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Maternal Genetic Effect on Expected Genetic Response of Selection Indices for Milk Production of Friesian Cows in Egypt

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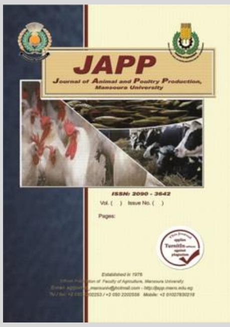

ABSTRACT

The present study aimed to estimate the genetic parameters of first lactation milk yield (FLMY), first lactation period (FLP), first dry period (FDP) and first calving interval (FCI) and inclusion these studied traits in selection indices through different animal models. The data utilized in this study were obtained from 1821 normal first lactation of Friesian cows belong to Sakha and EI-Karada Experimental stations of Animal Production Research Institute (APRI), Dokki, Cairo, Egypt. Data were collected during the period from 1990 to 2016 and analyzed using the MTDFREML program. Covariance components were used to construct the different selection indices for FLMY kg, FLP day, FDP day and FCI day with four multiple animal models. Means for FLMY, FLP, FDP and FCI were 2425 kg, 304 d, 170 d and 474 d, respectively. Direct heritability (h^2_a) for the above-mentioned traits were 0.32, 0.29, 0.27 and 0.18, respectively. The corresponding estimates of the maternal heritability (h^2_m) for the same traits were 0.25, 0.22, 0.30 and 0.27, successively. Estimates of direct genetic correlations among studied traits ranged from -0.52 to 0.61. The phenotypic correlations among investigated traits were ranging from -0.20 to 0.23. Animal model number two that included the additive and permanent effects had the highest accuracy. On the contrary, model number three that included additive and maternal effects. The ranking correlations among four animal models were higher than 0.93. This indicates that using one of the studied models can be achieved the genetic improvement. We would however recommend that included the permanent environmental effects on analytical models when selection for these traits in Friesian cows under Egyptian condition.

Keywords: Maternal genetic effect, Selection indices, milk production, Friesian cows.

INTRODUCTION

Over the past two decades, significant emphasis has been put on the importance of Friesian cattle in Egypt for milk production, which has resulted in an increase in the number of large Friesian herds either in government or commercial farms through imports from Europe and the United States (Farrag *et al*., 2017). Milk production in dairy farms can either be improved by increasing the number of milking animals or by rising the quantity of milk per animal by improving the environmental conditions, management practices and genetics. There are various mating techniques for enhancing the dairy animal's genetic ability.

The estimation of variance components and genetic parameters is necessary for the determination of an optimal breeding strategy seeking the genetic improvement of the dairy cows' performance traits (Pantelić *et al*., 2011; Zink *et al*., 2012). Weppert and Hayes (2004) reported the importance of genetic parameters evaluation for increasing the selection programs efficient. Selection is mainly based on accurate expectation of genetic parameters for selected traits and applications of practical breeding programs (Kumlu, 2003; Şahin *et al*., 2014). The first lactation milk yield was a reliable indicator of the productive life length in dairy cattle (Sawa and Krężel-Czopek, 2009). Heritability of first lactation milk yield has shown the possibility of genetically improved Brown Swiss dairy cattle by selection (Şahin *et al*., 2014). The selection indices were the better efficient methods for selection in the farm animal (Hazel and Lush, 1942). Selection in which several useful traits based on indices are an important for guiding the breeder to implement effective breeding strategy (Hazel, 1943). Hayes *et al*. (2009) reported that each country should develop its own selection index because the success of the selection index in different countries cannot be compared, notwithstanding breeding goals are more similar. VanRaden (2002) reflected that the selection indices are better measures of profit today than those published before three decades earlier. In many countries breeding goals included longevity, health, fertility, conformation and yield traits. Miglior *et al*. (2005) shown that the selection indices have been developed in various countries, a modifying focus on production to be the more balanced breeding goal of improving production.

The major objectives of the present research work were to estimate the direct and maternal genetic parameters for first lactation milk yield (FLMY), first lactation period (FLP), first dry period (FDP) and first calving interval (FCI) and construct different selection indices for these studied traits through different animal models.

MATERIALS AND METHODS

Data

The data utilized in this study were obtained from first lactation of Friesian cows belong to Sakha and EI-

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Karada Experimental stations of Animal Production Research Institute (APRI). Data were collected during the period from 1990 to 2016. Number of records and sires were 1821 and 118, respectively. Cows were kept under the same system of feeding and management practiced in the farms (El-Awady, 2013).

Statistical Analysis

Data were analyzed by using the MTDFREML program of Boldman *et al*. (1995) to valuation of covariance components of considered traits, i.e., first lactation milk yield (FLMY kg), first lactation period (FLP day), first dry period (FDP day) and first calving interval (FCI day) with four multiple animal models that included fixed effects of month and year of calving and farm and random effects for animal.

Model 1: $Y = X\beta + Za + e$

Model 2: $Y = X\beta + Za + Wpe + e$

Model 3: $Y = X\beta + Za + Mm + e$

Model 4: $Y = X\beta + Za + Mm + Wpe + e$

Where: Y= a vector of observations, β = a vector of fixed effects, a = a vector of additive genetic effects, m = a vector of maternal genetic effects, M = the incidence matrix relating records to maternal genetic effect, pe = a vector of environmental effects contributed by dams to records of their progeny (permanent environmental), W = the incidence matrix relating records to permanent environmental effects and e = a vector of the residual effects. X and Z are incidence matrices relating records to fixed and genetic effects, respectively.

The estimation of the accuracy (R_{IH}) correlation between the index variance and the aggregate genotype variance, partial regression coefficients (b,s), and the assumed genetic change (ΔG) per generation for studied traits in order to construct selection indices were performed via MATLAB software (Mathworks, 2002).

The economic weight for each trait was calculated according to December 2016 prices relying on the final net profit (Khattab and Sultan,1991 and Abu El-Naser, 2014) as the following steps: (1) the net profit/kg of milk =1.10 Egyptian pounds (LE), (2) the net profit/day of the lactation period: calculated via net profit/kg of milk*average daily milk yield =8*1.10 = 8.80 LE, (3) losses in the net profit/day due to increased dry proud one day =16 LE and losses in net profit/day due to increased calving interval one day =13 LE.

Table 1. The relative economic values of different studied traits in present investigation.

Traits	Net profit	Actual economic value
FLMY	1.10	1.00
FLP	8.80	8.00
FDP	-16	-14.55
FCI	-13	-11.82

FLMY= first lactation milk yield, FLP= first lactation period, FDP= first dry period, FCI= first calving interval and one of Egyptian pound (LE) = 0.06$

The index value was calculated as:

$$I = b_1P_1 + b_2P_2 + \ldots\ldots\ldots + b_nP_n = \sum_{i=1}^{n} b_iP_i$$

Where:

p_i **= phenotypic value of traits** b_i **= partial regression coefficient.**

Regression coefficients (b) of selection indices estimated as follows:

$$Pb = Ga \text{ or } b = P^{-1}Ga$$

Where:

P **= the phenotypic variance-covariance matrix,**

G **= the genetic variance-covariance matrix,**

b **= a vector of partial regression coefficients to be used in the index,**

a **= a vector of constants representing the economic values of the traits, and**

P^{-1} **= the inverse of phenotypic variance-covariance matrix.**

Calculate index variance as σ^2_I =b´ P b = b´ G a where b´ is the transpose of (b) vector of partial regression coefficients.

Variance of the total aggregate genotypic (σ^2_H) was estimated as σ^2_H =a´Ga, where, a´ is the transpose of the economic value column vector. Accuracy of the index (R_{IH}) defined as the correlation between σ^2_H and σ^2_I , was $\sigma^2_{IH} = \sigma_I / \sigma_H /(\sigma_I * \sigma_H)$ since $\sigma^2_{IH} = \sigma^2_I$ .The expected genetic gain (ΔG) for any one of the traits was $i\, R_{IH}\, \sigma_I$, where i is the selection intensity, which was set to 1.00 for the purpose of comparisons, construct selection indices use of Henderson's modifications of Hazel's method (1943).

RESULTS AND DISCUSSION

Descriptive statistics

The coefficients of variation for studied traits in current investigation ranged from 23.21 % to 58.24 % (Table 2). The current results are nearest to the results observed on Friesian cows by (El–Awady and Abu El-Naser, 2017) .

The mean of FLMY was lower (2425.3kg) than that calculated by Hammoud (2013) and Goshu *et al.* (2014) in Holstein Friesian being 10341.8 and 3019 kg, respectively. Furthermore, the mean of the FLP was 304 days that shorter than the estimate of 391.2 days given by Hammoud (2013). On the other hand, Goshu *et al.* (2014) found that the FLP (299 days) in Holstein Friesian.

Table 2. Means, standard deviation (SD) and coefficient of variation (CV%) for first lactation milk yield (FLMY), first lactation period (FLP), first dry period (FDP) and first calving interval (FCI) for Friesian cows.

Trait	Mean	SD	CV
FLMY, kg	2425	986	40.66
FLP, d	304	102	33.55
FDP, d	170	99	58.24
FCI, d	474	110	23.21

The presented means of FDP and FCI were 170 and 474 days, respectively. These results were longer than the estimates that reported by Ibrahim (2006) in Holstein Friesian being 72 and 394 days, respectively. Contrarily, shorter estimates in Holstein Friesian reported by Goshu *et al.* (2014).

Variances and heritabilities

The estimates of direct heritability (h^2_a) for FLMY, FLP, FDP and FCI were moderate being 0.32, 0.29, 0.27 and 0.18, respectively (Table 3). Noticeable the estimates of h^2a for FLMY and FLP were lower than observed by Hammoud (2013) in Holstein Friesian cattle (0.44 and 0.48), in succession. Also, the present result of h^2_a for FMLY was lower than value that obtained by Ibrahim *et al.*, (2020) in Friesian (0.35). While, the immediate estimates of h^2_a for FLMY, FLP, FDP and FCI were higher than estimates that found in Friesian cattle by Shalaby *et al*. (2013) were 0.141, 0.04, 0.109 and 0.104, successively. The valuation of maternal heritability (h^2_m) for FLMY, FLP, FDP and FCI were moderate 0.25, 0.22, 0.30, and 0.27, respectively (presented in table 3). These results were higher than that shown by El–Awady and Abu El-Naser (2017) of (h^2_m) for the same traits in Friesian cows being 0.11, 0.15, 0.14, 0.23 and 0.10, successively.

Table 3. Estimation of variance components and heritabilities for studied traits

Estimates	Traits			
	FLMY	FLP	FDP	FCI
σ^2_a	70667.04	224.87	455.15	192.76
σ^2_m	55208.63	170.59	505.72	289.14
σ^2_{pe}	17666.76	116.31	539.44	353.39
σ^2_e	77429.06	265.91	193.50	239.60
σ^2_p	220834.50	775.41	1685.74	1070.88
σ_{am}	-136.98	-2.27	-8.07	-4.01
r_{am}	-0.002	-0.012	-0.017	-0.017
h^2_a	0.32	0.29	0.27	0.18
h^2_m	0.25	0.22	0.30	0.27
c^2	0.08	0.15	0.32	0.33
e^2	0.35	0.34	0.11	0.22

σ^2_a = additive genetic variance, σ^2_m= maternal variance σ^2_{pe} = permanent environmental, σ^2_e = residual (temporary environmental variance σ^2_p = phenotypic variance, σ_{am} = direct maternal genetic covariance, h^2_a = direct heritability, h^2_m = maternal heritability, c^2 = fraction phenotypic variance to permanent environmental e^2 = fraction phenotypic variance due to residual effects.

Correlations

The actual estimates of r_{am} were negative for different studied traits as shown in table (3). Comparable the r_{am} results with those reported by El–Awady and Abu El-Naser (2017). The valuation of genetic correlations among FLMY, FLP, FDP and FCI were varying from (-0.52 to 0.61). Respecting, the genetic correlation between FCI both of FLP and FDP were positive (0.35 and 0.36), respectively. While, genetic correlations between the FDP and both of FLMY and FLP were negative (-0.16 and -0.52), consecutively (Table 4). Şahin *et al*. (2014) in Brown Swiss noticed that the genetic correlations among FLMY, FLP, and FCI were highly positive and varying from 0.69 to 0.93. They also showed the genetic correlations between the FDP and every of FLMY, FLP and FCI were 0.10, -0.31 and 0.44, consecutively. Goshu *et al*. (2014) noticed that genetic correlations between the FDP and both of FLMY and FLP were negative in Holstein Friesian cows (-0.84 and -0.15), in succession. Ibrahim (2006) noticed that the genetic correlations among 305dMY, LP, and CI in first lactation were positive and varying from (0.31 to 0.43) in Holstein cattle in Egypt.

The assessment of phenotypic correlations among FLMY, FLP and FCI were positive and varying from 0.11 to 0.23. While phenotypic correlations between the FDP and both of FLMY and FLP that given in table 4 were negative -0.08 and -0.20, consecutively. Şahin *et al.* (2014) in Brown Swiss cattle observed positive phenotypic correlations between FLP and every of FLMY and FCI were 0.55 and 0.20, consecutively. Also, they found phenotypic relation between FCI and FDP was positive 0.73.

Table 4. Different correlations and ratios among studied traits.

Traits		r_{a1a2}	r_{m1m2}	r_{pe1pe2}	r_{e1e2}	r_{p1p2}
FLMY	FLP	0.61	0.07	-0.05	0.16	0.23
	FDP	-0.16	0.05	-0.01	-0.22	-0.08
	FCI	-0.13	-0.04	-0.15	-0.22	0.11
FLP	FDP	-0.52	-0.01	-0.29	0.34	-0.20
	FCI	0.35	0.19	-0.37	0.03	0.12
FDP	FCI	0.36	-0.42	0.46	-0.82	0.17

r_{a1a2} = genetic correlation between trait1, 2 and so on, and r_{m1m2}= maternal genetic correlation between traits1, 2 and so on, r_{pe1pe2} = permanent environmental ratio between traits 1, 2 and so on, r_{e1e2} = residual environmental ratio between traits 1, 2 and so on r_{p1p2} = phenotypic correlation between traits 1, 2.

Ibrahim (2006) clarified that first lactation phenotypic correlations between DP and every of the LP and CI were -0.179 and 0.139, consecutively. The present permanent environment ratio among FLMY, FLP, FDP and FCI were varying from -0.37 to 0.46. Corresponding the residual environmental ratio varying from -0.82 to 0.34. Permanent and residual ratios of the mentioned traits being (-0.17 to 0.37) and (-0.09 to 0.49), successively in Friesian cows (El–Awady and Abu El-Naser, 2017).

Selection index

Selection indices (I,s) of four different animal models are shown in Tables 5, 6, 7 and 8. Comparisons between different selection indices from the model (1) be perceived that the selection index I_1 (full index) was the best indices (R_{IH} = 0.64 and RE%=100), following by the index I_2 (dropped FLP from the full index). The lost accuracy and relative efficiency (R_{IH} = 0.40 and RE%=62.50) were in the index I_7 included (FLP and FCI). Resulted in dropping FLMY and FDP from the full index reduced about 37.5% of selection index accuracy. The highest expected genetic gain in generation for FLMY found through selection index I_6 which lead to improvement 150.84kg, following by 140.98kg in selection index (I_5). While, the lowest genetic gain in generation for FLMY observed in the selection index (I_7) was 69.01kg.

Table 5. Estimation of accuracy (R_{IH}), partial regression coefficients (b,s), relative efficiency (RE%) and the expected genetic change (ΔG) in selection indices (I,s) within generation of studied traits from model 1.

Selection indices	Traits								R_{IH}	RE%
	FLMY		FLP		FDP		FCI			
	b	ΔG	b	ΔG	b	ΔG	b	ΔG		
I_1	0.46	127.38	3.63	7.1	-5.57	-11.63	-3.91	-4.99	0.64	100
I_2	0.44	133.72	-	4.28	-6.76	-11.07	-2.44	-2.14	0.62	96.88
I_3	0.46	132.68	-5.74	7.7	-5.74	-11.68	-	1.9	0.61	95.31
I_4	-	80.50	3.69	9.3	-5.84	-14.01	-4.00	-3.92	0.53	82.81
I_5	0.49	140.98	4.89	8.15	-	-6.26	-	3.36	0.50	78.13
I_6	0.48	150.84	-	2.55	-	-1.81	-1.26	-5.10	0.51	79.69
I_7	-	69.01	7.18	11.38	-	-8.76	-4.58	-11.53	0.40	62.50
I_8	0.45	135.59	-	5.63	-6.49	-11.29	-	3.8	0.60	93.75
I_9	-	71.40	-	5.91	-7.04	-13.55	-2.51	-13.54	0.49	76.56

The present results inducted that the best of expected genetic gain for FLP, FDP, FCI were in selection indices I_7, I_4 and I_9, which lead to improvement were 11.38, -14.01 and -13.54 days, respectively.

Estimates of different selection indices through the model (2) in the table (6) shown that the highest accuracy (R_{IH} = 0.70 and RE%=100) in I_1 (original index), following by I_3 (dropped FCI from the full index).

Table 6. Estimation of accuracy (R_{IH}), partial regression coefficients (b,s), relative efficiency (RE%) and the expected genetic change (ΔG) in selection indices (I, s) within generation of studied traits from model 2.

Selection indices	Traits								R_{IH}	RE%
	FLMY		FLP		FDP		FCI			
	b	ΔG	b	ΔG	b	ΔG	B	ΔG		
I_1	0.60	104.72	6.87	15.32	-4.72	-14.80	-4.59	-6.61	0.70	100
I_2	-4.90	110.39	-	5.75	-4.90	-11.98	-2.85	-8.01	0.57	81.43
I_3	0.69	95.27	4.90	15.83	-4.04	-17.14	-	1.7	0.63	90.0
I_4	-	74.63	7.35	16.60	-4.93	-16.07	-5.06	-4.21	0.60	85.71
I_5	0.71	130.60	.40	14.59		-8.80		-1.9	0.51	72.86
I_6	0.72	161.05		3.62	-	3.66	-1.93	-14.34	0.41	58.57
I_7	-	74.40	-4.23	15.68		-6.35	-4.23	-7.85	0.40	57.14
I_8	0.72	103.73	-	7.62	-4.40	-14.47	-	-1.19	0.52	74.29
I_9	-	60.00	-	5.33	-5.17	-13.80	-3.25	-5.08	0.49	70.0

Furthermore, the lowest accuracy and relative efficiency found in I_7 (R_{IH} = 0.40 and RE%=57.14), which dropping FLMY and FDP from the original index caused reduce of accuracy more than 40 %. The highest expected genetic gain for FLMY in generation observed through selection index I_6 (included FLMY and FCI) which lead to improve 161.05kg and the best expected genetic gain for FLP through I_4 (16.60 days). The best expected genetic gain for FDP and FCI noticed through selection indices I_3 and I_6, which lead to improve -17.14 and -14.34 days, respectively.

Estimation of selection indices of model 3 (table 7) showed the selection index I_1 (full index) was the best indices (R_{IH} =0.55 and RE%=100), following by the index I_3 (dropped FCI from the full index) which were R_{IH}=0.53 and RE%=0.96.36. While, the lowest accuracy and relative efficiency (R_{IH} = 0.28 and RE%=50.91) were in I_7 included (FLP and FCI), which dropping FLMY and FDP from the original index give rise to reduce about 50% of selection index accuracy. The highest expected genetic gain of FLMY and FLP in generation found in index I_5 (included FLMY and FLP) were 161.20kg and 13.45d, successively. While, the best of genetic improvement for FDP and FCI observed in selection indices I_8 included (FLMY and FDP) and I_9 included (FDP and FCI) were -16.39 and -8.28 days, respectively.

Table 7. Estimation of accuracy (R_{IH}), partial regression coefficients (b,s), relative efficiency (RE%) and the expected genetic change (ΔG) in selection indices (I,s) within generation of studied traits from model 3.

Selection Indices	Traits								R_{IH}	RE%
	FLMY		FLP		FDP		FCI			
	b	ΔG	b	ΔG	b	ΔG	B	ΔG		
I_1	0.35	107.67	3.18	7.45	-4.19	-13.92	-2.10	-1.93	0.55	100
I_2	0.37	109.73		1.39	-4.30	-14.92	-2.04	-2.55	0.51	92.73
I_3	0.35	121.42	3.10	8.10	-4.56	-15.32	-	2.04	0.53	96.36
I_4	-	81.70	3.55	8.00	-4.14	-14.59	-2.185	-3.97	0.47	85.45
I_5	0.35	161.20	3.41	13.45	-	-2.27		3.34	0.35	63.64
I_6	0.37	146.30	-	1.37	-	-2.03	-2.15	-4.15	0.33	60.00
I_7	-	70.00	3.83	12.29	-	-0.86	-2.01	-6.65	0.28	50.91
I_8	0.38	124.18	-	1.95	-4.66	-16.39	-	1.57	0.50	90.91
I_9	-	60.89	-	0.90	-4.27	-16.38	-2.12	-8.28	0.42	76.36

Ranking of the selection indices from model 4 in the table (8) noticed that the best selection indices of accuracy (R_{IH} = 0.61 and RE%=100) in I_1 (full index) and following by I_3 (dropped FCI from the full index). While, the lowest accuracy and relative efficiency (R_{IH} = 0.37 and RE% = 60.66) were observed in I_9, that reduced of accuracy about to 40% due to dropping FLMY and FLP from the original index. The highest genetic change from FLMY and FLP in different selection index observed in selection indices (I_6 and I_1) were 164.78kg and 8.80 days, respectively. While, the best improvement of FDP and FCI found in the selection index (I_9) were -10.80 and -1.86 days, respectively. Also, the lowest genetic chance of FLMY and FLP in the selection index (I_9) were 60.20kg and 3.80 days, respectively.

The present results indicated that the accuracy of full selection indices in different animal models were varying from (0.55 to 0.70) for FLMY, FLP, FDP and FCI. Where, the highest accuracy (R_{IH}=70) observed in model 2, while the lowest accuracy (R_{IH}=55) observed in model 3.

The accuracy decreased from 14 to 17% with omitting FLMY from original indices in different models. Abu EI-Naser (2014) shown that the genetic change (ΔG) from different three animal models for milk yield were varying from (13.4 to 226.9). Also, He found that the highest value of ΔG for milk yield and the accuracy of selection indices were in the model included (σ^2a, σ^2pe and σ^2e) in Egyptian buffalo. Hussein (2004) on Friesian cows found that the accuracy of different selection indices were varying from (0.51 to 0.71) for MY, FY and PY and the relative accuracy decreased 20% by omitting MY from different indices. El-Awady (2009) reported that genetic gain for milk yield was ranged from 110 to 304 on Friesian cows. Prata *et al.* (2015) included that betterment the economic genetic efficiency on farms in Brazil with regard to selection for fat and protein yields additionally milk yield for selection plan in Gir dairy cattle. Ashmawy and Khalil (1990) and (Khalil and Soliman (1993) indicated that the genetic change of MY ranged from 157.6 to 194.6 in dairy cows. El-Arian (2005) shown that the highest values of relative efficiency and accuracy of the selection index included (MY, FY, PY, CI and AFC) and followed by the selection index (MY, FY, CI and AFC) in Friesian cattle. The present results indicated that the ranking correlation coefficients among four models were ranged from 0.97 to 0.93.

Table 8. Estimation of accuracy (R_{IH}), partial regression coefficients (b,s), relative efficiency (RE%) and genetic change (∆G) in selection indices (I,s) within generation of studied traits from model 4.

Selection indices	Traits								R_{IH}	RE%
	FLMY		FLP		FDP		FCI			
	b	∆G	b	∆G	b	∆G	b	∆G		
I_1	0.40	142.4	5.03	8.80	-3.36	-9.12	-0.65	3.37	0.61	100
I_2	0.41	122.83	-	6.28	-4.12	-8.40	0.013	2.35	0.53	86.89
I_3	0.35	133.61	5.09	8.54	-3.50	-9.16	-	3.0	0.60	98.36
I_4	-	74.18	6.41	8.07	-3.61	-10.7	0.13	3.43	0.51	83.61
I_5	0.36	151.5	0.53	8.4	-	-5.03	-	2.3	0.53	86.89
I_6	0.52	164.78	-	5.9	-	-2.6	1.07	1.9	0.45	73.77
I_7	-	90.10	7.5	8.48	-	-6.52	1.03	3.57	0.42	68.85
I_8	0.41	122.63	-	6.27	-4.13	-8.40	-	2.34	0.53	86.89
I_9	-	60.20	-	3.80	-4.60	-10.80	-0.72	-1.86	0.37	60.66

Table 9. Ranking Correlation coefficients among four animal models under investigation

Item	Model 1	Model 2	Model3
Model 2	0.96		
Model3	0.97	0.95	
Model4	0.94	0.95	0.93

Where, the highest correlation was between first and third models, but the lowest correlation was between third and four models. At which noticed that quite similarity of cow's selection indices values for different animal models in table 9. Abu EI-Naser (2014) showed that the ranking correlation coefficients among three animal models were ranged from (0.96 to 0.90) in Egyptian buffalo.

CONCLUSION

The current results indicated that the additive and maternal heritability estimates of FLMY, FLP, FDP, and FCI reflected the ability to achieve a plausible rate of genetic improvement for studied traits. The accuracy reduced about from 37.5 to 50% as a result of omitting FLMY and FLP or FLMY and FDP from the original selection index. The ranking correlations among four animal models were higher than 0.93. This indicates that genetic improvement can be achieved using one of the studied models. While, the inclusion maternal effects due dam in the animal models lead to upturn expected genetic gain in selection indices.

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التأثير الوراثي الأمي على العائد الوراثي المتوقع من الأدلة الانتخابية لإنتاج اللبن من أبقار الفريزيان فى مصر

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تهدف الدراسة الحالية إلي تقدير المعايير الوراثية لمحصول اللبن فى أول موسم و طول أول موسم حليب وأول فترة جفاف وأول فترة بين ولادتين، وإدخال هذة الصفات فى الأدلة الانتخابية خلال نماذج الحيوان المختلفة. البيانات المستخدمة فى الدراسة جمعت من ١٨٢١ أول موسم حليب لأبقار الفريزيان الموجودة فى محطات بحوث الإنتاج الحيوانى بسخا والقرضا التابعين لمعهد بحوث الإنتاج الحيوانى وذلك خلال الفترة من ١٩٩٠ حتى عام ٢٠١٦م، والبيانات حللت باستخدام برنامج MTDFREML. واستخدم التغاير فى بناء الأدلة الانتخابية المختلفة لمحصول اللبن فى أول موسم حليب، طول أول موسم حليب، أول فترة جفاف وأول فترة بين ولادتين خلال أربع نماذج للحيوان. وكانت المتوسطات للصفات المدروسة هى ٢٤٢٥كجم و٣٠٤ يوم و١٧٠ يوم و٤٧٤ يوم على التوالي. وكان المكافئ الوراثي المباشر للصفات السابقة ٠,٢٣، ٠,٢٩، ٠,٢٧، ٠,١٨ بينما كان المكافئ الوراثي الأمي لها ٠,٢٥، ٠,٢٢، ٠,٣٠، ٠,٢٧ على التوالي. وكانت الارتباطات الوراثية بين الصفات المدروسة تتراوح من -٠,٥٢ الى ٠,٦١ بينما الارتباطات المظهرية تتراوح من -٠,٢٠ الى ٠,٢٣. وكانت أعلى دقة فى نموذج الحيوان رقم ٢ المحتوى على التاثيرات البيئية الدائمة وعلى العكس من ذلك نموذج الحيوان الثالث المحتوي على التاثير الوراثي المباشر والأمي و ارتباطات الرتب بين نماذج الحيوان الأربعة كانت أعلى من ٠,٩٣ وذلك يظهر إمكانية التحسين الوراثي بالانتخاب بأى نموذج من هذه النماذج. ولكن يقترح إدخال التأثيرات البيئية الدائمة فى نماذج التحليل عند الانتخاب لهذه الصفات فى أبقار الفريزيان تحت الظروف المصرية.