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COMPARISON BETWEEN SINGLE AND MULTIPLE TRAITS ANIMAL MODEL FOR SOME FERTILITY AND MILK PRODUCTION TRAITS IN FRIESIAN COWS IN EGYPT

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Abstract

A total of 2810 normal lactation records of Friesian cows belonging to Animal Research Institute, Ministry of Agriculture, Cairo, Egypt during the period from 2002 to 2007 were analyzed. Single and multiple trait analysis of fertility and milk yield traits was investigated as a method to estimate fertility breeding values when culling or selection based on milk yield in early lactation. Fertility traits are days open (DO) and calving interval (CI). Milk production traits are 305 day milk yield (305 d MY), 305 day fat yield (305 d FY), 305 day protein yield (305 d PY) and lactation period (LP). The model of the analysis included the fixed effects of month and year of calving and parity and the random effects of individuals, permanent environmental and errors. The estimates of heritability (h^2) were similar for two types of analysis. For fertility traits range of estimates of h^2 was 0.01 to 0.03 and for milk production traits ranged from 0.14 to 0.17. However, the accuracy of breeding values for two trait analysis was higher than those of single trait analysis. As single trait method is biased due to selection on milk yield, a multi trait evaluation of fertility with milk yield is recommended.

Keywords: breeding value estimation, animal model, Holstein-Frisian cattle, reproduction traits, milk production, Egypt

Introduction

Days open (DO) is the interval between calving and conception and considered an important measure of fertility. It is of practical value to milk producers and effect on milk yield is largely environmental (*Schaeffer and Henderson, 1972*). Early postpartum breeding in dairy animals resulted in



more calves and high milk per unit of time throughout the herd life. The range of h^2 estimate from the literature for various fertility traits (days open and calving interval) is from 0.00 to 0.12 (Khattab and Atil, 1999; Atil et al. 2001 and Atil and Khattab, 2005), and indicating that little genetic improvement for fertility traits can be expected. Also, the same authors concluded a negative influence of level of milk production on fertility. Estimated of genetic parameters and breeding values for milk yield and fertility traits using single and multiple trait animal model. Single – trait analysis, ignoring information on selective treatment of cows with different genetic potential for milk yield, would lead to biased genetic parameters, which in turn, would result in inappropriate predictions based on multi-trait national selection indexes (Kadarmideen et al., 2003).

The main objectives of the present study are (1) estimate genetic parameters for fertility and milk production traits and (2) estimate and compare breeding values for various fertility measures from single–trait evaluation of fertility and multiple–trait evaluation of fertility with milk yield as a correlated trait in a herd of Friesian cows in Egypt.

Materials and methods

Data

Data of the present study were collected from the history sheets of Sakha experimental farm, belonging to the Animal Production Research Institute, Ministry of Agriculture, Dokki, Cairo, Egypt and comprising 2810 normal lactation records during the period from 2002 to 2007. Animal were mainly grazed on Egyptian clover (*Trifolium alexandrinum*) during December–May. They were fed on concentrate mixture along with rice straw and limited amount of clover hay when available during the rest of the year. Cows pregnant in the last two months were supplemented with extra concentrate. Artificial insemination (AI) was used at random for both farms. Heifers were first inseminated at 18 months of age. In subsequent lactations, cows were initially inseminated 60 -70 days postpartum. Cows were machine milked twice daily. Milk yield were recorded daily and both fat and protein percents are estimated weekly in laboratory by using system of Milko–Scan 130 series, type 10900. Maintained at International Livestock Management Training Center (ILMTC) related to Animal Production Research Institute (APRI), this set have special program to estimate milk composition (fat, protein and lactose). Productive traits studied are 305 day milk yield (305 d MY), 305 day fat yield (305 d FY), 305 day protein yield (305 d PY) and lactation period (LP) and reproductive traits are days open (DO) and calving interval (CI). Lactations that began with an abortion or in which milking was interrupted by injury or sickness were excluded. Days open was computed as the interval between parturition and the date of successful mating.



Statistical Analysis

Data were analyzed by Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) according to *Boldman et al. (1995)*, using repeatability animal model single and multiple trait analysis. Two types of fertility analysis were set up. Single trait analysis for all traits and two trait analysis of each fertility trait jointly. Starting values for variance components for two–trait analyses were obtained from single–trait analyses on individual traits. The model of the analysis included animals, permanent environmental and errors as random effects, month and year of calving and parity as fixed effects. Parameters such as, ratio of additive genetic variance to the total phenotypic variance (that is, heritability (h^2), ratio of permanent environmental variance to the total phenotypic variance (c^2) and genetic correlations r_g between fertility traits and milk yield were estimated using the statistical software package, MTDFREML (*Boldman et al., 1995*). Best linear unbiased predictor (BLUP) of breeding values (EBV's) for fertility traits from single–trait and two–trait analysis with milk yield were obtained from the same (single–or two trait) MTDFREML variance component analyses. The characteristics of this data set and means of different traits studied are given in *Table 1*.

Table 1: Structure of data used in the analysis, unadjusted means, standard deviation (SD) and CV% for different traits studied

Traits	Means	SD	CV%
305 day milk yield (305 dMY), kg	2806	949	33.82
305 day fat yield (305 dFY), kg	102	36	45.29
305 d protein yield (305 dPY),.kg	79	28	35.44
Lactation period (LP), d	294	86	29.25
Days open (DO), d	141	91.17	64.62
Calving interval (CI), d	415	89.64	21.81
Observations			
Records in data	2180		
Cows in data	513		
Sires in data	91		
Dams in data	879		
Animals in Pedigree	1483		

Results and discussion

Unadjusted means and standard deviation (SD) for 305 dMY, 305 dFY, 305 dPY, LP, DO and CI are 2806 kg, 102 kg, 79 kg, 294 d, 141 d and 415 d, respectively (Table 1). Estimates of coefficient of variations (CV%) are given in Table 1. The large CV % value for DO (64.62 %) reflects a great variation between individuals in such an important reproductive trait.

The heritability (h^2) and ratio of permanent environmental variance (c^2) for production traits and fertility traits from single-trait and two-trait analysis for fertility with milk yield are given in Table 2. Heritability estimates for 305 d MY, 305 dFY, 305 dPY and LP are 0.17 (0.07), 0.15(0.01), 0.14(0.01) and 0.15(0.05), respectively, Table 2. The present estimates are agree with the estimates reported by de Jager and Kennedy (1987), El-Awady et al. (2002) and Atil and Khattab (2005) which ranged from 0.14 to 0.25.

Table 2: Heritability (h^2) and ratio of permanent environmental variance (c^2) of production and fertility traits obtained from single – and two – trait genetic analyses (with milk yield as a correlated trait).

Traits	Single – trait model		Two - trait model	
	h^2 (S.E)	c^2	h^2 (S.E)	c^2
305 day milk yield (305 dMY)	0.17(0.07)	0.09		
305 day fat yield (305 dFY)	0.14(0.01)	0.01		
305 d protein yield (305 dPY)	0.14(0.01)	0.01		
Lactation period (LP)	0.15(0.05)	0.07		
Days open (DO)	0.02(0.01)	0.01	0.01(0.01)	0.06
Calving interval (CI)	0.03(0.01)	0.002	0.02(0.01)	0.10

The present results concluded that the genetic improvement in milk production and its composition can be achieved through selective breeding program. Single-trait (or two-trait) estimates of heritability for fertility traits were generally much lower (range from 0.02 to 0.03) for single-trait and range from 0.01 to 0.02 for two traits). Similar results are reported by Khattab and Atil (1999), Atil et al. (2001), Kadarmideen et al. (2003) and Atil and Khattab (2005) working on different breeds of dairy cattle, found that h^2 for DO and CI ranged from 0.01 to 0.05. The present results indicated that the most variation in DO and CI is due to non genetic additive genetic factors. Therefore, improving the managerial techniques should lead to a considerable decrease in length of DO and CI. Makuza and McDaniel (1996) suggested that the low h^2 for DO indicated that temporary environmental influences



were much greater than genetic influences or permanent environmental effects. Estimates of h^2 and c^2 and their standard errors from single –trait and two- trait analysis were similar.

Genetic correlation between 305 d MY and each of DO and CI were negative and highly significant and being -0.40(0.02) and -0.71(0.01), respectively, while the genetic correlation between DO and CI were positive and highly significant (0.70(0.05)). The present results indicated that selection against days open and calving interval would increase milk yield. Also, genetic selection for reduced DO would result in reduced CI. Therefore a reduction DO and CI are the desirable goal of dairymen. *Khattab and Atil (1999), Atil et al. (2001), Kadarmideen et al. (2003), Atil and Khattab (2005)* and *Zakizadeh and Sabzali (2010)* came to the same conclusion.

Estimates of predicting breeding values from sires (EBV' S), minimum, maximum, predicted standard error (SE) and their accuracy (R_{it}) for single trait and two traits of milk yield with fertility traits are presented in *Table 3*. Range of predicted sire breeding values for single - trait ranged from -391 to 700 kg for 305 dMY, from -14.74 to 22.06 kg for 305 dFY, from -11.09 to 21.80 kg from 305 dPY, from -41.20 to 47.13 d for LP, from -4.05 to 8.44 d for DO and, from -11.11 to 23.04 d for CI. While, the range of predicted sire breeding values for two–trait analyses ranged from -1.69 to 3.67 d for DO and from -.126 to 0.75 for CI (*Table 3*). The present estimates showed large genetic differences between sires for productive and reproductive traits which indicate the high potential for rapid genetic improvement in 305 dMY, 305 dFY, 305 dPY, LP, DO and CI through sire selection. A Similar trends were found by different works on different countries are given in the literature (i.e., *E–Arian et al., 2003; Atil and Khattab, 2005 and Sawalha et al. 2005*).

The present estimates of sire breeding values for milk traits are lower than those estimates reported by different authors working on different breeds of dairy cows in different countries, in this respect, *El–Arian et al., (2003)* working on Holstein Friesian cows in Egypt, found that the range of sire breeding values for 305 d MY was 1289 kg. *Atil and Khattab (2005)* in a study based on 1780 normal first lactation records of Holstein Friesian cows kept at five herds in Turkey, using multi Trait Animal Model (MTAM), found that the range of sire transmitting ability of 305 d MY was 2186kg. In US, *Sawalha et al. (2005)* with 12,071 first lactation Holstein cows, using animal model, found that the average of sire predicted breeding values for milk yield, fat yield and protein were 540 kg/lactation, 26.6 kg/lactation and 15.7 kg/lactation, respectively.

Table 3: Range, standard errors (SE) and accuracy (R_{it}) of predicted sire breeding values (EBV's) for single-trait and two-trait fertility evaluation with milk yield.

Traits *	Single – trait EBV's				Two – trait EBV's			
	Min	Max	SE	R_{it}	Mi n	Ma x	SE	R_{it}
DO, d	-4.05	8.44	9.49 to 10.74	0.12 to 0.15	- 1.6 9	3.6 7	4.41 to 4.42	0.18 to 0.23
CI, d	- 11.1 1	23.0 4	13.71 to 11.42	0.32 to 0.61	- 1.2 6	0.7 5	0.01 to 0.02	0.86 to 0.94
305 d MY, kg	-391	700	18.37 to 29.40	0.61 to 0.87				
305 d FY, kg	- 14.7 4	22.0 6	7.29 to 7.63	0.83 to 0.85				
305 d PY, kg	- 11.0 9	21.8 0	5.52 to 5.79	0.84 to 0.85				
LP, d	- 41.2 0	47.1 3	18.04 to 18.39	0.81 to 0.82				

* DO, CI, 305 d MY, 305 d FY, 305 PY and LP are days open, calving interval, 305 day milk yield, 305 day fat yield, 305 day protein yield and lactation period, respectively

Table 3 shows that the standard errors and accuracy of predicted sire breeding values were higher for single-trait than for two-trait analyses. Therefore, multiple trait analyses improve accuracy of estimated breeding values for each trait involved by reducing variances of prediction error. Schaeffer (1984) showed that the percentage reduction in predicting breeding values (hence increase in accuracy) depends on the absolute difference between error and genetic correlations. The greater the absolute difference in correlations, the greater is the accuracy for both traits. When error correlation is less than the genetic correlation, traits with low h^2 achieve a greater increase in accuracy. Also, Abdelharith et al. (2002) estimated breeding values for 305 dMY of Friesian cows in Egypt, using multiple and single trait animal models, reported that the accuracy was higher in the multiple trait analysis by 6.33 % than in single trait analysis. They concluded that using the multiple trait analysis is recommended to obtain more accurate breeding values for 305 d MY. The reason of it, that it makes use of all information about the lactations and the covariances among them as well as the relationships between the relatives in the different traits.



Conclusions

A single trait evaluation for fertility would be biased due to selection or culling on milk yield information, two-trait evaluation of fertility with milk yield is highly recommended, especially for traits with low genetic correlations.

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