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ESTIMATES OF DIRECT AND MATERNAL GENETIC EFFECTS FOR MILK TRAITS IN FRIESIAN COWS

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ABSTRACT

Direct and maternal genetic effects on milk traits in dairy cows are very important elements for estimating the best genetic parameters. The present work aimed to estimate phenotypic and genetic parameters for productive and reproductive traits. Variance components and genetic elements were estimated, using records of 2166 lactations of Friesian cows' progeny of 92 sires and 882 dams from 2014 to 2020. Two animal models were constructed, and whether or not maternal genetic effects were considered. The variables studied are ten-month milk production (10 MMP), ten-month fat production (10 MFP), ten-month protein yield (10 MPP), lactation length (LL), days dry (DD), age at first parturition (AFP), days open (DO) and calving interval (CI). Phenotypic and genetic correlations among all variables studied were calculated. Estimated direct heritability (h2d) ranged from 0.23 to 0.25 for 10 MMP, from 0.20 to 0.27 for 10 MFP, from 0.19 to 0.26 for 10 MPP, from 0.03 to 0.06 for LL, from 0.03 to 0.06 for DD, from 0.01 to 0.04 for AFP, from 0.06 to 0.10 for DO and from 0.04 to 0.05 for CI. The estimates of maternal heritability (h2m) were 0.23, 0.20, 0.19, 0.03, 0.03, 0.04, 0.06 and 0.05 for the above variables studied, respectively. Therefore, maternal genetic effects should be considered in the animal model for genetic evaluation of milk production and its components. Therefore, the current study recommends improvement of milk production efficiency and milk component variables through selective breeding strategies targeting both bulls and cows. While direct h2 estimates showed that the greatest difference in fertility variables is influenced by environmental elements, which can be improved by using a better feeding system and controlling heat stress.

Key words: Direct, maternal, genetic, Friesian cows

INTRODUCTION

Milk traits attained from Friesian cows are affected by many environmental and physiological elements (i.e. month and year

Corresponding author: Adel Salah Khattab *E-mail address:* <u>adelkhattab@yahoo.com</u> *Present address:* Animal Production Department, Faculty of Agriculture, Tanta University, Egypt of parturition and parity) and heritable elements (heritability, phenotypic and genetic association). Corrected milk traits for environmental and physiological elements are essential to obtain the best estimates of genetic parameters and genetic progress. Estimates of heritability of milk production differed from 0.12 to 0.49, for days in milk ranged from 0.02 to 0.22, for days dry ranged from 0.03 to 0.27, for days open ranged 0.02 to 0.19, for calving interval ranged 0.01 to 0.19, and for number of mating per conception ranged from 0.01 to 0.03 as reported by (Salem et al., 2006; Mostafa et al., 2013; Sanad and Hassanane, 2017; Abou El- Naser et al., 2020).

Moderate heritability estimates for milk yield in dairy cows indicated the possibility of genetic improvement through selection of bulls and cows (Sanad and Gharibe, 2017; Zahed et al., 2020).

Low heritability estimates for reproductive parturition variables (days from to conception (OP) days open, calving parturition calving (CP) and number of mating per conception (NMPC) are calculated by some workers in Friesian cows in different regions (Salem et al., 2006; Mostafa et al. 2013; Sanad and Hassanane, 2017 and Abou El- Naser et al., 2020) and ranged from 0.01 to 0.19 and indicated that little genetic progress for fertility variables can be expected.

In livestock, environmental variation of the progeny is partially due to genetic variation of some variables from the dams, such that quantitative traits can be influenced by two genetic components, animal genotype (direct genetic effect) and dam genotype (maternal genetic effect). Maternal additive genetic effects have frequently been observed in dairy cows (Ajili et al., 2007; Mostafa et al., 2013; Abu El- Naser et al., 2020).

The current investigation was carried out to calculate phenotypic and genetic parameters associated with direct and maternal genetic effects on productive and reproductive variables of Friesian cows in Egypt.

MATERIALS AND METHODS

A total of 2166 lactations of Friesian cows' progeny of 92 sires and 882 dams collected from Sakha Experimental Farm, which belonged to Animal Production Research Institute, Ministry of Agriculture, during the period 2014 to 2020. In the winter, the animals were fed a concentrate combination of wheat or rice straw, as well as Egyptian clover and in the summer, they were fed clover hay and concentrate ration. Friesian heifers weighing roughly 350 kg and were artificially inseminated with verified Pregnancy Friesian sires' sperm. was detected after 60 days of service. The animals were milked by machine twice a day. Variables studied are ten month milk production (10 MMP), ten month fat production (10MFP), ten month protein production (10 MPP), lactation length (LL), days dry (DD), age at first parturition (AFP), days open (DO) and calving interval (CI).

Data were analyzed using linear mixed model SAS (2000). The model includes main effects of month and year of parturition, and parity and random effects of bulls and cows nested within bulls and errors.

In addition, all variables studied were analyzed by using multiple traits animal models (MTAM) according to (Boldman *et al.*, 1995).

Two animal models were used. Model 1 (full model), includes main effects of month and year of parturition and parity, permanent and direct genetic, maternal genetic, covariance between direct and maternal genetic and error as random effects. Model 2 is equal to model 1, while removing maternal and covariance between additive direct and maternal genetic effects.

In matrix notation, the following model 1 was used

 $Y = Xb + Za + M_m + Wp_e + e$

Where:

Y = vector of observations, b = v vector of fixed effects including month (12 levels), year (7 levels) and parity (8 levels),a= vector of direct additive genetic effect, m = vector of random maternal (indirect) genetic effect, p_e = vector of permanent environmental effect, e = vector of random error effects and X, Z, M and W are incidence matrices relating records to fixed, direct genetic, maternal genetic and permanent environmental effect, respectively.

In matrix notation, the following animal model 2 was used:

$Y = Xb + Za + Wp_e + e$ Where:

Y= vector of observations, b = vector of fixed effects including month (12 levels), year (7 levels) and parity (8 levels), a = direct genetic effect, p_e = permanent environmental effect and e = error effect vector and Z and Ware incidence matrices.

The heritability, phenotypic, and genetic correlations among all variables studied were estimated using the multiple traits animal models (Boldman *et al.*, 1995).

RESULTS

Means, Standard Deviation (Std) and Coefficient of Variability (CV%) for all studied variables 10 MMP, 10 MFP, 10 MPP, LL, DD, AFP, DO and CI are shown in Table (1).

Non genetic effects

The Least squares analysis of variance for non-genetic factors affecting productive and reproductive variables is presented in Tables (2 and 3).

Month and year of parturition and parity had a major fixed influence on all variables in the study (Tables 2 and 3, P<0.05 or P<0.01). While months of parturition have very little effect on 10 MFP and 10 MPP (Table 2).

Random effects

Bulls of the cows and cows nested within bulls are very important random effects on all variables in the study (Tables 2 & 3, P<0.01). Our results were explained the possibility of genetic improvement of productive and reproductive variables through selection of bulls and cows.

Genetic parameters

Direct heritability estimates

Estimates of direct heritability (h_d^2) , genetic associations (r_g) and phenotypic associations (r_p) among different variables studied are presented in (Table 4).

Estimated direct heritability for 10 MMP, 10 MFP and 10 MPP, LL, DD, AFP, DO and CI were 0.25, 0.27, 0.26, 0.06, 0.06, 0.01, 0.10 and 0.04, respectively (Table 4).

Estimates of maternal h_m^2 for 10 MMP, 10 MFP, 10 MPP, LL, DD, AFP, DO and CI were 0.23, 0.20, 0.19, 0.03, 0.03, 0.04, 0.06 and 0.05, respectively (Table 5).

Correlations

Phenotypic correlation (r_p)

Estimated phenotypic correlation among different variables studied is presented in Table (4). Phenotypic correlations among 10 MMP, 10 MFP, 10 MPP and LL were positive and ranged from 0.69 to 0.90 (Table 4). Phenotypic correlations among 10 MMP, 10 MFP, 10 MPP, LL with DD, DO and CI were negative and went between -0.19 to -0.45 (Table 4), expect the r_p between LL and each of DO and CI were positive. Phenotypic correlations among 10 MMP, 10 MFP, 10 MPP and LL with AFP were positive and ranged from 21 to 80. Phenotypic correlation between DO and CI was positive (1.00, Table 4).

Genetic correlation (rg)

Estimated genetic correlations (r_g) between different variables are presented in Table (4). Hereditary associations between 10 MMP, 10 MFP, 10 MPP and LL were positive, highly significant and ranged from 0.66 to 0.84 (Table 4), respectively. Also, genetic correlations between 10 MFP, 10 MPP was 0.69 and hereditary association between LL and each of 10 MFP and 10 MPP were 0.68 and 0.66, respectively.

Genetic correlations among 10 MMP, 10 MFP, 10 MPP and LL with AFP, DD, DO and CI are negative and ranged from -0.07 to -0.70 (Table 4), while r_g between DO and CI was positive (1.00, Table 4).

Maternal genetic correlations among different variables are presented in Table (5).

Maternal genetic correlation between 10 MMP, 10 MFP, 10 MPP and LL were of positive significance and ranged from 0.18 to 0.31 (Table 5). While the maternal genetic correlation between milk traits and reproductive traits were of negative significance and raged from -0.09 to -0.69, while r_g between DO and CI was positive, 0.20 (Table 5).

Table	1:	Means,	Standard	Deviation	(Std)	and	Coefficient	of	Variability	(CV%)	for	all
		studied '	variables									

Variables	No.	Mean	Std	CV%
10 MMP, kg	2166	2809	94.90	33.78
10 MFP, kg	2166	102.31	36.79	35.96
10 MPP, kg	2166	79.14	28.04	35.43
LL, d	2166	294	86.30	29.34
DD, d	2166	122.07	78.68	64.45
AFP, mo.	2166	32.89	4.50	13.68
DO, d	2166	141.22	90.90	64.37
CI, d	2166	414.87	89.60	21.60

Table 2: The Least squares analysis of variance for factors affecting productive variables in Friesian cows.

SOV	4 6	10 MMP		Ι	L	10	MFP	10 MPP	
5.0.V	u. 1	MS	p > r	MS	p > r	MS	p > r	MS	p > r
Bull	91	14937	< 0.0001	16481	< 0.0001	2164	< 0.0001	1557	< 0.0001
Cow (Bull)	790	9083	< 0.0001	8915	< 0.0001	1414	0.0029	851	< 0.0001
Month of calving	11	17504	0.0006	29249	< 0.0001	798	0.7653	469	0.7227
Year of calving	6	212331	< 0.0001	153374	< 0.0001	2277	0.0745	1419	0.0434
Parity	7	89808	< 0.0001	20706	0.0001	2826	0.0202	1883	0.0055
Residual	1260	5845		4893		1186		654	

Table 3: The Least squares analysis of variance for factors affecting reproductive variables in Friesian cows.

SOV		AFP		DD I			DO CI		
5.0.1	df	MS	p > r	MS	P>r	MS	P>r	MS	p > r
Bull	91	57.43	< 0.0001	14662	< 0.0001	10544	< 0.0001	14279	< 0.0001
Cow(bull)	790	42.18	< 0.0001	8009	0.0669	5702	0.4488	7287	0.4754
Month of calving	11	5.27	< 0.0001	23250	0.0003	11090	0.0289	16044	0.0121
Year of calving	6	40.99	< 0.0001	133792	< 0.0001	148262	< 0.0001	120263	< 0.0001
Parity	7	37.21	< 0.0001	8054	0.3563	18201	0.0022	25637	0.0009
Residual	1260	1.0583		7278		5657		7261	

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Table 4: Estimated heritability (on diagonal), genetic correlation (below diagonal) and phenotypic correlation (above diagonal) among all variables studied.

Variables	10 MMP	10 MFP	10 MPP	LL	DD	AFP	DO CI
10 MMP	0.25±0.03	0.77±0.10	0.88±0.10	0.80±0.20	40±0.10	0.80±0.02	40±0.01 - 0.45±0.02
10 MFP	0.72±0.02	0.27±006	0.90±0.02	0.79±0.09	25±0.01	0.25±0.01	-0.25±0.09 - 0.26±0.09
10 MPP	0.84±0.02	0.69±0.01	0.26±0.09	0.69±0.09	19±0.09	0.21±0.02	-0.30±0.09 - 0.34±0.10
LL	0.76±0.07	0.68±0.02	0.66±0.03	0.06±0.02	-0.45±0.10	0.30±0.10	0.20±0.09 0.21±0.10
DD	-0.20±0.10	-0.18±0.02	-0.19±0.02	19±0.01	0.06±0.02	0.25±0.09	0.10 ± 0.09 0.15 ± 0.09
AFP	70±0.10	-0.45±0.02	-0.34±0.02	07±0.01	08±0.02	0.01±0.002	0.24±0.09 0.22±0.09
DO	23±0.01	-0.13±0.02	-0.12±0.02	09±0.01	1.0±0.01	09±0.02	0.10±0.030 0.4±0.01
CI	24±0.02	-0.20±0.02	-0.19±0.02	10±0.01	1.0±0.01	-0.10±0.03	1.00±0.09 0.04±0.01

Table 5: Estimates of maternal heritability (on diagonal) and maternal genetic correlation (below diagonal) among all variables studied.

Variables	10 MMP	10 MFP	10 MPP	LL	DD	AFP	DO	CI
10 MMP	0.23±0.02							
10 MFP	0.31±0.02	0.20±0.08						
10 MPP	0.26 ± 0.04	0.24 ± 0.02	$0.19{\pm}0.02$					
LL	0.29±0.10	0.19 ± 0.05	0.18 ± 0.06	0.03±0.07				
DD	-0.09 ± 0.01	-0.09 ± 0.01	-0.07±0.01	-0.05 ± 0.01	0.03±.06			
AFP	-0.10 ± 0.01	-0.02 ± 0.01	-0.04 ± 0.01	-0.10±0.01	-0.01±0.01	0.04±0.012		
DO	-0.43 ± 0.02	-0.30±0.06	-0.29±0.06	$-0.69 \pm .01$	-0.12±0.02	0.02 ± 0.01	0.06±0	.01
CI	-0.06±0.02	-0.04±0.03	-0.04±0.03	0.03±0.02	-0.45 ± 0.05	01±.01	0.2±0.01 0.	05±0.01

DISCUSSION

The present estimates of 10 MMP, 10 FP and 10 PY are lower than those stated by some researchers in Friesian cows. In this respect, in Ireland, the average 10 MMP, 10 MFP and 10 MPP were 6557 kg, 246 kg and 222 kg, respectively, in Holstein Friesian cows (Buckley et al., 2003). In Egypt, the average 10 MMP, LL and DD were 9038 kg, 407 d and 64 d, respectively, in Holstein Friesian cows (Salem et al., 2006). Mostafa et al. (2013) analyzed another set of that herd, found that the average 10 MMP and LL were 3558 kg and 301 days, respectively. Amina Habib et al. (2020) studied an Egyptian Holstein Friesian cow and stated that the average 10 MMP, 10 MFP and 10 MPP were 8370 kg, 266 kg and 219 kg,

respectively. Zahed et al. (2020) investigated a herd of Friesian cows and reported that the average 10 MMP and LL were 2680 kg and 302 d, respectively. Kassab et al. (2024) found that Holstein Friesian cows averaged 10 MMP and LL were 9710 kg and 357 d, respectively.

On the other hand, our averages of 10 MFP and 10 MPP were higher than those reported by Ajili *et al.* (2007), who revealed that Tunisian Holstein Friesian cows averaged 10 MFP and 10 MPP were 180.23 kg and 167.83 kg, respectively.

Our averages of AFP, DO and CI are higher than those reported by many researchers who also studied Friesian cows. In Egypt, the average AFP and CI were 29 mo., and 470 d, respectively (Salem *et al.*, 2006). In Sudan, the average CI was 445 d (Eid *et al.*, 2012). The means of AFP and DO were 27.2 mo., and 113,1 d, respectively (Salem and Hammoud, 2016). Abu El-Naser *et al.* (2020) with another set of that herd found that the average DD and CI were 170 d and 474 d, respectively.

The present estimates of CV % are inside the array reported by some authors with different strains of Friesian cows (Boujenane *et al.*, 2020; Mostafa *et al.*, 2013; Salem and Hammoud, 2016; Abu–El Naser *et al.*, 2020; Kassab *et al.*, 2024) and ranged from 34.40 to 38.96 for 10 MMP, from 26.50 to 37.61 % for 10 MFP, from 30 to 38.04 % for 10 MPP from 31.90 37.86 % for LL, from 31.72 to 58.22 % for DD, from 9.1 to 13.2 % for AFP, from 40.30 to 68.12 % for DO and from 19.40 to 23.21 % for CI. The higher CV % for DD and DO reflects low accuracy in estrus detection and high insemination.

The differences between month and year of parturition may be due to changing management practices from year to year, culling old and weak cows, different feeding systems, heat stress and phenotypic trend. The increase of milk traits across parity may be due to the increase in age and body size of cows. Similar results are reported by many authors on Friesian cows in Egypt (Atil and Khattab, 2000; Yener *et al.*, 2006; Sanad and Afify, 2016; Zahed *et al.*, 2020; Khattab *et al.* 2021).

The middle direct h_d^2 estimates for 10 MMP, 10 MFP and 10 MPP indicated the possibility of using selection methods (direct, indirect and selection indexes) to improve milk yield and its components in dairy cows. Similarly, Boujenane (2002) found that h^2 estimates for 10 MFP and 10 MPP were 0.33 and 0.32, respectively. Marina Lazarevic *et al.* (2018) analyzed data of Holstein Friesian cows in Belgrade, using sire model, found that the heritability of 10 MMP, 10 MFP and MPP were 0.293, 0.319 and 0.272, respectively. Amina Habib *et al.* (2020) with Holstein Friesian cows in Egypt, using MTAM, found that direct h^2 estimates for 10 MMP, 10 MFP, 10 MPP were 0.08, 0.23 and 0.26, respectively. In Thailand, from 168,124 records of Holstein Friesian, the direct h^2 estimates for milk yield and fat/protein ratio were 0.347 and 0.293, respectively (Boonkum *et al.*, 2024).

Lower h² estimates for LL, DD, AFP, DO, and CI means that these variables are influenced by environmental factors. Improving the feeding system, management, detection of animals in heat and their insemination at proper time by good quality would help for decrease semen of reproductive variables. Also, low heritability estimates for LL, DD, AFP, DO and CI were reported by many authors (Eid et al., 2012; Mostafa et al., 2013; Salem and Hammoud, 2016; Sanad and Afify, 2016; Zahed et al., 2020; Kassab et al. 2024).

The present results in Table (4) show that the direct h^2 estimates for reproductive variables were generally lower than those for milk traits. This is expected due to the larger environmental influences on the reproduction variables regardless of their relationship with milk yield.

Maternal heritability for milk yield and it is component ranged from 0.10 to 0.23 (table 5) and indicated the important of maternal genetic effects for milk yield and it is components and it is necessary to include the maternal genetic effect in the model, before estimated sire transmitting ability. In addition, little quantity of additive maternal genetic effects for LL, DD, AFP, DO and CI, it could be determined that the additive maternal genetic effects and the covariance between additive maternal and direct genetic effects had very low important effects on reproductive variables. Also, Al- Anbari (2005) with Holstein Friesian cows in Iraq, found that maternal genetic effect for milk production, lactation length and calving interval were very low. Mostafa et al. (2013) analyzed 3748 normal lactation records of Friesian cows, found that the maternal h^2 calculated for 10 MMP, LL, F% and P % were 0.04, 0.01, 0.05 and 0.06, respectively. Sanad and Afify (2016) with two herds of Friesian, using MTAM, found that maternal heritability for total milk production (TMP), 10 MMP and LL were 0.07, 0.06 and 0.04, respectively for governmental herd and 0.9, 0.12 and 0.08, respectively for private herd. The same authors concluded that maternal h² estimates of milk traits were considerably less than direct h² estimates expect maternal h^2 of 10 MMP was higher in private farm (0.12) than its direct h² value. These results may indicate the genetic effect of sires on milk traits in both herds. In addition, Sanad and Gharib (2017) worked on Friesian cows, using six animal models, found that maternal h² estimates ranged from 0.01 to 0.028 for LL, ranged from .015 to 0.032 for 10 MMP and ranged from 0.006 to .031 for DO.

Positive rp correlations between 10 MMP, 10 MFP and 10 MPP and negative rp between milk traits and reproductive traits agree with those of other dairy cattle breeds. In this respect, Holstein Friesian cows in Morocco, the rp between milk yield and fat yield was positive (0.96) (Boujenane, 2002). In Iraq, the rp between 10 MMP, LL and CI were positive and ranged from 0.51 to 0.61 in the sire model of Holstein cows (Al-Anbari, 2005).

In Sudan, the Friesian cows' rp between milk production and LL and AFP were 0.480 and -0.116, respectively and rp between LL and AFP was -0.075 (Eid et al., 2013). In Friesian cows, the rp between 10 MMP, AFP and DO were 0.362, 0.157 and 0.257, respectively (Salem and Hammoud, 2016). In Egypt, the Friesian cows' rp between 10 MMP and both DD and CI were -0.08 and 0.11, respectively, rp between LL and DD and CI were -0.20 and 0.12, respectively, rp between DD and CI was 0.17 (Abu El-Naser et al., 2020). The present results indicated that cows producing higher milk yield tend to have longer LL, a little longer DO and a younger age at first calving.

In Holstein Friesian cows, the r_p between 10 MMP, 10 MFP and 10 MPP were positive and ranged from 0.425 to 0.886. The phenotypic correlation between milk yield and DO and CI were positive and ranged from 0.587 to 0.947 (Amina Habib *et al.*, 2020).

Positive rg between 10 MMP, 10 MFP, 10 MPP with LL shows that great yielding cows and milk components also have the longer LL and also indicates that assortment for high milk yield will be connected with genetic progress of fat yield, protein yield and days in milk. In addition, milk yield variables were predicted to be controlled by the same number of genes. Improving these variables could be through selective breeding. Therefore, selecting cows for high milk yield will also increase fat yield, protein yield and lactation length. Also, negative hereditary associations between 10 MMP, 10 MFP, 10 MPP and AFP suggested that selection for high-yielding milk, fat and protein would cause a correlated decrease in their AFP. Therefore, a lower AFP is a desirable goal of dairymen and will help minimize the cost of raising breeding heifers and maximize the number of lactations per cow. In addition, the present results show that fat and milk protein are important tools to identify cows at risk of poor reproductive performance.

In addition, the negative genetic association between milk yield, milk composition and DO and CI, requires special attention to cow fertility at selection for milk production. Also, the selection of cows for high milk production may lower both AFP and DO. Our results ranged from 0.35 to 0.96 and agree with those stated before (Boujenane, 2002; Al-Anbari, 2005; Salem and Hammoud, 2016; Usman et al., 2012; Mostafa et al., 2013; Sanad and Hassanane, 2017; Amina Habib et al., 2020 and Kassab et al., 2024).

The present results agree with some authors working on different breeds of dairy cows. In this respect, Salem and Hammoud (2016)

found that Holstein cows' rg between 305 d MY and LL, AFP and DO were positive and were 0.815, -0.035 and 0.999, respectively. Sanad and Gharib (2017) found that Friesian cows' rg among 305 d MY, LP and DO were positive and ranged between 0.31 and 0.99. Amina Habib et al. (2020) found that Holstein Friesian cows' rg between 10 MMP, 10 MFP and 10 MPP ranged from 0.995 to 0.998. Genetic correlations between 10 MMP and DO and CI were positive and values of 0.942 and 0.673 and the genetic correlation between DO and CI was 0.481. They concluded that high genetic correlation among productive traits, genetic selection for all traits can be achieved through selection for any of them.

CONCLUSION

The findings of the current study concluded that the maternal h2 estimates for milk yield and its components reflected the ability to achieve a plausible rate of genetic improvement for milk traits. The additive mothering genetic effects and the covariance between additive mothering and direct genetic effects had less importance for reproductive variables.

Therefore, the current study recommends improvement of milk production efficiency and milk component variables through selective breeding strategies targeting both bulls and cows. While direct h2 estimates showed that the greatest difference in fertility variables for LL, DD, AFP, DO and CI is influenced by environmental elements. Therefore, days dry, days open, calving interval and age at first parturition can be improved by using a better feeding system and controlling heat stress.

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Competing interests

No potential conflict of interest relevant to this article was reported.

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Availability of data and material

Upon reasonable request, the datasets of this study can be available from the corresponding author.

Authors' contributions Contributed by

Conceptualization: Alla, E. Gado and Anas, A. Badar, Syhmaa El – Komy; Khattab A S. Data collected: Alla, E. Gado and Anas Formal analysis: Khattab, A.S Methodology; Khattab, A.S. Alla, E. Gado and Anas Badr Validation: Khattab AS, Shymaa El- Komy Investigation: Khattab, A.S. Alla, E. Gado and Anas Badr: Gharab, M Writing - original draft: Alla, E. Gado and Anas, A. Badar, Syhmaa El – Komy; Khattab A S Writing - review & editing: Khattab A S Ethics approval and consent to participate This article does not require IRB/IACUC approval because there are no human and animal participants

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قدرت مكونات التباين والتأثير الوراثي باستخدام 2166 سجلا انتاجيا لابقار الفريزيان الناتجة من 92 طلوقة و 882 بقرة خلال الفترة من 2014 الى 2020م. استخدم عدد 2 نموذج حيوان أشتمل احدهما التأثير الوراثي الأمي . الصفات التي درست انتاج اللبن خلال عشرة أشهر , كمية الدهن خلال عشرة أشهر ، كمية البروتين خلال عشرة أشهر, طوّل موسم الحليب , فترة الجفاف , فتر التلقيح والفترة بين ولادتين. تراوحت قيم المكافىء الوراثي المباشر ما بين 23و 25- ، 2 و 27- ، 19و 26- ، 30و 06- ، 10و 04- ، 66و 1- ، 04 و 05- للصفات السابقة على التوالي. كانت قيم المكافىء الوراثي الأمى 23 ، 20 ، 19 ، 03 ، 03 ، 04 ، 06 , 05 للصفات السابقة على التوالي. أظهرت النتائج أهمية تقدير التأثير الوراثي الأمي عند التقييم الوراثي لانتاج اللبن ومكوناته. كذلك قدرت قيم الاتباطَّات الوراثية والمظهرية للصفات السابقة. لذلك، توصى الدراسة الحالية بتحسين كفاءة إنتاج الحليب ومتغيرات مكوناته من خلال استراتيجيات تربية انتقائية تستهدف كلاً من الثيران والأبقار. في حين أظهرت تقديرات h2 المباشرة أن أكبر فرق في متغيرات الخصوبة يتأثر بالعوامل البيئية، وهو ما يمكن تحسينه باستخدام نظام تغذية أفضل والتحكم في الإجهاد الحراري.