



A Comparison Between Single-Trait Statistical Model and Multi-Traits Model for The Genetic Evaluation of Dairy Cattle Populations Raised in Egypt

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ABSTRACT

Key words:

Macro-morphological, Micro-syrinx, Holstein-Friesian cattle, animal models, milk yield traits, fertility traits, Akaike Information Criterion, Model fitting

The incorporation of modern animal models become imperative for planning breeding strategies of dairy populations. The present study was designed to compare between single-trait and multi-traits animal models in estimating genetic parameters and breeding values for some milk yield and reproductive traits of Holstein-Friesian dairy cattle. A total of 9450 records of dairy cows calved in the period between 2007 and 2018 were included in the analyses by using the datasets of the first four lactations. Mixed model methodologies have been applied through applications of restricted maximum likelihood estimation algorithms. The heritability estimates for investigated traits were found be 0.26 for lactation milk yield (LMY), 0.42 (0.45) for milk fat percentage, 0.41 (0.44) for milk protein percentage, 0.13 (0.14) for lactation length (LL), 0.14 (0.15) for age at first calving, 0.17 (0.18) for calving interval, and 0.10 (0.13) for days open as denoted by single-trait (multi-traits) models, respectively. The genetic correlations between lactation milk yield and fertility traits ranged from 0.41 to -0.74. The highest genetic correlation was found between LMY and LL which was 0.84. The Akaike Information Criteria (AIC), the model evaluation measure were estimated for both models and its values were 59245.56 and 58598.23 for single-trait model and multi-traits model, respectively. Therefore, the multi-traits model, the model with the lowest value of AIC was selected as the model of choice for model's evaluation and preference. In conclusion, the current estimates and results indicate the possibility of genetic improvements for studied traits of Holstein-Friesian cows. Moreover, the multi-traits models are highly recommended for future analyses of complex livestock traits and for construction of selection plans.

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1. INTRODUCTION

Milk production traits are necessary for genetic enhancement programs of Holstein-Friesian dairy cattle (Zhang et al., 2022). It is extensively admitted that the performance of dairy herds is mostly affected by productive ability of the cows. The yield traits such as total milk yield, lactation length, as well as, fertility records of age at first calving, days open and calving interval are the core traits essential for dairy cattle breeders. Hence, recording accurate estimates for both genetic and phenotypic characteristics for such traits will support better improvements and planning effective breeding policies in dairy populations (Choudhar et al., 2003; Aynalem, 2006; Wasana et al., 2015).

The reproductive ability of dairy cows is considered as one of the main determinants influencing the profitability of milk yield in dairy cows (Aynalem, 2006). Economically, indigent fertility measures lead to an increase in the value paid for milk yield due to the need of a large number of services required for conception, elongated lengths of calving intervals, increased culling rates and high cost of medications and instruments required for treating reproductive diseases. It was noticed that a prolonged improvement of milk production traits caused a decline in fertility performance, particularly, in high producing cows. The cause is the existence of antagonistic relationship and inverse genetic correlation between fertility and milk yield traits (Kadarnideen

et al., 2003; Liu et al., 2007; Komlasi et al., 2010; Yamazaki et al., 2014; Brzakova et al., 2019). Recently, dairy improvement schemes work on assessing and enhancing fertility traits of dairy cattle since disregarding reproductive characteristics of the cows will minimize the economic gain of the herd (Abe et al., 2009; Zinc et al., 2012). Thus, it is recommended to involve reproductive traits along with yield traits in improvement programs to retard or prevent cows' impairment to gain females with good fertility (Weller et al., 2022). The most fertility traits that have been evaluated in previous studies and subsequently incorporated in breeding strategies were age at first calving, days open, calving interval, calving to first service period, conception rate and the number of inseminations for conception (Gonzalez-Recio and Alenda, 2005; Guo et al., 2014). However, these traits have still been insufficiently improved as reported by previous literature (Brzakova et al., 2019).

Until now, most breeding studies have been planned using multivariable statistical methods in order to achieve effective selection based on both yield and fertility traits. These multivariate approaches are beneficial in selection programs where the selection for a given trait could affect the other in an expected direction. Moreover, the incorporation of such models in analytical procedures will denote unbiased estimates with high reliability, due to the ability of complex models to handle huge amounts of information from the associated traits (Unalan and Cebeci, 2004; Mrode, 2005). Furthermore, analysis of many traits at the same time allows researchers to enhance the accuracy of prediction, improve the statistical power, as well as, minimize selection bias, particularly, for low heritable traits that show strong genetic correlations with those of high estimates (Jiang et al., 2015). However, still some researchers use univariate-fitted models to analyze breeding datasets. But the results of such univariate methods do not account for the covariance between investigated traits, which intern could output breeding values with low validity (Strabel et al., 2001; Ayalew et al., 2017).

Previous studies applied single-trait and multi-traits statistical analyses to compute genetic parameters and, hence, breeding values of dairy cows, such as those reported by Chen and Zhang (2009) and Xu et al. (2009). These models have been evaluated for many years and still need more confirmatory results to accredit the most effective methodology for

selection programs. Most of the previous investigations indicated that the multivariate methods are more sufficient for genetic assessment of dairy cows' traits than those assumed single trait. The superiority of multi-traits methods is derived from its ability to estimate genetic parameters with high precision so that some authors such as Aguilar et al. (2011) and Jia and Jannink (2012) revealed that the accuracies resulted by multivariate techniques that used in estimating BVs were twice those recorded by univariate models. Moreover, other studies (Guo et al., 2014; Miar et al., 2014; Jiang et al., 2015) have exhibited the superiority of multivariate methods in breeding plans. This study therefore was designed to use the single-trait and multi-traits statistical models to compute genetic characteristics, breeding values and genetic trends of milk production and fertility traits of Holstein-Friesian dairy cows in Egypt. In addition, to compare the two statistical methods in order to employ the information obtained in breeding strategies and selection indices for genetic amelioration of such dairy herds.

2. MATERIALS AND METHODS

2.1. Data and animals

Data for the present study were collected from five commercial dairy herds located in Alexandria governorate, Egypt. Lactation records of Holstein-Friesian cows were surveyed representing the period from 2007 to 2018. A number of 9450 lactation records were analyzed, but at first, data has been edited for missing values, incomplete lactations, distribution-free datasets, outliers, and for number of sires and dams involved. Specifically, records with incomplete or missing information were excluded from the final analyzed file. Only data that followed normal distributions were applied. To compute genetic parameters, as well as, to evaluate the single-trait and multi-traits statistical models, the following traits were investigated; lactation milk yield (LMY, kg), lactation length (LL, days), milk fat percentage (MFP, %), milk protein percentage (MPP, %), age at first calving (AFC, months), calving interval (CI, days) and days open (DO, days). The datasets were edited to be ready for variance components estimation procedures. To overcome any bias in the estimated parameters, pedigree files were edited in a way that inconsistent records were removed from the analyzed datasets. In addition, milk yield and fertility traits were managed for every own trait so that the data were retained according to standard ranges (Ayied et al., 2011). Records representing

the first four lactations have been involved in analytical procedures of such traits' structures. Cows with missed number of sires or dams did not used in the fitted animal models. Hence, investigation has been conducted on cows originated from a total of 112 valid sires.

2.2. Genetic indices

The variance and covariance structures and genetic parameters have been estimated for all investigated traits via the single-trait and multi-traits models. The maximum likelihood estimation procedures were applied using REML (restricted maximum likelihood)-based models that have been carried out through VCE 6.0.2 software (Groeneveld et al., 2008). In all models, mixed design approaches were adjusted including both fixed and random effects. The fixed effects were the season of calving, parity, and calving year of cows. While, the random effects were the animals, sires, dams, permanent effect of the environment, the direct genetic effects of cows and the random effect of residuals. Heritability was calculated as the ratio of additive genetic variance to the total phenotypic variance of such trait. The estimation equation can be summarized as follows (Gonzalez-Recio and Alenda, 2005):

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

Where h^2 is the heritability estimate; σ_a^2 is the value of additive genetic variance; σ_{pe}^2 is the permanent environmental variance while σ_e^2 is the error variance due to residuals. In which, the total phenotypic variance (σ_p^2) can be calculated as follows: $\sigma_p^2 = \sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2$. Moreover, the standard error (SE) of heritability is denoted by the following equation (Strabel et al., 2001):

$$SE(\text{heritability}) = \left[\frac{\sigma_a^2}{\sigma_p^2} \right] \left[\frac{\text{var}(\sigma_a^2)}{(\sigma_a^2)^2} + \frac{\text{var}(\sigma_p^2)}{(\sigma_p^2)^2} - \frac{\text{cov}(\sigma_a^2, \sigma_p^2)}{\sigma_a^2 \sigma_p^2} \right]$$

Where, SE is the estimated standard error of heritability; σ_a^2 is the direct additive genetic variance and σ_p^2 is the total phenotypic variance.

Phenotypic and genetic correlations among each couple of studied traits have been calculated using the multi-traits animal model. For the given seven traits, the correlation coefficients were computed for every two possible combinations of

incorporated traits. Phenotypic correlation is the relationship between two traits in the herd, and accounts for both genetic and environmental factors. For the X and Y traits, the phenotypic correlation is the ratio of the traits' covariance to the standard deviations of these traits. The phenotypic correlation (r_p) can be written as follows (Strabel et al., 2001):

$$r_p = \frac{\text{Cov}(X,Y)}{\sqrt{\sigma^2_X} \sqrt{\sigma^2_Y}}$$

Genetic correlation (r_g) is the association between the additive estimated breeding values (EBVs) of the two incorporated traits (gEBV1 and gEBV2), and can be written as follows (Legates and Warwick, 1990):

$$r_g = \frac{\text{Cov}[(\text{gEBV1})(\text{gEBV2})]}{\sqrt{(\text{Var gEBV1})(\text{var gEBV2})}}$$

Where, Cov [(gEBV1) (gEBV2)] is the genetic covariance between the additive breeding values of two traits; Var gEBV1 is the genetic variance of the first trait; Var gEBV2 is the genetic variance of the second trait. Furthermore, breeding values of cows were estimated for studied traits via the single-trait and multi-traits models. The best linear unbiased prediction (BLUP) procedures were used as the best solution to compute breeding values for all animals in the pedigree based on the dataset of their relatives. The BLUP procedures have been produced from the VCE, 6.0.2. In addition, the accuracy of EBVs, which is the association between the true and estimated breeding values have been obtained from single-trait and multi-traits statistical models in order to evaluate the process of prediction and to compare the performance of both statistical methodologies. The output cows' EBVs were presented in the form of standard deviation, minimum and maximum values of EBVs along with their accuracies.

2.3. Fitting the single-trait and multi-traits models

The present study showed applications of different statistical-genetics models for estimating genetic parameters and breeding values of the seven implemented traits. All investigated models were adjusted to be mixed so that some fixed effects and other random effects were fitted in each model (Aguilar et al., 2011). The fixed effects were: season of calving (summer, winter, autumn, and

spring); calving year (1 = 2007, 2 = 2008, ..., 12 = 2018) and parity (1 = first, 2 = second, 3 = third, ..., 4 for ≥ fourth lactation). Also, the random effects of animals, sires, dams, repeated records representing permanent environment and random errors were taken into account in the analyses. The single-trait assumed only one trait in the analysis, while the multi-traits statistical model in this study was conducted using two traits in each analysis, estimating genetic parameters. The following is the model applied for single-trait and multi-traits analyses, particularly, for traits assumed no permanent environmental effects, or with no application of repeated records, such as AFC (Aguilar et al., 2011):

$$Y = Xb + Zu + e \quad (1)$$

Where, Y is the vector of observed trait' values; X is the incidence matrix covered the fixed effects; b is the vector represents the fixed effects; Z is the incidence matrix of the additive genetic random effects of cows; u is the vector of additive genetic effects of animals; e is the vector of the residuals which is randomly independently distributed.

In addition, the model for traits which assumed the existence of permanent environmental influences was summarized in matrix formula as shown below. Such traits incorporate the repeated records in analytical models, both for single-trait and multi-traits statistical models. Examples of traits with repeated records were LMY, LL, MFP, MPP, CI and DO:

$$Y = Xb + Zu + Mpe + e \quad (2)$$

In which, Y is the vector of given values for studied variables; X is the incidence matrix for the fixed effects; b is the vector represents the fixed factors; Z is the incidence matrix of the random additive genetic impacts of cows; u is the vector of additive genetic effects of animals; M is the incidence matrix for permanent environmental effects; pe is the vector of repeated records' observations; e is the vector of the errors, which is also randomly and independently distributed.

Specifically, the model used in bivariate analysis (Y_1 and Y_2) for the seven traits' evaluations can be presented as follows:

$$\begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} M_1 & 0 \\ 0 & M_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

The random effects in the models should be normally distributed with an average of zero according to the variance - covariance (var-cov) matrix given below:

$$\text{Var} \begin{bmatrix} Pe \\ u \\ e \end{bmatrix} = \begin{bmatrix} I * P & 0 & 0 \\ 0 & A * G & 0 \\ 0 & 0 & I * E \end{bmatrix}$$

Where, Pe is the vector of permanent effects of environment due to repeated records; u is the vector of direct genetic effects of animals; e is the vector of random errors; I is the identity matrix; P is the var-cov matrix of permanent environmental effects; A is the numerator relationship matrix; G is the var-cov matrix representing the direct effects of animals and E is the diagonal matrix of random errors.

The followings are some of the model definition and properties:

$$\begin{aligned} \text{Expected value (y)} &= Xb \\ \text{Variance (u)} &= G \\ \text{Variance (e)} &= R \\ \text{Variance (Y)} &= ZGZ' + R \end{aligned}$$

2.4. Evaluation characteristics of the two models

The single-trait and multi-traits statistical models investigated in this study were compared on the basis of the estimates of heritability given by each model, the accuracy of prediction using the EBVs of each trait, as well as, the values of standard deviation and range (maximum value - minimum value) of EBVs. Furthermore, the two models were compared and evaluated using one of the most accredited model selection indices, named, the Akaike Information Criterion (AIC). The most important property of AIC is that it produces unbiased estimation of the tested model from the real model (Maniatis et al., 2013). To compute the AIC, one should first calculate the deviance (d) as follows (Strabel et al., 2001):

$$d = - 2 \text{Log} (P (Y | \hat{\theta})) = - 2 \text{Log likelihood}$$

Where θ is the vector of the parameters included in the model; $P (Y | \hat{\theta})$ is the probability of the observations of Y estimated via the maximum likelihood function. Thus, the AIC can then be calculated as recorded by (28) as follows:

$$\text{AIC} = - 2 \text{Log L} + 2P$$

Where, P is the number of parameters for each model. A model showed lower AIC is used as the best model of choice (Greven and Kneib, 2010). In other words, the selected model could be validated

for genetic evaluation of the studied traits and perform better if the AIC is minimum.

3. RESULTS AND DISCUSSION

3.1. Trait's description

The process of estimating variance and covariance structures, genetic parameters and subsequently, the breeding values of the productive and fertility traits of Holstein dairy cattle is considered as the main essential requirement for constructing effective breeding plans, particularly, for traits of economic impact. This study was undertaken to evaluate the genetic progress in Holstein-Friesian dairy cows using single-trait and multi-traits models. Table 1 shows the number of observations (N), means, standard deviations (SD) and coefficient of variations (C.V %) for the milk yield and fertility traits. Numerical data of all traits verified the normality assumption. In general, the descriptive statistics of studied traits were close to those have been reported by other investigations (Ibrahim et al., 2002; M'hamdi et al., 2010), but were higher than the observed values revealed by Olesen et al. (1999) and Bajwa et al. (2004) who conducted similar studies connected with Holstein-Friesian cow populations. In particular, the averages of milk yield traits in this study were similar to the findings of previous authors (Hatungumukama et al., 2007). Moreover, the current phenotypic values of fertility traits were higher than those recorded by Zaabza et al. (2016) and Liu et al. (2017). A study has been carried out by Weller et al. (2022) on Holstein population in order to compute genetic parameters for reproductive traits using univariate and multivariate methods. They found the averages of CI, AFC and DO to be 400 days, 25.6 months and 124.5 days, respectively. Some authors such as Worku and Ayalew (2021) conducted similar

research in regard to the dairy cattle breed, studied traits and the implemented statistical models. The current averages were higher than their findings in terms of LMY, LL and DO, but lower for AFC, while as CI showed similar results in the two studies. Moreover, the means of fertility traits in this study were slightly higher than those published by previous authors (Gonzalez-Recio and Alenda, 2005; Guo et al., 2014). In addition, recent research conducted by Zhang et al. (2022) showed lower means and variations for production traits. The value of C.V % of milk yield (close to 40 %, Table 1) indicates that the current herd showed remarkable variability so that a possible improvement and selection plan could be considered for future breeding strategies.

3.2. Computation of co-variance structures and heritability

Table 2 presents the values of variance components and the corresponding heritability estimates for both yield and fertility traits of Holstein-Friesian cows as computed by single-trait and multi-traits models. The results of single-trait model were presented for all traits including the variance structure and heritability estimates. On the other hand, no estimates were found for LMY in multi-traits model, because LMY was used as a covariate or a correlated trait in combination with other traits. Overall, the heritability estimates for the milk yield and reproductive traits were higher in multi-traits models than those computed from the single-trait models. The highest increase was observed for milk production traits, may be due to the incorporation of LMY as a correlated trait in bivariate analyses.

Table (1): Structure and summary measures for analyzed traits utilized in further estimation of genetic parameters

Investigated trait	N	Mean	SD	C.V%
LMY (kg)	9145	8743	3422	39.14%
MFP (%)	8784	3.12	0.62	19.89%
MPP (%)	8784	2.54	0.47	18.52%
LL (days)	8678	363.3	111.6	30.67%
AFC (month)	3689	28.36	3.45	12.17%
CI (days)	8545	424.8	103.1	24.21%
DO (days)	8595	166.9	122.9	73.69%

LMY, lactation milk yield; MFP, milk fat percentage; MPP, milk protein percentage; LL, lactation length; AFC, age at first calving; CI, calving interval; DO, days open

Considering the milk yield traits, it was noticed that the estimates of heritability for LMY,

MFP and MPP were moderate to high and ranged between 0.26 and 0.45. The heritability estimates for

milk yield traits were the same as those estimated by Zhang et al. (2022), who computed heritability using multi-traits models for MY, fat and protein yields to be 0.39, 0.40 and 0.49, respectively. The large values of heritability for yield traits indicate that the additive genetic variances were high and, hence, the current herd showed reasonable genetic variations which could suggest a possible improvement of such traits. This finding is in agreement with those reported by Worku and Ayalew (2021), who conducted a similar study on Holstein-Friesian cows with an application of univariate and bivariate models. Moreover, the heritability values for productive traits came in accordance with most of published literature using the same cattle breed (Zinc et al., 2012; Goshu et al., 2014; Wasana et al., 2015; Ayalew et al., 2017). On the other hand, the current estimates for LMY, MFP and MPP were higher than the findings of Seangjun et al. (2009) and Saha et al. (2010) who evaluated the genetic parameters for such traits in tropical dairy cattle herds. In conclusion, the heritability computations for yield traits (LMY, MFP and MPP) in this research explain the existence of feasible genetic diversity in this herd which allows beneficial selection on the basis of such traits to enhance milk yield in Holsteins-Friesians.

The heritability for LL was measured to be 0.13 as calculated using the single-trait model. The multi-traits model denoted an estimate for the same trait to be 0.14, with a slight increase when fitting LMY as a covariate trait in the bivariate analysis. The low heritability of LL (close to 0.1) indicates that the error variance was high relative to the direct additive genetic variance, compared with other yield traits. The heritability values for LL were in accordance with those recorded by Gebreyohannes et al. (2013) and Ayalew et al. (2017). They suggest that the low heritability for LL may be caused by varied management and environmental conditions among different parities. Comparing the two models, Worku and Ayalew (2021) estimated low heritabilities for LL by both animal models (0.12 and 0.13, respectively).

Regarding the estimated heritabilities of fertility traits, it was observed that the heritability estimates for AFC, CI and DO were ranged between 0.10 and 0.18, both for single-trait and multi-traits models. Although, the heritability values of fertility traits were low to moderate, the multi-traits analyses showed a slight improvement in the heritability estimates. The heritability values for AFC were 0.14 and 0.15 using the single-trait and multi-traits

models, respectively. AFC is one of the most economic traits of dairy cows because a cow with early maturity and good fertility is highly connected with replacement rates and milk production performance (Gonzalez-Recio and Alenda, 2005; Gavan et al., 2014). Therefore, like other fertility traits, AFC is highly influenced by breeding programs and management strategies on the farm. However, the current estimates for AFC suggest that genetic improvement could be achieved if selection was made on AFC, considering herd variation. This finding was in agreement with those reported by Divya (2012) who evaluated the same traits. The present heritabilities of AFC were higher than those calculated by Brzakova et al. (2019) who reported a value of 0.031 in Czech Holsteins, but lower than previous investigations such as (Makgahlela et al., 2008; Montaldo et al., 2010; Worku and Ayalew, 2021) who estimated heritability values for AFC to be ranged from 0.26 to 0.55. Furthermore, our estimates were within the range of Pirlo et al. (2000) who computed a wide range of heritabilities for AFC from 0.05 to 0.75.

Heritability values for CI were 0.17 and 0.18 using the two models. These estimates were higher than the value (0.034) reported by Brzakova et al. (2019), 0.04 by Gonzalez-Recio and Alenda (2005), 0.056 by Guo et al. (2014), 0.01 by Semagn et al. (2022), and 0.022 by Kadarmideen et al. (2003) who applied their researches on Holstein cows. Contrary, our estimates for CI were lower than the higher value of 0.35 observed by Saha et al. (2010). Similarly, some authors (Ayalew et al., 2017; Worku and Ayalew, 2021) found the heritability values of CI within the range of 0.12 to 0.17 with a slight increase using the multiple trait models. The heritabilities of DO were 0.10 and 0.13 using the univariate and bivariate models, respectively. Previous studies (Liu et al., 2008; Zinc et al., 2012; Guo et al., 2014; Weller et al., 2022) showed lower estimates (ranged from 0.026 to 0.053) for heritability of DO as a vital trait determining pregnancy rates in dairy cows. Using the same models, Worku and Ayalew (2021) estimated similar heritabilities for DO to be 0.14 by the two models. The present heritabilities for fertility traits, according to Toghiani Pozveh et al. (2009), Bahonar et al. (2009) and Norman et al. (2009) indicates the existence of additive genetic variance directly by cows which subsequently could be used in efficient breeding programs.

Table 2. Estimates of variance components and heritability for the yield and fertility traits using single-trait model and multi-traits model

Model	Estimates	Studied traits						
		LMY	MFP	MPP	LL	AFC	CI	DO
Single-trait model ^(a)	σ_a^2	2136	0.105	0.049	81.92	2.37	181.56	113.6
	σ_{pe}^2	1810	0.052	0.031	23.58	-	71.29	62.83
	σ_e^2	4495	0.095	0.041	505.83	13.98	772.45	978.56
	σ_p^2	8441	0.252	0.121	611.33	16.35	1025.3	1155
	h^2	0.26	0.42	0.41	0.13	0.14	0.17	0.10
Multi-traits model ^(b)	σ_a^2	-	0.111	0.053	45.39	2.85	188.26	105.97
	σ_{pe}^2	-	0.043	0.021	19.56	-	137.28	74.62
	σ_e^2	-	0.098	0.047	259.25	15.55	720.36	634.65
	σ_p^2	-	0.252	0.121	324.2	18.41	1045.9	815.24
	h^2	-	0.45	0.44	0.14	0.15	0.18	0.13

(a), univariate model; (b) multivariate model

 σ_a^2 : additive genetic variance; σ_{pe}^2 : permanent environmental variance; σ_e^2 : error variance; σ_p^2 : total phenotypic variance; h^2 : heritability estimates

LMY: lactation milk yield; MFP: milk fat percentage; MPP: milk protein percentage; LL: lactation length; AFC: age at first calving; CI: calving interval; DO: days open

Table (3): Estimates of genetic correlations (above diagonal) and phenotypic correlations (below diagonal) between the studied traits using the multi-traits statistical model

Trait	LMY	MFP	MPP	LL	AFC	CI	DO
LMY		- 0.39	- 0.52	0.84	0.41	- 0.74	0.56
MFP	- 0.04		0.77	- 0.15	0.72	0.65	0.81
MPP	0.02	0.08		- 0.35	0.76	0.61	- 0.24
LL	0.61	- 0.81	- 0.68		- 0.16	0.08	- 0.74
AFC	0.09	0.79	0.79	- 0.04		0.21	0.42
CI	- 0.52	- 0.14	- 0.18	- 0.17	0.04		0.34
DO	0.46	0.18	0.06	- 0.89	0.07	0.19	

LMY: lactation milk yield; MFP: milk fat percentage; MPP: milk protein percentage; LL: lactation length; AFC: age at first calving; CI: calving interval; DO: days open

3.3. Correlations between traits

Table 3 demonstrates the phenotypic and genetic correlations estimated between all traits as resulted the bivariate analyses. The phenotypic correlations between production traits and fertility traits were ranged between 0.02 and - 0.89, suggesting a wide range of variability and association between the original traits in the population. Genetic correlations among LMY and reproductive traits were medium and ranged from 0.41 to - 0.74. Genetic correlations between fertility traits were low to slightly moderate and ranged between 0.21 and 0.42. The highest genetic correlation was observed between LMY and LL (0.84), followed by a correlation of 0.81 between MFP and DO, then a correlation of 0.77 between MFP and MPP. It was observed that LMY showed the highest positive genetic correlation with LL (0.84) which implies that both traits are associated with the same genes, also, cows with prolonged LL will yield more milk. Therefore, selection on the basis of many traits will lead to multiple genetic

improvement schemes. This finding is in accordance with those reported by other authors (Goshu et al., 2014; Ayalew et al., 2017; Worku and Ayalew, 2021; Zhang et al., 2022). Interestingly, the favorable genetic correlations in this study along with the heritability estimates of traits conclude that there is a likelihood of an effective genetic improvement of the current herd via selection plans. This conclusion agrees with the results published by similar researches (Zinc et al., 2012; Brzakova et al., 2019). In other words, the moderate to high genetic correlations found between studied traits indicates that an effective selection plan could be applied for the current herd early in the breeding programs. In addition, the results showed that milk yield traits and fertility were genetically associated; hence, incorporation of such traits in selection indices would be beneficial.

3.4. Estimated breeding values and model comparisons

The animals' estimated breeding values for tested traits, which have been calculated by single-trait and multi-traits models, are presented in Table 4. The first observed result using the EBVs for each trait was the range and standard deviation of EBVs. The SD of EBVs (Table 4, Figures 1-6) showed that the variations in traits' EBVs using multi-traits analyses were larger than the findings recorded by the single-trait model. This implies that the multi-traits methods utilize more information from the associated traits, as well as, the large variations in EBVs of the studied traits denoted by this multivariate method provide a wide range for selection on the farm. The second noticed finding, as denoted by Table 4, was the accuracy of prediction of EBVs. The accuracy measures of prediction for all traits were higher in multi-traits model relative to the single-trait one. This indicates that the results of multivariate approach were more reliable than those estimated by univariate method. The study of Zhang et al. (2022) revealed that the reliability of EBVs given by multiple trait model were also higher than the corresponding outcome denoted by the single-trait model. Negussie et al. (2006) conducted a study to calculate genetic

indices of udder health characteristics using single and multi-traits models and their results implied that the multi-traits model is robust in predicting BVs for upcoming pedigrees of cows.

Furthermore, Table 4 presents another criterion for comparing the two models. The AIC values for the single-trait and multi-traits models were 59245.56 and 58598.23, respectively. Based on AIC, it was concluded that the multi-traits model which has the lowest AIC was the best suited for the current data. Many authors (Maniatis et al., 2013; Corrales et al., 2015; Yousuf et al., 2017) fitted different models in their studies and concluded that models with more information and large number of effects denoted more accurate results and the value of AIC decreased. Also, several researchers (Maniatis et al., 2013; Yousuf et al., 2017; Zhang et al., 2022) compared single-trait versus multiple traits models in different areas and fields of animal sciences, and their results revealed that the models that contained multiple traits have been chosen as the best models than the single-trait models because the multiple traits models contributed with the lowest AIC values.

Table (4): Summary information (SD, minimum and maximum values) of animals estimated breeding values (EBVs) along with the accuracy of prediction for the studied traits using single-trait and multi-traits models

Trait	Animals EBVs							
	Single-trait model				Multi-traits model (using LMY as correlated trait)			
	Accuracy	SD	Min	Max	Accuracy	SD	Min	Max
LMY	0.63	745.23	-2257	+2250	-	-	-	-
MFP	0.74	0.36	-0.55	+1.13	0.75	0.39	-0.53	+1.28
MPP	0.81	0.25	-0.39	+0.72	0.83	0.29	-0.38	+0.95
LL	0.61	15.39	-39.43	+44.72	0.63	16.89	-37.8	+57.1
AFC	0.57	0.91	-2.29	+4.12	0.58	0.94	-2.19	+3.59
CI	0.60	26.15	-53.59	+55.43	0.62	34.25	-74.01	+112
DO	0.59	15.38	-31.86	+30.08	0.64	28.44	-57.3	+115
Evaluation Criteria	AIC = 59245.56				AIC = 58598.23			

LMY: lactation milk yield; MFP: milk fat percentage; MPP: milk protein percentage; LL: lactation length; AFC: age at first calving; CI: calving interval; DO: days open

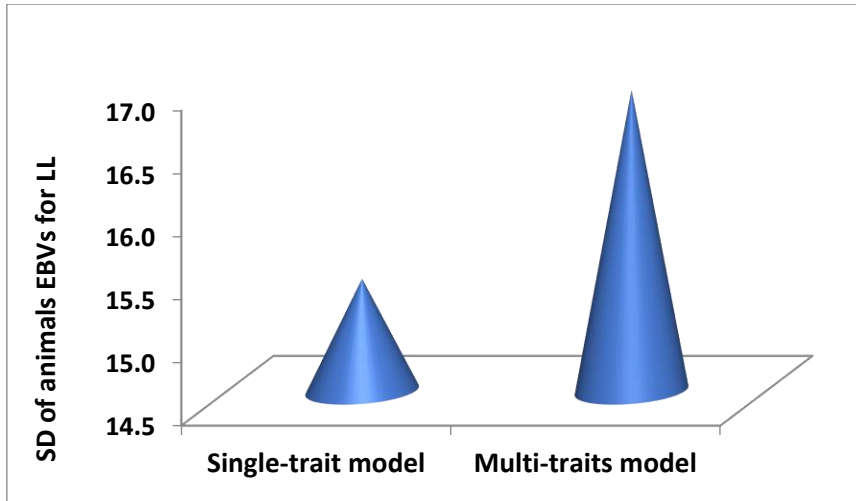


Figure 1. Graphical presentation of SD of animals' EBVs for lactation length using the single-trait and multi-traits statistical animal models.

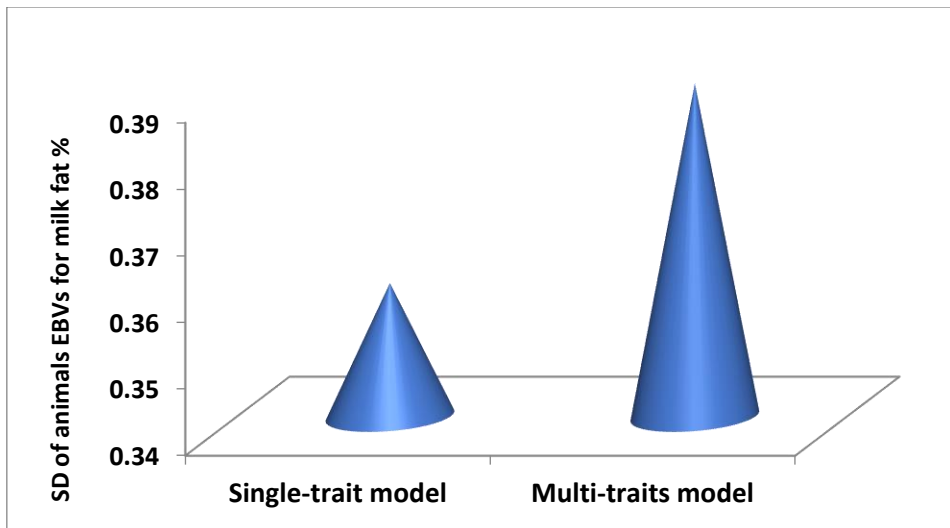


Figure 2. Graphical presentation of SD of animals' EBVs for milk fat percentage using the single-trait and multi-traits statistical animal models.

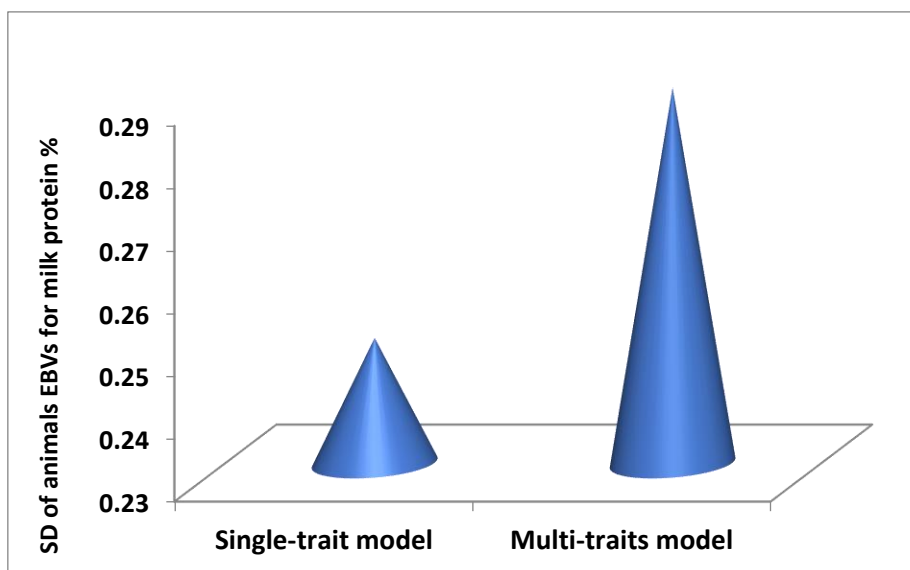


Figure (3): Graphical presentation of SD of animals' EBVs for milk protein percentage using the single-trait and multi-traits statistical animal models.

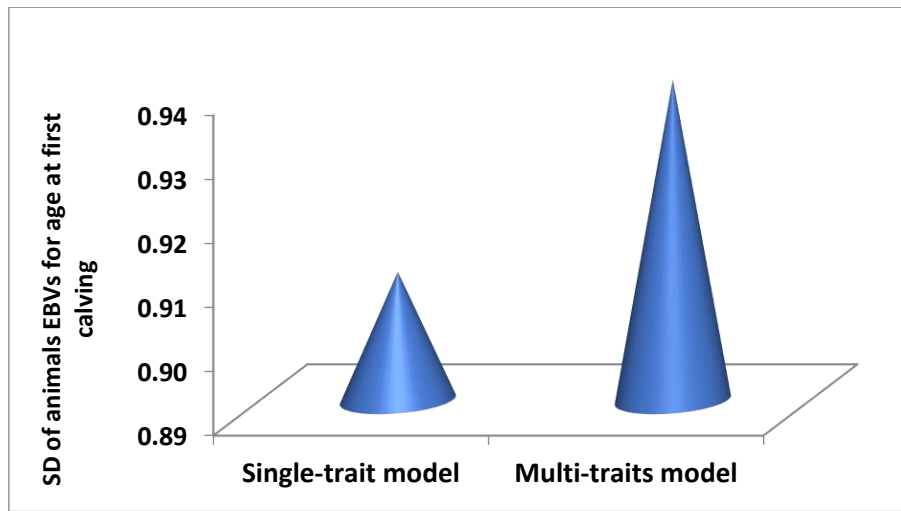


Figure 4. Graphical presentation of SD of animals' EBVs for age at first calving using the single-trait and multi-traits statistical animal models.

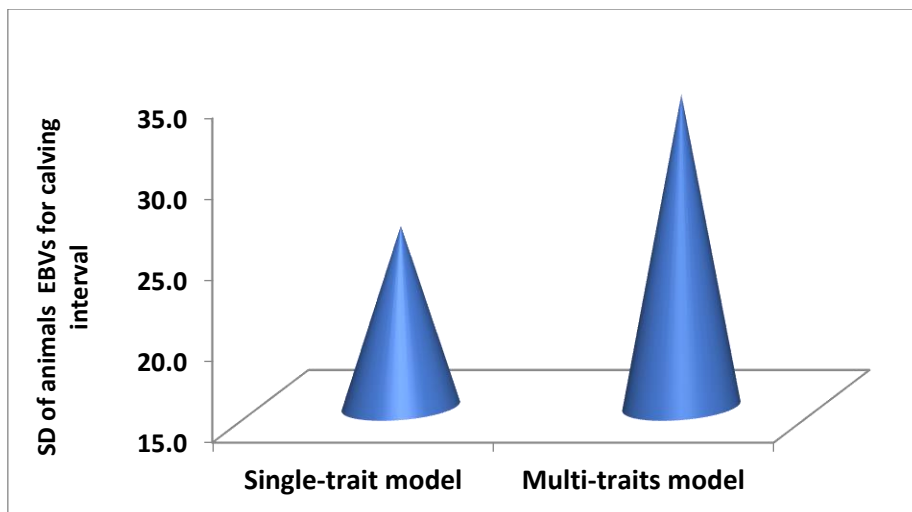


Figure (5): Graphical presentation of SD of animals' EBVs for calving interval using the single-trait and multi-traits statistical animal models.

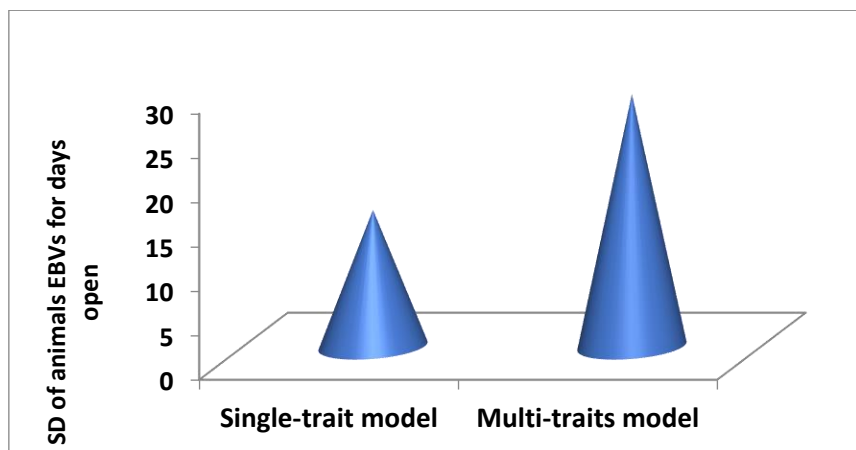


Figure 6. graphical presentations of SD of animals' EBVs for days open using the single-trait and multi-traits statistical animal models.

4. CONCLUSION

In conclusion, the estimates of heritability, breeding values and genetic correlations in this study indicate that the incorporation of many traits in analytical models could enhance the process of genetic evaluation of dairy cattle traits, indicating the superiority of multi-traits models over the single-trait models. The results revealed the multi-traits models improved such estimates both for yield and fertility traits. Therefore, the inclusion of more traits, and hence more parameters in statistical analyses is advantageous to provide optimum genetic parameters and highly accurate breeding values. Genetic correlations also emphasize the effectiveness of multi-traits models to take into account the covariances between studied traits. Overall, the heritabilities and genetic parameters in this study, particularly for milk yield traits revealed that the direct additive genetic variances for such traits are sufficient enough to construct selection plans and genetic improvement of Holstein dairy populations. In addition, the insertion of fertility traits along with milk yield traits in animal models and selection indices can improve the longevity and productivity of dairy cattle in Egypt. Hence, this would positively impact the milk yield of these cows as well as enhance fertility and health status of the whole herd.

AUTHORS' DECLARATIONS

PUBLICATION CONSENT

Each author has demonstrated his or her consent for the publication of the current manuscript.

DATA AND MATERIAL AVAILABILITY

All data of this study is provided.

CONFLICT OF INTEREST

All authors have stated the absence of any conflicts of interest.

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AUTHORS' CONTRIBUTIONS

S.A.M.: Study Design, Conceptualization, Data Collection, Statistical Analysis, Investigation, Writing the original draft, Review and Editing.

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