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CORRECTIVE MATING FOR LINEAR TYPE TRAITS IN DAIRY CATTLE

by

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CORRECTIVE MATING FOR LINEAR TYPE TRAITS

IN DAIRY CATTLE

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Corrective Mating for Linear Type Traits in Dairy Cattle

Octavio Martínez-Huerta, Ph.D.

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Adviser: Jeffrey F. Keown

The degree of negative assortative mating for 18 linear type traits was investigated in a corrective mating program. To evaluate the degree of assortative mating used, Pearson-Newman correlations between (PTAs) of sires recommended to correct the worst fault trait of the cow and actual scores of cows for worst fault traits were estimated for 18 linear traits. Correlations were obtained by using PTAs from the three recommended sires, or an average obtained from the same three PTAs. When the three PTAs were used, the largest correlations were for rear legs side view (-.69), rump side view (-.60), and basic form (-44). Correlations for the rest of the traits were essentially zero. Correlations were practically zero for all traits when an average of PTAs of the three recommended sires was used. The lack of association between PTAs of recommended sires and scores of cows was due to a large variation among PTAs of recommended sires or a low selection intensity for linear traits of recommended sires. A more carefull assigning of sires for recommendations was needed. No evidence of negative assortative mating was found for most of the linear traits in the corrective mating program using scores of cows and PTAs of recommended sires.

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Introduction

Traits of economic importance in the dairy cattle industry are currently grouped by production traits, e.g. milk, fat, and protein yields, and non-productive traits, also called type traits, e.g. stature, body depth, and udder attachment. Non-productive traits are used in defining the so-called "functional cow", or the type of cow that will remain in the herd a long time while maintaining high production.

Herdlife and lifetime performance are also traits of importance in dairy cattle. Type traits have been used to predict herdlife because type scores are available earlier than herdlife. However, accuracy of prediction of breeding values for survival, by using production records on the individual being selected, has more than twice the accuracy of prediction by using type scores (Brotherstone and Hill, 1991). Thus associated response in herdlife when selecting cows based on type is limited. It is unknown if non-productive traits are associated with lifetime performance. Lifetime performance is usually expressed as a function of one or more production traits.

Selection only for production traits can have a negative impact on some type traits, for example udder traits. Udder traits may be important when selecting for

production, if deep or shallow udders are associated with low production.

Many artificial insemination units in the United States and other nations around the world evaluate grade and registered cows for a number of type traits. The objective of evaluation for type traits is the estimation of breeding values for type traits of sires that are undergoing progeny test for production traits. Some companies have developed programs to "correct" type traits of progeny of cows with scores that deviate greatly from an optimum score, defined as a specific score on a linear scale. These programs, called corrective mating programs, are designed to use negative assortative mating by mating cows with low (high) scores for a given trait to sires with high (low) predicted transmitting ability for the same trait. With most systems the mating decision is based on the trait receiving the lowest score, the worst fault of the cow, as scored by evaluators from the companies in the field. Sires used to correct type traits typically are preselected for production traits.

Objectives

In this study, an attempt was made to document the degree of assortative mating used in the Mating Appraisal for Profit (MAP) program currently in use, by 21st Century Genetics. The MAP program is based on the worst fault of the cow when the cow is evaluated under field conditions.

Single and multiple trait estimates of (co)variance components were also obtained using sire and animal models.

Grouping of traits was also investigated by clustering procedure based on genetic correlations between traits.

Literature Review

Corrective Mating and Assortative Mating

Assortative mating is a mating system in which selection of individuals for mating is achieved through the phenotypic expression of a character. There are two kinds of assortative mating: positive (mating of like phenotypes); and negative (mating of unlike phenotypes). Assortative mating changes the phenotypic and genetic variation in the resulting progeny from that observed in the parents (Van Vleck et al. 1987). Breese (1956) showed that the degree to which positive assortative mating increases genetic variability between families of tobacco plants depends on the phenotypic correlation between parents, the degree to which genetic expression is affected by environmental fluctuations, and the complexity of the genetic control of the character.

The idea of mating individuals with contrasting phenotypes to produce more uniform progeny has been used for a long time by breeders. For example, breeders expect a reduction in variation for stature of progeny if tall sires are mated to short dams. The mating of individuals with contrasting phenotypes also has been used to compensate for faults of cows. This type of mating is called negative assortative mating, and was defined by Lush (1945) as the mating of unlike individuals to increase the uniformity of the population with a larger percentage of intermediate

offspring and fewer extremes. Allaire (1977) also defined negative assortative mating as "the mating of potential parents by divergent phenotypes similar in absolute deviation, above and below the mean or about another intermediate point on a trait scale".

Sewall Wright (1921) showed that the consequence of assortative mating was a reduction in the percentage of heterozygotes at the cost of an increase of the percentage of homozygotes in the population. The author reported that the degree of reduction in heterozygosis for traits determined by a few loci depends on the correlation between the genotypes of the two mating individuals, given by the expression $m = r_{pp}h^2$, where r_{pp} is the correlation between mated individuals, based on their phenotypic resemblance, and h^2 is the trait's degree of determination by heredity. Under perfect negative assortative mating ($m= -1$), with no presence of dominance and only 4 loci involved, reduction in fraction of heterozygotes can be as much as 47%. If dominance is important in determining the performance of an individual for a trait, or if negative assortative mating is not perfect, then reduction in the percentage of heterozygotes would be considerably smaller.

Changes in phenotypic and genetic variances for both Mendelian and quantitative traits, through several generations of assortative mating may be a viable method of evaluating such a mating system. In the case of quantitative

traits, reduction in variance of breeding values from one generation to the next generation can provide a measure of the effectiveness of assortative mating (Allaire 1980).

Negative assortative mating is not widely used because it usually is used as a method to produce less variation rather than a method to maximize total merit or total return. Also, the efficacy of negative assortative mating is low since no more than a 25 to 33% reduction in the variance of breeding values and a 15% reduction in phenotypic variation are expected under perfect negative assortative mating (when phenotypic correlation of mates equals -1 (Soller and Genizi, 1975). Allaire (1977) pointed out that only temporary reductions of no more than 5% in phenotypic variation can be expected from negative assortative mating. When negative assortative matings are discontinued, the reduction in phenotypic variation is likely to disappear.

A possible way to compare methods of corrective mating is to compare variances of breeding values of progeny resulting from different strategies developed to select mating pairs. The mating method producing progeny with the lowest variance of breeding values would be regarded as an "efficient" corrective mating method.

Corrective mating has been designed to use both selection and assortative mating (Hay et al., 1983; Thomas et al., 1986). The value of corrective mating depends on how selection is practiced, and subsequently, on how the mating

pairs are chosen. For traits where both extremes are suboptimal, selection and negative assortative mating are expected to produce an intermediate or more nearly optimum phenotype (Thomas et al., 1986). When total genetic merit is composed of several traits, with at least one related nonlinearly to overall merit, a benefit from negative assortative mating and selection can be expected. Examples of traits which are likely to have a nonlinear relationship with total economic merit and scale of measurement are traits describing condition, shape, or pregnancy an animal (Allaire, 1977).

Evaluation of Corrective Mating for Type Traits

Burnside et al. (1977) analyzed scores from maternal half-sisters of 53 AI Holstein-Friesian sires to compare progeny distributions from "Improver" sires vs. "Non-Improver" sires. Progeny from "Improver" sires differed dramatically for size, rump, dairy character, and body capacity, from progeny of "Non-Improver sires". Less differences were observed for legs and feet and udder components. Correlation between sire progeny test and mate's conformation was used as a measure of the extent of use of corrective mating.

In evaluating the worst fault of a cow ignoring basic form, Berger et al. (1986) found that the seven traits listed most often were legs (16.9%), fore udder, rump, feet, rear udder, fat test and scale, ranging from 8.5% to 9.6%.

The authors also found evidence of negative assortative mating for basic form through correlations between basic form scores of sires and dams in the mating appraisal for profit program (MAP) of 21st Century Genetics. Improvement in feet and mammary scores of progeny of specified matings as compared to scores of the dams was observed as compared to scores for progeny from unspecified matings. The improvement in progeny from assortative mating may be due to regression toward the population mean, because the scores of progeny of a cow scoring at one or the other extreme can be no worse than the score of the cow and generally would be be an improvement.

Thomas et al. (1986) used a sire's predicted differences for linear type traits and four measures of a dam's merit to predict offspring scores for 13 linear type traits. The four measures of dam's merit were phenotypic score deviated from overall mean, phenotypic score deviated from herd mean, a cow index, and one-half her sire's Predicted Difference. They concluded that the cow index combined with sire's predicted difference is the best predictor of offspring scores compared to other measures studied. However, for a set of 14,721 scores of cows on which no specific goal was determined, correlations between sire and dam measures were close to zero (lowest being for stature -.033, and highest for rear udder width .045) indicating a very low degree of corrective mating.

Corrective Mating for Linear Traits and its Effects on Production Traits

Only two studies have addressed the effects of corrective mating on production traits. Berger et al. (1986) reported that progeny from matings designed to correct the worst fault of the dam produced less milk (-144 kg) than progeny of matings in which the dam was not evaluated for linear traits by the MAP program. This comparison, however, may not be reliable because the fact that a dam had no evaluation in the MAP program does not mean that the breeder did not use type information to select a mate for a particular cow.

Misztal et al. (1992) showed that selecting only for milk yield, provided that the response in milk per year is around 181 kg, would decrease udder depth and fore udder attachment by 4.4 and 4.9 points, respectively, while increasing dairy form by 10.8 points, body depth 3.1 points, and rear udder width by 4.6 points, in a time period of 25 years. The author also showed that the cost of maintaining udder depth at its current value would result in a decrease of 15% in genetic gain for milk.

Mate Selection to Increase Total Genetic Merit

A distinction between mate selection and corrective mating is necessary because, in mate selection, "correcting" the phenotype of progeny may not be important. The problem in mate selection is centered on choosing a set of mating pairs from a population of possible pairs. Mate selection

can be regarded as a stage of corrective mating, where the first stage consists of an "unconditional" selection of one parent, in this case, a dam, and the second stage would be the selection of a sire depending on the phenotype of the first parent already selected (Allaire, 1977).

Selection of mating pairs to improve overall merit of progeny implies that the objective of selection is to increase merit of progeny. Then, the selected population is the resulting progeny (Smith and Allaire, 1985). Selecting a pair of parents is equivalent to choosing an action in decision theory. The problem is to determine the action **a** among a set of actions **A**, that minimizes the loss, **-M(a)**, associated with making a decision. According to Berger (1980), Bayesian decision rules to find an action $\mathbf{a}^*$ which minimizes the conditional expectation of the loss given data, **E[-M(a)/y]**, can be summarized as follows,

a) Listing of parents or mating pairs

b) Computing expected total genetic merit, **E[T/y]**, for each individual resulting from the matings. Total phenotypic merit may be defined as $\mathbf{T} = \sum f_i \mathbf{P}_i$, where $\mathbf{P}_i$ is the phenotype for the i-th trait, and f_i is the economic weight for the trait. In comparing different values of **T**, obtained by using different sets of weights, it is possible to determine how important economic weights are in selecting mating pairs. Variance of **T** for different sets of weights can be an aid in eliciting the appropriate set of weights.

Variance of **T**, in matrix notation, can be defined as

$$V(\mathbf{T}) = f'Pf$$

where f is the vector of weights and P is phenotypic covariance matrix for the traits. Here, it is assumed that the **T** is linear.

c) Identifying action $\mathbf{a}^{*}$. Integer linear programming can be used in this case to maximize:

$$\Sigma_{ij} x_{ij} c_{ij}$$

Subject to : $\Sigma_i x_{ij} = 1$, $j = 1,2,...,m$ (number of cows).

$\Sigma_j x_{ij} \leq n_i$, $i = 1,2,...,n$ (number of sires). The quantity n_i is number of units of semen available for the i-th sire. The value x_{ij} is an integer quantity taking values of 1 or 0. If $x_{ij} = 1$ when the solution id found, then the j-th cow is mated with the i-th sire. The variable c_{ij} is expected total economic phenotypic merit (T) of progeny produced by mating the i-th sire to the j-th cow.

Mate selection becomes necessary when independent selection of mates is not effective due to lack of constant change in economic value expected along the scale of measurement of a trait (Allaire, 1980), i.e., the relationship between the metric of the trait and its economic value is not linear. Allaire (1980) proposed that economic traits in dairy cattle contributing to net merit of an individual have linear relationships (e.g., milk solids yield), or non-linear relationships (e.g., fertility, udder conformation, disease resistance) with total merit, when

total merit is defined as

$$I_p = e_1 [1/2(I_1^{\bullet} + I_1^{'})] + e_2 [1/2(I_2^{\bullet} + I_2^{'})] + \ldots + e_k [1/2(I_k^{\bullet} + I_k^{'})]$$

where e_i and $I_i^{\bullet}$ and $I_i^{'}$ are expected economic return per unit and estimated breeding value of an individual for the i-th trait. The value I_p is the total economic merit for k traits of a progeny predicted from the mean parent predictions for each trait. Allaire (1980) found that when the economic values of traits changed with each potential mate, as a result of the expected breeding value of the progeny from a given mating pair, mate selection was preferable to individual selection. Selection of parents of the next generation, then, should be based on the ranking of mating pairs rather than on the ranking of individuals. Ranking of mating pairs would be achieved by using expected total predicted merit of progeny from each mating pair.

Mate selection can be useful as a mating strategy for short term gain mating strategy (Smith and Allaire, 1985); however, used sequentially, it can be of value to improve in the long term merit.

Bayesian selection rules previously defined fail to minimize the loss when means of traits and phenotypes of progeny cannot be predicted accurately. Thus, mixed model procedures can be adapted to estimate means and phenotypes, as shown by Smith and Allaire (1985).

MATERIALS AND METHODS

Corrective Mating for Worst Fault of Cow

In evaluating corrective mating a strict system to identify cows undergoing corrective mating is necessary. In order to classify matings, identification of cows for which recommendations were made needs to appear in the pedigree of their progeny. If the score of a cow for which recommendations were made is available, adjustment for contribution of mate can be made when evaluating the efficacy of the recommendation. Identification of mates is important for investigation of how well a given sire solved the problem for which the sire was recommended and compare the kind of progeny obtained and expected from such a mating.

The mating appraisal for profit (MAP) program of 21st Century Genetics was designed to assist farmers when choosing a sire to mate to a cow with problem type traits, in order to produce more uniform progeny for type while maintaining a high level of production for milk, fat, and protein. The MAP program uses evaluators for type, who visually score cows in the field using a linear scoring system with a range of values from 1 to 50. The system of linear scoring initiated in 1979 having 18 linear type traits scored. Table 1 provides a description of type traits scored using a linear scoring system in the MAP program. The trait which is used as the first basis for recommendations

TABLE 1. Description of linear type traits.

Trait	Score of 1	Score of 50
Basic form	Angular	Thick
Strength of body	Narrow and frail	Wide and strong
Dairyness	Undesirable	Outstanding
Stature	Short	Tall
Body depth	Shallow body	Deep body
Rump side view	Pins higher than hips	Extreme slope
Rear legs side	Posty	Sickle hocked
Foot angle	Low angle	Steep angle
Fore udder attachment	Broken	Tight
Udder depth	Deep	Shallow
Rump width	Narrow	Wide
Rear legs rear view	Severe toe out	No toe out
Rear udder height	Low	High
Rear udder width	Narrow	Wide
Suspensory ligament	Negative cleft	Extreme cleft
Teat placement	Base of teats wide	Base of teats touching
Disposition	Extreme problem	Excellent
Milkout	Extremely slow	Extremely fast