GENETIC ANALYSIS FOR SOME PRODUCTIVE TRAITS OF HOLSTEIN FRIESIAN COWS IN EGYPT THROUGH MTDFREML PROGRAM

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SUMMARY

A total of 2096 normal lactation records of Holstein Friesian cattle kept at Dalla farm in Egypt during the period from 1988 to 1992 were used in this investigation. Data were analyzed by Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) using repeatability animal model. The model included individual, permanent environment and errors as random effects, month and year of calving and lactation number as fixed effects and days open as a covariate. Genetic parameters and breeding values of cow, sire and dam for 305 day milk yield (305dMY) in kg, lactation period (LP) and dry period (DP) in days were estimated.

Estimates of heritability were 0.32, 0.07 and 0.03 for 305dMY, LP and DP, respectively. Repeatability estimates were 0.93, 0.78 and 0.27 for the same traits, respectively. The genetic correlation between 305dMY and LP was positive and high (0.97), whereas the genetic correlation between 305dMY and DP and between LP and DP was negative, -0.51 and -0.71, respectively. Cow breeding values, (CBV) ranged from -735 to 1579 kg for 305dMY, from -1.9 to 5.5 d for LP and from -2.4 to 6.1 d for DP. Likewise sire estimated breeding values, (SBV), were from -628 to 661 kg, from -1.9 to 4.6 d and from -3.2 to 5.5 d for the same traits, respectively. Dam breeding values, (DBV) ranged between -1225 and 878 kg, -3.3 and 6.4 d and -3.6 and -5.0 d for the above mentioned traits, respectively.

Keywords: Breeding values, milk traits, Holstein Friesian, multiple traits

INTRODUCTION

For dairy cattle improvement, prediction of breeding values with an animal model instead of the computation of separate genetic evaluation for cows and bulls is becoming common, Suzuki and Van Vleck (1994). Its calculation starts with the cow as source of production information. Prediction records on cows are influenced by effects shared by a management group within a herd, effects shared by daughters of a sire in a herd and permanent environmental effects peculiar to all records of a particular cow. Such environmental effects are usually accounted for in the model (repeatability model) to ensure accurate prediction of breeding (Mrode, 1996).

Genetic variance might be underestimated if selection intensity is large for males than for females (Misztal *et al.*, 1992). Animal models take into account differential selection of males and females and, might provide more accurate estimates of parameters than do sire models.

The objective of this study was to estimate the genetic parameters and breeding values using all available sources of pedigree, cows, sires and dams for 305 day milk yield (305dMY), lactation period (LP), and dry period (DP), by using multivariate analysis (Multi Trait Animal Model).

MATERIAL AND METHODS

The data used in the present investigation were collected from the history sheets of Holstein Friesian cows maintained at Dalla Farm , 130 km North West of Cairo. The nucleus of this herd was imported to Egypt from United States as pregnant heifers in 1986. The data comprised 2096 normal lactation records spread over the period from 1988 to 1992, representing in parities from 1 to 6. Abnormal records of cows affected by diseases (such as mastitis and udder troubles) or reproductive disorders were excluded. Animals were kept loose under semi-open sheds all the year round. All cows were fed concentrate mixture, rice straw and grazed (*Trifolium alexandrinum*) during the year. The concentrate mixture used was composed of 45% cotton seed cake, 26% wheat bran, 17% yellow maize, 7% rice bran, 2% molasses, 1% sodium chloride and 2% calcium carbonate. Concentrates were offered twice daily before milking according to cows body weight and her milk production. Cows were machine milked twice a day (at 7 a.m. and 4 p.m.). Milk yield was recorded to the nearest 0.2 kg, for each cow. Cows producing more than 10 kg a day and those in the last two months of pregnancy were supplemented with extra concentrate rations. Cows were artificially inseminated by using frozen semen imported from USA. Assignment of sires to cows was at random. Heifers were served for the first time when they reached 24 months or 350 kg. Cows were usually served two months postpartum. Pregnancy was detected by rectal palpation 60 days after the last service.

Data were analysed by Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) according to Boldman *et al.* (1995), using repeatability animal model single and multiple trait analysis. Table 1. shows the data structure considered in the analysis, means of 305 day milk yield (305dMY) in kg, lactation period (LP) and dry period (DP) in days, number of mixed model equations and number of iterations.

Firstly, traits were analysed through single trait animal model using mean literature values reported by Suzuki and Van Vleck (1994) for 305 d MY and Makuza and McDaniel (1996) for LP and DP as starting values.

Secondly, variances of genetic, permanent and residual effects obtained from the analysis of single trait animal model were used as start values in multiple trait animal model analysis. In addition permanent environmental effects for each cow were used to calculate the permanent covariance between each two traits, while the genetic and residual covariances were obtained using the Mixed Model Least Squares and Maximum Likelihood (LSMLMW) computer program of Harvey (1990) for all traits. The Multi Trait Animal Model was used to analyze 305dMY, LP and DP included individual, permanent environment and errors as random effects, month and year of calving and lactation number as fixed effects and days open as a covariate.

Table 1. Structure of data used in analysis, unadjusted means, standard deviation (SD) and CV% for 305 day milk yield (305 d MY), lactation period (LP) and dry period (DP)

	$\bar{x}$	SD	CV%
Traits			
305dMY, kg	5021	1368	27.3
LP, d	286	64	22.6
DP, d	108	65	59.5
Observations			
No. of records	2096		
No. of cow	606		
No. of sires	259		
No. of dams	434		
Animals in relationship matrix	1299		
Mixed model equations, no. MME	5787		
No. of iterations	5659		

In matrix notation the animal model used was:

$Y = Xb + Za + Wp + e$

Where:

Y = observations vector of records, b = fixed effects vector (e. g, parity from 1 to 6 , years from 1988 to 1992 and month of calving from January to December) , a = animal direct genetic effect vector, p = permanent environmental effect vector, and e = residual effect vector. X, Z and W are incidence matrices relating records to fixed animal and permanent environmental effects respectively.

Vector **a** only includes additive random animal effects; consequently, non-additive genetic effects are included in the **p** term. It is assumed that the permanent environmental effects and residual effects are independently distributed, with means of zero and variances σ^2_p and σ^2_e respectively. Therefore

$\text{Var}(p) = I\,\sigma^2_p$

$\text{Var}(e) = I\,\sigma^2_e = R$

$\text{Var}(a) = A\,\sigma^2_a$

$\text{Var}(y) = ZA\acute{Z}\,\sigma^2_a + WI\,\sigma^2_p W' + R$

The variance and covariane structure for the model was as follows:

$$
\begin{bmatrix} a1 \\ a2 \\ a3 \\ P1 \\ P2 \\ P3 \\ e1 \\ e2 \\ e3 \end{bmatrix} =
\begin{bmatrix}
A\sigma^2 a_1 & \alpha_1 a_2 & \alpha_1 a_3 & 0 & 0 & 0 & 0 & 0 & 0 \\
\alpha_2 a_1 & A\sigma^2 a_2 & \alpha_2 a_3 & 0 & 0 & 0 & 0 & 0 & 0 \\
\alpha_3 a_1 & \alpha_3 a_3 & A\sigma^2 a_3 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & I\sigma^2 p_1 & \sigma p_1 p_2 & \sigma p_1 p_3 & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma p_2 p_1 & I\sigma^2 p_2 & \sigma p_2 p_3 & 0 & 0 & 0 \\
0 & 0 & 0 & \sigma p_3 p_1 & \sigma p_3 p_2 & I\sigma^2 p_3 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & I n_1 \sigma^2 e_1 & \sigma e_1 e_2 & \sigma e_1 e_3 \\
0 & 0 & 0 & 0 & 0 & 0 & \sigma e_2 e_1 & I n_2 \sigma^2 e_2 & \sigma e_2 e_3 \\
0 & 0 & 0 & 0 & 0 & 0 & \sigma e_3 e_1 & \sigma e_3 e_2 & I n_3 \sigma^2 e_3
\end{bmatrix}
$$

Where:
A = the numerator relationship matrix,
σ^2_{a1}, σ^2_{a2} and σ^2_{a3} = the direct genetic variance for trait 1, 2 and 3,
σ^2_{p1}, σ^2_{p2} and σ^2_{p3} = the variance due to permanent environmental effects,
Each of I_{n1}, I_{n2} and I_{n3} is an identity matrix of order equal to the records of traits 1, 2 and 3,
σ^2_{e1}, σ^2_{e2} and σ^2_{e3} = the residual variance effects and
$\sigma_{ai\,aj}$ = the direct genetic covariance items between any pair of the three traits studied.
$\sigma_{pi\,pj}$ = the permanent environmental covariance items between any pair of the three traits and
$\sigma_{ei\,ej}$ = all the residual covariance items between any pair of the three traits.
To estimate heritability (h^2) and repeatability (t) , the following equations were used:
$h^2 = \sigma^2_a / (\sigma^2_a + \sigma^2_p + \sigma^2_e)$, and
$t = (\sigma^2_a + \sigma^2_p) / (\sigma^2_a + \sigma^2_p + \sigma^2_e)$
Where:
σ^2_a = additive genetic variance; $\sigma^2 p$ = permanent environmental variance and σ^2_e = the random residual effect associated with each observation.
The mixed model equation (MME) for the best linear unbiased estimator (BLUP) of estimable functions of **b** and for the best linear unbiased prediction (BLUP) of **a** and **p** in matrix notation were as follows:

$$
\begin{bmatrix}
X'X & X'Z & X'W \\
Z'X & Z'Z + A^{-1}\alpha_1 & Z'W \\
W'X & W'Z & W'W + I\alpha_2
\end{bmatrix}
\begin{bmatrix} \hat{b} \\ \hat{a} \\ p \end{bmatrix} =
\begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}
$$

Where $\alpha_1 = \sigma^2_e/\sigma^2_a$ and $\alpha_2 = \sigma^2_e/\sigma^2_p$

RESULTS AND DISCUSSION

Unadjusted Mean and standard deviation (SD) for 305dMY in kg and LP and DP in days were 5021±1368 kg, 286±64 and 108±65d., respectively (Table 1). Estimates of coefficient of variations (CV%) are given in table 1. The large CV% value for DP (59.5%) reflects a great variation between individuals in such an important productive trait.

The average number of Mixed Model Equations (MME) and iterations recorded were 5787 and 5659, respectively. The present results are higher than those estimated from single trait animal model reported by Khattab *et al.* (2003) being 3200 and 1950, respectively. In addition, Salem (1998) using another herd of Holstein Friesian cattle in Egypt, using single trait animal model , found that the number of iterations for 305 d MY , LP and DP were 153 and 127 for 305 d MY and LP, respectively. The higher number of iterations in the present study may be due to using three traits in the same analysis and taking into consideration the genetic, permanent and errors covariances among these traits. In this respect, Swalve and Van Vleck (1987) used records of 4000 cows to estimate genetic parameters for milk yields of first, second and third lactations with an animal model, only 18 rounds of iteration were realized, while, Albuquerque *et al.* (1995) indicated that some runs stopped after 300 rounds of iteration. In general, number of iterations required to reach convergence could be affected by the number of animals, the number of random effects in the model and traits studies.

The heritability estimates were 0.32, 0.07 and 0.03 for 305dMY, LP and DP, respectively (Table 2). The present estimate of 305 d MY was higher than that estimated with a sire model by Hussein (1996), being (0.25±0.05) and is within the range of recorded values with an animal model (Van Vleck and Dong 1988, Van Vleck *et al.*, 1988 , Suzuki and Van Vleck , 1994 and Makuza and McDaniel, 1996), ranging from 0.30 to 0.36. The moderate estimate of heritability for 305 d MY, suggests that more efforts could be made to bring about improvement 305day milk trait through individual selection as well as better managerial practices.

Published estimates for h^2 of 305 d MY in dairy cattle in Egypt, using animal model are few. Abdel-Salam *et al.*(2001) analyses 2245 lactation records of Holstein herd of the International Company for Animal wealth, reported that h^2 for 305 d MY was 0.05 and concluded that the low h^2 estimates for 305 d MY, may be due size of the data set and nature of editing of the data. Mousa *et al.* (2002) using two programs of animal model; Gibbs Sampling (GS) and MTDFREML, found that h^2 for 305 d MY were 0.22 and 0.38, respectively. In addition, Alnajjar *et al.* (2002) reported h^2 estimate of 0.28 and 0.13 for 305dMY of Holstein-Friesian cattle in Syria for first and second lactation, respectively by using Random Regression Model.

Low h^2 estimates for LP (0.07) and DP (0.03) indicate that these traits are affected mainly by environmental factors. Improvement of feeding, management, detection of animal in heat and their insemination at proper time by good quality semen would help in improving CI, which comprises LP and DP. Makuza and McDaniel (1996) working on Holstein Friesian cattle in Zimbabwe, using animal model, found that h^2 for DP were 0.05 and 0.08 for 2nd and 3rd lactations, respectively.

In general, heritability estimates obtained in the present study are higher than those obtained with sire model i.e., Khattab *et al.* 1987 (0.27) deJager and Kennedy.1987 (0.28) and Visscher and Goddard, 1995 (0.20). However, Cue *et al.*

1987, using a sire model with Canadian data, reported h^2 estimates of 0.36 for milk yield. h^2 estimates obtained with animal model vary, but most are higher than those obtained with sire model Albuquerque et al. (1995).

Table 2. Estimates of variance and covariance components, heritability (h^2), repeatability (t) and genetic correlation (r_G), for 305 day milk yield (305 d MY), lactation period (LP) and dry period (DP)

Estimate	Traits		
	305dMY, kg	LP, d	DP, d
Additive variances and covariances			
σ^2_a	32429	528	68
σ_a 305dMY with LP or DP		4011	-754
σ_a LP with DP			-133
Permanent variances and covariances			
$\sigma^2 p_e$	62120	5098	582
σp_e 305dMY with LP or DP			-3800
σp_e LP with DP			-13
Environmental variances and covariances			
σ^2_e	7249	1597	1786
σ_e 305dMY with LP or DP		1385	-1621
σ_e LP with DP			-153
Heritabilities and repeatabilities estimates			
h^2	0.32	0.07	0.03
t	0.93	0.78	0.27
Genetic correlations			
r_G 305dMY with LP or DP		0.97	-0.51
r_G LP with DP			-0.70

σ^2_a = additive genetic variance; σ_a = additive genetic covariance, σ^2_{pe} = permanent environmental variance, σ_{pe} = permanent environmental covariance, σ^2_e = temporary environmental variance and σ_e = temporary environmental covariance.

Repeatability estimates (Table 2) were higher than those reported by Khalil et al. (1992) working on 1646 lactation records of two commercial Friesian herds in Egypt, being 0.37 , 0.23 and 0.11, for 305 d MY , LP and DP, respectively. The authors concluded that, according to moderate t for productive traits, culling of cows based on a single record, as commonly practiced by commercial breeders of dairy cattle, would be recommended from a genetic standpoint. Therefore, assessment of several records are not required before selecting cows for lactation. The higher estimates of repeatability in the present study, indicate that the permanent environment fractions of variance were high. Therefore, the first lactation of each cow would lead to an accurate prediction of future performance, promises efficient selection and also would afford an opportunity for a faster return of sires to service if their evaluation can be made early.

Genetic correlation

The results in (Table 2) show that the genetic correlation between 305dMY and LP was positive and high (0.97) and in the desirable direction indicating that high yielding cows are also having the longer LP, whereas the genetic correlation between 305dMY and DP was negative (-0.51) which was quite expected since the high yielding cows usually have longer LP and shorter DP.

Similarly, the genetic correlation between LP and DP was negative and high (-0.71). The results lead to suggest that the selection for higher producer cows or higher productivity cows would cause a correlated increase in LP and shorter DP.

Predicted Breeding Values (PBV)

Estimates of minimum and maximum predicted breeding values (PBV) and their accuracies for 305dMY, LP and DP estimated from cow breeding values (CBV'S), sire breeding values (SBV'S) and dam breeding values (DBV'S) are given in Table 3. The range of cow breeding values for 305dMY, LP and DP was 1314 kg, 7.4 d and 8.5 d, respectively and that of SBV'S for the above mentioned traits were 1289 kg, 6.5 d and 8.7 d, respectively. Where was the range of dam breeding values (DBV'S) was 2103 kg for 305dMY, 9.7 d for LP and 8.6 d for DP. Similarly , Abdel-Salam *et al.* (2001) working on another herd of Holstein Friesian cattle in Egypt, using multi - trait animal model , found that the range of sire breeding values for 305 d MY were large and ranged from - 396 to 259 kg, and cow breeding values for the same trait ranged from - 409 to 447 kg. Results in Table 3 shows the importance of dam, since it gave the higher range of breeding values for 305dMY, LP and DP. Thus, selection of dams for the next generation would lead to higher genetic improvement in the herd. Also, Table 3. shows that the accuracy of the estimates of sire breeding value was higher than the accuracy of cow breeding values, which may be due to the higher number of daughters per sire.

The accuracy of minimum and maximum estimates of sire breeding values (SBV's, Table 3) for 305 d MY are higher than those compared to single - trait animal model obtained by Khattab *et al.* (2003) using another set of that herd, ranging from 0.00 to 0.71. This may be due to considering the covariance among traits studies. In this respect, Hanaa Abdelharith *et al.* (2002) estimated breeding values for 305 d MY of Friesian cattle in Egypt, using multiple - trait and single trait animal models, found that the accuracy was higher in the multiple - trait analyses by 6.33 %than in single -trait analyses. The authors concluded that using the multiple - trait analysis is recommended to obtain more accurate breeding values for 305 d MY. Because it makes use of all information about the lactations and the covariances among them as well as the relationships between the relatives in the different traits. In addition, Makuza and McDaniel (1996) concluded that multiple - trait analysis is needed to incorporate the genetic, residual and phenotypic correlations between traits studied to increase accuracy and precision of estimates.

Table 3. Range of predicted breeding values of cows (CBV's), sires (SBV's) and dams (DBV's) and their accuracy for 305 d MY, LP and DP

Trait	CBV's				SBV's				DBV's			
	Min.	Max.	Range	Accuracy	Min.	Max.	Range	Accuracy	Min.	Max.	Range	Accuracy
305dMY, kg	-735	579	1314	0.58-66	-628	661	1289	0.00-0.81	-1225	878	2103	0.52-0.68
LP, d	-1.9	5.5	7.4	0.00-0.63	-1.9	4.6	6.5	0.00-0.78	-3.3	6.4	9.7	0.53-0.64
DP, d	-2.4	6.1	8.5	0.00-0.57	-3.2	5.5	8.7	0.00-0.73	-3.6	5.0	8.6	0.33-0.65

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التحليل الوراثى لبعض الصفات الانتاجية فى أبقار الهولشتين فريزيان فى مصر باستخدام برنامج الـ MTDFREML

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اشــتملت هــذه الدراسة على ٢٠٩٦ من سجلات الحليب لأبقار الهولشتين الفريزيان بمزرعة دله فى مصر خــلال الفــترة مــن ١٩٨٨ حتى ١٩٩٢. تم تحليل البيانات بواسطة نموذج الحيوان باستخدام برنامج الـ MTDFREML واشتمل نموذج التحليل على الحيوان ، التباين البيئى الدائم والأخطاء كعوامل عشوائية ، ســنة وشــهر الــولادة وترتيب موسم الحليب كعوامل ثابتة وفترة الأيام المفتوحة كانحدار . وقدرت المعايير الوراثـية والقيم التربوية للأبقار والطلائق والأمهات لناتج لبن ٣٠٥ يوم بالكجم ، طول موسم الحليب باليوم وفترة الجفاف باليوم.

كانت تقديرات المكافئ الوراثى ٠,٣٢ ، ٠,٠٧ و ٠,٠٣ لصفات ناتج اللبن فى ٣٠٥ يوم، طول موسم الحليب وفتــرة الجفاف على التوالى. بينما كانت تقديرات المعامل التكرارى ٠,٩٣ ، ٠,٧٨ و ٠,٢٧ لنفس الصفات الســابقـــة على التوالى و كان الارتبــاط الوراثي بين ناتج لبن ٣٠٥ يوم وطول موسم الحليب موجبا وعاليا (٠,٩٧) فــى حيــن كان الارتباط الوراثى بين ناتج لبن ٣٠٥ يوم وفترة الجفاف وبين طول موسم الحليب وفتــرة الجفـاف سالبا (-٠,٥١ و -٠,٧١) على التوالى . تراوحت القيم التربوية للأبقار من -٧٣٥ إلى ١٥٧٩ كجــم لناتج لبن ٣٠٥ يوم ومن -١,٩ إلى ٥,٥٠ يوم لطول موسم الحليب ومن -٢,٤ إلى ٦,١ يوم لطول فترة الجفاف. وبالمثل تراوحت القيم التربوية للطلائق من -٦٢٨ إلى ٦٦١ كجم ومن -١,٩ إلى ٤,٦ يوم ومن -٣,٢ إلى ٥,٥٠ يوم لنفس الصفات السابقة على التوالى. كما تراوحت القيم التربوية للأمهات من -١٢٢٥ إلى ٨٧٨ كجم لناتج لبن ٣٠٥ يوم ومن -٣,٣٠ إلى ٦,٤ يوم لطول موسم الحليب ومن -٣,٦ إلى ٥,٠٠ يوم لطول فترة الجفاف.