Assiut Veterinary Medical Journal | Assiut Vet. Med. J. Vol. 71 No. 186 July 2025, 1-15

10.21608/AVMJ.2025.344734.1522 | Assiut University web-site: www.aun.edu.eg

TRENDS AND GENETIC EVALUATION OF ECONOMIC TRAITS IN FRIESIAN CATTLE MANAGED UNDER EGYPTIAN CONDITIONS

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Received: 5 February 2025; **Accepted:** 30 April 2025

ABSTRACT

This study aimed to investigate the impact of both genetic and non-genetic factors on the productive and reproductive traits of Friesian cattle, as well as to track genetic and phenotypic trends over the years of calving in Egypt. Records were gathered from the lactation records of Friesian cattle at the Sakha Experimental Station. During a span of ten years, from 2008 to 2017, which situated northwesterly of the Nile Delta in the Kafr El-Sheikh governorate. The herd is managed by the Animal Production Research Institute (APRI), which operates under the Agricultural Research Center (ARC) in Giza, Egypt. In total, 1,609 lactation records were collected from 384 Friesian cows, which were 290 dams and 95 sires offspring. Friesian cattle productive traits include Total Milk Yield (TMY), 305-Day Milk Yield, Lactation Length (LL), Days Open (DO), and Calving Interval (CI). A univariate animal model was used to assess variance components, heritability, and repeatability, using Wombat software. The productive qualities examined had moderate direct heritability (h^2a) estimations. For 305-DMY, TMY and LL were estimated to be 0.28 and 0.30, respectively. Current h^2a estimates implied that selective breeding efforts in future generations can result in genetic improvements in TMY, 305-DMY, and LL traits. In terms of reproductive traits, h^2a estimates were low. The estimate of h^2a for DO was 0.02 and for CI was 0.03. Better management strategies can help reduce environmental variation, while also improving reproductive features in medium and high-milk-producing cows. The genetic trend (GT) for TMY and 305-DMY fluctuated over time, with some years showing an improvement in these features and others showing a decline. In terms of reproductive qualities, the anticipated negative GT was attained in most research periods for both DO and CI, with negative annual genetic gains of around -0.09 and -0.14 days/year for DO and CI, respectively. To improve herd productivity, it's important to enhance both genetic potential and management practices. These aspects are crucial for overcoming low heritability in reproductive traits and increasing the overall herd performance.

Keywords: Cattle, genetic, heritability, repeatability, environment.

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INTRODUCTION

Egypt imports 1.068 million tons of milk to meet the demand that exceeds local production, as domestic milk production accounts for just 86.1% of total consumption (MALR-EAS, 2011). This gap is primarily due to the relatively low productivity of dairy animals (Khalil and Ahmed 2013). Therefore, to enhance the dairy sector, the production of dairy animals needs to be improved (Shoukry, 2021). Dairy cow selection was formerly based on milk yield and composition (Prata *et al*., 2015), but now includes other features, such as reproductive traits, due to their relationship with economic return (Stavetska & Dynko, 2021). The productivity of dairy farms can be improved in two main lines: by increasing the number of cows or boosting the milk yield per cow through improved management practices, better environmental conditions, and genetic advancements (Shehab El-Din 2020). In this regard, Friesian cows are regarded as one of the most popular dairy breeds in Egypt (Osman *et al*., 2013). Genetic improvement of dairy cows is a key element of a holistic strategy to enhance the profitability and sustainability of dairy operations. Identifying traits that impact genetic improvement in a population is required for assessing genetic enhancement and pinpointing areas for progress (Sarakul *et al*., 2011). Understanding genetic factors, such as heritability, is crucial for genetic evaluations, predicting selection responses, and guiding producers in choosing the appropriate breeding systems for future development (Sitkowska *et al*., 2024).

Genetic gain must be evaluated in each breeding program to determine genetic improvement in each generation and may be anticipated using criteria, such as genetics, proportion of animals selected, degree of selection, and population variance (Ratwan *et al*., 2021). Furthermore, it is critical to examine the success of breeding programs to evaluate their progress and make appropriate changes. The greatest approach for tracking genetic changes in a population is the calculation of genetic trends (Dash *et al*., 2016). Estimating genetic and phenotypic trends is critical for animal breeders because it provides them with the essential data to design more successful breeding programs or make beneficial alterations in the future (Solemani-Baghshah *et al*., 2014).

MATERIALS AND METHODS

Data: -

This study utilized data gathered from the lactation records of Friesian cattle at the Sakha experimental station, located to the northwest of the Nile Delta in Kafr El-Sheikh governorate. The herd is managed by the Animal Production Research Institute (APRI), which is part of the Agricultural Research Center (ARC) in Dokki, Giza, Egypt. The analyzed traits in this study are presented in Table (1). A total of 1,609 valid lactation records were collected from 384 Friesian cows, the offspring of 290 dams and 95 sires. These records were compiled over 10 consecutive years, from 2008 to 2017. Data were adjusted to exclude cows with unknown parentage or those with non-traditional drought origins. Additionally, records were discarded if the first calving age was below 24 months or above 40 months, or if the cows had fewer than 150 days in milk due to health issues such as injury, disease, reproductive or udder problems.

Table 1: Structure of the data.

ITEM	N
Records of productive features	1609
Records of reproductive features	1342
Sires of cows.	95
Dams of cows.	290
Cows.	384

* Reproductive periods were computed starting with the second parity.

Feeding and management:

Cows were managed and fed using a system developed by the Ministry of Agriculture's Research Centre. Dietary requirements depending on weight, reproductive state, and milk production were provided by daily allowances. Dried-off cows consumed berseem from November to mid-May. Cows graze on clover during the herd's daily milking period, which lasts for four hours, beginning at 10:00 a.m. They were then given 4 kg of rice straw per animal. Feed was a mixture of concentrate and rice straw, covering 60% of dietary needs. During the summer, depend on the concentrate mixture. Bricks made of mineral mixes were freely distributed as sold mineral mixtures in front of the animals. Basins of clean water were accessible. The open barns where the animals are housed have roofs between 3.5 and 4 meters high. When the heifers weighed 350 kg or were 18 months old, they were served. Artificial insemination was carried out within 12 to 15 hours of heat detection, using frozen semen sourced from the United States and Canada. Cows were artificially inseminated no earlier than 60 days before calving. Rectal palpation was used 60 days following the previous service to diagnose pregnancy. The cows were milked until they spontaneously dried out or until two months before the anticipated calving date. Two times a day, milking cows were machine-milked, and the amount of milk produced was noted every day.

Studied traits: -

The analyzed traits included total milk yield (TMY, kg), 305-day milk yield (305-DMY, kg), and lactation length (LL, days). The reproductive traits considered were days open (DO, days) and calving interval (CI, days).

Data analysis:

The GLM algorithm was used to analyze the data to identify fixed effects in SAS (2011). Season, calving year, and cow parity were all incorporated into the mixed model. The non-genetic components' non-significant interaction was eliminated.

The statistical mixed model employed was as follows:

$$Y_{ijklm} = \mu + SI_i + PA_j + YE_k + SE_l + e_{ijklm},$$

Y_{ijklm}: either TMY; 305-(DMY); LL; DO and CI; μ= overall mean for each trait; SI_i= the random effect of i^{th} sire; PA_j= the effect of j^{th} parity j, (j=1, 2,3… 5); YE_k= the effect of k^{th} year of calving k, (k=2008, 2009…., 2019),

SE_l=the effect of l^{th} calving season l, (l= 1, 2,3… 4) and e_{ijklm} = It is assumed that the random residual is independent, normally distributed, with a variance of σ^2e and a mean of zero.

Genetic parameters

The genetic parameter studies included significant fixed effects. Using a univariate animal model using Wombat software, variance components, heritability, and repeatability were determined (**Meyer, 2006**). In matrix form the model was represented as follows:

$$Y = X\beta + Z_1a + Z_2\,pe + Z_3m + e, \text{ with Cov } (a,m) = 0$$

And
$$Var\begin{pmatrix} a \\ m \\ pe \\ e \end{pmatrix} = \begin{pmatrix} A\sigma^2{}_a & 0 & 0 & 0 \\ 0 & A\sigma^2{}_m & 0 & 0 \\ 0 & 0 & I_d\sigma^2{}_{pe} & 0 \\ 0 & 0 & 0 & I_n\sigma^2{}_e \end{pmatrix}$$

y = vector of observations; β= vector of fixed effects with an incidence matrix X; a: = vector of random animal effects with incidence matrix Z1; pe: = vector of random permanent environmental effects with incidence matrix Z2; m: = vector of maternal effects with incidence matrix Z3 and e: = vector of random residual effects with mean equals zero and variance σ^2e. The vector of additive effects (a) was assumed to be N~(0, A σ^2a), where A is the numerator relationship matrix among animals in the pedigree file and σ^2a is direct genetic variance. The vector of maternal effects (m) was assumed to be N~(0, A σ^2m), where m is the numerator relationship matrix among animals in the pedigree file and σ^2m = variance due to maternal genetic. The vector of random permanent environmental effects (p_e) was assumed to be N~ (0, Id σ^2pe), where Id = identity matrix with order equal to the number of cows, and σ^2pe represents the permanent environmental effects variance.

The vector of residual effects (e) was assumed to be N~ (0, I_n σ^2_e), where I_n. The identity matrix had the same order as the number of entries, whereas σ2e represented the environmental variation. Heritability (h^2_a) was estimated as: -h^2_a = σ^2_a / σ^2_p.

Maternal heritability (h^2_m) was computed as: - h^2_m =σ^2_m/ σ^2_p.
Repeatability (Re) was computed as: Re = σ^2_a + σ^2_{pe} / σ^2_p.

The genetic (GT) and phenotypic (PT) trends were computed using SAS regression techniques of SAS (2011). By regressing the average breeding values of cows by year of calving, the yearly GT for the attributes under study was determined. A linear regression of each trait's phenotypic averages on the calving year was used to determine PT. The regression coefficient (b) of the genetic trends was divided by the total phenotypic mean of the trait in the assessed population, and the result was multiplied by 100 to get the percentage of yearly genetic gains (%G) (Carvalho *et al*., 2023).

RESULTS

Means and variance statistics

Table (2) displays the mean and standard deviation (SD), as well as the phenotypic coefficient of variability (CV%) for the examined characteristics.

The actual means for productive traits were 3339 kg, 2950 kg and 308 days for TMY,305-DMY and LL, respectively. In terms of reproductive features, the average for DO and CI were 149.27 and 448.85, respectively. CV% for all productive qualities shows a higher amount, ranging from 32% to 37%. While the CV% for the reproductive interval (DO and CI) were almost similar and mild, at 24.6 and 26.7%, respectively.

Table 2: Descriptive means and variance statistics for Friesian cow features under study.

Traits	Mean	SD	CV%
Productive traits			
TMY	3339	1235.43	37
305-DMY	2950	944	32
LL	308	104.72	34
Reproductive traits			
DO	149.27	36.72	24.6
CI	448.85	119.8	26.7

Table (3) displays the significance of fixed and random influences examined characteristics in Friesian cattle. The study found a substantial impact of calving year ($P \leq 0.01$ or $P \leq 0.001$) on all attributes examined. The season of calving showed a substantial influence on productive qualities (TMY, 305-DMY, and LL). In contrast, it had no significant influence on CI or DO levels.

Parity had a huge impact on TMY, 305-DMY, LL, and DO. On the contrary, inequalities among parities had no significant influence on CI.

Table (3) shows that the cow's sire had a substantial ($P \leq 0.001$) influence on milk production characteristics TMY, 305-DMY, and LL and DO ($P \leq 0.005$).

Genetic analysis

Table (4) shows the estimated variance components, as well as direct (h^2a), maternal (h^2m), permanent (pe^2), and repeatability (R) for the qualities under consideration. The productive traits examined had modest direct heritability

(h^2a) estimations. For 305-DMY, TMY and LL were estimated to be 0.28 and 0.30, respectively. In terms of reproductive qualities, h^2a estimates were low. The estimate of h^2a for DO was 0.02 and for CI was 0.03.

The maternal heritability (h^2m) for all productive and reproductive variables tested was low, ranging from 0.001 to 0.05. All examined reproductive and productive characteristics had modest maternal heritability (h2m), which ranged from 0.001 to 0.05.

Table 3: The significance of fixed and random influences examined characteristics in Friesian cattle.

Trait	Unit	Fixed effect			Random
		Year	Season	Parity	Sire of cow
TMY.	Kg.	**	**	**	***
305-DMY.	Kg.	***	***	***	***
LL.	Day.	***	*	***	***
DO.	Day.	***	NS	**	*
CI.	Day.	***	NS	NS	NS

*=P≤0.05, **=P≤0.01, *** = significant at P≤ 0.001, NS=non-significant

Table 4: The variance components and genetic parameters of univariate models derived for productive & reproductive variables in cattle.

	Productive features			Reproductive features	
	TMY	305-DMY	LL	DO	CI
Variance components					
σ^2_a	17.5	12	16	0.84	1.8
σ^2_m	2.5	1.5	3	0.3	0.09
σ^2_{pe}	0.2	0.2	0.3	0.015	0.012
σ^2_e	41.5	27	37	54	57.6
σ^2_p	61.7	40.7	56.3	55.155	59.502
Genetic parameters					
h^2_a	0.28±0.047	0.30±0.045	0.28±0.001	0.02±0.004	0.03±0.001
h^2_m	0.04±0.044	0.04±0.041	0.05±0.001	0.01±0.003	0.001±0.001
pe^2	0.003±0.03	0.005±0.03	0.01±0.001	0.001±0.004	0.001±0.002
e^2	0.67±0.042	0.66±0.039	0.65±0.001	0.97±0.004	0.97±0.0020
R	0.28	0.30	0.29	0.02	0.03

σ^2_a = additive direct genetic variance; σ^2_m=additive maternal genetic variance; σ^2_{pe}= permanent environmental maternal variance; σ^2_p=phenotypic variance; σ^2_e=residual variance; h^2_a= direct heritability; h^2m= maternal heritability and R= Repeatability.

Genetic trend (GT)

Table (5) displays the genetic trend (GT) of the studied traits and is represented as a trendline in Figures (A to E). A study of a herd of Friesian cattle found a negative yearly genetic trend of around -38.3 kg, -35.4 kg, and -0.38 days per year for TMY, 305-DMY, and LL. GT for TMY and 305-DMY fluctuated throughout time, with some years showing improvements and others showing declines. Regarding LL, it was noticed that the GT for LL was positive in 2008 and 2013. In contrast, negative GT was seen in 2010, 2016, 2017, and 2018 (Chart C). In terms of reproductive traits, the anticipated negative GT was attained in most research periods for both DO and CI, with negative annual genetic gains of around -0.09 and -0.14 days/year for DO and CI, respectively (Charts d and e).

Genetic gains (G%)

Given the negative GT observed in the studied traits, the findings related to genetic gains (G%) exhibited a similar pattern. Over the whole time, the measured yearly G% of around -1.15 %, -1.2%,-0.12%, -0.06%, and -0.03% per year for TMY, 305-DMY, LL, DO and CI, respectively.

Table 5: Genetic (GT), phenotypic (PT) trends and genetic gain (G%) of productive and reproductive traits of Friesian cattle

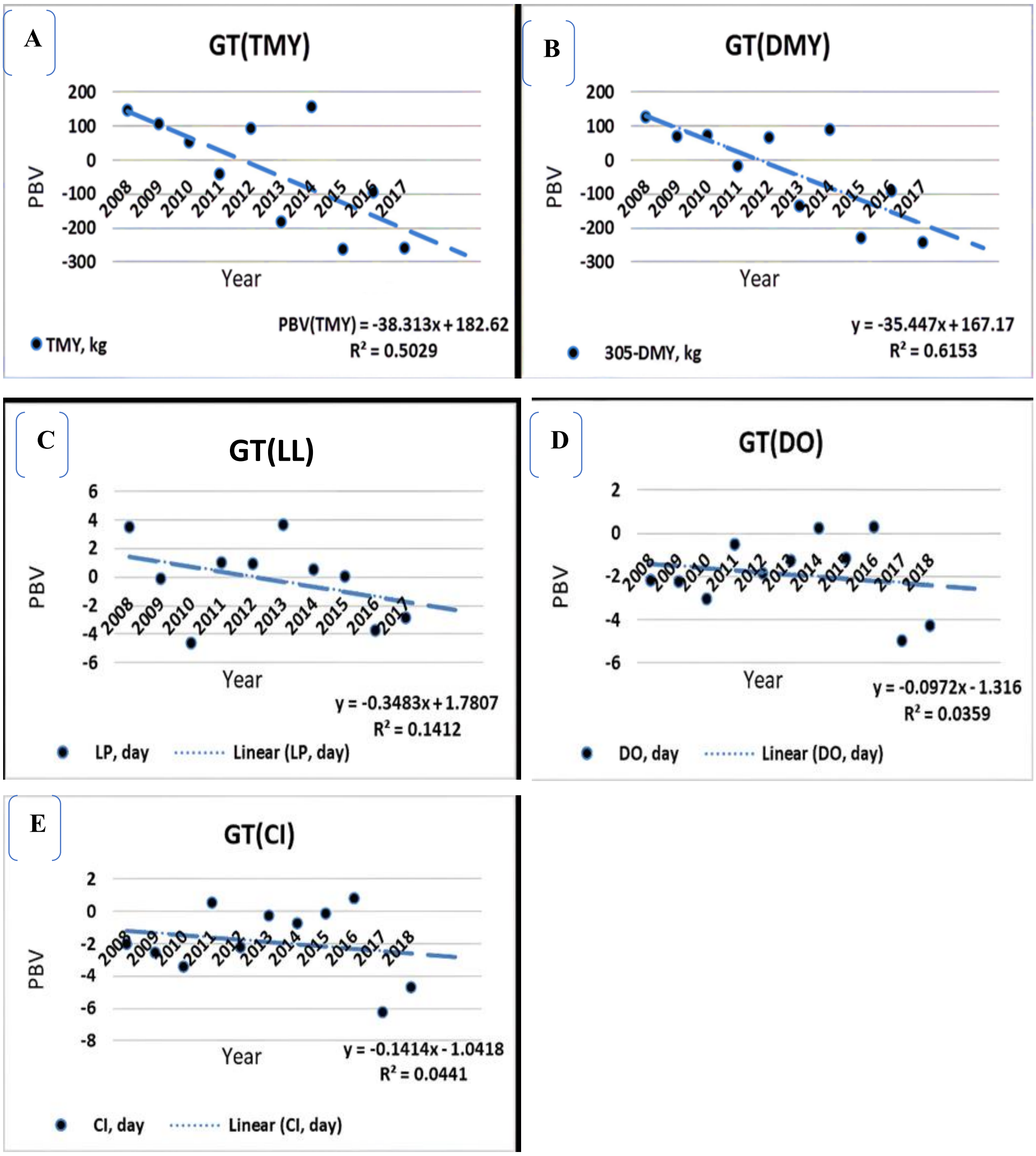
		Regression equation	R2	
Phenotypic trend (PT)				
Value/Year	TMY	=3671.2-59.0X[1]	0.16	
	305-DMY	=3236.8-57.7X	0.17	
	LL	=308.47-1.56X	0.27	
	DO	=152.47-1.15X	0.11	
	CI	=457.33-2.25X	0.12	
Genetic trend (GT)				G%*
PBV[1]/Year	TMY	=182.6-38.3X	0.50	-1.15
	305-DMY	=167.17-35.4X	0.61	-1.2
	LL	=1.78-0.380X	0.14	-0.12
	DO	=1.32-0.09X	0.03	-0.06
	CI	=1.04-0.14X	0.04	-0.03

[1]x=represented year; R^2: coefficient of determination and * G%= genetic gain/year

DISCUSSION

The previous trend (Table 2) agrees with those recorded in previous Egyptian studies, for Frisian cattle under state farm (Abo-Elenin, 2018; Shahab El-Din, 2020) and was lower than other studies for the same Friesian genotype (El-Awady *et al*., 2016; Sanad and Hassanane, 2017). The current herd's LL mean was 308 days, which is nearly identical to the usual 305 days, despite the lower total TMY. This shows a possible discrepancy between the herd's genetic capability and the environmental or management practices they face. In this regard, Abo-Elenin, (2018) demonstrates how climatic and administrative circumstances, as well as genetic and phenotypic variables, may all contribute to production variations.

In the current study, DO exceeded the optimal value of 90 days, as well as values reported by Shalaby *et al*. (2013) (121 days) and El-Awady *et al*. (2016) (120 days). However, it is within the greater range reported in previous Egyptian research Hammoud, (2013); Ayalew *et al*. (2017); Abo-Elenin, (2018). Similarly, the CI of 448.8 days, while within the range reported by Sanad 2006 and Abo-Elenin (2018) surpasses the ideal of 365 days and falls between the estimates of other studies (El-Tarabany and Nasr, 2015; El-Tarabany and El-Bayoumi, 2015 and Farrag *et al*., 2017). While it was lower than 470 and 484 days for the Holstein commercial herd in Egypt, reported by Salem *et al*. (2006) and Ibrahim *et al*. (2009), respectively. These protracted means for both DO and CI imply that the current herd has a relatively low fertility rate. This condition might be caused by a combination of physiological reasons, such as delayed postpartum ovarian reactivation and management methods, such as insufficient oestrus detection, and improper remating decisions. Additionally, mineral imbalances may also be contributing factors or insufficient healthcare.



Figures A to E . Genetic trends for (TMY), (305-DMY), (LL), (DO), and (CI).

A higher CV% for all productive qualities, ranging from (Table 2), in contrast to earlier Egyptian research on Friesian cows at state farms Shalaby *et al.* (2013) suggests a broader range of performance among individual cows within the herd. While the CV% for the reproductive interval falls within the range of Friesian cattle in Egyptian studies for DO report by Faid-Allah 2015 a &b (22.6%) and CI reported by Shalaby *et al*., (2013), Osman *et al*., (2013), El-Awady *et al.* (2016), Abo-Elenin, (2018), which ranged from 20.02 to 26.2%. Higher and intermediate CV% estimations in the current study may imply an increase in productive and reproductive qualities across animals in that herd, increasing the prospect of capitalizing on this variation through successful phenotypic selection programs and management approaches.

A substantial impact of the calving year ($P \leq 0.01$ or $P \leq 0.001$) on all attributes examined is consistent with prior reports by Faid-Allah (2015a), Hussein *et al*. (2016), Salem and Hammoud (2016), and Abo-Elenin (2018). Consistent with previous research, the inter-annual variations observed in this study could be attributed to fluctuations in environmental conditions, particularly those associated with managerial practices, weather patterns, nutritional status, and feeding regimens, all of which are demonstrably subject to change over time. Furthermore, herd size dynamics, animal age demographics, and phenotypic trends may all contribute to inter-annual trait variability (M'hamdi *et al*., 2012).

Moreover, the season of calving showed a substantial influence on TMY, 305-DMY, and LL. These findings support the reports of (Alhammad, 2005; Sanad, 2006; Rushdi *et al*., 2014; and Sanad, 2016). However, it showed that the season of calving had no significant influence on CI or DO levels. These findings support the reports of (Mohammed, 2011; Mengistu *et al*., 2016; Sanad, (2016).

A similar pattern for a huge impact of parity on TMY, 305-DMY, LL, and DO was seen by (Motlagh *et al*., 2013; Hunde *et al*., 2015; Wassie *et al*., 2015; Rushdie, 2015; Mengistu *et al*., 2016; Salem and Hammoud, 2016; Sanad and Gharib, (2017). On the contrary, inequalities among parities had no significant influence on CI. These findings were discovered by Amasaib *et al*. (2011) and Ashour *et al*. (2014).

In general, the present strong effect of non-genetic effect on most features, particularly productive ones, emphasises the need to consider these factors when managing dairy herds for maximum output.

Table (3) showed that the cow's sire had a substantial ($P \leq 0.001$) influence on milk production characteristics TMY, 305-DMY, and LL and DO ($P \leq 0.005$). These results align with the findings of Pantelic *et al*. (2014), Faid-Allah (2015a), Ayalew *et al*. (2015), Ratwan *et al*. (2016) and El-Awady *et al*. (2016). So, these investigations, as well as the current study, reveal that there exist genetic differences for qualities, particularly productive ones, and point to the possibility of selection to achieve genetic advancement for examined traits through sire selection. While the sire impact on CI was not substantial in accordance with Zein Elabdeen (2004), Abdel-Gader *et al*. (2007), and Suhail *et al*. (2010) all concurred.

However, Hammoud *et al*. (2010) found a highly substantial sire impact on both DO and CI, indicating the possibility of genetic improvement through sire selection. This disparity between our findings on CI might be attributed to variances in population size, environmental variables, or analytical methodology.

Table (4) shows the estimated variance components, as well as direct (h^2a), maternal (h^2m), permanent (pe^2), and repeatability (R) for the qualities under consideration.

The productive traits (TMY, 305-DMY, and LL) had modest direct heritability (h^2a) estimations ranging from 0.28 to 0.30. Similar ranges for Friesian cattle varied from 0.22 to 0.35 for TMY, 0.25 to 0.36 for 305-DMY, and 0.22 to 0.35 for LL reported. By (Pritchard *et al*., 2013; Faid-Allah, 2015a; El-Bayoumi *et al*., 2015, Al-Samarai, 2015; Sanad 2016 and Radwan *et al*., 2017).

Current h^2a estimates imply that selective breeding efforts in future generations can result in genetic improvements in TMY, 305-DMY, and LL traits. However, the h^2a

obtained in this investigation was lower than the values according to Hammoud (2013) for TMY, as well as Hussein *et al*. (2016) and El-Awady *et al*. (2016) for 305-DMY, the estimates were higher than those published by Abdel-Gader *et al*. (2007), Eid *et al*. (2012), Rushdi *et al*. (2014), and Sanad and Hassanane (2017) for TMY and 305-DMY, which varied from 0.10 to 0.19. The study also discovered that the h^2a estimate for LL was greater than the low values of 0.003 to 08 informed by (Eid *et al*., 2012; Al-Samarai *et al*., 2015; Sanad 2016). The current investigation discovered greater h^2a estimates for 305-DMY compared to TMY, generally with lower error variance.

Hammoud *et al*. (2014) ascribe this to the cutoff of lactation data at 305-DMY or the use of average daily output, which may diminish the transient environmental variance associated with daily swings in milk supply, particularly near the end of lactation. This increases genetic variety in relation to the environment.

In terms of reproductive qualities, h^2a estimates were low. In contrast to these low values, the error variance effects contribute significantly to the overall variation, leading to low heritability estimates for these traits. In this context, most previous studies have shown that additive genetic variation for reproductive traits is minimal relative to phenotypic variation, resulting in heritability estimates close to zero. Therefore, selection to improve these traits would likely be ineffective. The same ranges for Friesian cattle were noted by (El-Awady *et al*., 2011; Guo *et al*., 2013; Pritchard *et al*., 2013; Solemani-Baghshan *et al*., 2014; El-Bayoumi *et al*., 2015; Sanad and Gharib, 2017) with estimates varying from 0.01 to 0.07 for DO and from 0.02 to 0.07 for CI.

Better management methods can help improve cattle production systems' low reproductive efficiency (Cardoso Consentini *et al*., 2021). Farmers can benefit from accurate knowledge on how to care for their cows, such as excellent heat detection, high-quality semen and insemination procedures, efficient health programs, and enough feed. These methods can decrease environmental variance, while also improving reproductive features in medium and high-milk-producing cows.

The maternal heritability (h^2m) for all productive and reproductive variables tested was low (from 0.001 to 0.05, Table 4). Similar findings were reported by Gudex *et al*. (2012), Radwan *et al*. (2015), Sanad and Hassanane (2017), Sanad and Gharib (2017), Radwan *et al*. (2017), and Ismail (2018). Their estimations for productive traits (TMY, 305-DMY and LL) were modest or minor, ranging from 0.00006 to 0.05, and for reproductive traits (DO and CI) ranging from 0.00 to 0.02. These findings indicate that maternal factors have minimal effect on observed variance in these traits.

A successful breeding program in a herd relies on favorable genetic trends (Dash *et al*., 2016). A study of a herd of Friesian cattle found a negative yearly genetic trend for TMY, 305-DMY, and LL (Table 5), which fluctuated throughout time, with some years showing improvements and others showing declines.

Breeding better animals and employing effective selection strategies may result in a positive trend in milk yield during some periods of study. However, ineffective breeding strategies at the herd level have resulted in adverse annual genetic changes. Negative genetic trends in milk production features can be produced by a lack of efficient selection programs, infrequent monitoring of genetic development, and use poor genetic potential sires (Shehab El-Din, 2020).

In terms of reproductive traits, the anticipated negative GT was attained in most research periods for both DO and CI, with negative annual genetic gains (Charts d and e). Sahin *et al*. (2012) discovered that the yearly genetic trend for 305-DMY and LL was -2.46 kg/year and -0.4006 days/year, respectively. This was because the selection focused on phenotype rather than genetics.

Effa *et al*. (2011) found negative annual GT in Ethiopian dairy cows for TMY, 305-DMY, LL, and CI. The study indicated that changes in environmental components resulted in negative genetics in productive and fertility attributes, showing that reproductive efficiency increased with time. Amimo *et al*. (2007) discovered a negative GT of -2.1 kg/year for 305-DMY in Ayrshire cattle due to limited sample size, the inclusion of new sires and cows, advanced age at first calving, longer CI, and dairy operation traits such as diet and milking management.

Several factors may contribute to GT reductions. These include the absence of selection and breeding techniques for animal evaluation, small herd size, inbreeding, inaccurate recording, government austerity policies to reduce spending (including research budget), poor nutritional management, random mating, use of bulls with unknown breeding values, and reliance on pedigree information and phenotypic observations, rather than more reliable estimates of breeding value (Sahin *et al*., 2012; Solemani-Baghshan *et al*., 2014; Chawala *et al*., 2017; El–Awady *et al*., 2016; Abdel-Hamid *et al*., 2017).

CONCLUSION

To enhance herd productivity, it is essential to focus on both improving genetic potential and implementing effective management practices. Genetic selection should prioritize high-yielding individuals to boost production traits. At the same time, management strategies that improve reproductive efficiency are crucial. These strategies include maintaining optimal temperature control, using quality insemination techniques, and ensuring adequate nutrition. Addressing these factors can help overcome the low h^2 of reproductive traits and significantly improve overall herd performance.

Acknowledgments

The data for this study were provided by the Animal Production Research Institute (APRI)-the Agricultural Research Center (ARC), Egypt, and we sincerely appreciate their support.

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الاتجاهات والتقييم الوراثى للصفات الاقتصادية في الأبقار الفريزيان المُدارة تحت الظروف المصرية

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تم جمع البيانات المستخدمة في هذه الدراسة من سجلات إنتاج الحليب لأبقار الفريزيان في محطة سخا، التابعة لمعهد بحوث الإنتاج الحيواني(APRI) ، مركز البحوث الزراعية (ARC) ، محافظة كفر الشيخ، مصر. شملت البيانات ١٦٠٩ سجل حليب تم جمعها من ٣٨٤ بقرة فريزيان، من أمهات عددها ٢٩٠ وأباء عددهم ٩٥. تم جمع السجلات على مدار عشر سنوات، من ٢٠٠٨ إلى ٢٠١٧. تهدف الدراسة إلى دراسة تأثير العوامل الوراثية وغير الوراثية على الصفات الإنتاجية والتناسلية لأبقار الفريزيان، مثل إجمالي إنتاج الحليب (TMY)، وإنتاج الحليب في ٣٠٥ يوم (305-DMY)، وطول فترة الإدرار(LL) ، وفترة الأيام المفتوحة (DO)، والفترة بين الولادات(CI) . تم تقدير المعالم الوراثية مثل المكافئ الوراثي والمعامل التكراري باستخدام نموذج حيواني أحادي المتغير عبر برنامج Wombat (Meyer, 2006) ، بالإضافة إلى تحليل الاتجاهات الوراثية والمظهرية عبر سنوات الولادة للتنبؤ بالعائد الوراثي المحتمل للصفات المدروسة.

أظهرت النتائج أن تقديرات المكافئ الوراثي للصفات الإنتاجية المدروسة كانت متوسطة. بالنسبة لإنتاج الحليب في ٣٠٥ يوم وإجمالي إنتاج الحليب وفترة الإدرار، تراوحت تقديرات المكافئ الوراثي بين ٠,٢٨ و٠,٣٠. وتشير هذه التقديرات إلى أن برامج الانتخاب المستقبلية قد تساهم في تحسين هذه الصفات الوراثية في الأجيال القادمة. أما بالنسبة للصفات التناسلية، فقد كانت تقديرات المكافئ الوراثي منخفضة، حيث بلغت تقديرات المكافئ الوراثي ٠,٢٠ و٠,٠٣ وذلك لفترة الأيام المفتوحة والفترة بين الولادات على التوالي. يمكن تحسين الكفاءة التناسلية المنخفضة في أنظمة الإنتاج الحيواني من خلال إدارة أفضل، والاستفادة من ممارسات رعاية فعّالة، مثل بما في ذلك توفير درجات الحرارة المثلي، وتقنيات التلقيح عالية الجودة، والرعاية الصحية، والتغذية الكافية. هذه الممارسات قد تساهم في تقليل التباين البيئي وتحسين الصفات التناسلية في الأبقار ذات الإنتاج المتوسط والعالي.

كما أظهرت الدراسة أن الاتجاه الوراثي (GT) لإنتاج الحليب في ٣٠٥ يوم وإجمالي إنتاج الحليب كان متغيرًا عبر السنوات، حيث أظهرت بعض السنوات تحسنًا في هذه الصفات بينما أظهرت سنوات أخرى انخفاضًا. في المقابل، كانت الاتجاهات الوراثية للصفات التناسلية سلبية في معظم فترات الدراسة، حيث كانت التقديرات السنوية للزيادة الوراثية السلبية تقدر بحوالي -٠,٠٩ و-٠,١٤ يومًا/سنة للأيام المفتوحة والفترة بين الولادات على التوالي.

للعمل على رفع إنتاجية القطيع محل الدراسة يستلزم الامر تحسين الجانب الوراثى من خلال عملية انتخاب موجهة للأفراد ذات الإنتاجية المرتفعة مقارنة بمتوسط القطيع، مع توفير جانب رعائي أمثل يمنح تلك الافراد إمكانية لإظهار أدائهم ورفع متوسط إنتاجية القطيع في المرحلة القادمة.

الكلمات الرئيسية: أبقار- وراثة -المكافئ الوراثى-المعامل التكراري- البيئة