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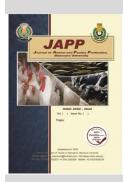
Genetic Assessment for some Productive and Fertility Traits Using Maximum Likelihood (REML) Of Friesian Cows in Egypt

Ebrahim, S. Z. M.*

Animal Production Research Institute, Dokki, Giza, Egypt.



ABSTRACT



This study aimed to evaluate the genetic improvement program of the Friesian cows. SAS program was used to calculate averages and significant effect, and (REML) program was used to estimate genetic parameters for productive traits lifetime milk yield (LTMY), daily milk yield (DMY), Lactation Length (LL) and Lactation number complete (LNC), and fertility traits days open (DO) and calving interval (CI). The least square means of LTMY, DMY, LL, LNC, DO and CI were 17546 (Kg), 12(Kg), 304 (d), 3.5 (lactations), 78 (d) and 379(d), respectively. The effect of the month, year of calving and age at first calving (AFC) were significant for all the traits except, the farm was non-significant to DMY. Estimates of the heritability (h2a) were 0.09, 0.44, 0.24 and 0.34 for LTMY, DMY, LL and LNC, respectively, whereas 0.13 and 0.17 for DO and CI, respectively. High h2a of productivity traits, particularly DMY, emphasized the possibility of achieving a significant rate of genetic improvement in this trait through selection program. The genetic correlations were positive ranging from 0.02 to 0.76, except CI with (DMY, LL and LNC) were negative and ranging from -0.07 to -0.76. The highest genetic and phenotypic correlation between DMY and LTMY. The low genetic value of these fertility traits reflected the lack of patients' genetic advancement for these traits while, phenotypic correlation estimates were positive except reproductive traits with some productive traits. Repeatability estimates are few and close to the heritability value due to the small presence of permanent environmental variation, confirming the unpredictability of the cow from its current records of fertility traits.

Keywords: Friesian cows, fertility traits. Genetic parameters, productive, variance component.

INTRODUCTION

The main challenge in expanding the range of breeding programs, especially government farms in Egypt, is lack of capabilities to cover ideal agricultural and animal needs that can be compared to the needs of foreign countries.

In order to develop breeding programs, they must be concerned with the administrative side through the work of courses and missions to familiarize themselves with the latest technologies abroad and devise the latest breeds (Oudah *et al.*,2013).

To develop a sustainable breeding program, it is important to estimate the components of variance and genetic parameters, such as heritability and repeatability of production and fertility characteristics. The components of variance and genetic parameters are key factors in predicting the selection response to a particular breeding program. The heritability (h²a) of fertility characteristics in dairy cattle is less economic than many others important attributes (Chawala et al., 2017). Decreased the heritability (h²a) of fertility traits indicate that the herd effect, Management and other environmental impacts is higher than the genetic background. This was as mentioned by both of Schaeffer and Henderson, (1972) and Ulutas and Sezer, (2009) .Fertility qualities are one of the major factors affecting the profitability of dairy cows. Fertility factors increase the cost of milk by a higher execution rate, higher veterinary costs, higher number of inseminations and longer calving interval. Prolonging milk periods increased the economic return. Which in turn leads to a decrease in physiological performance in high-yielding cows. Because of the direct genetic relationship between productive and reproductive (Yamazaki *et al.*, 2014).

The destinations of the present investigation were to:

- (1) Estimate the effect of some non-genetic factors for lifetime milk yield (LTMY), daily milk yield (DMY), lactation length (LL), Lactation number complete (LNC), days open (DO), and calving interval (CI).
- (2) The estimate of variance component and (3) Estimates the genetic and phenotypic parameters for the same traits studied.

MATERIALS AND METHODS

Data

The present investigation employed more than 27 years (1990-2018) data and got from the history sheets of Friesian research crowds kept up at Sakha and El-Karada experimental Farms having a place with the Animal Production Research Institute, Ministry of Agriculture and Land Reclamation, Egypt. A total of 2795 records were obtained from Sakha station (1590 records)and 1205 records from El-Karada station Kafr El-Sheikh governorate cows presenting 55 sires and 875 dams as indicated in (table1). The productive traits examined are lifetime milk yield (LTMY), daily milk yield (DMY), lactation length (LL) and Lactation number complete (LNC) while, fertility traits were days open (DO) and calving interval (CI).

* Corresponding author.

E-mail address: ebrahim.samah@yahoo.com DOI: 10.21608/jappmu.2019.76681

Management:

The animals were they are fed according to the recommended governmental requirements. The animals were kept in the farm according to the production of dairy cows. Cows were fed on Egyptian clover (Trifolium alexandrinum) during the period (December to May) with the concentrated mixture and rice straw with different amounts of feeding according to milk production, while the period (June to November) was fed on the mixture of rice straw concentrate and a limited amount of hay or silage.

The milking cows, which produce more than 10 kg of milk, are increased their nutrient concentrations according to the milk production. Cows were artificially inseminated after 60 days postpartum, while cows were artificially inseminated for the first insemination at more than 350 kg of in vivo weight or 18-24 months using frozen semen from the APRI Dairy Services Sakha, Kafr El-Sheikh, the government. Diagnoses of pregnancy at 60 days after insemination were by rectal contact as a routine. Cow's milk is delivered twice daily during the lactation period by the milking machine, and the milk yield is recorded to the nearest 0.1 kg of daily feeding.

Statistical analysis:

Model1 data were analyzed by SAS, version 9.3 2011 .The program was used to prepare data from sorting, formatting, merging and calculating new variables. Abnormal data is excluded and lactation length of cows that was less than 100 days were excluded in the analysis.

Records included number of the daily milk yield are calculated by dividing the total milk yield by the cow-days in milk. While, lifetime milk yield was determined by taking the total days from the first calving date to the last (culling). Calving interval, it is the period between two consecutive calving or includes collection of the days open and the gestation length. Days open, computed as the interval between parturition and the first date of successful fertilization or by deducting the mean of GL (gestation length) estimated from the present date as 285 days from the normal calving if the date of fertilization was not known. The analysis included fixed effects for both month, year of calving, farm and age at first calving.

The following model was:

$$Y_{ijkmn} = \mu + M_i + Y_j + F_k + A_m + e_{ijkmm}$$

Where: $Y_{ijklmn}=$ observation value; $\mu=$ overall mean; $M_i=$ fixed effect of the ith month of calving; $Y_j=$ fixed effect of jth year of calving $F_k=$ fixed effect of a kth farm, A_m=fixed effect of mth age at first calving and $e_{ijkmn}=$ random error

Model 2 data analyzed by the multiple animal model (REML) procedure using the MTDFREML program (Boldman *et al.*, 1995). To estimate the variance and covariance component and heritability for productive and feritility traits.

$$Y = X\beta + Za + Wpe + e$$

Where:

Y= a vector of phenotypic observations; $\beta=$ a vector of impact effects included (year of calving, month of calving ,farm and parity); a= a vector of additive genetic effects, p= a vector of environmental

permanent (environmental) effects contributed by dams to records of their progeny, W= the incidence matrix relating records to permanent environmental effects and e= a vector of the residual effects. X and Z are respective incidence matrices.

Heritability was calculated as (h^2a)= σ^2a / ($\sigma^2a + \sigma^2pe + \sigma^2e$) where: σ^2a = means additive genetic variance, σ^2pe = means permanent environmental variance, σ^2e = means residual. and Repeatability was calculated as (R)= ($\sigma^2a + \sigma^2pe$)/ ($\sigma^2a + \sigma^2pe$)+ σ^2e).

Table 1. The properties of the dataset used for genetic parameter estimates.

Description	Total	_
Number of records	2795	_
Records of Sakha	1590	
Records of El-Karada	1205	
Number of Sires.	55	
Number of dams	875	
Parity	10	
Years (1990-2018)	27	
Month	12	

RESULTS

Descriptive statistics of different traits in(table2). The means of LTMY, DMY, LL, LNC, DO and CI were 17546Kg, 12Kg, 304d, 3.5 lactations, 78 d and 379d, respectively. The current mean of LTMY was 17546 kg. Studies conducted in Egypt reported a higher mean of LTMY of 26935kg, 21796kg and 18309kg, respectively by Abou-Bakr, (2009), Oudah et al., (2013) and Salem and Hammoud (2019), respectively. However, smaller means were 6970kg and 8831kg reported by Khattab et al., (2009) and Rahbar et al., (2016), respectively. In this study, the coefficient of variation (CV %) for productive traits (table 2) ranged from 37.05 to 68.74. and were 25.21 and 99.93 for fertility traits (CI and DO), respectively. The present estimate is comparable with the values for productive traits ranged from 57 to 66 % for lifetime milk yield, lifetime fat yield, lifetime protein yield, and the number of lactations completed reported by Khattab et al., (2009).

The overall mean of DMY was 12Kg, and higher reports on Friesian cattle in Egypt were 18.63kg and 13.6 kg reported by Oudah *et al.*, (2013) and Salem and Hammoud (2019), respectively. The overall mean LL for all lactations was 304d lactation length was generally similar compared by standard 305 days. The ongoing study was higher than previous studies on Mpwapwa dairy cattle and Holstein Friesian cattle were 271.4d and 299d, respectively recorded by Chawala *et al.*, (2017) and Ulutas and Sezer (2009).

However, higher means of 407 was reported for the same breed by Salem *et al.* (2006). Faid-Allah (2015) found that means for LL was found ranged from 286 to 407 on Friesian Holstein cattle.

The overall mean of LNC was 3.5 lactations. This result is according to the overall mean of Friesian cattle in Egypt reported by Sadek *et al.*, (2009) and Abou-Bakr (2009). While the smallest means for LNC was 2.48 lactations recorded by Khattab *et al.*, (2009). But, the highest the means were 4.04 lactation and 5.26 lactation they reported by Salem and Hammoud (2019) and Khattab and Atil (1999). The overall mean of DO was 78 d. Higher estimates were reported by several other authors from different production environments ranged from 124.26 to 255 reported by (Abou-Bakr *et al.*, (2000), Abou-Bakr *et*

al. (2006), Faid-Allah (2015), Rahbar *et al.*, (2016) and Brzakova *et al.*,(2019).

The overall mean of CI was 379d. This is in close agreement 371d reported for Simmental Cattle in Turkey by Ulutas and Sezer (2009). On Iranian Holstein Dairy Cattle was 386.8d recorded by Aghajari *et al.*, (2015).

However, it is higher than the means reported for the same breed in other countries (Salem *et al.*, (2006), Rahbar *et al.*, (2016), Chawala *et al.*, (2017) and Brzakova *et al.*, (2019).

Table 2. Descriptive statistics of different traits.

Variable	Mean	Std Error	Std Dev	CV.%
LTMY(Kg)	17546	228.30	1206.20	68.75
DMY(Kg)	12	0.11	6.02	50.87
LL(d)	304	2.13	112.54	37.05
LNC(lactations)	3.5	0.039	2.078	59.75
DO(d)	78	1.47	77.62	99.93
CI(d)	379	15.06	95.55	25.21

LTMY: lifetime milk yield, DMY: daily milk yield, LL: lactation length, LNC: Lactation number complete, DO: days open, and CI: calving interval.

Fixed effects(Non-genetic effects):

The month of calving effect had a significant (P<0.05) for all traits studied (LTMY, DMY, LL, LNC, DO and CI) respectively (table 3), Similar effects on LTMY of Holstein cows in Egypt was significant but, non-significant for CI were documented by Abou-Bakr, (2009). This result

is identical to the traits of TMY, 305-DMY, LP, DP and DO where the significant effect was found for both of them reported by Faid-Allah (2015). On contrast, Salem, and Hammoud (2019) found that the Season of calving had no significant effect on LTMY, DMY, and LNC. While, year of calving was high significant (P<0.01) for all traits, but was significant only for LTMY (table 3). Similar effects were found in the year of calving, which had a significant effect on traits of LTMY, DMY, and LNC, respectively in Egypt by Salem and Hammoud (2019). While was a highly significant effect on CI and only significant for LTMY by Abou-Bakr, (2009). Which is similar the effect of month and year of calving on traits is explained by significance because it is related to changes in both climatic factors and successive management system each year.

Effect of the farm had a highly significant for LTMY and LNC but, significant only for LL, DO and CI in contrast was non-significant for DMY.

Effect of the age at first calving(AFC) was high significant (P<0.01) for all traits (DMY, LNC, DO and CI), except LTMY and LL were significant only. Salem, and Hammoud (2019) point to age at first calving was significant effect(P<0.05) on DMY, but had non-significant effect on LTMY and NLC. Abou-Bakr, (2009) revealed that AFC was highly significant excluding for CI was non-significant .

Table 3. fixed effect of the month, year of calving, farm and age at first calving on the studied traits

Factors -	Traits					
	LTMY	DMY	LL	LNC	DO	CI
Month of calving	2.26*	2.47*	1.70*	2.64*	1.53*	1.40*
Year of calving	1.33*	3.50**	5.46**	13.71**	5.23**	5.53**
Farm	81.85**	0.08^{ns}	2.38*	52.40**	14.81*	12.82*
age at first calving	1.28*	4.21**	1.65*	17.98**	4.52**	4.45**

^{*} Significant (P<0.05), ** High significant (P<0.01) and NS non-significant (P>0.05)

Genetic parameters: Heritability (h²a):

The estimate of variance components, heritability (h^2a) and repeatability (R) for studied traits on (table 4). In this study, DMY showed greater additive genetic variance (σ^2a) related to LNC as a bilateral trait. DMY and LNC were much larger than other features and they reached (549 and 273). The assessment of permanent environmental variance (σ^2pe) was higher for DO, LNC and LL than for the other traits. Heritability estimates in this study were 0.09, 0.44, 0.24 and 0.34 for productive traits LTMY, DMY, LL and LNC, respectively and were 0.13and 0.17 for fertility traits (DO and CI, respectively).

Heritability estimate for LTMY was 0.09. The current heritability values of LTMY in this study indicate little genetic variation in the population.

This estimate is similar to the values of 0.10 as reported by Al-Samarai *et al.*, (2013). On the other hand, higher h²a estimates for LTMY were 0.24, 0.29, 0.26, and 0.27 reported by Abou-Bakr, (2009), Sadek *et al.*,(2009), Oudah *et al.*,(2013) and Salem and Hammoud (2019),respectively. Differences in the estimation of h²a may be the result of some differences in the size of data and environmental conditions and management and methods used to calculate and genetic diversity between animals and biased virtual selection and loss of some high-value animals

through slaughter or exclusion all directly contributed to the decline in the genetic value of the animal.

The h^2a estimate of DMY was 0.44. Lower estimates of h^2a for DMY were 0.02 and 0.12 reported by Oudah *et al.*,(2013) and Salem and Hammoud (2019) ,respectively. The h^2a estimate for LL was 0.24. Heritability estimate was very high for Friesian cattle where they reached 0.10, 0.04, 0.07 and 0.11 they reported by Khattab and Atil (1999), Ulutas and Sezer, (2009), Salem *et al.*, (2006) and Faid-Allah (2015) ,respectively. On Ethiopian Holstein, the estimates of heritabilities for this trait were between 0.03 \pm 0.03 and 0.08 \pm 0.03 reported by Ayalew *et al.*, (2017).

The h^2 a estimate for LNC was 0.34. The present result is lower than estimates of 0.40 for Egypt Friesian cows reported by Oudah *et al.*,(2013). In contrast, it is higher than the estimates of 0.02 and 0.12 reported for the same breed reported by Al-Samarai *et al.*, (2013) and Salem and Hammoud (2019). While relatively less on the same herd 0.25 advertised by Sadek *et al.*,(2009).

Heritability estimate for DO was 0.13. However, slightly lower estimates were reported by several authors for Egyptian Holstein Friesian cattle where they reached (0.10 and 0.09±0.03)by Faid-Allah (2015) and Ayalew *et al.*, (2017), respectively. On the other side, it is lower than heritability estimates of 0.38 for the Czech Holstein population by Brzakova *et al.*, (2019). But, it is higher than

heritability estimates of 0.02 in the north of Iran by Rahbar *et al.*, (2016).

The heritability estimates obtained in this study for CI was 0.17. It is slightly higher than heritability estimates of 0.022 for Simmental Cattle in Turkey reported by Ulutas and Sezer (2009). However, lower estimates have been reported by many other authors from different production environments (Abou-Bakr, (2009), Salem et al., (2006), Rahbar et al., (2016) and Brzakova et al., (2019). The current estimates were higher than estimates of Ayalew et al., (2017) who used different models for analysis and decided that h²a estimate for CI was 0.11±0.04 from univariate, and 0.13±0.04 from two trait and three trait models. The current study showed that the highest heritability estimate was for an DMY trait followed by LNC then LL. This indicates that the productive traits of heritability have higher genital traits while, fertility traits with low h²a estimates Suggest that a large part of the difference in these qualities they were environmental and the selection would not be effective at achieving genetic improvement it can play an important role in improving this trait. Therefore, the management style that will lead to dependency should be improved to the length of reproductive traits. This is comparable with Khattab and Atil (1999).

Repeatability(R):

In the current study the repeatability (R) estimate for productive traits LTMY, DMY, LL, and LNC were 0.48, 0.51, 0.77 and 0.73 respectively, while were 0.42 and 0.24 for fertility traits DO and CI ,respectively (table 4). On the contrary, higher estimates of days open and calving interval have been reported in Ethiopian Holstein and Czech Holstein population by Ayalew *et al.*, (2017) and Brzakova *et al.*, (2019). However, lower estimates for LP of 0.31 in Friesian cows in Egypt by Salem *et al.*, (2006). The difference in R for each attribute assessed it can be the cause of the difference Permanent environmental variation followed by genetic variation between animals or use another statistical model in the analyzes used. This is comparable with Brzakova *et al.*, (2019).

Estimate	Traits						
Esumate	LTMY	DMY	LL	LNC	DO	CI	
σ^2 a	57	549	159	273	195	282	
σ^2 pe σ^2 e	233	84	351	309	437	125	
	309	611	152	209	875	1291	
$\sigma^2 p$	599	1244	662	791	1507	1698	
h^2a	0.09	0.44	0.24	0.34	0.13	0.17	
R	0.48	0.51	0.77	0.73	0.42	0.24	
C^2 e^2	0.39	0.67	0.53	0.39	0.28	0.73	
e^2	0.52	0.49	0.23	0.27	0.57	0.76	

 $\sigma^2 a=$ additive genetic variance, $\sigma^2 p=$ permanent environmental, $\sigma^2 e=$ residual $\sigma^2 p=$ phenotypic variance, $h^2 a=$ heritability, R=repeatability,

 c^2 = Part of the phenotypic variation due to permanent environmental variation and e^2 = part of the phenotypic variance due to residual effects

Genetic correlation

Milk production traits were higher in genotypes than in other traits, with the highest genetic correlation between DMY and LTMY 0.76 and the lowest was 0.04 between LL and DMY (table 5). This is comparable with what was found in Ethiopian Holstein genetic correlation was highest

between LMY and 305-d MY 0.99±0.01 reported by Ayalew *et al.*, (2017). Milk production features a higher genetic relationship reported by Falconer and Mackay (1996) and Ayalew *et al.*, (2017). In general, the extremely high correlation between these two traits indicates the fact that the use of daily milk yield with some productive traits was studied for the selection of milk animals.

Genetic correlations between LTMY with (LL, LNC, DO, and CI) were in general positive (Table 5). The highest genetic correlation between milk production traits TMY, DMY, and LNC ranging from 0.98 to 0.99 for Holstein cattle in Egypt by Sadek *et al.*,(2009). Similarly, the genetic correlation for the same traits found to be 0.26 to 0.99 on Friesian cattle in Egypt by Oudah *et al.*,(2013). However, higher and negative genetic correlations of - 0.687 between LTMY with CI were reported for the same breed in Egypt by Abou-Bakr (2009).

Table 5. Estimates of heritability (on diagonal) and phenotypic (above diagonal) and genetic correlation (below diagonal) correlation traits for different traits studied .

Trait	LTMY	DMY	LL	LNC	DO	CI
LTMY	0.09	0.80	0.67	0.05	-0.06	0.08
DMY	0.76	0.44	0.24	0.20	-0.05	-0.09
LL	0.50	0.04	0.24	0.02	0.32	0.35
LNC	0.05	0.09	0.41	0.34	-0.02	-0.01
DO	0.08	0.24	0.64	0.02	0.13	0.06
CI	0.35	-0.07	-0.28	-0.76	0.42	0.17

Genetic correlations between DMY with (LL, LNC and DO) were positive and ranging from 0.04 to 0.24 while, Genetic correlations between DMY with CI were negative and low -0.07(Table 5). In this study, a higher milk production rate was genetically correlation with the length of both LL, LNC and DO.

Similarly, the genetic correlation between DO and CI found to be 0.42 (Table 5). This result accords with a 0.99±0.01correlation estimate of Ethiopian Holstein by Ayalew *et al.*, (2017). In this ongoing study, the positive genetic relationship indicates that there are genetic and physiological factors that control these traits.

The genetic correlation between LL and each of (LNC and DO) were positive and high 0.41 and 0.64 respectively, while it was negative -0.28 between LL and CI. This is in close agreement with the genetic correlation between LL and DO found to be positive 0.882±0.035 in Egypt by Faid-Allah (2015). This is comparable and positive for the genetic correlation between LL and DO in Ethiopian Holstein by Ayalew *et al.*,(2017). Positive and very high for Genetic correlation between LL and CI were 0.89±0.076 by Ulutas and Sezer (2009).

The genetic correlation between LNC with reproductive traits DO was positive (0.02) while, was high and negative with CI and being (-0.76). Most investigations of the relationship between milk yield and reproductive traits in dairy cows indicated a negative relationship among them.

Phenotypic correlation

The highest phenotypic correlations in the present study were between milk production traits where it was the highest among DMY and LTMY was 0.80 and the lowest phenotypic correlations were 0.02 between LL and LNC

was (table 5). The current study thus indicates that most of the productive traits are affected by the same genetic and environmental factors and therefore there are positive phenotypic correlations. This is comparable with the highest phenotypic correlation among productive traits that were in agreement with crossbreeds dairy cattle in Egypt registered by Ahmad *et al.*, (2001) and Shalaby *et al.*, (2001).

Phenotypic correlation among LTMY with (LL, LNC, DO, and CI) was positive except, the phenotypic correlation between LTMY and DO was negative and low - 0.06 (Table 5). The phenotypic correlation between LTMY and LNC in the present study was lower than Sadek *et al.*, (2009).

The Phenotypic correlations between DMY with (LL and LNC) were positive relationships and it reached 0.24 and 0.20, respectively (Table 5). Contrast correlations between DMY with reproductive traits (DO and CI) were negative and low -0.05 and -0.09.

The phenotypic correlation between LL with (LNC, DO and CI) was generally positive and it reached 0.02, 0.32 and 0.35, respectively. This result accords with Phenotypic correlation between LL with DO reported by Ayalew *et al.*, (2017). However, a higher and positive Phenotypic correlation between LL with DO of 0.89 was reported for the same breed in Egypt by Faid-Allah, (2015). While the Phenotypic correlation between LL and CI it was positive and relatively higher 0.78±0.084 for Simmental Cattle in Turkey by Ulutas and Sezer, (2009).

The phenotypic correlation was negative and low between LNC with reproductive traits DO and CI and it reached -0.02 and -0.01, respectively (Table 5). Phenotypic correlation reproductive traits between CI and DO were positive 0.06. However, higher and positive phenotypic correlations of 0.98±0.01 were reported for the same breed in Ethiopia by Ayalew *et al.*, (2017).

CONCLUSION

The high heritability of production traits, especially DMY followed by LNC and then LL on the possibility of achieving significant genetic improvement of these traits through a selection program. While the selection with great interest in DMY traits on LNC and LL is because the genetic associations with these traits were positive and high. Estimates of low heritability of reproductive traits were mainly due to differing administrative, nutritional and climatic conditions. Milk production traits were higher in genetic and phenotypic correlation than in reproductive traits, with the highest genetic and phenotypic correlation between DMY and LTMY. The low genetic value of these reproductive traits reflected the lack of patients' genetic advancement for these traits. Overall, the results indicate that improved Friesian cattle traits can be obtained through a selection program and improved management and good feeding conditions.

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التقييم الوراثي لبعض الصفات الإنتاجية والخصوبة باستخدام أقصى احتمال (REML) لماشية الفريزيان في مصر سماح زغلول محمود إبراهيم*

معهد بحوث الإنتاج الحيواني ، الدقى ، الجيزة ، مصر

هدفت هذه الدراسة إلى تقييم برنامج التحسين الوراثي لسلالة الأبقار الفريزيان في محطتي سخاوالقرضا التابعة لوزارة الزراعة خلال الفقرة من 1990 إلى 2018. بلغ العدد الإجمالي للسجلات من المزرعتين 2795. تم استخدام برنامج SAS لحساب المتوسطات وتم استخدام برنامج الاحتمال الأقصى (LTMY) ، ومتوسط انتاج اللبن في اليوم الاحتمال الأقصى (EMY) لتقدير المعالم الوراثية للصفات الانتاجيه وهي طول الحياه الانتاجيه (DMY) ، وطول موسم الحليب (LL) ، وعدد مواسم الحليب الكامله (LNC) وفتره الايام المفتوحة (DO) والفتره بين ولادتين (CI). بلغت قيمه المتوسطات LTMY ، LTMY ، LMC ، LNC (LD و CI كانت 17546م. 21 كجم, 304 يوم و 3.5 موسم , 78 يوم و 379 يوم على التوالي. تأثير شهر وسنة الولادة والعمر عند اول ولاده بين معنوى (1750 P0) وعالى المعنويه (P<0.01) بلميناء ، تأثير الوراثي قيم المكافىء الوراثي (h²a) من نموذج الحيوان متعدد المتغيرات 2004 ، 0.44 ، 0.09 و 0.24 ، 0.44 ، 0.09 وعالى الموات الإنتاجية الإرتباط الموات الإنتاجية المنافقة من خلال برنامج الانتخاب. كانت الارتباطات الإنتاجية الوراثية إيجابية تتراوح من 20.0 إلى 0.76 ، باستثناء المع صفات إنتاج الحليب (DMY ، على الصفات التناسلية وتتراوح من -0.70 إلى الوراثية إيجابية تتراوح من 20.0 إلى 20.7 ، باستثناء المطهري إيجابية باستثناء الصفات التناسلية (CI و CI) مع بعض الصفات الإنتاجية مرضى لهذه الصفات التناسلية ومظهري بين كالم (DMY و DM) مع بعض الصفات الإنتاجية مرضى لهذه الصفات التناسلية وكورية من قيمة المكافئ الوراثي نظرًا لوجود تباين بيئي دائم ، مما يؤكد عدم القدرة على التنبؤ للبقرة من خلال سجلاتها الحالية لخصائص الخصوبة.