

GENETIC EVALUATION OF MILK PRODUCTION AND REPRODUCTION TRAITS IN HOLSTEIN FRIESIAN RAISED IN HUNGARY USING SINGLE-AND MULTI-TRAIT ANIMAL MODEL ANALYSES

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ABSTRACT

A total of 3165 normal first lactation records of Holstein-Friesian cows kept at Mezoheges State Farm, Hungary collected during the period from 1982 to 1990 were used. The number of sires and the average number of daughters per sire were 281 and 11.3, respectively. The data were used to evaluate genetic parameters and breeding values for milk production and reproduction traits by using single-trait and multi-trait animal model. Each of reproduction trait, as well as persistency of milk yield was joined with milk yield. Spearman rank correlation based on EBVs of all animals (sires) for trait studied from single trait and two-trait analyses with milk yield were estimated. Production Traits studied were: 305-day milk yield (305-d My), 305-day fat yield (305-d Fy), maximum daily milk yield (MdMy); days in milk (DIM) age at first calving (AFC), days open (DO), number of services per conception (NSC) and persistency of milk yield (Per My).

Unadjusted means of AFC, DO, NSC, DIM, Per My, MdMy, 305-d My and 305-d Fy were 24.4 month, 133.6 day, 2.1, 334.9 day, 76.7%, 27.3 Kg, 6568 Kg and 243.9 Kg, respectively. Estimates of heritability (h^2) of AFC, DO, NSC were 0.06, 0.11 and 0.07, respectively; while for DIM, Per My, MdMy, 305-d My and 305-d Fy were 0.05, 0.08, 0.29, 0.26 and 0.29, respectively. The standard errors (S.E) of h^2 ranged from 0.02 to 0.04 for all traits studied, using single-trait analyses. Minor differences were observed in h^2 from single-trait versus two-trait genetic analyses. Estimates of genetic and phenotypic correlations between productive traits and reproductive traits were positive and medium to high; between Per My and each of DO and NSC were negative and low; between production traits and AFC were positive and moderate. The genetic and phenotypic correlation between AFC and Per My were positive and medium.

The results indicated higher breeding values (EBVs) for two-trait than single-trait analyses for all animals (sires). Low rank correlations between single-trait and two-trait analyses with milk yield of all animal or only sires (0.56 – 0.99 and 0.71 – 0.99, respectively) for sires indicated that re-ranking of sires would be considered between the two methods. The present results indicate the antagonistic relationship of production with reproduction traits. Therefore, evaluation of the sire role as well as cow on reproduction must be taken into consideration and subsequently incorporated into a multi-trait selection index.

Keywords: Holsteins, milk production, reproduction, persistency, breeding values, genetic parameters, single-and multi-trait animal model, Hungary.

INTRODUCTION

Selection for milk production over the last 50 years reduced reproductive efficiency and decline conception rate (Grosshans *et al.*, 1997; Dematawewa and Berger, 1998; Darwash *et al.*, 1999 and Castillo-Juarez *et*

al., 2000). Many studies have shown the antagonistic relationship between milk production and reproduction traits. The level of the antagonistic is influenced by level of production and management (Dematawewa and Berger, 1998; Castillo-Juarez *et al.*, 2000; Lucy and Crooker, 2001; Haile-Mariam *et al.*, 2003; Kadarmideen *et al.*, 2003 and Shalaby, 2005). The genetic antagonism between production and reproduction traits becomes more evident in high yielding cows, reflecting high culling rates. This concept must be considered especially the high yielding cows being at risk for involuntary culling for reproductive and health disorders (Vollena, 1998). Such involuntary culling leads to shorter lifetime production and increased replacement costs.

Despite including functional traits such as fertility, longevity and health traits in the breeding program, the effort to minimise the negative effect of selection for milk yield on fertility and health traits might be helped by considering persistency of milk yield (Haile-Mariam *et al.*, 2003). A related advantage of improving persistency of milk yield may be than more persistent cow with lower peak yield can be fed on cheaper roughage (Solkner and Fuchs, 1987) than cows with higher peak yield.

It is well known that if milk yield included as a covariate in the analysis of fertility traits only reproductive correction measures with respect to phenotypic differences in milk yield level may be achieved. Therefore, a multi-trait analysis of fertility with milk yield as an additional trait is a different approach which aims to improve accuracy of genetic evaluation for the trait involved by reducing variances of prediction error of estimated breeding values (Schaeffer, 1984).

The objective of this study is to evaluate the production, reproduction and persistency of lactation traits of Holstein Friesian in their first lactation under Hungarian conditions. Heritability as well as genetic and phenotypic correlations among these traits were estimated. Breeding values for these traits were estimated by single-trait and multiple-trait animal model.

MATERIALS AND METHODS

The data of 3165 normal first lactation records of 3165 Holstein-Friesian cows daughters of 281 sires, and 3165 dams in Hungary were collected from Mezoheges State Farm, Gödöllő, Hungary during the period from 1982 to 1990 and used in this study. The average number of daughters per sire was 11.3. Edits were performed to remove incomplete records and sires having less than five daughters. The animals were kept in shaded-stables and fed and managed according to system of Mezoheges State Farm. According to season of the year, the available rations were offered to the cows: hay, high moisture feedstuff silage (ear com, sugar beet-pulp, grass and molasses) green mixture (alfalfa, soybeans, sun flowers, red clover, hybrid Sudan grass, mixed com and ear-com). In addition, concentrate mixture (com, wheat bran, and corn meal) supplemented with mineral and vitamins was provided. The lactating cows were machine milked twice a day at 5.00 a.m. and 5.00 p.m. and were dried off about two months before the expected calving date. Milk yield and fat content for each cow

were checked monthly. Samples were taken from the two successive milkings (a.m. and p.m.) to determine fat percentage in milk. Persistency of milk yield for each cow was determined according to the Hungarian standard (MSZ 6801-58) according to the following formula:

$$\text{Persistency \%} = \frac{\text{Actual milk yield during the first 300 days}}{\text{Maximum daily milk yield} \times 300} \times 100$$

Heifers were inseminated artificially using frozen semen at the first time when they reached about 14 to 16 months of age. Cows were artificially inseminated at least 45 days after calving. Pregnancy was detected by rectal palpation 60 days after the last service and heifers or cows that failed to conceive were artificially inseminated again in the following heat. Traits studied were 305-day milk yield (305-d My), 305-day fat yield (305-d Fy), maximum daily milk yield (MdMy), days in milk (DIM), age at first calving (AFC), days open (DO), number of services per conception (NSC) and persistency of milk yield (Per My).

The statistical analyses were performed using the MTDFREML (multivariate derivative free restricted maximum likelihood, Boldman *et al.*, 1995) program. Models for single-and multiple trait evaluation were as follows:

$$Y_{ijkm} = \mu + A_i + M_j + YR_k + B_{AFC} + e_{ijkm}$$

Where:

Y_{ijk} is observations for all traits.

μ , is overall mean,

A_i , is random additive genetic effect of i^{th} animal,

M_j , is the fixed effect of j^{th} month of calving ($M = 1, 2, \dots, 12$)

YR_k , is the fixed effect of k^{th} year of calving ($YR = 1982, \dots, 1990$),

B_{AFC} , is the regression coefficient for age at first calving and

e_{ijkm} , is the random error term.

Initial analyses of each trait were conducted using a single trait animal model.

The vector presentation of this model is:

$$Y = xb + zu + e$$

Where: Y is the vector of observations for all traits, b is a vector of common fixed effects, u is a vector of random genetic effects and e is a vector of residuals and x and z are incidence matrices relating observations to the fixed and animal effects, respectively. Firstly, single-trait animal model analyses for all traits, secondly, two-trait animal model analysis of each reproduction, persistency and age at first calving traits jointly with milk yield.

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 two-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 analyses with milk yield. The standard error for the genetic correlation was calculated as described by Falconer and Mackay (1996). Additionally, the correlation among ranks of these estimates were calculated by Spearman (rs) rank correlation based on EBVs for traits studied from single-trait and two-trait analyses with milk yield.

RESULTS AND DISCUSSION

Unadjusted means, standard deviations (S.D) and coefficient of variations (C.V%) for production, reproduction and persistency traits in the 1st lactation are shown in Table 1. The mean of 305-dMy (6568 Kg) is fairly close to that obtained on the 1st lactation of Friesian cows in different countries El-Awady in Egypt (1998) reported 6641 Kg; Dematawewa and Berger (1998) 6359 Kg; and Aboul-Ela *et al.* (2001) 6587 Kg. Meanwhile, the estimate is higher than that reported by Haile-Mariam *et al.* (2003) 5553 Kg; Atil and Khattab (2005a) being 4642 Kg and Shalaby (2005) 5546 Kg. In contrast, the recorded 305-d My is lower than findings on the 1st lactation Mostafa *et al.* (1999) reported 6800 Kg, and Abdel-Salam *et al.* (2001) 7128 Kg. The mean of 305-d My in the present study mainly reflects high level of management of Holstein Friesian cows under Hungarian and several conditions.

Table 1: Unadjusted means (\bar{X}), standard deviations (S.D) and coefficients of variation (C.V%) for milk production, reproduction and persistency traits.

Traits	Abbreviations	\bar{X}	SD	C.V%
Age at first calving (month)	AFC	24.4	4.0	16.6
Days open (day)	DO	133.6	71.5	53.6
Number of services/conception	NSC	2.1	1.6	73.7
Days in milk (day)	DIM	334.9	77.1	23.0
Persistency of lactation (%)	Per My	76.7	8.7	11.4
Maximum daily milk yield (Kg)	MdMy	27.3	5.5	20.1
305-day milk yield (Kg)	305-d My	6568.0	1626.0	24.8
305-day fat yield (Kg)	305-d Fy	243.9	54.5	22.3

The obtained 305-dFy (243.9 Kg) is close to estimates reported by Mostafa *et al.* (1999) 246.2 Kg and Kadarmideen *et al.* (2003) 245 Kg, but it is higher than that found by Dematawewa and Berger (1998) 226.2 Kg and Olori *et al.* (2002) 204 Kg. Also, the present average maximum daily milk yield (MdMy) 27.3 Kg is close to the value found by Mostafa *et al.* (1999) 28.0 Kg and Aboul-Ela *et al.* (2001) 27.8 Kg on the same breed under Hungarian conditions, but slightly higher than that found by Coulon and Perochon (1998) 25.7 Kg. The present mean of days in milk DIM (335 day) is comparable to those reported by Abdel-Gilil (1996) 333 day, Mostafa *et al.* (1999) 335 day.

However, lower values was reported by El-Awady (1998) 292 day; Haile-Mariam *et al.* (2003) 303 day and Kadarmideen *et al.* (2003) 321 day. On the other hand, Shalaby (2005) reported higher values of DIM 354 days. The persistency of milk yield (Per My) value in the 1st lactation 76.6% is very close to the estimates of Mostafa *et al.* (1999) 77.5% and Aboul-Ela *et al.* (2001) 75.8%, but lower than that found by Shalaby (2005) 82.2%.

The mean of age at first calving (AFC) reported in the present study (24.4 months) is almost similar to that reported by Mokhtar (1993) and Grosshans *et al.* (1997) 23.7 and 23.9 months, respectively on Holstein Friesian. But it was lower than those reported by Oudah *et al.*, 2001 (27.0 months); Kadarmideen *et al.*, 2003 (26.4 months), Haile-Mariam *et al.*, 2003 (26.0 months), Wall *et al.*, 2003 (28.9 months) Atil and Khattab, 2005a (28.8 months) and Shalaby, 2005 (27.7 months).

The mean of days open (DO) found in the present study (133.6 days) is nearly similar to that found by Ali *et al.* (1999) on Holstein Friesian in Turkey (132.9 days). Also, the mean of DO is longer than that estimated by Simert *et al.* (1992) 120 days; Mokhtar (1993) 129 days; Grosshans *et al.* (1997) 101.1 days; Aboul-Ela *et al.* (2001) 122.6 days; Oudah *et al.* (2001) 124 days and Kadarmideen *et al.* (2003) 107 days, but it is lower than that estimated by Dematawewa and Berger (1998) 169.3 days; Abdallah and McDaniel (2000) 155 days and Shalaby (2005) 162.7 days. El-Keraby and Aboul-Ela (1992) attributed longer DO in dairy cows to several factors (e.g. silent estrus, missed estrus due to weak symptoms, frequency and timing of estrus detection, feeding season and level of milk production). Shalaby (2005) noticed the relation between longer DO (Lower reproductive efficiency) in the higher producing cows and the negative performance energy balance of nutrition state of the cow.

Consequently, the mean of number of service per conception (NSC) found in the present study (2.1) is close to that obtained by different authors (Aboul-Ela *et al.*, 2001 being 2.0; Oudah *et al.*, 2001 being 2.0; Kadarmideen *et al.*, 2003 being 2.0). On the other hand, this mean was slightly higher than that found by Grosshans *et al.* (1997) 1.5; Dematawewa and Berger (1998) 1.8 and Wall *et al.* (2003) 1.7. However, it is clearly lower than the value estimated by Mokhtar (1993) 2.6.

Estimates of C.V.% were higher in DO and NSC (53.6 and 73.7%, respectively) which reflect the large individual variation in reproductive performance. Similarly, the CV% of DO, NSC and AFC recorded by Mokhtar (1993) were 58.3, 59.2 and 5.4% and Oudah *et al.* (2001) to be 56.9, 61.0 and 12.7%. Moreover, Aboul-Ela *et al.* (2001) found that C.V.% of DO and NSC was 46.2 and 63.3%, respectively. Consequently such large C.V.% of reproductive traits are indicative for improvement opportunities in these traits.

Heritability (h^2):

The heritability (h^2) estimates and their standard errors (S.E.) for productive, reproductive and persistency of milk yield obtained from single- and two-trait analyses with milk yield as a correlated trait in the 1st lactation are given in Table 2. In the single-trait genetic analysis, the estimate of h^2 of 305-d My was 0.26. A similar h^2 estimate (0.28) was reported by

Kadarmideen *et al.* (2003) and (0.28) by Atil and Khattab (2005b). Higher h^2 estimates (from 0.33 to 0.56) were obtained Dematawewa and Berger, (1998); Aboul-Ela *et al.* (2001) and Olori *et al.* (2002). However, lower h^2 estimates were found by Mostafa *et al.* (1999) 0.22; and Abou-Bakr *et al.* (2000) 0.09. The moderate h^2 estimate obtained may be a relatively good opportunity for selection for 305-d My and by the way to genetic change in this trait.

Table 2: Heritability estimates (h^2) \pm S.E. of milk production, reproduction and persistency traits obtained from single- and two-trait genetic analyses (with 305-day milk yield as a correlated trait).

Trait	Single-trait model $h^2 \pm$ S.E.	Two-trait model $h^2 \pm$ S.E.
AFC	0.06 \pm 0.03	0.07 \pm 0.03
DO	0.11 \pm 0.03	0.12 \pm 0.02
NSC	0.07 \pm 0.03	0.07 \pm 0.02
DIM	0.05 \pm 0.02	0.08 \pm 0.02
Per My	0.08 \pm 0.03	0.12 \pm 0.03
MdMy	0.29 \pm 0.04	0.27 \pm 0.03
305-d Fy	0.29 \pm 0.04	0.32 \pm 0.04
305-d My	0.26 \pm 0.04

Single-trait and two-trait analysis estimates of h^2 for 305-d Fy were (0.29 and 0.32, respectively) fall within the range from 0.24 to 0.63 reported in the literature in the 1st lactation (Mostafa *et al.*, 1999 and Kadarmideen *et al.*, 2000). Also, Kadarmideen *et al.* (2003) reported that h^2 estimate by single-trait for 305-d Fy (0.21) was lower than those in the present study (0.29). However, the present estimates indicated that h^2 estimate for 305-d Fy was higher than h^2 for 305-d My (0.29 versus 0.26, Table 2). A similar trend was also observed by Dematawewa and Berger (1998) 0.30 versus 0.28 and Mostafa *et al.* (1999) 0.54 versus 0.22. In contrast, Kadarmideen *et al.* (2000) reported that estimate of h^2 for 305-d My was higher than 305-d Fy (0.40 versus 0.39) for multi-trait linear animal model. Also, Kadarmideen *et al.* (2003) found that the values of h^2 were 0.28 versus 0.21 for single-trait analysis.

The h^2 estimates obtained for MdMy were 0.29 and 0.27 by single- and two-trait analysis, respectively (Table 2). The values were lower than that obtained by Mostafa *et al.* (1999) 0.53 and Aboul-Ela *et al.* (2001) 0.51 in the 1st lactation in Holstein Friesian cows. It seems that the h^2 values were higher for 305-d Fy and MdMy than for 305-d My (0.32, 0.29 and 0.26, respectively).

The h^2 estimates for Per My were 0.08 and 0.12 for single- and two-trait analysis, respectively (Table 2). Similar values for h^2 of Per My were reported by Mostafa *et al.* (1999) 0.13; Aboul-Ela *et al.* (2001) 0.09; Haile-Mariam *et al.* (2003) 0.09 and Shalaby (2005) 0.08 on Holstein Friesian in 1st lactation. However, the h^2 estimates of Per My in the present study were slightly higher than those found by Gengler *et al.* (2001) 0.05 for USA

Holstein cattle, but lower than those reported by Amin *et al.* (1997) 0.22 and Muir *et al.* (2004) 0.18. Moreover, Danell (1982) stated that the level of h^2 for Per My was about half as high as those of milk yield when based on the same material (0.07 to 0.15).

The h^2 estimates of DIM in the present study was 0.05 and 0.08 for single-and two-trait analyses (Table 2). A nearly similar h^2 values were recorded by Mostafa *et al.* (1999) 0.06; Haile-Mariam *et al.* (2003) 0.08 and Atil and Khattab (2005b) 0.07; it was lower than that obtained by Aboul-Ela *et al.* (2001) 0.15 and Shalaby (2005) 0.27. Low estimate of h^2 for DIM in the present study, indicate that inclusion of DIM in selection program may not be useful.

The h^2 estimate for AFC in the present study were 0.06 and 0.07 by single-and two-trait analyses, respectively (Table 2). It seem to be in accordance with the estimate found by Seykora and McDaniel (1983) 0.05, but lower than that by Grosshans *et al.* (1997) 0.13, Oudah *et al.* (2001) 0.16; Atil and Khattab (2005a) 0.75 and Shalaby (2005) 0.19 and 0.18 by single-and two-trait analyses, respectively. The lower h^2 and small genetic coefficient of variation of AFC in the present study (0.06 and 4.01%, respectively), did not support AFC as suitable trait for selection. Meanwhile, Shalaby (2005) reported on the basis of moderate h^2 estimate for AFC (0.19), the genetic improvement can be achieved through selection for this trait.

The h^2 estimate for DO was 0.11 and 0.12 (Table 2) by single-and two-trait analyses, respectively. The present values were close to the h^2 estimate by Dematawewa and Berger (1998) 0.12 and Shalaby (2005) 0.11 and 0.13 by single-and two-trait analyses, respectively; but, it could be considered higher than that obtained by Amin *et al.* (1997) 0.07 and Abdallah and McDaniel (2000) 0.03.

The h^2 estimate for NSC in the present study was 0.07 for both single-and two-trait analyses (Table 2), slightly higher than that of Dematawewa and Berger (1998) 0.03; Kadamideen *et al.* (2003) 0.02 and Wall *et al.* (2003) 0.02. However, it was lower than that of Amin *et al.* (1997) 0.14 and Oudah *et al.* (2001) 0.10.

It could be noticed that the h^2 estimates obtained by either single-trait or two trait analysis of examined traits were nearly similar. However, the h^2 for reproductive traits which were generally much lower (range 0.06 – 0.11 and 0.07 – 0.12, respectively) than h^2 of milk yield traits (range 0.08 – 0.29 and 0.12 – 0.32, respectively) by the two method. In spite of the h^2 estimates of the two system of analyses were nearly similar, the reproductive traits (AFC, DO and NSC) as well as some of the productive traits (DIM and Per My) could be considered as a low h^2 traits. On the other side, the productive traits (MdMy, 305-d My and 305- d Fy) are considered as high h^2 traits. Thus, improving the management system for low h^2 traits and selection for the high h^2 traits would be the effective ways for improving these traits.

Genetic and phenotypic (r_g & r_p) correlations:

Estimates of genetic (r_g) and phenotypic (r_p) correlations among the examined traits in this study are shown in Table 3. Generally, the estimates of both the r_g and r_p between productive traits (305-d My, 305-d Fy and MdMy) and reproductive traits (DO and NSC) were positive and medium to

high except r_p between 305-d Fy and NSC which was negative (Table 3). The estimates obtained for r_g and r_p were in range 0.44 to 0.78 and -0.22 to 0.63, respectively. However, r_g estimates between production and reproduction traits were positive and unexpected, in relation to early finding that selection for production alone is expected to lead to a genetic decline in fertility (Pösö and Mantysaari, 1996; Grosshans *et al.*, 1997; Haile-Mariam *et al.*, 2003 and Shalaby, 2005). It is concluded that fertility traits should be incorporated into selection programmes for dairy cows to counteract the antagonistic relationship between milk production and fertility. Therefore, the selection for peak milk yield is not a useful tool to improve reproductive traits. On the other hand, the cows with low fertility expressed in higher value of NSC and in the same time longer DO period, the effect of pregnancy will be delayed, and hence delaying the drying off, in other meaning prolong DIM with a net increase in total milk yield. Aboul-Ela *et al.* (2001) indicated that selection for high milk yield will be associated with undesirable results of prolonging in calving interval, and thus the number of calves and lactations that cow would give in its herdlife will be reduced. Additionally, the r_g correlation between milk production and fertility traits is generally influenced by level of production and management (Castillo-Juarez *et al.*, 2000 and Lucy and Crooker, 2001).

The genetic correlations between Per My and each of DO and NSC were negative and small (-0.19 and -0.17 , respectively) (Table 3), while the phenotypic correlations were -0.78 and 0.13 , respectively. Thus, the effort to minimise the negative effect of selection for milk yield on fertility and health traits could be obtained by considering Per My in breeding program. Solkner and Fuchs (1987) reached to similar conclusion. In the same trend, Aboul-Ela *et al.* (2001) reported that the genetic and phenotypic correlations between Per My and each of DO and NSC were rather poor (r_g -0.16 and -0.08 and r_p 0.04 and 0.05 , respectively). However, Shalaby (2005) recorded positive r_g and r_p correlations between Per My and DO (0.64 and 0.11 , respectively), which lead to undesirable longer DO.

The r_g and r_p estimates between production traits (305-d My, 305-d Fy and MdMy) and AFC were positive and moderate to high (range from 0.28 to 0.72 and from 0.21 to 0.38 , respectively) (Table 3). These results suggest that if the production is considered as the selection target the AFC will be increased too. Shalaby (2005) found that the r_g and r_p estimates between AFC and milk production (TMY, 305-d My and 70-d My) were positive and moderate to high (range from 0.83 to 0.93 and from 0.25 to 0.36 , respectively) and indicated that heifers with genetic potential for high milk yield would be older in age at 1st-calving, and these correlation depends on the level of production. Grosshans *et al.* (1997) reached to similar conclusion. In contrast, Atil and Khattab (2005a) reported that the r_g correlation between AFC and 305-d My was negative and significant (-0.22) and suggested that selection for high yielding cows would cause a correlated decrease in their AFC. Therefore, a reduction of AFC is a desirable goal of dairymen and will help in minimizing the cost of raising breeding heifers and maximizing the number of lactations per cow.

Estimates of r_g and r_p between AFC and Per My were positive and moderate 0.52 and 0.33, respectively (Table 3), indicating that younger age at first calving was genetically and phenotypically associated with higher Per My in the 1st lactation. In the other direction, Shalaby (2005) found that r_p correlation between AFC and Per My was negative and close to zero (-0.07), and the r_g correlations between the traits were positive (0.12). The r_g and r_p estimates between AFC and DIM was positive to moderate 0.22 and 0.12, respectively (Table 3), indicating that an older age at 1st calving was genetically associated with longer DIM in the 1st lactation.

The r_g estimate between AFC and DO (0.54) gave more advantages for the genetic improvement (Table 3). Similar results were obtained by Fatehi and Schaeffer (2003) and Shalaby (2005). In contrast, Grosshans *et al.* (1997) reported that the r_g and r_p between AFC and DO were -0.14 and -0.39, respectively. While, estimates of r_g and r_p correlations between AFC and NSC were -0.13 and 0.11, respectively (Table 3), is nearly similar to that estimated by Grosshans *et al.* (1997) 0.02 and 0.01, respectively.

Estimated breeding values (EBVs):

Table 4 shows, minimum, maximum, range and standard deviations (S.D) of estimated breeding values (EBVs) from single-trait and two-trait analyses. Regarding the breeding values obtained from single-trait analyses, the range of all pedigree animals for AFC, DO and NSC were 2.69 month, 53.80 day and 1.71, respectively. While, in the case of sire breeding values the range were 2.61 month, 34.50 day and 1.40, respectively (Table 4). Shalaby (2005) reported breeding values obtained from single trait analysis with the range of all pedigree animals for AFC and DO were 5.02 months and 99.7 days, respectively. While, the values of range of sire breeding value were 4.86 months and 61.6 days, respectively. In the other side, the breeding values obtained from two-trait analyses, the range of all pedigree animals for AFC, DO and NSC were 3.04 month, 75.40 day and 1.88, respectively. While, the range of sire breeding values only were 2.82 month, 38.50 day and 1.56, respectively (Table 4). Shalaby (2005) also found that the breeding values obtained from two-trait analyses, for all pedigree animals for the same traits were 6.42 months and 173.0 days, respectively. While, the range of sire breeding value for the same traits were 5.89 months and 99.6 days, respectively. The wide range of breeding values for all reproductive traits, suggests the existence of more genetic variation between both animal and sires and hence the possibility of sire selection for daughter fertility traits by using two-trait analyses than one single trait. In this respect, Kadarmiddeen *et al.* (2003) and Shalaby (2005) reported similar conclusion.

Furthermore, Table 4, showed that the breeding values from single-trait of all pedigree animals for 305-d My, 305-d Fy, MdMy, DIM and Per My were 4336, 184.46 and 12.91 Kg, 36.50 day and 31.0%, respectively. While the range of sire breeding values were 4366, 119.56 and 12.45 Kg, 33.45 days and 27.7%, respectively. However, the breeding values obtained from two-trait analyses of all pedigree animals for 305-d Fy, MdMy, DIM and Per My were 204.36, 13.38 Kg, 106.7 day and 31.7%, respectively. While the range of sire breeding values were 154.72 and 13.23 Kg, 42.71 day and 27.7%, respectively.

Table 3: Genetic correlations \pm S.E. (above diagonal) and phenotypic correlations (below diagonal) among milk production, reproduction and persistency traits.

Traits	AFC	DO	NSC	DIM	Per My	MdMy	305-d My	305-d Fy
AFC		0.54 \pm 0.13	-0.13 \pm 0.07	0.22 \pm 0.09	0.52 \pm 0.13	0.64 \pm 0.19	0.72 \pm 0.17	0.28 \pm 0.10
DO	-0.31		0.82 \pm 0.21	0.55 \pm 0.14	-0.19 \pm 0.08	0.78 \pm 0.20	0.78 \pm 0.18	0.44 \pm 0.15
NSC	0.11	0.72		0.33 \pm 0.07	-0.17 \pm 0.07	0.58 \pm 0.12	0.52 \pm 0.13	0.53 \pm 0.13
DIM	0.12	0.36	0.23		-0.28 \pm 0.14	-0.71 \pm 0.19	0.92 \pm 0.12	0.82 \pm 0.26
Per My	0.33	-0.78	0.13	0.14		0.15 \pm 0.09	0.51 \pm 0.14	-0.32 \pm 0.16
MdMy	0.35	0.52	0.52	-0.58	-0.78		0.88 \pm 0.21	0.64 \pm 0.20
305-d My	0.38	0.63	0.44	0.54	0.23	0.63		0.89 \pm 0.22
305-d Fy	0.21	0.42	-0.22	0.16	0.21	0.43	0.52	

Table 4: Minimum, maximum, range and standard deviations (S.D) of estimated breeding values (EBVs) from single-trait and two-trait analyses of reproductive traits and persistency of lactation evaluation with milk yield in all pedigree animals and sire of heifers only.

Traits	All pedigree animals												Sire of heifer only					
	Single-trait EBVs						Two-trait EBVs						Single-trait EBVs			Two-trait EBVs		
	Min.	Max.	Range	S.D	Min.	Max.	Range	S.D	Min.	Max.	Range	S.D	Min.	Max.	Range	S.D		
AFC	-1.39	1.30	2.69	0.28	-1.59	1.45	3.04	0.29	-1.39	1.22	2.61	0.28	-1.59	1.23	2.82	0.30		
DO	-9.90	43.90	53.80	83.87	-11.90	53.50	75.40	6.12	-6.20	28.30	34.50	5.31	-7.30	31.20	38.50	5.65		
NSC	-0.87	0.84	1.71	0.12	-0.91	0.97	1.88	0.14	-0.87	0.53	1.40	0.14	-0.91	0.65	1.56	0.16		
DIM	-18.78	17.72	36.50	0.72	-70.73	35.98	106.71	7.53	-15.73	17.72	33.45	2.98	-19.73	22.98	42.71	8.60		
Per My	-8.16	22.84	31.00	2.00	-8.37	23.33	31.70	2.04	-5.39	22.33	27.72	2.11	-5.83	21.84	27.67	2.38		
MdMy	-6.64	6.27	12.91	1.49	-6.66	6.66	13.28	1.52	-6.32	6.13	12.45	1.74	-6.61	6.62	13.23	1.83		
305-dMy	-2034	2302	4336	419.71					-1288	2078	4336	465.36						
305-dFy	-72.13	112.33	184.46	15.38	-85.28	119.08	204.36	16.23	-40.64	78.92	119.56	16.78	-73.28	81.44	154.72	17.98		

The results, showed great range among traits breeding values of animals and sires in different examined productive by single or two trait analysis. Thus, selection of both animals and sires for the next generation would lead to higher genetic improvement in these traits in dairy cattle. Shalaby (2005) arrived to similar conclusion; that the breeding values obtained from single-trait analyses, for all pedigree animals for 305-d My, 70-d My, DIM and Per My were 3917 and 1039 Kg, 176.04 days and 0.12%, respectively. While the range of sire breeding values were 2938 and 903 Kg and 142.82 days and 0.10%, respectively. Shalaby (2005) also found that the breeding values obtained from two-trait analyses, for all pedigree animals for the same traits 70-d My, DIM and Per My were 999.7 Kg, 171.66 days and 0.14%, respectively. While the range of sire breeding values for the same traits were 1024.9 Kg, 139.08 days and 0.10%, respectively.

Table 4, in general, showed that the standard deviation (S.D.) of EBVs for all different traits were higher for two-trait than single-trait analyses in both all animals as well as sire which indicate wide range of breeding values for reproductive and Per My traits. The differences in (S.D) values of EBVs between single and two trait may be due to high absolute differences between genetic and phenotypic correlations between milk yield and fertility traits. Kadarmideen *et al.* (2003) and Shalaby (2005) obtained similar results and reached to similar conclusion.

Correlation between ranking of all animal or only sires by single-and two-trait analyses:

Table 5 showed rank correlation between EBV's of all animals in pedigree or only sires by single-and two-trait analyses of the same trait with milk yield. The present results indicate that rank correlation of all animals in pedigree was different from and much lower than one (range 0.73 – 0.99) showing that two-trait genetic evaluation with milk yield provides information in estimating fertility and Per My breeding values. For sires, rank correlation was not as severely affected as for cows. However, correlation differed from one a range, 0.70- - 0.99 for rank. However, correlation of animal (sire) rankings between the two analyses were the highest for AFC and Per My (0.99 for both) and lowest for DIM and DO (0.56 and 0.70, respectively). This reveals that ranking of sire (animal) according to AFC was accurate as ranking using Per My. Thus, the evaluation using AFC trait could reduce the generation interval which in turn results in higher genetic gain. Similar results have been reported by Kadarmideen *et al.* (2003) rank correlation of all animal in pedigree was ranged from 0.69 to 0.83 and for sires with the range 0.89 to 0.95 for fertility traits. While, Shalaby (2005) found that rank correlation of all animal in pedigree and sires were ranged from 0.49 to 0.81 and from 0.58 to 0.90, respectively for reproductive and Per My traits.

Lower rank correlations (differed from unity) between ranking of all animals or only sires estimated by single-trait and two-trait analyses with milk yield indicated that re-ranking of sires would be considered between the two methods of genetic evaluation. Kadarmideen *et al.* (2003) and Shalaby (2005) reached similar conclusion. Therefore, the present results indicate that, breeders can choose the traits, which are economically important for

them and can rank animals based on the appropriate EBVs or index. Selection of the superior animals from this ranking allows breeders to make genetic progress in the chosen economically important traits.

Table 5: Correlation between rankings based on EBVs of all animal or only sires from single-and two-trait analysis of the same trait with milk yield.

Traits	All animals	Sires
AFC	0.89	0.88
DO	0.84	0.70
NSC	0.73	0.77
Per My	0.99	0.99
MdMy	0.76	0.93
305-d Fy	0.79	0.96
DIM	0.56	0.71

Conclusions

Results from the present study indicate that based on the moderate heritability estimates in this study for different traits, the genetic improvement can be achieved through selection. Minor differences were observed in heritability estimates from single-trait versus two-trait analyses. Antagonistic genetic correlation existed between milk production and reproduction traits. Fertility traits should be incorporated into selection programmes for dairy cows to counteract the antagonistic relationship between them. More genetic variation among animals (sire) in multi trait analysis caused change in of sires rank and hence increased the possibility of sire selection for daughters fertility. Therefore, two-trait evaluation of fertility as well as Per My with milk yield is recommended.

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التقييم الوراثي لإنتاج اللبن والصفات التناسلية في موسم الحليب الأول لماشية الهولستين فريزيان المرباه في المجر باستخدام نماذج الحيوان الفردية والمتعددة.

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استخدم في هذه الدراسة السجلات الإنتاجية والتناسلية لعدد ٣١٦٥ عجله هولستين فريزيان في موسم الحليب الأول تابعة لمزرعة ميروهيجنس بالمجر خلال الفترة من ١٩٨٢ وحتى ١٩٩٠ ناتجة من ٢٨١ أب و٣١٦٥ أم، كان متوسط عدد البنات لكل أب ١١,٣ عجله استخدمت البيانات في تقييم المعالم الوراثية والقيم التربوية للصفات الإنتاجية والتناسلية باستخدام نموذج الحيوان فردي الصفة وثنائي الصفة لكل من الصفات التناسلية والمثابرة على إنتاج اللبن مع صفة إنتاج اللبن، تم تقدير معاملات الارتباط الرتب (سبيرمان) بين النموذجين (الفردى والثنائي) للحيوانات والطلاق. كانت الصفات المدروسة هي إنتاج اللبن في ٣٠٥ يوم، إنتاج الدهن في ٣٠٥ يوم، أقصى إنتاج لبن يومي، طول موسم الحليب، العمر عند أول ولادة، طول فترة الأيام المفتوحة، عدد مرات التلقيح والمثابرة على إنتاج اللبن.

بلغت متوسطات العمر عند أول ولادة، طول فترة الأيام المفتوحة، عدد مرات التلقيح، طول موسم الحليب، المثابرة على إنتاج اللبن، أقصى إنتاج لبن يومي، إنتاج اللبن في ٣٠٥ يوم وإنتاج الدهن في ٣٠٥ يوم ٢٤ر٤ شهر، ١٣٣ر٦ يوم، ٢,١ تلقيحه، ٢٣٤ر٩ يوم ٧٦ر٧%، ٢٧ر٣، ٦٥٦٨، ٢٤٣ر٩ كجم على التوالي.

بلغت قيم المكافئ الوراثي (التحليل الفردي) للعمر عند أول ولادة، طول فترة الأيام المفتوحة وعدد مرات التلقيح ٠,٠٦، ٠,١١ - ٠,٠٧ على التوالي، بينما لطول موسم الحليب، المثابرة على إنتاج اللبن، أقصى إنتاج لبن يومي، إنتاج اللبن في ٣٠٥ يوم، إنتاج الدهن في ٣٠٥ يوم ٠,٠٥، ٠,٠٨، ٠,٢٩، ٠,٢٦ و ٠,٢٩ على التوالي. وتراوحت قيم الخطأ القياسي للمكافئ الوراثي للصفات المدروسة من ٠,٠٢ إلى ٠,٠٤. لوحظ بعض الاختلافات البسيطة بين قيم المكافئ الوراثي والخطأ القياسي الناتجة من التحليل الفردي والثنائي للصفات.

كانت قيم الارتباطات الوارثية والمظهرية بين الصفات الإنتاجية والتناسلية موجبة وكانت قيمها متوسطة - عالية، وبين المثابرة على إنتاج اللبن وكل من فترة الأيام المفتوحة وعدد مرات التلقيح سالبة ومنخفضة، وبين الصفات الإنتاجية والعمر عند أول ولادة موجبة ومتوسطة القيمة، وبين المثابرة على إنتاج اللبن والعمر عند أول ولادة موجبة ومتوسطة القيمة.

تشير النتائج إلى زيادة القيم التربوية الناتجة من تحليل نموذج الحيوان الثنائي عن التحليل الفردي للحيوانات والطلاق وانخفاض قيمة معامل ارتباط الرتب الناتج من تحليل نموذج الحيوان الفردي والثنائي لنفس الصفة مع اللبن إلى إختلاف الترتيب للطلاق (الحيوانات) وتشير هذه النتائج الحالية إلى العلاقة العكسية بين الصفات الإنتاجية والتناسلية. ولهذا فإن تقييم الطلائق والحيوانات