They are virtually identical between the models used, indicating comparable ranges of estimates. Because of differences in heritabilities among the various traits, the standard deviations among traits varied quite widely.

TABLE 6.--Standard Deviations of Sire Estimates Using All Progeny of Sires.

	Model	
Trait	Without Covariate (NOCOV)	With Covariate (WITHCOV)
General appearance	.140	.139
Breed character	.154	.155
Fore feet and legs	.124	.125
Rear feet and legs	.077	.077
Rump	.153	.153
Dairy character	.129	.129
Chest and body	.137	.175
Fore udder	.163	.163
Rear udder	.145	.145
Teats	.134	.134
Mammary system	.153	.152
Final score	.147	.146

If the distributions of daughter scores are similar between two traits, one would expect to find greater differences among sire estimates for the trait with a higher heritability. For traits with higher heritability, a greater portion of phenotypic variation is caused by sire effect, and it is subsequently easier to distinguish genetic ability among sires.

Rank correlations were calculated on all traits between the two sets of sire solutions corresponding to both models. These are shown in Table 7. All correlations between results of these two evaluations, for all traits, exceeded .995, which indicates little meaningful difference between the two sets of solutions; their rankings are not significantly changed due to the addition of dam's score.

4.3 Mates' Effect on Sire Rankings Based on Initial Daughter Samples

In practice, sires having few mates are more subject to random sampling variation, which could result in a bull having a non-representative sample of mates. Because young sires routinely are selected on evaluations based on few progeny, it is important to eliminate as much sampling variation as possible.

Three sets of correlations were computed to assess the value of including a dam covariate in a sire evaluation model when few data are available. First, for sire

TABLE 7.--Rank Correlations Between Models Including and Excluding Dam Covariate Using All Progeny of Sires.

Trait	Spearman's r
General appearance	.997
Breed character	.998
Fore feet and legs	.998
Rear feet and legs	.998
Rump	.995
Dairy character	.999
Chest and body	.996
Fore udder	.998
Rear udder	.999
Teats	.998
Mammary system	.998
Final score	.998

estimates calculated from few progeny, the rank correlations between the two models were examined. These correlations do not indicate whether differences caused by inclusion of a covariate constitute an improvement in accuracy, however. Therefore, each set of results was compared separately to results obtained using many more data, to determine whether inclusion of sires' mates' covariate results in an improvement in accuracy of rankings. It was assumed that rankings of sires as evaluated using all of their progeny were more accurate than rankings using only the first 20 daughters, so that higher values in the second set of correlations indicate better accuracy of the evaluations based on few progeny than do lower values.

Rank correlations between results of both models using few data are shown in Table 8. These correlations are weighted averages as described in section 3.4.2. Comparison with Table 7 shows that, for each trait, there is less agreement between rankings of the two models when fewer data are available than when all daughters are used. In general, however, the correlations are quite high.

In Table 9 the accuracies of the two models using few records are contrasted. In general, only moderate weighted rank correlations were found between evaluations based on few records and evaluations based on many,

TABLE 8.--Weighted Rank Correlations Between Models Including and Excluding Dam Covariate Using Initial Progeny of Sires.

Trait	Spearman's r
General appearance	.940
Breed character	.993
Fore feet and legs	.985
Rear feet and legs	.989
Rump	.992
Dairy character	.980
Chest and body	.980
Fore udder	.970
Rear udder	.990
Teats	.964
Mammary system	.988
Final score	.974

TABLE 9.--Weighted Rank Correlations of Both Models Using Initial Sample of Daughters to Model Without Covariate Using All Daughters.

	Model	
Trait	Without Covariate (NOCOV)	With Covariate (WITHCOV)
General appearance	.436	.348
Breed character	.134	.43
Fore feet and legs	.327	.365
Rear feet and legs	.235	.240
Rump	.295	.294
Dairy character	.316	.244
Chest and body	.640	.656
Fore udder	.276	.214
Rear udder	.293	.273
Teats	.238	.261
Mammary system	.172	.169
Final score	.512	.475

indicating that evaluations based on few data provide only a weak indication of a sire's true genetic rank.

If sire solutions are more accurate when their mates' covariate is included in the model, we would expect corresponding correlations to be higher. However, upon examination of Table 9, little difference can be seen between models in their ability to predict sire rankings. Among traits, however, a wide range of correlations can be seen, suggesting that evaluations of young sires may be more accurate for some traits, such as chest and body, than for others such as breed character or mammary system. While reasons for this are not clear, large phenotypic variances may influence young sire evaluation because a more balanced range of category frequencies for daughters exists, making it easier to distinguish between sires.

4.4 Examination of Covariate Regression Coefficients

Regression coefficients of the sires' mates' covariates using all of the data and only the first 20 daughters of each sire are reported in Table 10. They are all greater than zero, indicating a positive relationship between type score for dam and daughter in all traits. Standard errors were not computed for reasons given in section 3.3.5. Across traits, 95% confidence intervals about the mean regression coefficient were .008 ± .055 and .094 ± .087, using all of the data and the first 20

TABLE 10.--Regression Coefficients for Dam Covariates.

	Data Set	
Trait	All Daughters	Initial 20 Daughters
General appearance	.0989	.1492
Breed character	.0923	.0661
Fore feet and legs	.0773	.1036
Rear feet and legs	.0546	.0557
Rump	.1255	.0925
Dairy character	.0602	.0431
Chest and body	.1428	.1814
Fore udder	.0882	.0831
Rear udder	.0680	.0639
Teats	.0719	.1086
Mammary system	.0836	.0895
Final score	.0962	.0898

daughters of each sire, respectively. It appears that regression coefficients are not zero. Because the vast majority (nearly 85%) of all animals are classified in only two categories, very good or desirable, and because the heritabilities of these traits are generally moderate to low, these coefficients may be of little predictive value for daughter classification.

It is interesting to note that despite the paucity of information in the set of data FIRST (containing all sires' first 20 daughters) compared to the ALL data (including all sires' progeny), the correlation between regression coefficients computed from both data sets is .735, rather high in contrast to correlations of sire solutions between sets of data, which range from .179 for mammary system to .656 for chest and body.

5. CONCLUSIONS

Among Guernsey sires having at least 40 daughter appraisals, more than one-third (37.2%) are bred to mates which are not a random sample from the dam population with respect to final class ($p < 0.05$). However, it cannot be concluded from these results that, if left unadjusted for mates, these sires' evaluations would be biased. Though a sire's mates' distribution of final classes may differ from the population distribution, the mates' frequencies in each category may be such that there is negligible prejudice toward either extreme. Also, despite the bias of a sample of mates toward an extreme, its effect upon a sire's evaluation may not be significant.

After acknowledging these two possibilities, the goodness-of-fit test is seen to indicate only the potential for bias in an evaluation. Comparisons were made between results of evaluations adjusted and unadjusted for mates.

When sire solutions were compared between the two models, within each data set, rank correlations were high ($> .96$) for all traits. Within the large set of data (ALL), all correlations exceeded .99. There were essentially, no differences between sire solutions obtained with and without a covariate of mate's score when all sires had a large amount of daughter information available. When each sire had only 20 daughters, the correlations between sire solutions obtained from the two models were slightly smaller across traits, but still near unity.

Sire solutions obtained from the smaller set of data (FIRST) provided much smaller correlations than those obtained from ALL, regardless of model used. These correlations varied widely across traits, being highest for chest and body, and lowest for breed character. Possible reasons for these discrepancies were included in the Discussion. From the correlations, one may conclude that neither model was superior in predicting a later, presumably more accurate, sire solution.

If a covariate of mates' scores were to be included in a model to evaluate more Guernsey sires for conformation traits, then, we might not expect to see a great change in the ranking of sires with many progeny. If a sire having few daughters had been bred to a sample of mates very biased toward either extreme, however, we might expect a more noticeable change in his rank. From the results of this investigation, there is little indication that this change would improve the accuracy of the sire's evaluation.

When reviewing results of this investigation, it is imperative to consider its scope, especially in two areas: the sires included, and the use of somewhat subjective classification scores as records rather than more objective or continuous traits.

One must be careful when applying results obtained from examination of only the eighty Guernsey sires with the most daughters to additional bulls or to other breeds. When a sire has few daughters, his evaluation is more subject to sampling errors and therefore less precise. This imprecision is increased if the sire's progeny are in very few herds. Differences in philosophies among breed organizations about body conformation's desired relationship to production traits can affect sire selection among dairymen; non-random mating may not occur to the same degree as found in this study. Also, genetic parameters of body conformation traits can differ markedly among breeds.

It is also difficult to extend conclusions of this research to any continuously scored trait, such as milk or fat production or linearly measured conformation characteristics. Concerning production traits, the extent of non-random mating may be quite different than for type traits, possibly eliminating the need to adjust for mate's ability. When an appraiser uses linear scales for body conformation, some of his subjectivity may be reduced compared to a system using classification scores. In addition, by being scored on a more continuous scale, a more precise adjustment for covariate can be given to each observation. This may result in more normally distributed residuals. The increased continuity of production records, as well as the more objective assessment of cows, might have the same effect, but to a greater degree.

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