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Genetic And Phenotypic Evaluation of Lactation Curve Parameters for Holstein Cattle in Egypt

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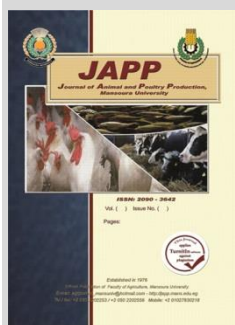


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ABSTRACT

This study examined lactation curve parameters and their genetic relationships in Holstein cows using 1,684 test-day milk yield records collected from 2017 to 2019 in Fayoum Governorate, Egypt. Wood's gamma function modeled lactation curves. Overall means for test-day milk yield (TDMY), initial yield (a), ascending phase (b), descending phase (c), persistency (P), days to peak yield (PY), and maximum yield (Ymax) were 25.98 kg, 12.72 kg, 0.401 kg, 0.008 kg, 6.76 kg, 50.12 days, and 29.43 kg, respectively. Heritability estimates ranged from 0.14 (persistency) to 0.36 (ascending phase), while TDMY, initial yield, and maximum yield showed moderate heritability's values (0.26, 0.23, and 0.29, respectively). Strong positive genetic correlations were found between TDMY and Ymax (0.97), and TDMY and persistency (0.79). Initial yield showed negative genetic correlations with ascending slope (-0.39) and days to peak milk (-0.64). The rate of milk yield increase (b) negatively correlated with persistency. Days to peak milk (PY) positively correlated with ascending slope (0.77) and negatively with descending slope (-0.55). These findings provide insights into the genetic control of lactation curve parameters in Holstein cows, offering potential for genetic improvement through selective breeding and developing effective strategies to enhance milk production efficiency and persistency in Egyptian dairy herds.

Keywords: Holstein cows, lactation curve, Wood's function, heritability, genetic correlations, test-day milk yield, persistency.



INTRODUCTION

The dairy industry is vital to Egypt's agricultural sector and economy, with milk yield significantly impacting farm income in developing countries (Bakri *et al.*, 2022). As the demand for dairy products continues to rise primarily driven by rapid population growth, there is an increasing need to improve the productivity and efficiency of dairy cattle (Njuki, 2022). In this regard, Holstein cattle, known for their high milk yield, have become a popular breed in Egyptian dairy farms. However, to maximize their potential in the local environment, it is essential to understand and optimize their lactation performance.

In the realm of milk performance analysis, researchers recognize the importance of examining not only overall milk yield but also the unique lactation patterns of individual cows (Innes *et al.*, 2024). To achieve this comprehensive understanding, mathematical models have become indispensable tools. Among these, the Wood model stands out as a particularly influential parametric mathematical model for describing lactation curves (Wood, 1967; Bouallegue and M'hamdi, 2020). Its widespread adoption stems from its ability to capture the essential characteristics of lactation activity: initial milk yield at the onset of lactation, the increase in production leading to peak lactation, and the subsequent decline in milk output. The Wood model's utility extends beyond mere description, offering valuable insights for dairy cow health monitoring, genetic evaluation, feeding strategy optimization, and economic analysis within the dairy industry (Bouallegue *et al.*, 2013).

By providing a quantitative framework for lactation dynamics, this model empowers dairy professionals to make

informed decisions about herd management and breeding programs, ultimately contributing to more efficient and productive dairy farming practices. The integration of such mathematical models into dairy science represents a significant step forward in combining rigorous analytical approaches with practical applications, enhancing our understanding of milk production and supporting the continued advancement of the dairy sector (Shamsuddoha *et al.*, 2023). Moreover, lactation curves serve as valuable tools in dairy animal management and breeding programs. These curves facilitate early milk yield predictions, enabling farmers to make informed decisions about culling low-producing animals. Additionally, they aid in resource allocation, allowing for more efficient planning of feed and farm resources (Cole *et al.*, 2023).

In the realm of genetic improvement, lactation curves contribute to a more accurate ranking of sires by utilizing their daughters' incomplete records. Furthermore, the ability to forecast milk output based on partial lactation data empowers farmers to make timely decisions regarding the retention or culling of cows. This approach enhances overall herd productivity and economic efficiency in dairy operations (Bermejo *et al.*, 2020; Lee *et al.*, 2020 and Mohamed *et al.*, 2021). Additionally, genetic analysis of lactation curve traits offers potential for improving cattle productivity through selective breeding. Understanding the heritability and genetic correlations of these traits is crucial for developing effective genetic evaluation and breeding programs (Moradi Shahrabak, 2001). This study employs the incomplete gamma function to model lactation curves in cows, aiming to estimate heritability and explore genetic and phenotypic

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correlations among key lactation parameters (a, b, c, Ps, PY, and Ymax/kg). In our study, we investigate the relationship between these curve characteristics and test-day milk yield (TDMY). By providing a comprehensive analysis of lactation patterns and their genetic basis, this research seeks to inform breeding strategies for optimizing milk production efficiency and advancing dairy cattle genetics.

MATERIALS AND METHODS

Dataset: This study analyzed test-day milk yield (TDMY) records obtained from 1,684 Holstein cows, collected monthly between 2017 and 2019. The data originated from the El-Lahhamy farm, operated by the Association of Livestock Development, situated approximately 30 km west of Fayoum Governorate, Egypt.

The research protocol received approval from the Fayoum University Institutional Animal Care and Use Committee (FU-IACUC) (AEC 2422). TDMY measurements followed an alternating morning-evening monthly recording scheme, with milking conducted twice daily at 7 am and 4 pm throughout the lactation period. The analysis employed an animal model that accounted for all known relationships among individuals in the herd. The dataset used in this study shown in Table 1 represents a sufficient sample size for analyzing lactation curves and genetic parameters in Holstein cows. With 1,684 test day records, the study likely has sufficient statistical power to detect meaningful patterns and relationships in milk production traits. The pedigree structure, including 947 animals and 105 sires, suggests a diverse genetic background which is beneficial for estimating genetic parameters such as heritability's values and genetic correlations. The presence of both base and non-base animals in the pedigree allows for the consideration of ancestral relationships in genetic evaluations.

Table 1. Structure of test day data analyzed for Holstein cow.

Item	Records number
Base animals number	768
Non-base animals number	179
Animals total number	947
Sires number	105
Dams numbers	434
Total number of lactation animals	1684

Estimating the curve parameters of milk yields:

To analyze the lactation curves of Holstein cows in this study, we utilized the gamma-type function proposed by Wood (1967), which has been shown to effectively model extended lactations (Abdel-Salam *et al.*, 2011). This function is expressed as:

$$Y_n = a n^b e^{-cn}$$

Where Y_n represents the test-day milk yield (kg) in the n^{th} month of lactation, 'a' indicates initial yield, 'b' describes the rate of yield increase to peak, and 'c' denotes the rate of yield decrease post-peak. The constants a, b, and c were determined using the general linear model (GLM) procedure in SAS software (SAS, 2014).

We employed the NLIN procedure in SAS to fit the gamma-type function to our data. Subsequently, we calculated additional lactation parameters as follows:

- Persistency of lactation: $P = -(b+1) \ln(c)$
- Days in milk (DIM) at peak yield: $PY = b/c$
- Maximum production during lactation: $Y_{max} = a(b/c)^b e^{-b}$

Genetic analysis for lactation curve parameters:

In our research, we employed a multi-trait repeatability animal model to evaluate various components of lactation curves. This approach allowed us to estimate variance and covariance elements, including:

- Direct additive genetic effects
- Permanent environmental
- Error components
- Phenotypic components

Additionally, we calculated heritability's values for the traits of interest. The analysis was conducted using the VCE6 software package (Groeneveld *et al.*, 2010).

$$Y_{ijklmno} = \mu + A_i + P_{e_j} + HTD_k + Y_{e_l} + P_{a_m} + S_n + b(A) + e_{ijklmno}$$

As: $Y_{ijklmno}$ denotes the observed trait, encompassing measures such as daily milk yield, initial production, lactation curve phases, persistency, peak timing, and maximum yield. The overall mean is represented by μ . A_i signifies the random additive genetic effect specific to each cow, assumed to follow a normal independent distribution (NID) with a mean of 0 and variance σ^2_a . The random permanent environmental effect, P_{e_j} is also assumed to be normally and independently distributed with a mean of 0 and variance σ^2_{pe} . HTD_k represents the fixed effect of the k^{th} herd-test-day, while Y_{e_l} denotes the fixed effect of the l^{th} year of calving. P_{a_m} accounts for the fixed effect of the m^{th} parity, and S_n indicates the fixed effect of the n^{th} season of calving. The covariate for days in milk is represented by $b(A)$. Lastly, $e_{ijklmno}$ signifies the random residual term associated with each observation, capturing unexplained variation in the model.

The repeatability animal model employed in our analysis can be expressed in matrix notation as follows:

$$y = Xb + Za a + Zc c + e$$

The vector y encompasses lactation observations. X is the matrix linking fixed effects to y , while b is a vector that includes the overall mean and fixed effects. These fixed effects comprise herd test day, parity, calving year and season, and days in milk (as a covariate). Za serves as the matrix connecting direct additive genetic effects to y . The vector a represents these random direct additive genetic effects, associated with Za . Zc is the matrix relating permanent environmental effects, and c is the corresponding vector of these effects, linked to Zc . The vector e denotes random residual effects, following a normal distribution $N(0, I\sigma^2_e)$, where I represents an identity matrix.

RESULTS AND DISCUSSION

Test-day milk curve parameters

The overall means of TDMY, a, b, c, P, PY, and Y_{max} were 25.98 kg, 12.72 kg, 0.401 kg, 0.008 kg, 6.76 kg, 50.12 day, and 19.53 kg, respectively. The results obtained for TDMY in the present study were notably higher than those reported by Boujenane and Hilal (2012) and Sanad and Gharib (2022). Regarding the initial milk yield (a), our findings surpassed those documented by Yilmaz *et al.* (2011) and Sanad and Gharib (2022), while remaining below the values reported by Farhangfar and Rowlinson (2007) and Boujenane and Hilal (2012).

Concerning the rate of increase to reach peak production during the ascending phase (b), the rate of decrease (c), and days in milk to peak (PY), our results were higher than those presented in the study of Boujenane and

Hilal (2012), yet lower than the findings reported by Sanad and Gharib (2022) and Bakri *et al.* (2022). It is worth noting that the persistency value obtained in our study (6.76) is closely aligned with that reported by Boujenane and Hilal (2012). Furthermore, our observed persistency exceeded that found in the study of Farhangfar and Rowlinson (2007). The peak yield observed in our research was higher than those reported by some previous studies on Holstein cows (Gradiz

et al., 2009; Bakri *et al.*, 2022), while aligning closely with the findings presented by Farhangfar and Rowlinson (2007). It is important to acknowledge that variations in production characteristic traits may be attributed to a combination of factors, including management practices, dietary regimens, climatic conditions, and genetic influences (Fleischer *et al.*, 2001; Macciotta *et al.*, 2006).

Table 2. Means, standard error (SE), minimum (min.) and maximum (max.) for test-day milk curve parameters of Holstein cows.

Item	Mean	Standard error	Minimum	Maximum
Test day milk yield (TDMY), kg	25.98	3.14	4.5	45.0
Initial milk yield (a), kg	12.72	1.87	5.13	19.07
Ascending slope yield (b), kg	0.401	0.03	0.121	0.692
Descending slope yield (c), kg	0.008	0.01	0.001	0.014
Persistency (P), kg	6.76	0.11	5.13	11.91
Days in milk to peak (PY), day	50.12	0.15	31.6	72.14
Maximum milk production (Ymax), kg	29.43	2.85	14.65	47.58

Variance components and heritability estimates:

The variance components and heritability estimates presented in Table 4 provide valuable insights into the genetic and environmental factors influencing milk production traits in Holstein cattle. Test-day milk yield (TDMY), initial milk yield (a), and maximum production of milk (Ymax) demonstrate moderate heritability's values of 0.26, 0.23, and 0.29, respectively, indicating significant potential for genetic improvement through selective breeding.

Among lactation curve parameters, the ascending slope (b) exhibits the highest heritability of 0.36, suggesting that the rate of increase in early lactation milk production is strongly influenced by genetics. In contrast, the descending slope (c) and persistency (P) show lower heritabilities of 0.17 and 0.14, respectively, indicating a greater influence of environmental factors on these traits.

Table 3. Variance components and heritability estimates for test-day milk traits as well as lactation curve parameters for Holstein cows.

Milk trait	σ^2_a	σ^2_{pe}	σ^2_e	σ^2_p	$h^2 \pm SE$
TDMY	1.294	3.528	0.09	4.912	0.26±0.03
a	0.552	1.702	0.14	2.394	0.23±0.03
b	0.045	0.066	0.015	0.126	0.36±0.04
c	0.019	0.064	0.03	0.113	0.17±0.03
P	0.813	4.934	0.14	5.887	0.14±0.03
PY	48.670	709.893	0.10	758.663	0.06±0.004
Ymax	4.816	13.007	0.87	18.693	0.29±0.04

σ^2_a = direct genetic variance; σ^2_{pe} = random permanent effect variance; σ^2_e = residual variance; σ^2_p = phenotypic variance; h^2_a = direct heritability. TDMY= Test day milk yield; a= Initial milk yield; b= Ascending slope (Yield); c= Descending slope (Yield); P= Persistency (Yield); PY= Days in milk to peak (Days); Ymax= Maximum milk production during lactation (Yield).

Our estimates of heritability for Wood's function parameters (a, b, c) were lower than those reported by Sanad and Gharib (2022), and higher than those obtained by Yilmaz *et al.* (2011). The persistency heritability estimate (0.14) aligns with findings by Rekaya *et al.* (2000), who used various indices across different dairy cow breeds in multiple countries. However, this estimate is considerably higher than that stated by Boujenane and Hilal (2012) in Holstein cows.

Heritability estimates for TDMY and Ymax were comparable to those reported by Sanad and Gharib (2022) and substantially higher than those reported by Boujenane and Hilal (2012). The variations in heritability estimates between the present work and previous research may be attributed to differences in models employed, breeds studied, and the environmental and genetic factors affecting various parameters

Table 4. The additive genetic correlations estimates and their standard errors (SE) (upper off-diagonal), and phenotypic correlations (lower off-diagonal) for TDMY and the lactation curve parameters in Holstein cows.

Milk yield	TDMY	a	b	c	P	PY	Ymax
TDMY	-	0.37±0.002	-0.22±0.009	-0.22±0.009	0.79±0.002	0.72±0.001	0.97±0.009
a	0.50	-	-0.39±0.009	-0.38±0.003	0.46±0.001	-0.64±0.009	0.76±0.001
b	-0.34	-0.75	-	0.35±0.001	-0.51±0.002	0.77±0.002	0.19±0.003
c	-0.17	-0.31	0.40	-	-0.29±0.004	-0.55±0.003	-0.27±0.001
P	0.49	0.54	-0.78	-0.21	-	0.84±0.005	0.69±0.005
PY	0.31	-0.42	0.33	-0.05	0.48	-	0.73±0.009
Ymax	0.87	0.19	0.11	-0.04	0.47	0.31	-

TDMY= Test day milk yield; a= Initial milk yield; b= Ascending slope (Yield); c= Descending slope (Yield); P= Persistency (Yield); PY= Days in milk to peak (Days); Ymax= Maximum production of milk during lactation (Yield).

Test Day Milk Yield (TDMY) emerges as a central trait, showed strong positive genetic correlations with persistency (0.79) and maximum milk production (Ymax) (0.97), indicating that cows with higher daily milk yields tend to maintain their production levels throughout lactation and achieve higher peak yields. This relationship is further supported by the moderate positive genetic correlations

between TDMY and both initial milk yield (0.37) and days to peak milk (0.72). However, Boujenane and Hilal (2012) reported this correlation as unity, differing from these findings. The observed interrelationships among the examined traits (DMY, PS, and Ymax) indicate that breeding programs targeting these characteristics may indirectly enhance other attributes through associated responses. This

pattern is consistent with findings from diverse studies, including those on Egyptian buffalo (Amin *et al.*, 2019) and Holstein cattle (Pangmao *et al.*, 2022), as well as earlier research by Yilmaz *et al.* (2011).

Initial milk yield (parameter a) shows strong positive genetic correlations with Ymax (0.76) and moderate positive correlations with persistency (0.46). However, it exhibits negative genetic correlations with the ascending slope (b) (-0.39) and days to peak milk (-0.64). This aligns with findings from Macciotta *et al.* (2006) and Amin *et al.* (2019) but differs from Boujenane and Hilal (2012).

An inverse relationship between parameters a and b suggests that cows with greater initial production tend to exhibit a more gradual rise to peak lactation (Chegini *et al.*, 2015). Furthermore, research by Moradi Shahrabak (2001) proposes that focusing breeding efforts on early lactation yield could result in more consistent milk production curves and expedited peak yield attainment. Our findings on the genetic (0.35) and phenotypic (0.40) correlation between parameters b and c contrast with previous studies. Unlike Boujenane and Hilal (2012) and Macciotta *et al.* (2006), we didn't observe that rapid-peaking cows experienced faster post-peak declines. The inverse relationship between lactation persistency and the rate of yield increase (b) suggests that emphasizing sustained production might slow the ascent to peak yield. These observations align with earlier reports by Tekerli *et al.* (2000) and more recent findings in Egyptian buffalo by Amin *et al.* (2019).

Days to peak milk (PY) shows interesting relationships with other traits. Its strong positive genetic correlation with the ascending slope (0.77) and negative correlation with the descending slope (-0.55) suggest that cows reaching peak production later often have steeper increases in early lactation but also experience more rapid declines afterwards. The genetic correlations between parameter c and both PY and persistency (-0.55 and -0.29, respectively) suggests that selection for maximum yield early in lactation could enhance persistency by reducing the decrease rate after peak yield. This in agree with results reported by Chegini *et al.* (2015) and Amin *et al.* (2019) in Egyptian buffalo.

CONCLUSION

Our investigation on the parameters of lactation curve in Holstein cattle reveals significant genetic variation in key milk production traits. Moderate heritability's values for test-day milk yield, initial yield, and maximum yield indicate potential for genetic improvement through selective breeding. Strong positive genetic correlations between daily milk yield, persistency, and maximum yield suggest that selecting for higher daily production could improve lactation persistency and peak yield. These findings have important implications for dairy breeding programs in Egypt and similar environments, enabling breeders to develop more effective strategies to enhance milk production efficiency and persistency.

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التقييم الوراثي والمظهري لمعايير منحى اللبن لماشية الهولشتاين في مصر

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المخلص

هدفت الدراسة الحالية إلى تقدير معايير منحى الحليب وعلاقتها الوراثية في أبقار الهولشتاين باستخدام 1,684 سجل إنتاج حليب يومي تم جمعها من 2017 إلى 2019 في محافظة الفيوم، مصر. تم استخدام دالة وود (جاما) لنمذجة معايير منحى الحليب. كانت المتوسطات الإجمالية لإنتاج الحليب اليومي (TDMY)، والإنتاج الأولي من الحليب (a)، ومرحلة الصعود (b)، ومرحلة الهبوط (c)، والمثابرة (P)، وعدد الأيام حتى ذروة الإنتاج (PY)، والإنتاج الأقصى من الحليب (Ymax هي 25,98 كجم، 12,72 كجم، 0,401 كجم، 0,008 كجم، 6,76 كجم، 50,12 يوم، و 29,43 كجم على التوالي. تراوحت تقديرات المكافئ الوراثي من 0,14 (للمثابرة) إلى 0,36 (لمرحلة الصعود)، مع إظهار إنتاج الحليب اليومي والإنتاج الأولي من الحليب والإنتاج الأقصى من الحليب لوراثية متوسطة (0,29، 0,23، 0,26). وُجدت ارتباطات وراثية إيجابية قوية بين إنتاج الحليب اليومي والإنتاج الأقصى (0,97)، وبين إنتاج الحليب اليومي والمثابرة (0,79). أظهر الإنتاج الأولي ارتباطات وراثية سلبية مع مرحلة الصعود (-0,39) وعدد الأيام حتى ذروة إنتاج الحليب (-0,64). ارتبط معدل زيادة إنتاج الحليب (b) سلبياً مع المثابرة. ارتبط عدد الأيام حتى ذروة إنتاج الحليب (PY) إيجابياً مع مرحلة الصعود (0,77) وسلبياً مع مرحلة الهبوط (0,55). توفر هذه النتائج رؤى حول التحكم الوراثي في معايير منحى الحليب في أبقار الهولشتاين، مما يتيح إمكانية التحسين الوراثي من خلال الانتخاب وتطوير استراتيجيات فعالة لتعزيز كفاءة إنتاج الحليب واستمراره في قطاع الألبان المصرية.