A STUDY ON THE PREDICTION OF SIRES BREEDING VALUE

By

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Approval Sheet

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Abstract

This study was carried out to evaluate 79 sires, each one had at least 10 daughters, each daughter had 305-day first lactation record. Sires evaluations were without and with using relationships among these sires (relationship inverse matrix A^{-1}).

Data were consisted of 4,318 305-day first lactation records in the period from 1960 through 1989 from two herds of Friesian cattle raised in Sakha and El_Karada experimental stations, belonging to Animal Production Research Institute, Ministry of Agriculture, Egypt. Two seasons of freshening were defined, November to April and May to October. A total of 97 herd-year-season subclasses were formed. Data editing left 1,812 records in the period from 1963 through 1989 in two herds of Friesian cattle within 94 herd-year-season subclasses. To account for genetic trend, five genetic groups were arbitrarily defined according to the year of birth of sires. Data were analyzed using Harvey (1990) program. Two analyses were done using the same model with and without utilizing A^{-1}. The model included herd-year-seasons, age at first calving, and groups as fixed effects and sires within groups as a random effect. The overall mean of milk yield was 1,967 kg with a standard deviation of 445 kg. The transmitting ability (TA) estimates predicted without using A^{-1} ranged from 182.22 to -142.76 kg with an average difference between sires of 4.1 kg. Estimates of TA when A^{-1} was used ranged from 197.40 to -143.09 kg with an average difference between sires of 4.3 kg. Whether A^{-1} was used or not, 52 % and 48 % of the sires had positive and negative TA estimates, respectively. The difference between TA estimates with and without using A^{-1}, appeared random and many were large. The greatest absolute change was 47.86 kg. There were 59 sires (74.7 %) showed an absolute difference of less than 10 kg and 20 sires (25.3 %) showed 10 kg or more. There were

44 sires (56 %) showed positive deviations by using A^{-1}, However, there were 35 sires (44 %) showed negative deviations. The rank of 65 sires (82 %) had been changed after using A^{-1}. The rank of 14 sires (18 %) had not been changed. It did indicated that using A^{-1} affected sires' rank. Product moment correlations and rank correlations among sires TA estimates with and without using A^{-1} were large .96 and .98 for milk, respectively. Rank correlations were .39 for top ten sires and .98 for the bottom ten sires. The first two sires in the top ten sires had the same rank with or without using A^{-1}. The remaining top ten sires ranked differently using A^{-1}. Some of the top ten sires showed large differences using A^{-1} in both the TA estimates and the rank. The maximum absolute difference among TA estimates with and without using A^{-1} for a sire from the top ten sires was 47.86 kg of milk and the rank for that sire changed from 4 to 3. The percentages of the variance components changed slightly using A^{-1}. The value of the heritability of milk yield estimated without using A^{-1} was .16, while its value using A^{-1} was .17.

KEY WORDS

Sire Evaluation
Breeding Value
Transmitting Ability
Best Linear Unbiased Prediction

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INTRODUCTION

The herd sire is half of the herd. In the past, it meant that half of the future herd genes would come from the sire and half from his mates. At present, it means that half of the future herds genes comes from the sire and the other half from cows that coincided with the spread of artificial insemination (AI) which gives the sire possibility of having daughters in many herds at the same time.

In Egypt, the majority of dairy cattle are owned by small farmers who have less than five heads each. Sires in such case are not selected based on their productive traits or their genetic merits but on their phenotypes, semen characters, and the ability to mount. Therefore, there is no appropriate opportunity for genetic improvement, besides the potentiality of using bad sires.

The accuracy of sire evaluation and consequently sires' rank depends to a large magnitude on the factors that are included in the statistical model. The resemblance between relatives has long been known as one of the most important phenomena in population genetics theory. Including the inverse of the relationship matrix in the statistical model, as a measure of resemblance among sires, provides relationship ties among contemporary groups. Relationship ties do the same things as reference sires having progeny in many different contemporary groups. It also gives predictions that include the paternal half-sib information that are available. This concept is equivalent to the selection index theory approach which combines sources of information into one predicted value. The lower the heritability of the trait, the more important this aspect of including the relationship inverse matrix becomes.

The objective of this study was to evaluate the effect of either neglecting or using the relationship matrix on sires' proofs accuracy and their rank using the best linear unbiased prediction (BLUP) method.

REVIEW OF LITERATURE

Sire Evaluation Methods:

The concept of sire evaluation means estimating a value for each sire representing its breeding value. The rank of these sires' values in an descending order permits the optimum choice of sires. Sires with highest values at the top of the rank have the highest breeding value. There are four basic information sources from which the breeding value can be estimated. These are: (1) the animal itself; (2) the animal's progeny; (3) the animal's ancestors; and (4) collateral relatives (Donald et al., 1978). Since sires do not have phenotype for milk, their daughters has to be used in the evaluation as the most important source of information.

Pedigree Evaluation:

Pedigree evaluation for the breeding value is based on studying records of an animal's ancestors. Its usefulness lies on the fact that each animal receives one half of its genes from one parent and the other half comes from the other parent. The most important identifiable relationships among sires used in AI are due to common sires and maternal grandsires (Henderson, 1975d). Pedigree information are most valuable for young bulls that have no progeny (Donald et al., 1978).

Robertson and Rendel (1950) found that the percent of the theoretical genetic gain was 43 % from sires of bulls, 33 % form dams of bulls, 18 % from sires of cows and 6 % from dams of cows in two thousand cows population under AI. Skjervold (1963) found that the percent of the theoretical genetic gain from the same four sources was 46 %, 24 %, 24 %, and 6 % respectively for 60,000 cows population under artificial insemination.

Most of these kinds of studies of the genetic gain were made considering selection for only a single trait. In real life, several traits are selected which reduces the genetic gain.

Van Vleck and Carter (1972) explained a two-stage selection method for AI bulls which has been widely used in dairy sire selection. In the first stage, young bulls are selected based on their three-point pedigree (sire, dam, and maternal grandsire) evaluations. In the second stage, the same young bulls are progeny tested in AI and the best group are returned to the active service when their daughters are evaluated. Pedigree evaluation and selection of young bulls to progeny test, the first stage, is probably the weakest point in dairy cattle improvement. Any increase in the accuracy of pedigree evaluation could result in faster progress and (or) less cost.

Progeny Test:

The importance of proving sires has increased with the growth of AI and many procedures have been proposed for evaluating sires used in AI programs based on the records of their progeny. In fact, the progeny test appears to be the most valuable tool by which sires can be chosen for heavy service (Van Vleck et al., 1961).

Progeny testing is valuable for traits of low heritability, sex-limited traits, and slaughter traits. Progeny testing is performed by different methods.

White et al. (1981) pointed out that dairymen have used sire evaluations based on Daughter-Dam Comparison, Herdmate Comparison , Contemporary Comparison, and Modified Contemporary Comparison, as well as by Best Linear Unbiased Prediction (BLUP) procedures.

Daughter-Dam Comparison:

Donald et al. (1978) reported that this method based on comparing the adjusted yield of a bull's daughters with the adjusted yield of their dams. They pointed out the advantages of the daughter-dam comparison. It attempted to take into account both the sampling nature of inheritance and the fact that environmental effects were important in determining the yield of the daughters and the dams. Its disadvantage lies in that there was about 2.5 years lapse between the time that dams and daughters made their first records and in that period environmental changes occur even within a single herd. Therefore, daughter-dam comparison is severely biased, the bias increases if the dam and her daughter made their records in different herds.