

DIFFERENT ANIMAL MODELS FOR ESTIMATING BREEDING VALUES USING EARLIER RECORDS IN A FRIESIAN HERD IN EGYPT

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SUMMARY

Different methods for evaluating sires, considering available information, were investigated. Multiple-trait and single-trait animal model analyses were employed to obtain predicted breeding values (PBVs) for all the sires in the herd for the first three lactations of Friesian cows in an institutional herd in Egypt. Three types of statistical analyses were investigated.

In the first analysis (analysis 1), the multiple-trait animal model with derivative free restricted maximum likelihood (DF-REML) was used to analyze the first three lactations simultaneously as three different traits where covariances between the three lactations and relationships between animals were taken into account. Different sets of fixed effects were fitted to each lactation.

In the second analysis (analysis 2), the single-trait animal model with DF-REML was used. Records of each lactation were analyzed separately ignoring the other two lactations. The third analysis (analysis 3), records of the three lactations were used in a repeatability model utilizing the single-trait animal model with DF-REML.

g values (PBVs) were higher in the multiple-trait analysis compared with the single-trait analysis (0.94, 0.89 and 0.97 between lactations 1,2, 1,3 and 2,3 vs. 0.46, 0.34 and 0.36), respectively. Accuracy was higher in the multiple-trait analysis by 6.33% than in the single-trait analysis. PBVs obtained from analysis 1 were weighted economically in a combined index to obtain one aggregate BV for each animal. The relative weights were 1, 0.95 and 0.63 for lactations 1, 2 and 3, respectively. Heritability and repeatability estimates obtained from the third analysis (analysis 3) were 0.14 and 0.34 respectively. It was concluded that using the multiple-trait analysis is recommended to obtain more accurate breeding values for the studied traits because it makes use of all the information about the lactations and the covariances among them as well as the relationships between the relatives in the different traits.

Keywords: Dairy cattle, Friesian, sire evaluation, multiple-trait, breeding values, animal model and DF-REML.

INTRODUCTION

Over the last 50 years, dairy breeders and other practitioners were often concerned with the problem of predicting sires' breeding values. The development of methods and techniques of evaluation of sires have passed through several stages and routines. The genetic values of sires are always of interest for the purpose of selection, estimating the genetic trend, and determining economic merits of the animals. Application of mixed linear models (MLM) to animal breeding has been justified on the grounds of best linear unbiased estimation and prediction (BLUP). Properties of those MLM require knowledge of the variance-covariance structures for traits and individuals in the population.

Maximizing genetic progress in a breeding program involves using the most appropriate method of evaluation to make optimum breeding decisions. These methods are based mainly on utilizing all the available information to increase the accuracy of evaluation of the animal's genetic value.

The objectives of this study were to compare three methods to evaluate sires using the animal model strategy protocol under single and multiple-trait procedures for the first three lactations of Friesian cattle.

MATERIAL AND METHODS

Data

Data utilized in this study were from the Friesian herd raised in Sakha and Alkarada experimental farms, Kafrelsheikh governorate in the Nile Delta which belong to the Animal Production Research Institute (APRI), Ministry of Agriculture. The herd was established by the import of 948 pregnant heifers and 19 bulls from The Netherlands in 1959. Data covered the period from 1960 to 1994 and consist of 9622 records on the first three lactations of 4459 Friesian cows progeny of 301 sires and 2400 dams. All cows were inseminated artificially using frozen semen locally prepared from sires produced in the same herd at Sakha and Alkarada farms.

Management and Nutrition

Animals were kept under the routine feeding and managerial system applied in Sakha and Alkarada animal experimental farms. Dried off cows were fed on Egyptian clover (berseem) (*Trifolium alexandrinum*) from November till mid- May. However, cows in milk grazed berseem from 10:00 hrs to 14:00 hrs, then were given rice straw at the rate of 4 kg/animal. Concentrate mixture were given to cover about 60% of their requirement. In summer (mid-May to November) the animals were fed on concentrate mixture, rice straw and berseem hay if available. Daily allowances were offered in amounts to cover the animal requirements according to their milk production, body weight and the reproductive status as recommended by APRI, 1968.

Predicted Breeding Values (PBVs)

Model 1:

Multiple-trait derivative-free restricted maximum likelihood (DF- REML) with animal model analysis (Boldman *et al.*, 1993) using records of the first three

lactations simultaneously taking into account the interrelationships among the lactations. In this analysis, the first three lactations were treated as three different traits and analyzed simultaneously to obtain three predicted breeding values. The distribution of records available at each parity, for this analysis, is shown in Table 1.

Table 1. Pattern of data distribution utilized in the multiple-trait analysis

Description	lactation		
	1	2	3
Records of cows with lactations 1,2 and 3	2028	2028	2028
Records of cows with lactations 1 and 2	956	956	-
Records of cows with lactation 1 only	1162	-	-
Records of cows with lactations 1 and 3	40	-	40
Records of cows with lactation 2 only	-	132	-
Records of cows with lactations 2 and 3	-	111	111
Records of cows with lactation 3 only	-	-	30
Total	4186	3227	2209

Also, in this analysis all possible relationships among the animals were considered following Quaas (1976). The assumed animal model was:

$$y = X\beta + Zu + e,$$

with the following mixed model equations:

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

where,

y is $N \times 3$ matrix of observations of 305-d milk yield in the first three lactations,

X is the incidence matrix that associates the fixed effects to the observations,

β is the vector of fixed effects including farm, year of calving and season of calving with one covariate term for age at calving,

Z is the incidence matrix that associates random effects to the observations,

u is the vector of animal random effects, and

e is the vector of random residual effects associated with each observation.

Assuming that:

$$E \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \quad V \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix}$$

where,

G is the direct additive genetic variance-covariance matrix of the traits; and

R is the residual variance-covariance matrix.

Convergence was obtained when assuming that the variance of the log likelihood values in the simplex reached $<10^{-19}$.

Model 2:

Single-trait DF-REML with animal model analysis (Boldman et. al, 1993) of records of the first three lactations separately each as a separate trait was used to obtain predicted breeding values for animals in each lactation was:

$$y = X\beta + Z u + e ,$$

where,

y is N*1 column vector of observation of 305-d milk yield records for each lactation; and

X, β , Z, u and e are defined as before.

The single-trait mixed model equations used were:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\lambda \end{bmatrix} \begin{bmatrix} \beta \\ u \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

where,

λ is the ratio of the residual variance to the additive genetic variance; and

A^{-1} is the inverse of the numerator relationship matrix between animals.

Model 3:

Single-trait DF-REML with animal model (Boldman et. al, 1993) analysis of the lactation records as one trait (repeatability model) was used. For analyzing the single trait, the animal model was:

$$y = X\beta + Z_a a + Z_p p + e$$

where:

y is N*1 column vector of observation of 305-d milk yield records;

X is the incidence matrix that associates the fixed effects to the observations;

β is the vector of fixed effects including farm, year of calving, season of calving, parity and one covariate term (age at calving);

Z_a is the incidence matrix that associates additive genetic random effects to the observations,

a is the vector of additive genetic effects of cows with mean=0 and variance = $A\sigma^2_g$;

Z_p is the incidence matrix that associates the random permanent environmental effects to the observations;

p is the vector of the permanent environmental effect of cows; and

e is the vector of random residual effects associated with each observation with mean=0 and variance = $I\sigma^2_e$.

Predicting the Aggregate Animal Breeding Value (APBV)

To combine the three breeding values resulting from the multiple-trait analysis into one value, the procedure of Meyer (1983), using an index that includes the predicted breeding value of each lactation and the lactation's relative economic weight, was followed. The relative economic weights used in this study were obtained according to Hill and Swanson (1983), who used the lactation relative frequency in the herd as its economic weight. Sakha and Alkarada farms had 12,195 records of which 28.1%, 26.66% and 17.64% were first, second and third lactations, respectively. Thus the relative economic weights, respectively, were: $a_1 = 1$, $a_2 = 0.95$ and $a_3 = 0.63$, respectively. The constructed index was:

$$ABV = a_1u_1 + a_2u_2 + a_3u_3$$

where,

ABV is the aggregate breeding value estimate,

u_i is the predicted breeding value for the i^{th} lactation, ($i=1, 2$ and 3)

a_i is the relative economic weight for the i^{th} lactation.

Accuracy

Accuracy of single-trait and multiple-trait animal models were calculated for analyses one and two according to Van der Wref (2001) depending on the selection index theory. Heritability estimates, genetic and phenotypic variances as well as correlations between lactations resulted from both analyses were used to apply the index theory. The same relative economic weights for the three lactations were also used.

Rank Correlation

A total of eight predicted breeding values were obtained for each animal included in the analysis (cows, sires and dams):

- three predicted breeding values for lactations 1, 2 and 3 resulting from the multiple-trait analysis (analysis 1);
- three predicted breeding values for lactations 1, 2 and 3 resulting from the single-trait analysis analyzing them separately (analysis 2); and
- one predicted breeding value resulting from analyzing the three records as a single trait analysis (repeatability model, analysis 3).
- one aggregate breeding value obtained from analysis 1.

Spearman rank correlation coefficients were estimated between all the eight breeding values including the aggregate breeding value. The Statistical Analysis System (SAS, 1989) package was utilized. The number of sires used in the rank correlations was 246 sires. Also, the rank correlation coefficients for the top 20% of sires (50 sires) were estimated.

RESULTS AND DISCUSSION

Accuracy of Multiple-trait vs Single-trait Models

Test of accuracy shows 6.33% more accuracy of utilizing the animal model with the multiple-trait procedure than that with the single-trait procedure as it accounts for the covariances among the traits, besides the relationships among the related animals

in all the three lactations simultaneously. Gengler and Coenraets (1997) and Dahlin *et al.* (1998) recommended the multiple-trait models for the higher accuracy than the single-trait models.

Predicted Breeding Values (PBVs)

Rank correlations between PBVs of the first three lactations are shown in Table 2. Rank correlations were higher in the multiple-trait analysis than their corresponding values from the single-trait analysis. Meyer (1983) reported a rank correlation of 0.55 between first and second lactation proofs from single-trait analysis and 0.98 between the same two lactations using multiple-trait evaluation as compared to 0.46 and 0.94, respectively in this study. Wickham and Henderson (1977) reported a rank correlation of 0.77 between the first two lactations' evaluation ignoring the selection. The difference between the estimates may be due to that in the single-trait analysis, each lactation is analyzed separately without considering the relationships among the related animals in the other two lactations nor the covariance structure among the lactations, which is in contrast to the multiple-trait analysis which takes into account all available relationships and covariances between traits under study. The rank correlations for the top 20% of sires obtained in the present study are reported in Table 2. The rank correlations between the BVs of the first three lactations are very low in the single trait analysis (ranging from -0.10 to 0.29) compared with the estimates from multiple trait analysis (from 0.54 to 0.87). As shown in Table 2, the rank correlation between the first and second lactation in the single-trait analysis, where each lactation was analyzed separately, was of a small magnitude (-0.01) while the corresponding correlation for the multiple trait analysis was 0.77. Correlations involving lactation 3 exhibited similar trend.

Table 2. Rank correlation coefficients between sire PBVs of 305-d milk production of the first three lactations using multiple and single-trait analyses for all sires and for top 20% of sires (probability of type I error)

Lactations	Multiple-trait evaluation (Analysis 1)		Single-trait evaluation (Analysis 2)	
	All sires	Top 20%	All sires	Top 20%
1,2	0.94 (.0001)	0.77 (0.0001)	0.46 (0.0001)	-0.01 (0.96)
1,3	0.89 (.0001)	0.54 (0.0001)	0.34 (0.0001)	-0.10 (0.50)
2,3	0.97 (.0001)	0.87 (.0001)	0.36 (0.0001)	0.29 (0.04)

Among the top 20% sires, the highest rank correlation was found between the second and third lactations (0.87), estimated from multiple-trait analysis, while it was only 0.29 when single trait results were used. These results show that top sires with high breeding values were highly affected by the amount of information and the structure of the data utilized in the analysis. Using the complete structure of the data and all pedigree information in the multiple-trait analysis, gave high correlations

between lactations, while in the single-trait analysis where the complete structure of the data is ignored, correlations between lactations were low.

In spite of the high rank correlation reported by Meyer (1983) between the first and later lactations' BVs, she concluded that there were changes in the BVs between lactations for individual sires. Pollak *et al.* (1984), in a simulation study, concluded that applying multiple-trait methodology increased the accuracy of prediction for the trait and in some cases eliminated bias due to selection. Gengler and Coenraets (1997) reported the same conclusion. Dahlin *et al.* (1998) recommended the multiple-trait animal model for obtaining most accurate prediction using data on 4000 Sahiwal cows. The animal model strategy for predicting breeding values for milk production of the first three lactations were used by many researchers (Van der Werf *et al.*, 1994 and Sigurdsson and Arnason, 1995).

Aggregate Predicted Breeding Value (APBV)

Nicholson *et al.* (1978) using multiple-trait evaluation method, pointed out that the resulting PBVs should be combined using a suitable method and weights to get single PBV for each sire. The three breeding values (PBVs) resulted from the multiple trait analysis were combined into one aggregate value for each sire based on the relative economic weights for each of the first three lactations. Some rank correlation coefficients involving these aggregate predicted breeding values are shown in Tables 3 and 4.

Table 3. Rank correlation between sire's BVs in the first lactation (single-trait) and other evaluations for all sires and for the top 20% of sires (probability of type I error)

Evaluation	First lactation as a singletrait Analysis 2	
	All sires	Top 20 %
First lactation in a multiple trait (analysis 1)	0.97 (.0001)	0.94 (.0001)
All 3-lactations as single trait (analysis 3)	0.80 (.0001)	0.42 (.0023)
An index from multiple-trait (aggregate PBVs)	0.90 (.0001)	0.77 (.0001)

Table 4. Rank correlation coefficients between the APBVs and other sire evaluations for all sires and for the top 20% (probability of type I error)

Evaluation	All sires	Top 20%
The APBV and first lactation – multiple trait	0.97 (.0001)	0.90 (.0001)
The APBV and repeatability model as a single trait	0.94 (.0001)	0.76 (.0001)

Meyer (1983) combined the sire proofs resulting from a multiple-trait evaluation describing them as partial breeding values using an index with suitable relative economic weights. She recommended using multiple-trait analysis for simultaneous evaluation to increase the accuracy.

Many dairy breeders depend on the first lactation records to evaluate sires. The first lactation is an easy and less costly information utilized in estimating genetic values, but Ufford *et al.* (1979) stated that utilizing more records than the first increases the accuracy. Wickham and Henderson (1977) concluded that ranking of sires based on first lactation evaluation could be different from that based on second lactation evaluation. They suggested constructing an index using relative economic values for each lactation as an optimal method.

The resulting rank correlations as shown in Table 2 between the first and second lactation when analyzed as separated traits was 0.46 while when the same two lactations treated in a multiple trait analysis allowing for the covariance between them to be accounted for, the rank correlation was 0.94. Although the first lactation record is an easy criterion for judging the later records, the second record is more valuable in predicting the third record than the first (Nicholson *et al.*, 1978). The rank correlation between the second and third lactations' BVs was only 0.36 using the single trait analysis and 0.97 in the multiple trait analysis.

Sire rank correlations between the first lactation evaluation (analysis 2) and the constructed index based on the relative economic weights of each of the first three lactations and other possible evaluations are shown in Table 3. The APBVs had a higher rank correlation with the all-3 lactation evaluation (repeatability model), as shown in Table 4, than the rank correlation between the first lactation single-trait evaluation and all-3 lactation (Table 3). The rank correlation was 0.76 i.e. as compared to that of (0.42) obtained from analyzing first-lactation as a single-trait.

The estimates of rank correlations between the index constructed depending on the multiple-trait breeding values and the evaluation based on the all-3 lactations (repeatability model) were higher in general for all sires and top 20% of sires than those estimates based on the first-lactation only (Table 4).

Table 5 shows that the association between the corresponding lactations from the analyses of single-trait and multiple-trait decreased with advancing the lactation. Ranking of sires according to the first lactation evaluation from single or multiple-trait evaluation had the highest rank correlation (0.97), while the third lactation had the lowest rank correlation coefficient (0.67). The rank correlation coefficient between the two analyses for the second lactation was in the middle (0.79).

Table 5. Rank correlation coefficients between the corresponding lactations from both single and multiple-trait analyses(probability of type I error)

Rank correlation between single and multiple-trait PBVs		
	All Sires	Top 20%
1,1	0.97 (.0001)	0.94 (.0001)
2, 2	0.79 (.0001)	0.68 (.0001)
3, 3	0.67 (.0001)	0.63 (.0001)

Predicting the sire breeding values for the second and third lactations from the first and second lactations for high ranking sires can be carried out more accurately based on multiple trait evaluation than on the single trait evaluation analysis.

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نماذج الحيوان المختلفة لتقدير القيم التربوية باستخدام السجلات المبكرة في قطيع فريزيان في مصر

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تم دراسة و مناقشة عدة طرق مختلفة لتقييم الطلائق مع استخدام جميع البيانات المتاحة على القطيع. تم التنبؤ بالقيم التربوية لكل الطلائق الموجودة في القطيع باستخدام نموذج الحيوان (Animal Model) في حالة نموذج متعدد الصفات (Multiple-trait) و أيضا في حالة نموذج احادى الصفة (Single-trait) و ذلك لصفة انتاج اللبن في ٣٠٥ يوم للمواسم الثلاثة الاولى لأبقار الفريزيان الموجودة في قطيع حكومى في مصر.

تم مناقشة ثلاث أنواع من التحليلات الإحصائية :

في التحليل الأول (تحليل ١) ، تم تحليل صفة إنتاج اللبن في أول ٣ مواسم كثلاث صفات مختلفة في آن واحد آخذين في الاعتبار العلاقات بين الأفراد و أيضا التغيرات بين المواسم و ذلك باستخدام نموذج الحيوان متعدد الصفات و تم إعتبار تأثيرات ثابتة لكل موسم على حدة.

في التحليل الثانى (تحليل ٢)، استخدم نموذج الحيوان أحادى الصفة وقد حلل كل موسم على حدة ولم يؤخذ في الإعتبار العلاقات بين المواسم. وفي التحليل الثالث استخدمت بيانات الثلاثة مواسم في نموذج الحيوان أحادى الصفة مع المعامل التكرارى (Repeatability Model).

وقد أظهرت النتائج أن ارتباط الرتب بين القيم التربوية المتوقعة للمواسم الثلاثة الأولى كان أعلى في القيمة في تحليل الصفات المتعددة عنه في حالة تحليل الصفة الواحدة و كان (٠,٩٤ ، ٠,٨٩ ، ٠,٩٧ بين المواسم ٢,١ ، ٣,١ ، ٣,٢ مقابل ٠,٤٦ ، ٠,٣٤ ، ٠,٣٦) على التوالي. و أيضا كانت دقة التنبؤ بالقيم التربوية أعلى في تحليل الصفات المتعددة ب ٦,٣٣ % عن تحليل الصفة الواحدة. كما استخدمت أوزان اقتصادية نسبية للثلاث قيم تربوية الناتجة من تحليل ١ في عمل دليل لحساب قيمة تربوية مجمعة. وكانت هذه القيم ١,٩٥ ، ٠,٦٣ ، ٣,٢ على التوالي.

كانت قيم المكافئ الوراثى و المعامل التكرارى للتحليل الثالث (تحليل ٣) هي ٠,١٤ و ٠,٣٤ على التوالي.

و قد أوصت نتائج هذه الدراسة باستخدام نموذج الحيوان في حالة الصفات المتعددة للتنبؤ بقيم تربوية أدق للصفات المدروسة و ذلك لأنه يستخدم جميع البيانات المتاحة على المواسم و أيضا يأخذ في الإعتبار التغيرات بينهم وكذلك يأخذ في الإعتبار العلاقات بين الأفراد في الصفات المختلفة.