

GENETIC EVALUATION FOR MILK PRODUCTION, REPRODUCTION AND SOMATIC CELL COUNT TRAITS IN EARLY LACTATION FOR FRIESIAN CATTLE IN EGYPT

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ABSTRACT

A total of 2396 records of 673 Holstein Friesian cows were collected from one commercial Holstein Friesian farm during the period from 1999 to 2004. Genetic, phenotypic correlations and breeding values for productive, reproductive and somatic cell count traits were analyzed by using single-trait and multi-trait animal model analyses. Traits studied were total milk yield (TMY, kg), days in milking (DIM, days), milk yield in first test of lactation after calving (M1, kg), days open (DO, days), number services per conception (NSC, services), age at first calving (AFC, month), and somatic cell count in the first test of lactation (SCC).

Unadjusted means of TMY, M1, DIM, SCC1, AFC, NSC and DO were 6716 kg, 17.39 kg, 319.8 day, 505.23x10³ cell/ml, 28.3 month, 1.97 services and 144.5 day, respectively. Estimates of heritability of TMY, DIM, M1, SCC1, AFC, NSC and DO were 0.34±0.028, 0.22±0.08, 0.10±0.026, 0.04±0.023, 0.20±0.113, 0.02±0.013 and 0.02±0.017 for single-trait. While, the obtained h² from multi-trait analysis were 0.40±0.12, 0.20±0.16, 0.16±0.02 and 0.10±0.08 for TMY, M1, DO and SCC1, respectively. The genetic correlations among TMY, M1, SCC1 and DO were positive and ranged from 0.19±0.06 to 0.84±0.08. The phenotypic correlations between milk production and reproduction traits were positive for all studied traits and ranged between 0.10 for correlation between SCC1 and TMY to 0.44 for correlation between M1 and DO.

The range of breeding values obtained from single-trait analysis for DO, TMY, M1, SCC1 and AFC were 20.9 day, 6006 kg, 229 kg, 57.7 x 10³ cell/ml and 3.83 month, respectively. While, the breeding values obtained from multi-trait analysis for all animals were 193.9 day, 10280 kg, 383.8, and 630x10³ cells/ml for DO, TMY, M1, and SCC1, respectively. The present results will help the farmers to select the best dairy cows based on a combination of production, reproduction and somatic cell count in early lactation.

INTRODUCTION

Mastitis is one of the most common dairy cow diseases. Therefore, it can cause considerable economic losses to dairy farmers, which are caused by ways factors, such as decreasing milk yield, marked compositional changes in milk lead to reduce milk quality, increasing labor costs, and increasing risk of early culling of cows. Hagnestam *et al.* (2007) estimated a reduction in 305-day milk production between 0.0-902 kg (11%) depending on parity and the week time of lactation at clinical onset (Veerkamp *et al.*, 1998). Somatic cell count in milk (mainly the number of white blood cells) is the most common way of measuring milk quality as well as udder health

(Harmon, 1994). Itavo *et al.*, (2001) found that mastitis has been the disease that causes the high costs in the milk production resulting in significant losses. Tsenkova *et al.* (2001) reported that somatic cell count is recognized as a good indicator of cows' health and milk quality. Also, somatic cell count reflects the level of infection and resultant inflammation in the mammary gland of dairy cows associated with mastitis.

Detilleux *et al.* (1997) suggested that the risk of intramammary infection from environmental pathogens, which lead to a brief increase in SCC, is high at the beginning of lactation when cows are metabolically stressed. Li *et al.* (2001) concluded that, in spite of such brief or short elevations in SCC observed in early lactation had very low heritability, they are highly genetically correlated (0.90–0.95) with overall lactation somatic cell score. Therefore, it is important to consider mastitis in dairy cattle breeding (Koivula *et al.*, 2005). So, the main objectives of the present study were: 1) To evaluate the productive, reproductive traits and somatic cell count of Holstein Friesian cows under commercial herd in Egypt, 2) to estimate heritability, genetic and phenotypic correlations among production, reproduction traits and somatic cell count by using single and multi-traits animal model, 3) to estimate breeding values for these traits which obtained from single and multi-traits and 4) to estimate the correlations between breeding values for all traits.

MATERIALS AND METHODS

Data on milk production, reproduction traits and somatic cell count were collected from one commercial Holstein Friesian herd. The herd is situated in the northern part of Delta, south Domiate government. Total of 2396 records of 673 (sired by 68 sire) Holstein Friesian cows in the first five parities were collected during the period from 1999 to 2004.

The animals were housed free in open yards, and the cows were fed on Egyptian clover (*Trifolium Alexandrinum*), rice straw and Sorghum as silage, in addition to concentrate mixture in winter according to their milk yield level.

In summer and autumn, the animals were fed on concentrate mixture, rice straw, clover hay and Sorghum as green fodder. Water was offered freely. Cows were machine milked three times daily at 4.00 a.m., 12.00 a.m. and 8.00 p.m. After calving, calves were suckled colostrums' from their dams for three days after then they were separated. The cows were dried when the daily milk production was reduced to less than 2 kg and/or at two months before the next calving. Cows were artificial insemination. Pregnancy diagnosis via rectal palpation was performed on day 60 after the last service. Traits studied were total milk yield (TMY), milk yield in the first test of lactation (M1), days in milking (DIM), somatic cell count in first test of lactation (SCC1), age at first calving (AFC), number of services per conception (NSC) and days open (DO).

Animal models were used for analyses for all data. The multiple-trait derivative-free restricted maximum likelihood (MTDFREML) suite of programs (Boldman *et al.* 1995) was used for univariate and multiple-trait analyses for

all traits. Effects of year and month of calving and parity were assumed to be fixed. Days open and age at first calving (AFC) were included in the model as covariate when total milk yield and days in milk were analyzed. Milk yield and AFC were included in the model as covariate when reproduction traits were analyzed, Days from parturition to the first test and AFC were included in the model as covariate when test day of milk yield and somatic cell count were analyzed and effects of animal, direct and permanent environmental effect and random residual effect considered to be random. In multiple traits general animal model used was:

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

Where:

Y = observations vector of records, β = the vector of fixed effects, pe = the vector of environmental effects contributed by dams to records of their progeny (permanent environmental), and e = the vector of residual effects. X, Z and W are incidence matrices relating records to fixed, direct genetic and permanent environmental effects, respectively.

Mixed-model equations in the analyses were solved iteratively. Based on the variance of the log-likelihood function values, the convergence criterion was 1×10^{-9} . In addition, several restarts were necessary until changes in the log-likelihood function values were less than 1×10^{-5} . Restarts were performed for all analyses, using the final results of the previous analysis, in order to locate the global maximum for the log likelihoods. Starting values for variance components for multi-trait analyses were obtained from single-trait analyses on individual traits. Best linear unbiased prediction (BLUP) of estimated breeding values (EBVs) were obtained by back-solution using the MTDFREML program for all animals in the pedigree file for single-trait and two-trait analysis with milk yield. Additionally, Spearman rank correlations between EBVs for traits were studied from single-trait and multi-trait analyses.

RESULTS AND DISCUSSIONS

Unadjusted means, standard deviations (S.D) and coefficients of variation (C.V%) of productive traits of Holstein Friesian cows are shown in table (1). The overall unadjusted mean of TMY (6716 ± 2355 kg) was nearly similar to that reported by Shalaby (2005) being 6733 kg using Friesian cows in Egypt. While, higher than those reported by Hegazy and Morsy (2005) being 2837, 2572, and 2780 kg for 1st, 2nd, and 3rd lactations; Tag-El-Dein and Hussein (2005) being 4857 kg. Coefficient of variation (CV%) was 35.07% for TMY higher than those reported by Aboul-Ela *et al.* (2001) being in the first three lactations were 24.1, 25.9, and 25.8%, respectively. Also, higher than those by Alemam (2002) being 26.7. The overall unadjusted mean of DIM (319.8 ± 128.0 days) was considerably lower than that reported by Shalaby (2005) showed that unadjusted mean of DIM was 353.9 days for using Friesian cows in commercial herds in Egypt.

Coefficient of variation (CV%) was 40.02% for days in milk. The present result was higher than those reported by Alemam (2002) being

24.7%. The overall unadjusted mean of milk yield in the first test after calving was 17.39 ± 8.10 kg. Coefficient of variation (CV%) was 46.6% for milk yield in the first test lactation after calving.

The overall unadjusted means, standard deviations (S.D) and coefficients of variation of reproductive traits of Holstein Friesian cows are shown in table (1). The overall unadjusted mean of NSC (1.97 ± 1.38 services). These value was nearly similar to that reported by Alemam (2002) being 1.96 services. Coefficient of variation (CV%) of NSC (70.05%) was considerably higher than reported by Oudah *et al* (2001) being 61.0%. While, lower than those reported by Alemam (2002) being 94.59%.

Table (1): Unadjusted means (\bar{x}), standard deviations S.D, and coefficients of variation C.V% for studied traits.

| Traits | Abbre. | \bar{x} | S.D | C.V% |
|--|--------|-----------|-------|-------|
| Total milk yield , Kg | TMY | 6716 | 2355 | 35.07 |
| Milk yield in the first test of lactation , Kg | M1 | 17.39 | 8.10 | 46.6 |
| Days in milking , Days | DIM | 319.8 | 128.0 | 40.02 |
| Somatic cell count in first test of lactation, 10^3 cell | SCC1 | 505.23 | 1059 | 209.6 |
| Age at first calving, Month | AFC | 28.03 | 3.29 | 11.74 |
| Number of services per conception, service | NSC | 1.97 | 1.38 | 70.05 |
| Days open, Days | DO | 144.5 | 81.5 | 56.40 |

Unadjusted mean of DO was 144.5 ± 81.5 days, these value was higher than reported by Alemam (2002) being 140.43 days. While, lower than reported by Shalaby (2005) being 162.7 day in dairy commercial Holstein Friesian herds. Coefficient of variation (CV%) was 56.45% for DO. These nearly similar to Oudah *et al* (2001) being 56.9.

The overall unadjusted mean of AFC was 28.03 ± 3.29 month. This value was nearly similar to Atil and Khattab (2005a) being 28.8 month and higher than Shalaby (2005) being 27.7 months. While, lower than Ashmawy (1986) being 32 month. A reduction in age at first calving can be achieved through better feeding, management, disease control and efficient heat detection and timely service programmed. Coefficient of variation (CV%) of AFC was 11.74%.

Unadjusted mean of somatic cell count was 505.23×10^3 cell/ml. This value was higher than reported by O'Rourke (1999). Also, Itavo *et al.*, (2001) showed that the somatic cell count level considered normal is less than 200,000 cells/ml of milk, although it may be less in the first lactation. Dohoo and Meek, (1982) showed that in dairy cattle both 400 000 and 500 000 cells/ml have been evaluated as possible thresholds, for classifying a quarter as being infected, but both will resulted in a high false negative rate. Coefficient of variation (CV%) of somatic cell count in milk was 209.6% for somatic cell count in milk. The large coefficients of variation are lead to opportunities for improvement in these traits. Holsteins in commercial herds in Egypt are showing high production performance under adequate management.

Heritability

Heritability estimates and their standard errors of milk production, reproduction traits and somatic cell count obtained from single-and multi-traits genetic analysis are shown in tables 2 and 3. Single-trait analysis of data gave an estimate of 0.34 ± 0.028 for the heritability of TMY and also by multi-traits analyses gave an estimate of 0.40 ± 0.12 . The heritability estimated of TMY in this study fall within the range of the available heritability estimates obtained in the literature. As that reported by Shalaby (2005) for heritability of 305days-milk yield and TMY were 0.34 ± 0.107 and 0.28 ± 0.139 using single-trait analysis for Holstein Friesian cows, Tag El-Dein (1997) being 0.38. El-Awady (1998) using Friesian cows of total milk yield was 0.43. While, it was higher than that reported by Alemam (2002) for total milk yield was 0.184.

It could be noticed that value of heritability of DIM for single-trait was 0.22 ± 0.08 (table 2). Abdel-Glil (1996) recorded nearly similar h^2 of 0.27 for DIM and Shalaby (2005) being 0.27 ± 0.091 using single-trait analysis for Holstein Friesian cows. The present result was higher than that reported by El-Awady (1998) being (0.14), Farrag *et al.* (2000) being 0.05, and Alemam (2002) being 0.062. But, it was lower than that reported by Tag El-Dein (1997) h^2 of DIM was 0.37.

Single-trait analysis gave an estimate of 0.10 ± 0.026 and also, multi-traits analyses gave an estimate of 0.20 ± 0.16 for the heritability of M1. Nearly similar findings was reported by Reents *et al.* (1995) that heritability estimates of SCS were from 0.10 in the first lactation to 0.13 in the third lactation. While, Amin *et al.* (2005) stated that heritability estimates for SCS did not showed clear trend of month of lactation with estimate 0.09 from zero day to three lactation months. In the other side, Mrode and Swanson (2001) reported that h^2 of SCS increased slightly with days in milk in all parities.

Table (2): Heritability estimates (h^2) and standard errors (S.E) for single-traits.

| Traits | h^2 | S.E |
|--------|-------|-------|
| TMY | 0.34 | 0.028 |
| M1 | 0.10 | 0.026 |
| DIM | 0.22 | 0.08 |
| SCC1 | 0.04 | 0.023 |
| AFC | 0.20 | 0.113 |
| NSC | 0.02 | 0.013 |
| DO | 0.02 | 0.017 |

It could be noticed that value of heritability of days open for single-trait was 0.02 ± 0.017 , and the value was 0.16 ± 0.02 using multi-traits. These results was nearly similar to that reported by Moore *et al.* (1999) being heritability ranged from 0.03 to 0.06. Also, Abdel-Glil (1996) recorded 0.12, Pryce *et al.* (1998) obtained 0.017 and 0.005 for the 1st and 2nd lactation, Oudah *et al.* (2001) being 0.105 ± 0.038 and Alemam (2002) being 0.176 ± 0.05 . similarly, Shalaby (2005) reported estimate of heritability of DO was 0.11 ± 0.064 using single-trait.

Single-trait analysis gave an estimate of 0.02 ± 0.013 for the heritability of NSC. The obtained present value fall within the range of the heritability of the available estimates reported in the literature. In this trend, Alemam (2002) recorded 0.036 and Estrada-Leon *et al.* (2008) obtained 0.04. The low estimates for above reproductive traits indicated that environmental effects are more important than additive genetic effect.

Single-trait analysis gave an estimate of 0.20 ± 0.113 for the heritability of AFC. Similar estimate reported by Estrada-Leon *et al.* (2008) being 0.28 on Brown Swiss cows. While, it was lower 0.36 than that reported by Toosi (2002) on Holstein cattle.

The results in the present study indicated to the differences in heritabilities obtained from single versus two-trait genetic analyses (Table 2 and 3). In this respect, Schaeffer (1984) compared accuracies of single- and multiple-trait analyses of milk and fat yields, he concluded that genetic and residual correlations between traits affect the choice of analysis and are more important than the number of animals. Moreover, multi-trait analysis of fertility with milk yield as an additional trait is a different approach which aims to improve accuracy of genetic evaluations for the traits involved by reducing variances of prediction error of estimated breeding values (Schaeffer, 1984). The value of h^2 from multi trait analysis reported in the present study indicated that the improvement of studied traits could be achieved through better management besides genetic selection.

Genetic and phenotypic correlations

Estimates of genetic correlations among TMY, M1, DO and SCC1 are shown in table (3). The genetic correlation between TMY and M1 were positive being 0.27 ± 0.15 . however, El-Awady (1998) recorded 0.81 and Shalaby (2005) obtained positive and high (0.85) in their studied on Holstein Friesian cows in Egypt. The high and positive genetic correlation between TMY, DIM and M1 indicated that selection for one trait would be associate with genetic improvement in the other.

It could be noticed that these correlations were positive and ranged from 0.19 ± 0.06 for correlation between M1 and SCC1 to 0.84 ± 0.08 between M1 and DO. In this trend, Shalaby (2005) obtained higher estimate (0.82) for genetic correlation between TMY and DO.

Table (3): Estimates of heritability (h^2) and standard errors (S.E) (diagonal), phenotypic correlations (above), and genetic correlations \pm S.E (below) among the traits.

| Traits | TMY | M1 | DO | SCC1 |
|--------|------------------|------------------|------------------|------------------|
| TMY | 0.40±0.12 | 0.19 | 0.40 | 0.10 |
| M1 | 0.27±0.15 | 0.20±0.16 | 0.44 | 0.177 |
| DO | 0.46±0.13 | 0.84±0.08 | 0.16±0.02 | 0.175 |
| SCC1 | 0.30±0.13 | 0.19±0.06 | 0.35±0.10 | 0.10±0.08 |

Estimates of genetic correlation between somatic cell count and milk yield in the first test was positive 0.19 ± 0.06 The obtained result was nearly similar with Rupp and Boichard (1999) that estimates of genetic correlation between yields and SCC were moderately unfavorable (from 0.11 to 0.27). In the same Monardes and Hayes (1985) found that the genetic correlations for

SCC between adjacent lactations vary considerably, from 0.44 to near unity; they added that genetic correlations tend to be lower as distance between lactations increases. In the other direction, Koivula *et al.*, (2005) showed that the genetic correlation between SCC and milk yield was positive in the first lactation, but negative or near zero in the second lactation. Estimate of genetic correlation between SCC and DO was positive and moderate being 0.35 ± 0.10 (Table 3).

The phenotypic correlations among TMY, M1, DO and SCC1 were positive and ranged from 0.10 for correlation between SCC1 and TMY to 0.44 for correlation between M1 and DO.

The phenotypic correlations between reproductive trait (DO) and milk production traits (TMY and M1) were positive (0.40 and 0.44, respectively) In this respect, Aboul-Ela *et al.* (2000) recorded 0.52 between production and reproduction traits in their study on Friesian cows, and Oudah *et al.* (2001) found 0.50 for Friesian cows. Also, Shalaby (2005) reported that the phenotypic correlation between DO and TMY was 0.49. These estimates indicated that higher-yielding animals were associated with undesirable longer DO. The effect of high milk production on the incidence of reproductive disorders may be related to the degree to which energy balance becomes negative in the early postpartum period. During early lactation, many high producing cows are unable to consume enough feed to meet their energy demands, which could result in reduced reproductive performance (Gröhn *et al.*, 1994).

Breeding values

Means, maximum, minimum, standard deviations, and range of estimated breeding values (EBV) of productive, reproductive and somatic cell count traits in all pedigree and for all animal obtained from single-traits analysis are presented in Table 4. Regarding the breeding values obtained from single-trait analysis, the range of all pedigree animals for DO, TMY, M1, SCC1 and AFC were 20.9 day, 6006 kg, 229 kg, 57.7×10^3 cell/ml and 3.83 month, respectively. While, the range of breeding value of DO, TMY, M1, and SCC1 of multi-trait were 193.9 day, 10280 kg, 383.8 and 630×10^3 cells/ml for all animals (Table 5). The present results indicate that the wide range of breeding values for all reproductive traits, suggests the existence of genetic variation between animal and hence the possibility of sire selection for daughter's productive traits by using multi- trait reproductive in the next generation is a goal of dairymen. In this respect Shalaby (2005) showed that the range of breeding value obtained from single-trait analysis for all pedigree animals for AFC, DO, 305-d MY, DIM and 70-d MY were 5.2 months, 99.71 days, 3917 kg, 176.4 days and 1039.1 kg, respectively, while the range of sire breeding value were 4.86 months, 61.59 days, 2938 kg, 142.82 days and 902 kg, respectively. Also, Atil and Khattab (2005b) reported that the range of sire breeding values were 388 kg and 4.64 days for 305-d MY and DIM, respectively. The same authors found that the rang of sire breeding value for 305-d MY was 2186 kg of Holstein Friesian cattle in Turkey. Atil and Khattab (2005a) found that the range of sire breeding value for AFC was 14.31 months.

Table (4): Means, maximum, minimum, standard deviations, and range of estimated breeding values (EBV) of productive, reproductive and somatic cell count traits for all animals obtained from single-traits analysis.

| Single-trait breeding value | | | | | | | | | | |
|-----------------------------|-------|------|-------|-------|--------|-------|--------|-------|--------|--------|
| TRAITS | DO | | TMY | | M1 | | SCC1 | | AFC | |
| | EBV | S.E | EBV | S.E | EBV | S.E | EBV | S.E | EBV | S.E |
| Means | 0.036 | 10.1 | 25.20 | 1026 | 45.12 | 6.33 | 13.13 | 20.2 | -0.033 | 1.01 |
| Max | 11.4 | 10.5 | 3174 | 1360 | 116.5 | 705 | 34.05 | 21.80 | 1.825 | -0.014 |
| Min | -9.4 | 7.6 | -2832 | 450 | -102.4 | 344 | -14.66 | 13.80 | -2.01 | 0.59 |
| S.D | 24.3 | 0.34 | 773.9 | 216.5 | 291.8 | 54.22 | 47.48 | 9.97 | 0.436 | 0.0758 |
| Range | 20.9 | 18.1 | 6006 | 1810 | 229.3 | 104.9 | 57.71 | 35.60 | 3.834 | 0.604 |

The present results showed higher estimates of standard deviations for multi-trait than single-trait analyses. The differences in distribution (S.D) of breeding values between single-trait versus multi-trait analyses may be due to high absolute differences between genetic and phenotypic correlations between milk yield, reproduction and somatic cell count traits. Higher standard deviations of breeding value for multi-trait than single-trait analyses obtained in the present study indicated the existence of more genetic variation among animals and hence increases the possibility of sire selection for the traits studies. Kadarmideen *et al.* (2003) reported similar results.

Table (5): Means, maximum, minimum, standard deviations, and range of estimated breeding values (EBV) of productive, reproductive and somatic cell count traits for all animal obtained from multi-trait analysis.

| Multi-trait breeding value | | | | | | | | |
|----------------------------|-------|------|-------|------|-------|-------|-------|------|
| traits | DO | | TMY | | M1 | | SCC1 | |
| | EBV | S.E | EBV | S.E | EBV | S.E | EBV | S.E |
| Means | 2.0 | 3.28 | 20 | 141 | 13.8 | 11.29 | 1.12 | 448 |
| Max | 117.3 | 42.6 | 5270 | 1830 | 203.2 | 13.86 | 4210 | 4700 |
| Min | -76.6 | 28.3 | -5010 | 1220 | -186 | 9.92 | -2096 | 2380 |
| S.D | 32.7 | 2.6 | 1460 | 0110 | 60.5 | 0.71 | 829 | 230 |
| Range | 193.9 | 70.9 | 10280 | 3050 | 383.8 | 23.78 | 6306 | 7080 |

In this respect, Togashi *et al.* (2004) concluded that multiple-trait evaluation appears desirable because it takes into account the genetic and environmental variance-covariance of all traits evaluated. For these reasons, multiple-trait evaluation would reduce bias from selection and achieve a better accuracy of prediction as compared to single-trait evaluation. They add that the number of traits included in multiple-trait evaluation should depend upon the breeding goal. In this respect, Pollak and Quaas (1983) found the same result; they reported that the multiple-trait model is usually preferred over the single-trait model as the former uses the covariance structure among traits and the records with missing information, both of which are ignored by the latter.

Correlations among EBVs from single traits analyses.

Correlations among EBVs provided by single-trait analysis are presented in table (6). Correlations among EBVs for traits studied of all animals in were positive, except that between DO and each of TMY, DIM , M1 and AFC. The negative estimates were between SCC1 and each of NSC and AFC, also the correlation between NSC and AFC was negative. In general, it could be noticed that the correlations among EBVs provided by single-trait analysis for studied traits were small, indicated that the selection for any trait lead to small change in the other.

Table (6): Correlations coefficients between actual EBVs all animals of the single traits studied.

| Traits | TMY | DIM | M1 | DO | NSC | AFC |
|--------|--------|--------|--------|--------|--------|--------|
| DIM | 0.616 | | | | | |
| M1 | 0.327 | 0.082 | | | | |
| DO | -0.205 | -0.178 | -0.016 | | | |
| NSC | 0.061 | 0.049 | -0.021 | 0.246 | | |
| AFC | 0.003 | -0.035 | 0.013 | -0.094 | -0.009 | |
| SCC1 | 0.090 | 0.080 | 0.239 | 0.065 | -0.016 | -0.052 |

Correlations between EBVs of somatic cell count with milk production were positive and ranged between 0.080 to 0.239, also, these correlation between somatic cell count and days open were positive (0.065).

Correlation between EBVs from multi-traits analyses.

Correlations between EBVs provided by multi-trait analysis for all animals are presented in table (7). Correlations between EBVs of all animals in pedigree were positive, except that between SCC1 and each of TMY and DO.

Table (7): Correlations coefficients between actual EBVs all animals of the multi-traits studied.

| Traits | TMY | M1 | DO |
|--------|--------|-------|--------|
| M1 | 0.271 | | |
| DO | 0.909 | 0.250 | |
| SSC1 | -0.083 | 0.077 | -0.057 |

Correlations between EBVs of TMY and DO was positive and high (0.909), and also positive correlation between days open and milk yield in the first test of lactation (0.250). The present study indicate that cows with higher milk yield during early lactation and cows with higher genetic merit for milk yield also have longer days open than do cows with mean yield during early lactation (Chauhan et al., 1994). The present findings confirm the antagonistic relationship of milk yield with reproduction under high producing Holsteins under production system of commercial herds.

Conclusions

The present study indicated that the Holstein dairy farming system in commercial herds in Egypt can show high production performance under

adequate management. The large coefficients of variation are indicative leaders for opportunities for improvement in these traits. The present results showed some differences in heritabilities obtained from single versus multi-trait genetic analyses. Higher standard deviations of breeding value for multi-trait than single-trait analyses obtained in the present study indicated the existence of more genetic variation among sires (animals). Also, the sire and cow evaluations for reproduction and somatic cell count in early lactation must be taken into consideration and subsequently incorporated into a multi-trait selection index. This will help the farmers to select the best heifers based on a combination of production, reproduction and somatic cell count in early lactation.

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التقييم الوراثي لصفات إنتاج اللبن و الصفات التناسلية و عدد الخلايا الجسدية في
الفترة الأولى من الإنتاج لأبقار الفريزيان في مصر.
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استخدم في هذه الدراسة ٢٣٩٦ سجلا خلال خمس مواسم إنتاج مختلفة لعدد ٦٧٣ بقرة هولستين فريزيان مراباة تحت نظام القطعان التجارية في منطقة شمال دمياط، جُمعت البيانات على سجلات الإنتاج والتاسل وكذلك قياسات الخلايا الجسدية لهذه الأبقار وتم أخذ العينات شهريا خلال الفترة من ١٩٩٩ حتى ٢٠٠٤م وذلك لدراسة تقييم الصفات الإنتاجية و التناسلية وكذلك عدد الخلايا الجسدية، وكانت أهم الصفات

المدروسة هي محصول اللبن الكلي وطول فترة الحليب و إنتاج اللبن وكذلك عدد الخلايا الجسدية خلال الاختبار الأول من موسم الحليب ، وكذلك العمر عند أول ولادة وعدد التلقيحات اللازمة للإخصاب والفترة من الولادة حتى الإخصاب. تم تقدير المعالم الوراثية والقيم التربوية للصفات المدروسة باستخدام نموذج الحيوان سواء بالتحليل الفردي للصفات، كما تم إجراء تحليل متعدد لصفات محصول اللبن الكلي وإنتاج اللبن وعدد الخلايا الجسدية خلال الاختبار الأول من موسم الحليب وكذلك الفترة من الولادة حتى الإخصاب معا. وكانت أهم النتائج المتحصل عليها كما يلي:

- بلغ متوسط كل من محصول اللبن الكلي وطول فترة الحليب و إنتاج اللبن وكذلك عدد الخلايا الجسدية خلال الاختبار الأول من موسم الحليب ٦٧١٥,٥ كجم، ٣١٩,٨ يوم، ١٧,٣٩ كجم / يوم و ٥٠٥,٢٣ $\times 10^3$ خلية/ملي، علي التوالي.

- بلغ متوسط كل من العمر عند أول ولادة وعدد التلقيحات اللازمة للإخصاب والفترة من الولادة حتى الإخصاب ٢٨,٣ شهر و ١,٩٧ تلقيحه و ١٤٤,٥ يوم، علي التوالي.

- بلغت قيم المكافئ الوراثي لكل من محصول اللبن الكلي وطول فترة الحليب و محصول اللبن خلال الاختبار الأول و عدد الخلايا الجسدية في الاختبار الأول من موسم الحليب والعمر عند أول ولادة وعدد التلقيحات اللازمة للإخصاب والفترة من الولادة حتى الإخصاب $0,08 \pm 0,22$ ، $0,028 \pm 0,34$ ، $0,017 \pm 0,02$ ، $0,013 \pm 0,02$ ، $0,113 \pm 0,20$ ، $0,023 \pm 0,04$ ، $0,026 \pm 0,10$ التحليل الفردي و بينما كانت قيم المكافئ الوراثي في التحليل المتعدد $0,16 \pm 0,20$ ، $0,16 \pm 0,40$ ، $0,08 \pm 0,10$ ، $0,02 \pm 0,16$ ، لصفات محصول اللبن الكلي وإنتاج اللبن خلال الاختبار الأول من موسم الحليب وكذلك الفترة من الولادة حتى الإخصاب و عدد الخلايا الجسدية خلال الاختبار الأول من موسم الحليب ، علي التوالي .

- بلغ قيمة الارتباط الوراثي بين محصول اللبن الكلي و إنتاج اللبن خلال الاختبار الأول $0,15 \pm 0,27$ و بينما كانت $0,08 \pm 0,84$ بين محصول اللبن خلال الاختبار الأول و الفترة من الولادة حتى الإخصاب.

- كانت قيمة معامل الارتباط الوراثي بين عدد الخلايا الجسدية في الاختبار الأول و محصول اللبن الكلي $0,13 \pm 0,30$. بينما كانت قيمة الارتباط الوراثي بين عدد الخلايا الجسدية في الاختبار الأول و الفترة من الولادة حتى الإخصاب $0,10 \pm 0,35$.

- قيم الارتباط المظهري بين الفترة من الولادة حتى الإخصاب وكلا من إنتاج اللبن الكلي وإنتاج اللبن خلال الاختبار الأول كانت موجبة ومتوسطة $0,40$ و $0,44$ ، علي التوالي.

- بلغ مدى القيم التربوية لكل الحيوانات الناتجة من التحليل الفردي لصفات الفترة من الولادة حتى الإخصاب و محصول اللبن الكلي و محصول اللبن خلال الشهر الأول و عدد الخلايا الجسدية في الشهر الأول و العمر عند أول ولادة $20,9$ يوم و $60,6$ كجم و $229,9$ كجم و $1 \times 10^5 \times 0,7$ خلية/ملي و $3,83$ شهر، علي التوالي. بينما كانت قيم المدى $193,9$ يوم و $1028,0$ كجم و $383,8$ كجم و 630×10^3 خلية/ملي لصفات الفترة من الولادة حتى الإخصاب و محصول اللبن الكلي و محصول اللبن خلال الشهر الأول و عدد الخلايا الجسدية في الشهر الأول في التحليل المتعدد للصفات معا.

أوضحت هذه الدراسة أن مزارع أبقار الهولستين فريزيان والمراباة تحت نظام القطعان التجارية في مصر تعطي إنتاج عالي تحت الرعاية المتميزة، وتؤكد أيضا نتائج هذه الدراسة العلاقة غير المرغوبة بين الصفات الإنتاجية والصفات التناسلية تحت مستوى الإنتاج العالي، قيم معاملات الاختلاف العالية وقيم المكافئ الوراثي المتوسط والمدى الواسع للقيم التربوية ، وزيادة قيم الانحرافات القياسية للقيم التربوية المتحصل عليها من التحليل المتعدد عن تلك المتحصل عليها من التحليل الفردي لنفس الصفة تشير إلى زيادة التباين الوراثي بين الحيوانات ، مما يزيد إمكانية الانتخاب. كما يجب أن تؤخذ في الاعتبار لاختبار الأول من موسم الحليب لإنتاج اللبن وعدد الخلايا الجسدية في التحسين الوراثي، وهذا يساعد المربين في اختيار أفضل الحيوانات في فترة مبكرة من الإنتاج.