

A Comparison of Linear Models for Estimating Co-Variance Components and Genetic Parameters in Holstein Dairy Cattle

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Abstract: The objective of this study was to compare four different statistical models for genetic evaluation of some traits of Holstein-Friesian dairy cattle raised in Egypt. Data were collected from Alexandria Copenhagen Company; a commercial dairy herd located in Egypt on Cairo-Alexandria desert road, and represented 2846 first three lactation records pooled from cows having 60 sires and 428 dams. The studied traits were; days open (DO), 305-days milk yield (305-DMY), fat yield (FY) and protein yield (PY). Models were discriminated according to random effects fitted in each model. The random effects were; direct additive genetic effects of animals, maternal additive genetic effects, permanent environmental effects, together with the covariance between direct and maternal genetic effects, and residuals. Comparisons of statistical models were based on (AG) Log Likelihood values and estimates of genetic parameters of traits. Co-variance components and genetic parameters were estimated with VCE-6 software package. Heritabilities obtained from all models were ranged from (0.07 to 0.10), (0.24 to 0.32), (0.25 to 0.42) and (0.24 to 0.33) for DO, 305-DMY, FY and PY, respectively. Also, for all traits, the best-fitted model was characterized by the highest Log Likelihood value, the highest maternal heritability and the existence of direct-maternal genetic covariance. Estimated breeding values (EBVs) showed high variations with positive spearman's rank correlations (≥ 0.83) among models. This study showed that the inclusion of maternal effects with direct-maternal genetic covariances in the statistical models for genetic evaluations would improve the current herd genetically.

Keywords: Statistical models, heritability, model selection, Log Likelihood values.

INTRODUCTION

Genetic evaluation of dairy cattle is influenced by a variety of factors such as additive genetic, maternal genetic and permanent environmental effects. Different studies made evidence that fitting a model with maternal effects would lead to a more precise estimation of (co)variance components and subsequently genetic parameters of both productive and reproductive traits of dairy cows (Miraei-Ashtiani *et al.*, 2007; Zamani and Mohammadi, 2008; Mohammadi *et al.*, 2013 and Jalil-Sarghale *et al.*, 2014). As a result, designing breeding programs and genetic evaluation systems require the use of more precise estimation of variance components and genetic parameters by adopting the best statistical models.

Unbiased animal model ranking for identification of genetic merit of individual animals need us to develop an operational model closer to the biological one considering recent advances computational capabilities. It is therefore, the search for the most suitable statistical model and the furthestmost advanced statistical tool is an important step in the development of genetic improvement schemes. Hence, the quality of the statistical models adopted for genetic evaluations of herd animals must be checked against other available models before being used in genetic evaluation procedures. Setting up a good statistical model is an essential concern for a reliable genetic computation and evaluation (Jorjani, 2003).

Recent model diagnostics and criteria could be used in evaluating the validity of statistical models to fit the best model among competitive ones. The most recent and familiar tools are; Akaike information criterion (AIC), the Schwarz Bayesian information

criterion (BIC), and the -2 log likelihood (Log L). Hence, the present study aimed to compare four statistical models based on AG Log likelihood values. In addition, to fit different models including additive genetic, maternal additive and permanent environmental effects for choosing the most appropriate statistical model to be largely used in genetic evaluation of dairy cattle herds.

MATERIALS and METHODS

Data collection and herd management

Data of the current study were collected from Alexandria Copenhagen Company, a commercial dairy herd located in Cairo-Alexandria desert road, about 80 km from Alexandria, Egypt. On the farm, all animals were kept in an open system under open sheds all over the year round, however supplied with a cool spraying system during hot climate. Animals had free access to clean water. The cows were fed on total mixed ration (T.M.R.) according to their production status. The ingredient compositions of rations were formulated through nutrient requirements of dairy cattle recommended by the National Research Council (NRC, 2001). Cows were machine-milked three times daily with 8 hours interval (at 6.00, 14.00 and 22.00 o'clock) in a herringbone parlor Alfa Lafal (40 point). Recording system used in the farm was a computer program system (Afikim and Dairy Comb 305). Heifers were inseminated when they reached an average of about 350 kg body weight. Inseminations were done artificially using frozen semen from the best 100 Total Predicted Index (TPI) Holstein bulls in U.S.A. and Canada assuming some reproductive and productive traits for Holstein-Friesian dairy cows. The studied traits were;

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days open (DO), 305-days milk yield (305-DMY), fat yield (FY), and protein yield (PY). The data used represented 2846 lactation records of cows with 60 sires and 428 dams, and born in the period from 2000 to 2010. Data were pooled for the first three lactations before analysis to construct repeated lactations for the permanent environmental effects and variance components estimation.

Statistical models fitting

Mixed linear models were used in all analyses applied in the present study. The fixed effects of models incorporated age at first calving (years), year of calving (from 2000 to 2010), season of calving (winter, spring, summer, and autumn). The random effects varied according to the model used for analysis. Animal, dam, and sires were fitted in all models. Variance components and genetic parameters for the investigated traits were estimated by VCE software, version 6.0.2 according to Groeneveld *et al.* (2008). Four models were used, and identified by two criteria; the first is the presence or absence of maternal genetic and permanent environmental effects; while the second is the existence or non-existence of direct- maternal additive genetic covariance. Model (1) was the least full animal model where only the additive genetic effect was fitted as the sole random effect of the model together with the residuals. Model (2) was increased by adding the permanent environmental effect as another random effect. Model (3) was adjusted to be as model (2), but the permanent environmental effect was replaced with maternal effects as a random effect, with the existence of direct-maternal genetic covariance. Model (4) was fitted to include three main random effects; additive genetic, maternal and permanent environmental effects, with the inclusion of direct-maternal genetic covariance. The tested models in matrix notation were as follows:

Model 1, was a full animal model:

$$Y = X\beta + Z_1a + e$$

Model 2, was a full animal model together with only maternal permanent environmental effects:

$$Y = X\beta + Z_1a + Z_2C + e$$

Model 3, was a full animal model with maternal additive genetic effects, but correlated with additive genetic one:

$$Y = X\beta + Z_1a + Z_3m + e, \text{ Cov}(a,m) = A\sigma_{a,m}$$

Model 4, was a full animal model with maternal additive genetic and permanent environmental effects, but both direct additive and maternal effects were uncorrelated:

$$Y = X\beta + Z_1a + Z_2C + Z_3m + e, \text{ Cov}(a,m) = 0$$

Where, Y is the vector of observations of studied traits; β , a, C, m, and e are the vectors of the fixed effects, animals additive genetic effects of, permanent environmental effects of dams of repeated lactations, maternal additive genetic effects, and residual effects, respectively. X, Z₁, Z₂, and Z₃ are the incidence matrices of the fixed effects, additive genetic effects of animals, permanent environmental effects of dams, and maternal additive genetic effects, respectively.

(Co) variance components were found to be as follows: $V(a) = A\sigma_a^2$, $V(m) = A\sigma_m^2$, $V(c) = \sigma_c^2 I$, $V(e) = \sigma_e^2 I$ $\text{Cov}(a,m) = A\sigma_{a,m}$ for Model (3).

The following is a general formula for the (co)variance components in matrix notation:

$$V \begin{pmatrix} a \\ m \\ c \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & A\sigma_{a,m} & 0 & 0 \\ A\sigma_{a,m} & A\sigma_m^2 & 0 & 0 \\ 0 & 0 & I\sigma_c^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{pmatrix}$$

Where, σ_a^2 is the additive genetic variance; σ_m^2 is the maternal additive genetic variance; σ_c^2 is the variance of maternal permanent environmental effects (because dams may have more than offspring in data); σ_e^2 is the residual variance; $\sigma_{a,m}$ is the covariance between direct and maternal additive genetic effects; while A is the numerator relationship matrix among animals and I is the identity matrix.

Also, $\begin{pmatrix} a \\ m \end{pmatrix} | A, G \sim N$

$$\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, G \otimes A \right)$$

Where, $G = \begin{pmatrix} \sigma_a^2 & \sigma_{a,m} \\ \sigma_{a,m} & \sigma_m^2 \end{pmatrix}$, and

\otimes is a direct product of matrix and,

$$C \sim N(0, I\sigma_c^2)$$

and,

$$e \sim N(0, I\sigma_e^2)$$

Additive and maternal heritabilities were estimated as follows:

$$h_a^2 = \frac{\sigma_a^2}{\sigma_p^2}, \quad h_m^2 = \frac{\sigma_m^2}{\sigma_p^2}$$

Where, h_a^2 is the additive genetic heritability; h_m^2 is the maternal additive genetic heritability according to the equation of (Willham, 1980); σ_a^2 , σ_m^2 , and σ_p^2 are the corresponding variance components estimated by each model.

RESULTS

Description of data

Summary of data used in the present study including number of records, overall means, standard deviations, minimum, maximum, and coefficients of variation of traits were presented in Table (1). Overall means of days open, 305 days milk yield, fat yield, and protein yield were; 166.02 days, 8478.59 kg, 267.92 kg, and 221.56 kg, respectively. In addition, standard deviations were estimated for these traits to be 124.64 days, 2333.84 kg, 102.78 kg, and 84.92 kg, respectively. The current data showed high variations of most of studied traits, which were ensured by the minimum and maximum values. Moreover, coefficients of variations were high especially for days open trait (75.07%).

Table (1): Summary statistics for studied traits of the first three pooled lactations

Trait studied	Number	Mean	SD	Minimum	Maximum	C.V. %
Days open, days	2846	166.02	124.64	19.00	965.0	75.07
305-days milk yield, kg	2846	8478.59	2333.84	524.00	16276.0	27.53
Fat yield, kg	2846	267.92	102.78	9.00	594.0	38.36
Protein yield, kg	2846	221.56	84.92	7.00	529.0	38.33

SD is standard deviation; C.V. % is the coefficient of variation

Variance components and genetic parameters estimates

Table (2) shows the estimates of (co) variance components and heritabilities with their standard errors of the four traits as estimated from different tested models. Generally, estimates of variance components and heritabilities varied for all traits by the model. Estimates of additive genetic variances of days open were 1377, 1095, 1402, and 1317 day²; of 305-days milk yield were 1378691, 1251960, 1536717, and 1310311 kg²; for fat yield were 2974, 2522, 3593, and 2859 kg²; for protein yield were 1692, 1401, 1967, and 1605 kg² as resulted from Model 1 through 4, respectively. These results showed that the highest additive genetic variances were attained from Model 3 for all traits (where the covariance between maternal effects exists).

Maternal variance components were estimated only in Models 3 and 4, but turned to become continuously higher in Model 3 for all traits. The estimates from Model 3 for days open, 305-day milk yield, fat yield, and protein yield were 612 day², 362731 kg², 708 kg², and 434 kg², respectively. On the other hand, estimates of maternal additive variances for Model 4 were relatively smaller and were 0.120 day², 32464.8 kg², 7.6 kg², and 24.9 kg², respectively for the same traits, respectively.

The permanent environmental variances as fitted in Model 2 and Model 4 were higher in Model 2 (where the maternal additive effects were absent) than Model 4. The component values were 326 day², 147360 kg², 387 kg², and 236 kg² in Model 2 for days open, milk yield, fat yield, and protein yield, respectively. The estimates for the same traits were 34.2 day², 35095 kg², 43.4 kg², and 36 kg² in Model 4. The present results showed also a negative covariances and correlations between additive and maternal effects in Model 3 for all tested traits. The direct-maternal genetic correlations were moderate to high and ranged from (-0.66) to (-0.87).

In the current study, estimates of phenotypic variances and ratios of permanent environmental variances to phenotypic variances were found to be slightly different from model to another. The differences were observed to be of the same magnitude for all the four traits, as presented in Table (2). In addition, the estimates of heritabilities were varied by the tested model. It was noticed that the greatest heritabilities for all traits were reported in Model 3. More detailed, heritabilities within range were (0.078-0.104), (0.241-

0.329), (0.259-0.429), and (0.214-0.335) for days open, 305-days milk yield, fat yield, and protein yield, respectively. Thus, maternal heritabilities were higher in Model 3 than in Model 4 for all studied traits. The highest maternal heritability was for fat yield (0.085) which was very small as compared to heritability. Maternal heritabilities of days open, 305-days milk yield, and protein yield in Model 3 were 0.045, 0.078, and 0.074, respectively.

Estimated Breeding Values of Traits

Standard deviations, minimum, maximum, and range of estimated breeding values (EBVs) are listed in Table (3). These estimates were used to study the effect of statistical models on their values. Among tested models, there were high variations in the values of breeding values of animals for productive and reproductive traits. The range of EBVs of days open and protein yield were the highest in Model 1, while the range of EBVs of 305-day milk yield and fat yield were the highest in Model 3 as compared to other models. The results of days open in Model 1 showed EBVs that ranged from - 65.06 day to 103.42 day, while those of protein yield from the same model were ranged from - 93.13 kg to 116.14 kg. In addition, 305-day milk yield and fat yield as a main productive traits, reported EBVs in Model 3 with a range of (-993.8 kg to 3211.7 kg), and (-116.08 kg to 169.5 kg), respectively.

Furthermore, to test the reliability of the four models, spearman's rank correlations among estimated breeding values obtained by different models are given in (Table 4). The results showed a high positive and significant ($P \leq 0.05$) spearman's rank correlations (≥ 0.83) among EBVs of studied traits in different models.

Models comparison and ranking

The present paper demonstrated different four linear models for genetic assessment of dairy cattle. Hence, these models were compared to obtain the most reliable parameter and (co)variance component estimates for the same trait. Model comparison section as presented in (Table 5) was depended on the analytical gradient (AG) Log Likelihood function. Based on the VCE results, the AG Log L values were 7625.63, 7549.71, 10368.37, and 10297.02 for Models 1, 2, 3, and 4, respectively. Models were ranked from the highest to the smallest Log L values. It was noticed that Model 3 was the highest, while Model 2 was the lowest in Log L values.

Table (2): Estimates of (co) variance components and genetic parameters for days open, 305-days milk yield, fat yield, and protein yield with different studied animal models

Trait	Model	σ_a^2	σ_m^2	σ_c^2	σ_{am}	σ_c^2	σ_p^2	$h_a^2 \pm SE$	$h_m^2 \pm SE$	$c^2 \pm SE$	$r_{am} \pm SE$
DO, days	1	1377		12708		14084		0.098±0.018			
	2	1095	326	12616		14038		0.078±0.008		0.023±0.003	
	3	1402	612	12620	-575	13484		0.104±0.016	0.045±0.014		-0.662±0.116
	4	1317	0.120	12650		14002		0.094±0.015	0.00001±0.000	0.002±0.003	
305-DMY, kg	1	1378691		3827942		5206634		0.265±0.018			
	2	1251960	147360	3801142		5200462		0.241±0.013		0.028±0.002	
	3	1536717	362731	3802236	-518911	4663862		0.329±0.024	0.078±0.022		-0.695±0.115
	4	1310311	32464.8	3821039		5198911		0.252±0.023	0.006±0.012	0.007±0.011	
FY, kg	1	2974		6875		9849		0.301±0.021			
	2	2522	387	6794		9703		0.259±0.014		0.039±0.005	
	3	3593	708	6826	-1384	8359		0.429±0.025	0.085±0.023		-0.867±0.062
	4	2859	7.6	6866		9776		0.292±0.019	0.0008±0.003	0.004±0.008	
PY, kg	1	1692		4956		6647		0.255±0.020			
	2	1401	236	4923		6561		0.214±0.012		0.036±0.004	
	3	1967	434	4914	-722	5872		0.335±0.024	0.074±0.024		-0.871±0.080
	4	1605	24.9	4943		6609		0.243±0.019	0.004±0.008	0.005±0.010	

σ_a^2 is additive genetic variance; σ_m^2 is maternal additive genetic variance; σ_c^2 is maternal permanent environmental variance; σ_{am} is covariance between additive and maternal additive genetic effects; σ_c^2 is residual variance; σ_p^2 is phenotypic variance; h_a^2 is additive heritability; h_m^2 is maternal heritability; c^2 is ratio of maternal permanent environmental variance to phenotypic variance; r_{am} is maternal genetic correlation; SE is standard error.

Table (3): Standard deviation (SD), minimum, maximum, and range of estimated breeding values of traits:

Model	Trait	SD	Minimum	Maximum	Range
Model 1	Day open, days	17.45	-65.06	103.42	168.48
	305 DMY, kg	549.63	-993.90	3120.50	4114.50
	Fat yield, kg	39.44	-123.43	160.68	284.11
	Protein yield, kg	28.39	-93.13	116.14	209.26
Model 2	Day open, days	15.81	-57.17	84.39	141.56
	305 DMY, kg	548.10	-997.50	2893.30	3890.80
	Fat yield, kg	35.38	-109.61	144.96	254.56
	Protein yield, kg	26.00	-81.37	105.36	186.74
Model 3	Day open, days	18.63	-60.50	81.54	142.05
	305 DMY, kg	583.90	-993.80	3211.70	4205.50
	Fat yield, kg	39.34	-116.08	169.50	285.58
	Protein yield, kg	29.34	-85.51	117.63	203.14
Model 4	Day open, days	18.15	-63.84	99.41	163.25
	305 DMY, kg	566.80	-979.50	2974.80	3954.30
	Fat yield, kg	38.42	-118.96	158.41	277.38
	Protein yield, kg	28.41	-88.60	114.44	203.04

Table (4): Spearman rank correlations among EBVs for all studied traits from different models

Models	Days open			305-days milk yield		
	Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
Model 2	0.99**			0.98**		
Model 3	0.83*	0.85*		0.89**	0.89*	
Model 4	1.00*	0.99**	0.84**	0.99**	0.98**	0.90**
	Fat yield			Protein yield		
Model 2	0.99**			0.99**		
Model 3	0.90*	0.90**		0.91*	0.91**	
Model 4	1.00**	1.00**	0.90**	1.00**	1.00**	0.91**

* Significant ($P \leq 0.05$).** Highly significant ($P \leq 0.01$).**Table (5):** Model rank based on the value of AG Log likelihood for model selection:

Model	Effects	Rank	AG Log likelihood values *
1	Only additive genetic	3	7625.6300
2	Additive genetic with permanent environmental	4	7549.7149
3	Additive genetic, maternal and covariance	1	10368.3710
4	Additive genetic, maternal, and permanent environmental (without covariance)	2	10297.02

* AG = the resultant of multiplying the relationship, A by genetic, G matrices)

* Log Likelihood values (Log L) for goodness of fit of the adopted statistical model

DISCUSSION

The present study showed large coefficients of variation with a range of (38-75%) for most of studied traits, especially days open then milk composition traits. These values may indicate a wide variation among animals of the current herd. Mostafa *et al.* (2013) conducted a similar study on Holstein-Friesian dairy herd. They revealed 40% as C.V for milk yield trait, and concluded that the high C.V. Percent may reflects a great variation between individuals.

The additive genetic variance as the common random effect in all models was fluctuating from model to another for milk yield traits. The present components were higher than those reported by many authors such as; Schutz *et al.* (1992) in USA; Olori *et al.* (2002) in Ireland; Adel *et al.* (2005) on the Friesian cows in Egypt; Edriss *et al.* (2006) on Holstein Friesian cows in Iran; and Mostafa *et al.* (2013) on the Egyptian native cows. These results indicate that the variance components may be affected by the characteristics of populations, herd structures and sample size. In addition, they depended on the statistical model used in analysis.

Based on the present results, both additive and maternal heritabilities of all traits were changed and affected by the random effects included in the model. It was found that the stepwise changes among maternal effects, permanent environmental effects, and the covariances between additive and maternal effects caused a fluctuation in heritability estimates. Additive heritabilities were observed with the greatest increase for all studied traits in Model 3 (where the maternal additive genetic effects were fitted in the models, together with the existence of -maternal genetic covariances). In contrast to the present findings, Mostafa *et al.* (2013) estimated narrow sense heritabilities from a full animal model (including; additive, maternal and maternal genetic covariances) for 305-DMY, fat yield and protein yield to be 0.33, 0.16 and 0.64, while from the model without maternal effects they were 0.34, 0.17 and 0.65 for the same traits. Mostafa *et al.* (2013) concluded that the removal of maternal effects and the direct-maternal genetic covariances from the model increased the estimates of narrow sense heritabilities (heritability in the narrow sense). Similar conclusion was reported by Albuquerque *et al.* (1998) who indicated that narrow sense heritabilities increased by 0.014 and 0.021 for milk and fat yields when the these effects were removed from the model. Nevertheless, the present estimates of narrow sense heritabilities of 305-DMY are within the range of Albuquerque *et al.* (1998), Yener *et al.* (2006), Usman *et al.* (2012), and Mostafa *et al.* (2013), but higher for fat and lower for protein yield. Different authors such as; Weigel *et al.* (1999), and Edriss *et al.* (2006) estimated narrow sense (additive) heritability for milk and fat yield to be (0.320 and 0.205); (0.23 and 0.17), respectively, from a model with only additive genetic effects.

Although, maternal heritabilities of this study were relatively small, but they increased by inclusion of direct-maternal genetic covariance (from model 4 to 3)

and the exclusion of permanent environmental effects from the statistical model. This result is in disagreement with the findings of Schutz *et al.* (1992), Albuquerque *et al.* (1998) and Edriss *et al.* (2006), but accordance with the results obtained by Zülkadir *et al.* (2009). On the other hand, the direct-maternal genetic covariances, and correlations estimated by Model 3 were all negative with moderate to high values, which suggest the inverse relationship between additive and maternal effects, and may play a role in the improvement of maternal heritabilities from Model 4 to Model 3. Different studies also recorded a negative correlation between additive and maternal additive genetic effects, such as Lee *et al.* (2003) to be -0.45; Adel *et al.* (2005) to be -0.45; Mostafa *et al.* (2013) to be -0.58. Other studied conducted by Albuquerque *et al.* (1998) and Edriss *et al.* (2006) recorded a positive correlation and covariances between additive and maternal effects.

Animal's breeding values (BVs) were high for all traits of the present study, which indicate that the genetic difference among individuals is a factor, which reflects the rate of expected genetic improvement that can be accomplished through individual selection. Breeding values of 305-day milk yield, fat and protein yield of the present study are somewhat higher than those estimated by Zutere (2008) and Ayied *et al.* (2011), and lower those reported by Mosharraf *et al.* (2014) except for milk yield trait. The high variances and ranges of BVs estimated by different models may indicate that these models gave a reasonable goodness of fit and accuracy for selection and genetic improvement of the current traits. Moreover, spearman rank correlations between estimated breeding values from the four models were high and positive (≥ 0.83). These correlations are higher than the findings of Cilek and Kaygisiz (2008) and Kaygisiz (2013) and similar to those reported by Kaya *et al.* (2003) and Seyedsharifi *et al.* (2008). Spearman rank correlations (≥ 0.97) obtained by Kaya *et al.* (2003) and Zutere (2008) indicate that for all studied traits, ranking of animals according to their estimated breeding values was closely correlated with each other and are in accordance with the present findings.

Model comparisons in the present investigation are mainly dependent on the values of the Log Likelihood of AG (*i.e.* the resultant of multiplying the relationship by genetic matrices) and the effect of model structure on the estimates of both (co)variance components and corresponding heritabilities. Many studies have shown that a higher Log Likelihood values (Log L) for goodness of fit of statistical model are preferable. For instance, Edriss *et al.* (2006) mentioned that animal models with higher Log Likelihood values are more accurate and concluded that by considering more parameters in the models, there would be more improvement for the animal models accuracy. In addition, Miroslav and Marija (2004) concluded that the best-fit model should have highest log likelihood and smallest 'Mendelian sampling' standard deviation. Furthermore, Posta *et al.* (2009) used VCE software for variance components estimation in sport horse; they mentioned that the model with the highest log-likelihood value was considered as the best fitting

model. On this basis, Model 3 with the highest AG Log L is considered the best-fit model for genetic evaluation of the current traits, followed by Model 4 then Model 1 and Model 2. Comparing Models 2, 3 and 4 versus Model 1 based on model structure and the impact of maternal effects, permanent environmental effects and the maternal additive genetic covariance, it was found that the presence of only maternal genetic effect (in Model 3) lead to increase in additive genetic variance and narrow sense heritabilities for all traits. On the other hand, when both maternal effects and permanent environmental effects fitted together (in Model 4), the result is the decrease in values of additive genetic variance and heritabilities as compared to Model 3. In addition, the inclusions of only permanent environmental effect (in Model 2) lead to the same result of decrease in estimates as occurred in Model 4. From these results, we can conclude that the existence of -maternal genetic covariance in Model 3, which included maternal additive genetic effects as the only random effect together with the additive one, resulted in the greatest increase in additive genetic variance and additive heritability estimates. Variety of studies such as those reported by Schutz *et al.* (1992), Albuquerque *et al.* (1998), Khattab *et al.* (2005), Edriss *et al.* (2006) and Mostafa *et al.* (2013) concluded that the inclusion of maternal effects in the model resulted in reduction in estimates of additive genetic variances and heritabilities especially for milk traits. In contrast to these findings, the present study showed that if the model was fitted with maternal effects together with the -maternal genetic covariance, this might improve the estimates of variance components and both additive and maternal heritability for studied traits. The moderate to high and negative correlations between direct and maternal effects and their negative covariances for all traits indicate the existence of negative relationship between additive and maternal additive genetic effects. In other words, selection on the base of animal's milk yield will subsequently decrease the maternal performance. Similarly, Tawah *et al.* (1993) reported that the negative correlations between additive and maternal effects may reflect the adaptation of animals to a dry tropical environment. In addition, negative direct and maternal genetic correlations may suggest that both additive and maternal effects could be selected for breeding programs.

Moreover, both Models 2 and 4 included the permanent environmental effects, which were not clear in this study, as the ratio of permanent environmental variances to the total phenotypic variances were small and may have non-significant contribution in improvement of heritabilities as compared with Model 3. This may be attributed to the fact that the present data included only the first three lactations with small number of records; hence, the permanent environmental effect may appear much effectively, if more repeated records were used.

CONCLUSION

One of the most significant and effective applications of statistics in animal breeding is to provide and fit a more accurate and applied models for

estimating genetic parameters in dairy cattle. The present study demonstrates some criteria for evaluating four statistical models with different structures. A comparison between AG Log Likelihood values, (co) variance components, heritability estimates revealed that Model 3 in this study was the best and suitable model for genetic improvement of the current herd. The moderate heritabilities of studied traits suggest the importance of these traits in selection programs and good practices. The results showed that the inclusion of maternal additive genetic effects with additive genetic effects together with the covariance between them give the best estimates rather than using the model with permanent environmental effects or the absence of direct-maternal genetic covariance. In addition, the negative correlations and covariances between direct and maternal effects could probably have indirect contribution in genetic improvement of dairy farms with attention to number of records and number of daughters per dam, because the maternal heritability increased in the presence of these effects in the model. Moreover, the permanent environmental effects may be effective and reasonable if later lactations could be used in further investigation.

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مقارنة بين النماذج الخطية المستخدمة في تقدير مكونات التباين والمعالم الوراثية لأبقار حلاب الهولشتين

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هدفت الدراسة الحالية إلى مقارنة أربعة نماذج إحصائية مختلفة لتقييم بعض صفات أبقار حلاب الهولشتين- فريزيان المرباة في مصر. وقد تم تجميع بيانات هذه الدراسة من مزارع إسكندرية - كوبنهاجن، إحدى قطعان الألبان التجارية المتواجدة في مصر على طريق القاهرة - الإسكندرية الصحراوي، والتي مثلت عدد ٢٨٤٦ سجلا للثلاثة مواسم الأولى مجمعة من إنتاج اللبن لأبقار لها ٦٠ أبا و ٤٢٨ أما. الصفات المدروسة كانت: الفترة المفتوحة، إنتاج ٣٠٥ يوم من اللبن، كمية الدهون و كمية البروتين. تم التمييز بين النماذج بناءا على التأثيرات العشوائية التي اشتملت عليها كل نموذج. كانت التأثيرات العشوائية هي، التأثير الإضافي الوراثي المباشر للحيوان، التأثير الإضافي الوراثي الأموي، التأثير البيئي الدائم، إضافة إلى التباين بين كل من التأثير المباشر للحيوان والتأثير الأموي وكذلك التأثير العشوائي للأخطاء. اعتمدت المقارنة بين النماذج الإحصائية على قيم لوغاريتمات الإمكان الأكبر وقيم المعالم الوراثية الناتجة من كل نموذج لجميع الصفات المدروسة. تم استخدام الحزمة الإحصائية في سي إي الإصدار السادس. المكافآت الوراثية المتحصل عليها من جميع النماذج تراوحت من (٠.١٠ إلى ٠.٢٤)، (٠.٢٤ إلى ٠.٣٢)، (٠.٢٥ إلى ٠.٤٢) و (٠.٢٤ إلى ٠.٣٣) لكل من الفترة المفتوحة، إنتاج ٣٠٥ يوم من اللبن، كمية الدهون و كمية البروتين، على التوالي. كذلك، لجميع الصفات كان النموذج الإحصائي المفضل يتميز بأعلى قيمة من لوغاريتم المكان الأكبر، قيم المكافآت الوراثية الأموية الأعلى وكذلك تواجد التباين بين كل من تأثير الحيوان والتأثير الأموي. القيم التربوية المقدره أظهرت وجود تباينات عالية وكذلك كانت معظم الارتباطات بين القيم التربوية بين كل النماذج الإحصائية موجبة ومرتفعة (أكبر من ٠.٨٣). أظهرت هذه الدراسة أن احتواء النموذج الإحصائي على التأثيرات الأموية وكذلك التباين بين كل من التأثير الوراثي للحيوان وتأثير الأم المضاف يمكن أن يؤدي إلى زيادة التحسين الوراثي لهذا القطيع محل الدراسة.