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Genetic Evaluation of First Lactation and Lifetime Production Traits in Friesian Cattle in Egypt

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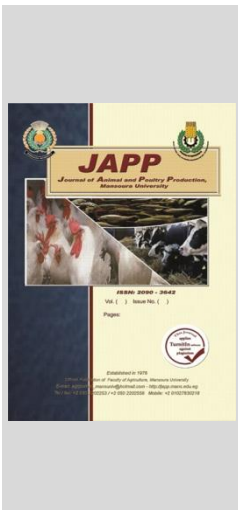
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ABSTRACT

Research on the longevity of dairy cattle has been extensively explored, yet it remains a subject under active investigation due to its significant implications for farm economics. Therefore, the aim of this study was to estimate the genetic parameters of first lactation and lifetime productivity traits in Friesian cattle, in order to identify avenues for genetic enhancements in these traits. The dataset encompassed 2837 records from 1243 cows, offspring of 835 dams and 108 sires, spanning the years 2000 to 2015 and sourced from two experimental stations, Sakha and El-Karada, managed by the Animal Production Research Institute, Egypt. The heritability estimates stood at 0.17, 0.26, 0.24, 0.12, 0.16, 0.31, 0.27, and 0.10 for FDIM (first days in milk), FLMY (first lactation milk yield), FLSMY (first lactation standard (305 days) milk yield), FDP (first dry period), LTDIM (lifetime days in milk), LTMY (lifetime milk yield), LTSMY (lifetime standard (305 days) milk yield), and LTDP (lifetime dry period), respectively. Significant positive genetic correlations were found between lifetime production traits. Also, positive genetic coefficients were observed between lifetime milk production traits and both of FLMY and FLSMY. Sire's breeding values displayed a wide range for FLMY, FLSMY, LTMY, and LTSMY. In conclusion, the moderate heritability estimates of first and lifetime milk production traits suggest that enhancing these traits through selection is feasible. The positive genetic correlation observed between these traits indicates a shared genetic influence, suggesting that progress in these traits can be simultaneously pursued through early selection processes in sires.

Keywords: first lactation; lifetime performance; genetic evaluation; Friesian cattle



INTRODUCTION

Dairy cattle genetic improvement programs prioritize specific selection criteria aimed at enhancing milk production efficiency while minimizing herd maintenance costs. A critical focus for milk producers is ensuring that both of heifers and cows are raised to be healthy, fertile at the right age, and capable of realizing their full genetic potential over an extended productive lifespan (Langford and Stott 2012; Hutchison et al. 2017; Fabris et al., 2025). Despite these goals, the dairy industry faces a persistent challenge in the form of limited animal longevity. Longevity, a crucial trait for sustained productivity, proves difficult to assess accurately due to the delayed recording of phenotypic data, which in turn can extend the generation interval (Albarrán-Portillo and Pollott, 2013). A decrease in the number of calvings directly affects the duration of a cow's longevity in the herd, thus significantly influencing the overall profitability of dairy industry (Hu et al., 2021). The limited longevity of cows not only curtails selection prospects for future generations but also leads to considerable financial losses as well as raising concerns about animal welfare (Najafabadi et al., 2016). In light of the dairy industry's global importance, it is imperative to identify not only the most productive animals but also those that excel in production, longevity, reproduction, and conformation. Generally, such animals play a crucial role in improving the profitability of production system (Tamboli et al., 2022). Given the impracticality of selecting depending on lifetime performance due to the lengthy generation interval, a more viable approach involves evaluating animals using the performance of earlier lactations instead of traits manifesting

later in life (Chaudhari, 2015). The effectiveness of breeding animals, including cattle, within a managed herd chiefly hinges on their productive performance (Pirlo et al., 2008; Toghiani et al., 2012). Notably, traits observed during the first lactation serve as reliable indicators of subsequent lactation performance, given the high inter-correlation between them in cattle (Eastham et al., 2018). Economic traits with high heritability can be used for genetic improvement by progeny testing as well as other programs for genetic improvement. Therefore, selecting animals based on these highly heritable traits, which contribute to lifetime performance, is crucial for achieving comprehensive enhancement through correlated responses (Albarrán-Portillo and Pollott, 2013; Birhanu et al., 2015; Hossein-Zadeh, 2016; Mirhabibi et al., 2018). Hence, the objective of this study was to estimate genetic parameters of first lactation traits and lifetime productivity in Friesian Cattle in Egypt, with the aim of exploring opportunities for genetic improvements in these traits.

MATERIALS AND METHODS

Dataset description and herd Management:

The data analyzed in this research originated from two Friesian cattle experimental herds, El-Karada and Sakha, affiliated with the Animal Production Research Institute, Agriculture Research Center, Ministry of Agriculture and Land Reclamation, Dokki, Giza, Egypt. The study emphasized first lactation traits, including FDIM (first days in milk), FLMY (first lactation milk yield), FLSMY (first lactation standard (305 days) milk yield), and FDP (first dry period), alongside lifetime production traits, such as LTMY (lifetime milk yield), LTSMY (lifetime standard (305 days)

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milk yield), and LTDP (lifetime dry period). The dataset comprised 2837 records from 1243 cows, offspring of 108 sires mated with 835 dams, collected between 2000 and 2015. Both experimental herds adhered to similar feeding and management conditions. The cows were kept in open sheds and fed Total Mixed Ration (TMR) consistently throughout the year. Rations were incorporated following the guidelines of the National Research Council (NRC). Heifers were inseminated once they reached the appropriate age and weight range between 350 and 375 kg, while cows were inseminated after the 45th day during the initial post-partum heat cycle; rectal examination was used for pregnancy confirmation. Veterinary oversight ensured vaccinations and medical attention for the livestock. Cows were machine milked twice daily, in the morning and evening, until two months before their expected calving date.

Variance components and genetic parameters:

Before evaluating the genetic parameters and breeding values of the traits under investigation, the dataset underwent thorough validation to confirm its suitability for fitting the analytical model. Both of sires with fewer than three offspring and data points with residual standard deviations (SD) exceeding 3.5 or falling below -3.5, SD were removed from the analysis (Buzanskas et al., 2013; Tramonte et al., 2019). All traits under examination were analyzed using the multi-trait animal model through the DFRAML program (Boldman et al., 1995). A mixed model approach was utilized to evaluate the genetic parameters and breeding values of the examined traits, incorporating random effects as well as fixed effects such as herd (2 herds), parity order (seven parities), calving year (16 years), calving season (4 seasons), and the interaction between calving year and calving season. The utilized model was as following:

$$y = Xb + Za + e$$

Here, y signifies the vector containing phenotypic data; b represents the vector of aforementioned fixed effects; a stands for the vector of random additive effects; and e denotes the vector of residual effects related to the investigated trait. The matrices X and Z correspond to the incidence matrices of fixed and additive genetic effects, respectively.

Direct heritability (h^2_d), genetic correlation (r_g), and phenotypic correlation (r_p) were computed using the following equations:

$$h^2_d = \frac{\sigma^2_d}{\sigma^2_p}$$

$$r_g = \frac{\sigma_{aij}}{\sqrt{\sigma^2_{ai} \sigma^2_{aj}}}$$

$$r_p = \frac{\sigma_{pij}}{\sqrt{\sigma^2_{pi} \sigma^2_{pj}}}$$

Here, σ^2_{ai} and σ^2_{aj} represent the additive genetic variance for traits 'I' and 'J', respectively; σ^2_{pi} and σ^2_{pj} are the phenotypic variance for the two traits 'I' and 'J'; and σ_{aij} and σ_{pij} are the additive genetic and phenotypic covariance between the two traits mentioned earlier.

RESULTS AND DISCUSSION

Descriptive statistics

Table 1 displays the unadjusted phenotypic means, standard deviations (SD), and coefficients of variation (CV, %) for the traits under investigation. The current LTMY (8257.10, kg) and LTDIM (706.64, days) were found to be lower compared to the values reported by Alhammad et al. (2008), which were 10542, kg and 2042, days, respectively. Also, Khattab et al. (2009) reported higher values of LTMY in Friesian cattle (9670, kg). The LTMY value in the current study closely approximated the reported mean of 8831, kg for LTMY in Holstein Cattle (Sadek et al., 2009). In addition, the FLSMY in this study (3293, kg) closely aligns with the value (3396, kg) reported by Meseret et al. (2015) for Holstein Friesian cattle in Ethiopia, surpassing the mean (2326, kg) noted by Sadek et al. (2009) but falling short of the figure (3661, kg) documented by Goshu et al. (2014) in Holstein Friesian cattle. The FDP in our study corresponds to 79.59 ± 2.220 , days, as noted by Şahin et al. (2014), and is lower than the estimate of 129.50, days provided by Shashikant et al. (2024). The discrepancies between our results and those reported by other researchers could be attributed to variations in management practices, climatic conditions, and/or genetic differences across herds. Notably, the higher coefficient of variation values for the traits under study (ranging from 25.33% to 80.07%, as shown in Table 1) signify significant variability among individuals in these crucial production traits.

Table 1. Descriptive statistics for lifetime production traits in Friesian dairy Cattle

Items	FDIM, days	FLMY, kg	FLSMY, kg	FDP, days	LTDIM, days	LTMY, kg	LTSMY, kg	LTDP, days
Mean	286.95	3105.11	3293.19	82.43	706.64	8257.10	8162.95	191.48
S.D	85.02	1285.77	913.88	20.88	512.68	6611.70	5957.93	123.80
CV (%)	29.63	41.41	27.75	25.33	72.55	80.07	72.99	64.65
No. of records	2837							
No. of cows	1243							
No. of sires	108							
No. of dams	835							

FDIM, first days in milk; FLMY, first lactation milk yield; FLSMY, first lactation standard (305 days) milk yield; FDP, first dry period; LTDIM, lifetime days in milk; LTMY, lifetime milk yield; LTSMY, lifetime standard (305 days) milk yield; LTDP, lifetime dry period.

Heritability:

The heritability estimates for first lactation and lifetime production traits in Friesian dairy cattle are presented in Table 2. Heritability estimates were relatively low for FDIM (0.17 ± 0.02) and LTDIM (0.16 ± 0.01). These findings align with those of Salem and Hammoud (2019), who reported a lower heritability estimate of 0.137 ± 0.09 for LTDIM in Holstein-Friesian cattle. Similarly, Dash et al. (2018) observed a low heritability estimate of 0.10 ± 0.08 for production life in Karan Fries cattle. Furthermore, Dash et al. (2016) reported a heritability estimate of 0.13 ± 0.06 for FDIM in Karan Fries cattle. Meanwhile, Tamilarasan et al. (2024) in composite Vrindavani cattle reported moderate heritability

estimate for FDIM (0.229 ± 0.044). The low heritability values observed in this study for both first and lifetime lactation lengths suggest that these traits are predominantly influenced by non-genetic factors, as evidenced by the lower genetic to environmental variance ratios. The heritability estimates for dry period traits in this study were also relatively low, with values of 0.12 ± 0.03 for FDP and 0.10 ± 0.03 for LTDP. These findings suggest that the majority of the variation in dry period traits is due to environmental factors, indicating that improvements in environmental conditions, such as nutrition and management practices, could lead to notable changes. Kumar et al. (2015) reported similarly low heritability estimates for dry period in Frieswal dairy cattle

(0.009). Şahin et al. (2014) observed low heritability for lactation and dry periods in Brown Swiss cattle, with estimates of 0.10 and 0.06, respectively. Generally, the heritability of lactation length and dry period in dairy cattle is lower than that of many other economically significant traits, such as LTMY and LTSMY (Şahin et al., 2014). This suggests that direct selection to enhance these traits may not be efficient. Instead, genetic progress for these traits is more effectively achieved through indirect selection based on correlated responses when selecting for other associated traits (Alhammad et al., 2008).

In contrast; variance components for first and lifetime milk production showed relatively high additive genetic variance (σ^2_a), resulting in moderate heritabilities for these traits. The heritability estimates for FLMY, FLSMY, LTMY, and LTSMY were moderate, at 0.26 ± 0.05 , 0.24 ± 0.06 , 0.31 ± 0.07 , and 0.27 ± 0.06 , respectively. These values suggest

that genetic improvement of lifetime milk traits can be achieved through selective breeding. The present results are consistent with those of Dash et al. (2016), who reported moderate heritability estimates for FLMY and FLSMY of 0.26 and 0.25, respectively, which are similar to the estimates in this study. Additionally, Sadek et al. (2009) reported moderate heritability estimates for LTMY (0.29) and FLMY (0.21) in Holstein cattle. Salem and Hammoud (2019) working on Friesian cattle in Egypt found a moderate heritability estimate of 0.272 ± 0.018 for LTMY. In contrast, Alhammad et al. (2008) and Dash et al. (2016) reported lower heritability estimates for LTMY (0.12 ± 0.05) and higher estimates for FLSMY (0.39 ± 0.09). Also, Ward et al. (2018) reported lower heritability estimates of 0.18 for LTMY. The discrepancies in heritability estimates between studies may be attributed to differences in breed, sample sizes of data, and statistical models used in the analyses.

Table 2. The estimates of variance component and genetic parameters lifetime production traits in Friesian dairy cattle

Items*	σ^2_a	σ^2_e	σ^2_p	h^2
FDIM, days	13997.33	68339.92	82337.25	0.17±0.02
FLMY, kg	2506845	7134866	9641711	0.26±0.05
FLSMY, kg	2602827	8242285	10845112	0.24±0.06
FDP, days	815.56	5980.79	6796.36	0.12±0.03
LTDIM, days	79893.64	419441.6	499335.2	0.16±0.01
LTMY, kg	21135710	47043999	68179709	0.31±0.07
LTSMY, kg	17991117	48642649	66633766	0.27±0.06
LTDP, days	3666.32	32996.90	36663.22	0.10±0.03

*, See abbreviations in Table 1; σ^2_a , additive genetic variance; σ^2_e , residual variance; σ^2_p , phenotypic variance; h^2 , heritability.

Genetic and phenotypic correlation:

Table 3 presents the genetic and phenotypic correlations between lifetime production traits in Friesian dairy cattle in Egypt. Generally, genetic correlation coefficients were slightly higher than the corresponding phenotypic correlations. The estimates of genetic correlation provided insights into the degree to which these traits were affected by the same set of genes (Dash et al., 2018). This study identified a notably high genetic correlation between FDIM and FLMY (0.834), as well as between FLMY and FLSMY (0.668), what in general agreement

with the findings of Sahin et al. (2012) and Tamboli et al. (2022). The genetic correlation of FDIM exhibited negative relationships with all lifetime production traits except for LTDIM and LTDP, which displayed positive associations ($r=0.244$ and 0.013 , respectively). Significant positive genetic and phenotypic correlation coefficients were found among lifetime production traits, ranging from 0.972 (LTDIM-LTSMY) to 0.870 (LTMY-LTDP) for genetic correlation and from 0.819 (LTDP-LTMY) to 0.936 (LTMY-LTDIM) for phenotypic correlation.

Table 3. Genetic correlations (below diagonal) and phenotypic correlations (above diagonal) lifetime production traits in Friesian dairy cattle

Items*	FDIM, days	FLMY, kg	FLSMY, kg	FDP, days	LTDIM, days	LTMY, kg	LTSMY, kg	LTDP, days
FDIM, days	---	0.798	0.108	0.130	0.211	-0.240	-0.072	0.006
FLMY, kg	0.834	---	0.577	-0.033	0.167	0.277	0.143	0.018
FLSMY, kg	0.127	0.668	---	-0.519	0.121	0.296	0.278	0.023
FDP, days	0.196	0.056	-0.006	---	-0.021	-0.083	-0.094	0.119
LTDIM, days	0.244	0.202	0.150	-0.019	---	0.936	0.903	0.875
LTMY, kg	-0.193	0.331	0.335	-0.023	0.945	---	0.899	0.819
LTSMY, kg	-0.032	0.205	0.315	-0.047	0.972	0.970	---	0.908
LTDP, days	0.013	0.021	0.037	0.154	0.879	0.874	0.920	---

*, See abbreviations in Table 1

This positive genetic correlation between traits implies that selecting for improvement in one trait can lead to enhancements in another trait as a correlated response. The present findings correspond with former research studies (Alhammad et al., 2008; Khattab et al., 2009; Sahin et al., 2014; Dash et al., 2016). Also, El-Saied (2008) noted significant correlations among lifetime traits (productive life and herd life) and lifetime milk production (ranging from 0.92 to 0.97) in Holstein Friesian cattle in Egypt. The results of this study suggest that older cows also tend to have higher genetic potential as high producers. Furthermore, cows with extended herd life exhibit a genetic advantage in terms of lifetime performance traits. Interestingly, positive correlation coefficients were observed between FLMY and all lifetime milk production traits under investigation, with correlation coefficients varied between 0.021 and 0.331. Similarly,

FLSMY displayed positive correlation coefficients with all first and milk production traits, except for a negative correlation coefficient detected with FDP ($r=-0.006$). The genetic correlation between first lactation performance and lifetime traits suggests that these traits may be influenced by similar genes and cellular pathways (Seno et al., 2007; Barros et al., 2016; Ramadan, 2018). With regard to FDP, negative correlation coefficients were observed between this trait and all lifetime traits, except for a positive correlation coefficient with LTDP ($r=0.154$). The negative genetic and phenotypic correlations between lactation length and the dry period suggest that cattle with shorter dry periods tend to have longer lactation periods.

Breeding values:

Table 4 presents estimates for predicting breeding values across sires and their accuracies for first and lifetime

production traits. Breeding companies and farmers heavily depend on selection indices to pinpoint sires that are anticipated to improve the profitability of the production system (Lopez-Villalobos et al., 2019). The breeding value denotes the overall genetic capacity of an animal for a specific trait, representing its worth in a breeding program. Practically,

breeders seek insights into the anticipated performance levels of progeny from particular individuals (Salem and Hammoud, 2016). In this study, expected breeding values of sires exhibit a wide range for FLMY, FLSMY, LTMY, and LTSMY, with values of 1237.04 kg, 1046.62 kg, 3134.94 kg, and 2869.25 kg, respectively.

Table 4. Minimum, maximum, accuracy, and range of sire's breeding values for first lactation and lifetime production traits in Friesian dairy cattle.

Traits*	Minimum	Accuracy	Maximum	Accuracy	Range
FDIM, days	-59.73	51.23	32.56	54.11	92.29
FLMY, kg	-510.86	74.16	726.18	77.69	1237.04
FLSMY, kg	-474.70	81.34	571.92	78.92	1046.62
FDP, days	-9.92	41.25	14.47	46.10	24.39
LTDIM, days	-47.02	51.37	46.89	49.99	93.91
LTMY, kg	-1269.84	84.61	1865.10	88.37	3134.94
LTSMY, kg	-1359.20	81.01	1510.05	79.82	2869.25
LTDP, days	-22.68	41.26	41.96	39.91	64.64

*, See abbreviations in Table 1

The present results corresponded with former studies observed wide ranges for lifetime production traits in Friesian cattle in Egypt (Khattab et al. 2009; Salem and Hammoud, 2019). Consequently, the selection of sires for the upcoming generation is poised to drive notable genetic enhancements within these herds. Furthermore, the increased accuracy of sire breeding value estimates for the mentioned traits might be attributed to a larger number of daughters per sire. Salem and Hammoud (2016) highlighted that the substantial ranges of expected breeding values for milk production traits are reasonable, given the inclusion of high-producing animals in the herd formation process. However, this strategy could encounter a challenge as high-producing cows often exhibit reduced fertility traits.

CONCLUSION

The moderate heritability estimates of first and lifetime milk production traits suggested that improving these traits may be achievable through selective breeding. On the other hand, improvements in the lactation period and dry period may rely more on optimizing environmental and managerial practices due to their lower heritability estimates. Furthermore, the strong positive genetic correlation observed between first lactation and lifetime milk production traits indicates a shared genetic control, implying that advancements in these traits can be concurrently pursued through selective breeding practices. Also, this study underscores the importance of assessing fertile sires based on their genetic breeding values and prioritizing those with the highest positive breeding values for selection.

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التقييم الوراثي لصفات الحليب في الموسم الأول وخلال العمر الإنتاجي في أبقار الفريزيان في مصر

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المخلص

لقد تم دراسة طول العمر الإنتاجي لماشية اللبن على نطاق واسع، ومع ذلك فهي لا تزال موضوعاً قيد البحث النشط نظراً لآثارها الكبيرة على اقتصاديات المزرعة. الهدف من هذه الدراسة تقييم المعايير الوراثية لصفات الحليب في الموسم الأول وخلال العمر الإنتاجي في أبقار الفريزيان في مصر من أجل تحديد سبل التحسين الوراثي في هذه الصفات. تم استخدام 2837 سجل إنتاج لعدد 1243 بقرة نتاج ل 835 أم و 108 أب خلال الفترة من عام 2000 حتى عام 2015 من قطيعين لأبقار الفريزيان بمحطتي بحوث سخا والقرضة التابعين لمعهد بحوث الإنتاج الحيواني، مصر. بلغت تقديرات المكافئ الوراثي 0.17 و 0.26 و 0.24 و 0.12 و 0.16 و 0.31 و 0.27 و 0.10 لأيام الحليب في الموسم الأول وإنتاج الحليب الكلي في الموسم الأول وإنتاج اللبن المعدل عند 305 يوم في الموسم الأول وطول فترة الجفاف الأولى وعدد أيام الحليب خلال العمر الإنتاجي وإنتاج اللبن الكلي خلال العمر الإنتاجي وإنتاج اللبن المعدل عند 305 يوم خلال العمر الإنتاجي وطول فترات الجفاف خلال العمر الإنتاجي. كان هناك ارتباط وراثي موجب بين جميع صفات العمر الإنتاجي. أيضاً كان هناك ارتباط وراثي موجب بين صفات إنتاج اللبن خلال العمر الإنتاجي وبين كلا من إنتاج اللبن الكلي وإنتاج اللبن المعدل عند 305 يوم خلال الموسم الأول. في الخاتمة، من خلال تقديرات المكافئ الوراثي المتوسطة لصفات إنتاج اللبن خلال العمر الإنتاجي وخلال الموسم الأول يمكن تحسين هذه الصفات وراثياً عن طريق الانتخاب. الإرتباط الوراثي الموجب بين إنتاج اللبن في الموسم الأول وخلال العمر الإنتاجي يشير إلى وجود تأثير وراثي مشترك، مما يشير إلى أنه يمكن تحسين هذه الصفات في وقت واحد من خلال الانتخاب المبكر في الذكور.

الكلمات الدالة: إنتاج الحليب في الموسم الأول، الأداء خلال العمر الإنتاجي، التقييم الوراثي، الماشية الفريزيان.