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GENETIC CHANGES FOR DAILY MILK YIELD AND MILK CONTENTS IN EGYPTIAN BUFFALO BULLS

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SUMMARY

Predicting the characteristics of buffalo milk lactation curves is more important for sustaining the genetic diversity in Egyptian native populations. The Wood's function was fitting for individual test-day records over the entire range of calving, from 1999 to 2021, in three experimental buffalo herds at the Animal Production Research Institute of the Agricultural Research Center. Wood's daily milk yield (WM), daily peak milk yield (PM), days to peak milk yield (DP), persistency (PS), fat percentage (FP), and protein percentage (PP) were estimated using the best linear unbiased prediction (BLUP) approach for predicting daily genetic values of the studied bulls. Genetic changes for the studied traits were obtained as the regressing the average estimated daily breeding values (EDBVs)of bulls on birth year of their daughters over three generation interval for assessing the genetic progress. The average EDBVs for the investigated traits were found to be lower and insignificant. EDBVs varied from -0.30 to 0.31 for WM, -0.23 to 0.19 for PM, -0.14 to 0.25 for PS, -2.5 to 6.63 for DP, -0.56 to 0.09 for FP, and -0.44 to 0.21 for PP over the three separated lactations. Chiefly, bulls' genetic responses are either positive or negative and insignificant over the study period. These findings suggested implementing sustained straight-breeding schemes for the experimental native Egyptian buffalo populations.

Keywords: Egyptian native buffalo, Test-day records, Wood's function, genetic progress, sustained straight-breeding schemes

INTRODUCTION

The Egyptian River buffaloes (*Bubalus bubalis)* are mainly reared for milk production with the global aim of promoting economic efficiency, which is one of the major reasons for maintaining genetic diversity. They were classified as endangered, using alternative foreign germplasm (cross-breeding) to improve production without scientific guidance from small holders. Moreover, breeding decisions using the available phenotypic data for ranking individual animals on their estimated daily breeding values (EDBVs) and for measuring the genetic progress which can be early predictors of genetic merit towards reducing the generation interval, which result in increasing the amount of genetic gain (Ashmawy, 1990).

Consequently, using longitudinal information along the trajectory can help in determining the shape of milk lactation curve based on measures derived from lactation specific variables such as peak yield, and persistency on a limited number of TD records during lactation (Wood, 1967; Olds *et al*., 1979, and Ptak and Schaeffer, 1993). Previous studies have focused mostly on characterizing the lactation curves of various species using Wood's function (1967). According to Rekaya *et al*. (2000), the Wood's model has the benefit of providing a small set of parameters with an evaluated direct connection to the main characteristics of individual lactation curves. Samak *et al*. (1988), and Mansour *et al*. (1993) mentioned that Wood's function of Egyptian buffalo data showed greater flexibility than other methods for predicting milk yield lactation curves.

Additionally, El-Bramony *et al*. (2016) fit Wood's function on other data in Egyptian buffalo populations and, based on certain criteria, predict the same trend. Similarly, Lazaro *et al*. (2024) stated that Wood's function was the most appropriate model to predict lactation curve patterns in Murrah dairy buffaloes.

The available knowledge to fit Wood's equation of test-day records (TDR) for milk yield in the experimental Egyptian buffalo stations is relatively limited. Based on all these considerations, we aim to use Wood's model to fit daily milk yield (WM), and to predict its derived variables in terms of peak milk yield (PM), days to peak milk yield (DP), and persistency (PS). This information and milk constituents; in terms of fat and protein percentage, were used to explore their implications on the subsequent predicating of estimated daily breeding values in bulls and for investigating the genetic progress from the base birth year of 1995 to 2013 of their daughters in the first three lactations.

MATERIALS AND METHODS

Data set:

Data on test-day milk yield and its percentages of the fat and protein records were collected at monthly intervals over the period between 5 and 305 days in milk (DIM) and were classified according to DIM into eleven classes (DIM1 to DIM11). Buffaloes with less than three TDR / lactation were excluded from the data file to insure better estimation of the typical lactation curve. Days in milk 10 classes starting with one for DIM between five and after 305-d were discarded from the data set.

All records of buffaloes whose bulls had less than two daughters were removed, and calving between 1995 and 2013 in three experimental herds utilized in this study are purebred herds and, under hygienic conditions, belonged to the Animal Production Research Institute (APRI), Agricultural Research Center. Moreover, lack test-day recording for economical daily milk yield traits (milk, fat and protein) has made it difficult to construct the complete lactation curve (typical). Lactating buffaloes were milked once or twice a day throughout the lactation period by either humans or machinery. Fat and protein percentages were measured by the automated method of infrared absorption spectrophotometry (Milk-o-Scan); at the Dairy Services Unit, APRI, Sakha, Kafr El-Sheikh Governorate. Lactating buffaloes were milked once or twice daily during the lactation period by machine or hand. Morning and evening milk yields were recorded and composite samples of the two milking were taken to determine fat and protein percentages. More detailed consideration of the dataset and management of this experimental buffalo herd was conducted by EL-Bramony *et al.* (2017). Data were classified according to the month of calving into two seasons: hot (April through September) and mild (October to March). Structure of the data file for daily milk yield of lactations from one to three are presented in Table1.

Table1. Structure of the dataset

Item	Full data
TDMR[1], no.	8529
TDMR/typical lactation curves, no.	7688
Lactations with typical curve, no.	3
TDMR / lactation, mean	5.2
Herd, no.	3
Buffaloes with records, no.	913
Days in milk classes, no.	11
Bull, no.	160
Years of birth of buffaloes	1995 to 2013
Years of calving of buffaloes	1999 to 2021

[1]TDMR: test-day milk records.

Wood's *model fit:*

The Wood's model was used to fit daily milk yield on day time of lactation, the following nonlinear form:

$$\mathbf{Yt = at^{b} exp^{-ct}}, \{1\}$$

Where Y_t is the expected daily milk yield in DIM t, a is a scalar factor, b is related to the rate of increase prior to the peak and c is related to the rate of decrease after the peak. The day at peak production was defined as tmax=b/c, which means that b and c are parameters that define the pre-peak and postpeak slope of the curve, respectively. Peak values are independent of a, which represents a scale factor and "exp" is the constant refers to the natural exponential function.

Daily milk yield can be fitted of nonlinear Wood's model for each lactating buffaloes by Quasi-Newton iteration method and the convergence criterion has a precision of 5×10−5 as follows using of SAS version 9.0 (SAS Institute Inc.2004). The parameters of Wood' model were used to compute lactation curve characteristics namely peak milk yield (PM = a $(b/c)e^{(-b)}$), days to peak (DP = b/c) and persistency (PS = -(b+1)ln (c). As an alternative, the compound symmetry structure (CS), usually adopted in repeated measures design (Littel, 1998), was imposed to R in order to estimate the average TD variance and the mean correlation among TD pairs within lactation. The adjusted R-square is used to evaluate typical lactation curves with ≥ 0.75 (Macciotta *et al.*, 2005).Estimates of the breeding values for the studied traits of bulls were predicted from their daughters based on birth years and considering all available pedigree information generated from their ancestors (parents, grandfather, and grandmother) applied the best linear unbiased prediction (BLUP) procedure {2}, using the software PEST 4.0, as described by Groeneveld and García Cortés (1998), fitting a multivariate animal model of 3 lactations separately as repeated measures.

In matrix notation, the model and its respective assumptions can be described as follows:

$$\mathbf{y = X\beta + Z\alpha + Wc + e} \quad \{2\}$$

Where, y is the vector of daily traits; β is the vector of an overall mean and fixed effects of herd, year-season of calving, age at calving, milking type, and the linear regression coefficients of studied traits on age at calving and on DIM at TD_1; α is the vector of random animal additive genetic effect, normally and independently distributed as[0, Iσ2a]; c is the vector of random permanent environmental effect of the buffalo cows normally and independently distributed as[0, $I\sigma^2c$] and X, Z and W are incidence matrices for fixed and random effects and e is the vector of random residual effects, normally and independently distributed as (0, $I\sigma^2e$).

Genetic changes for the tested traits were estimated as the regression in the average estimated daily breeding values (EDBVs) of bulls on the birth year of their daughters, assuming a 6-year/generation interval over birth years from 1995 to 2013.Generation interval, defined as the average age of parents at the birth of their progeny kept for reproduction (James 1977), were estimated.

RESULTS AND DISCUSSION

Fixed effects:

Based on a preliminary analysis of the fixed effects (herd, year-season of calving, milking type, and the linear regression coefficients of studied traits on age at calving and on DIM at TD_1) using a linear mixed model structured to repeated measures within lactations, the former showed a better approximation significant to a univariate normal, which was declared at P<0.05 and then was included in genetic analysis. The descriptive statistics of means, standard deviations, and coefficients of variation for the editing data set (n = 7688; TDR) over the entire range of calving years from 1999 to 2021 of lactations from one to three are presented in Table 2.

Table2. Means (M), standard deviations (SD) and coefficients of variation CV (%) of the first three lactations for the studied traits

Traits[1]	Lactation1			Lactation 2			Lactation 3		
	M	SD	CV (%)	M	SD	CV (%)	M	SD	CV (%)
WM, kg	5.49	0.81	14	7.59	1.02	15	7.10	1.21	17
PM, kg	5.64	0.68	12	7.79	0.88	13	7.50	1.00	14
DP, d	80.82	32.53	40	76.57	50.26	66	76.41	45.08	59
PS, kg	2.76	0.22	8	2.81	0.31	11	2.79	0.28	10
FP, %	6.54	1.53	23	6.61	1.67	25	6.68	1.60	24
PP, %	3.80	0.53	14	3.75	0.57	15	3.77	0.58	15

[1] WM, Wood daily milk yield; PM, daily peak milk yield; DP, days to peak milk yield; PS, persistency; FP, fat percentage, and PP, protein percentage.

Estimated parameters of Wood's model:

Concerning averages of lactation curves for WM and the variables derived in terms of PM, DP, and PS using fitting Wood's model {1} (Table 2), in the range of the low to close values reviewed by Catillo *et al.* (2002) and Ludmilla *et al.* (2020), working on Italian buffaloes. Whereas averages for FP and PP, Table (2) were low to moderate, in accordance with those reported by Catillo *et al.* (2002) and Rosati and VanVleck (2002).

Pattern of changes in WM at selected DIM (TD1 to TD11) along the lactation trajectory from 1 to 3 separated are given in Fig. 1. When comparing lactations,1st lactation exhibited lower averages for initial daily yield (*a*)just following calving, the rate of ascending slope to peak, (*b*) and the descending slope after peak yield (*c*). The averages (±standard errors) were 6.72±0.15, 0.36±0.04 and 0.13±0.01 for *a*, *b*, and *c* parameters, respectively of the 1stlactation. Ludmilla *et al.* (2020) stated a higher average of (a= 8.52) than found in this study while in the range for both (b= 0.59) and (c= 0.19) during 1st lactation. Moreover, a higher pattern of parameters showed as lactation order advanced from 2nd to 3rd. The values were 8.06, 0.17, 0.36, 0.04, and 0.14, 0.01, and 8.28, 0.19, 0.50, 0.05, and 0.18, 0.01 of the parameters a, b, and of the first three lactations, respectively.

Wood's model does not have the same satisfactory to fit change in the first three lactations separated in Fig. (1), according to assessment over DIM for the expected daily milk yield that follow the typical buffalo pattern. Actually, the estimate of the third lactation curve may be corrupted by a lack of numbers TD in the end lactation. Considering values, WM peaked at the 3rd DIM, with days ranging from 76.41 to 80.82. And estimates ranged from 2.76 to 2.81, respectively, where persistency is defined as the extent to which peak yield is sustained (Grossman *et al.*, 1999; Table 2 and Fig. 1) for PS. Among the lactation patterns, the first lactation exhibited persistence, a longer time to attain peak, and a lower daily production, which trended upward as the lactation order increased. Similar findings with Italian water buffaloes were previously reported by Dimauro *et al.* (2005).

Predication of breeding values and genetic trends:

Plotted in figs. 2 to 5 during the studied lactations separately are the average estimated daily breeding values (EDBVs) of bulls for the current variables, based on the birth years of their daughters between 1995 and 2013. In the base year of 1995, the mean EDBVs for WM, PM, PS, DP, FP, and PP were 0.30, 0.17, 0.25, 6.36, -0.41, and 0.15 were 0.24, 0.08, 0.01, 1.73, -0.56, and -0.44 were -0.30, -0.23, 0.08, -2.50, 0.00, and -0.05, in that order.

As expected, the 1st lactation estimates for WM, PM and PS in kg/d and DP/d, showed similar trend of declining shapely in irregular fluctuated patterns, as indicated by the mean EDBVs of bulls for WM and PM up until the end of the birth years, concerning PS and DP values tended to rise above zero in a linear fashion (Figs. 2-5). However, the genetic changes that were found to be insignificant ($P > 0.05$) ranged from 0.01 to 0.10 for WM, from 0.01 to 0.06 for PM, from -0.11 to 0.01 for PS, and from -0.67 to 0.08 d for DP. The results for WM, PM, and PS indicated genetic change that was economically unfavorable, while there was little pattern for DP. These might have been caused by the impacts of commonly utilized bulls that had lower or higher BV along the study period.

However, EDBVs values for WM and PM showed similar response values that tended to increase gradually in a small parallel gain, whereas the average EDBVs for both PS and DP tend to increase in the altered response of the 2nd lactation, as (Figs. 3-5). Also, the regressed genetic values showed a negative and insignificant genetic change ranging from -0.36 to 0.07, -0.29 to 0.03, -0.14 to 0.06, and from -0.37 to 1.62 for WM, PM, PS, and DP. However, regressed values of WM, PM, and PS revealed an adverse genetic response. In spite of DP, it satisfied the genetic pattern.

In the same context, the average EDBVs of the 3rd lactation vary greatly depending on the year of birth; sharply irregular estimates followed, increasing above reaching zero. With the continued small and insignificant genetic change varying from -0.14 to 0.14 for WM and from -0.14 to 0.11 for PM, kg/d were obtained. Clearly, a negative response of the average EDBVs in an inconsistent pattern was found for PS and DP (Figs. 4 and 5). And, consistently insignificant regressed values ranged from -0.04 to 0.05 kg/d to -0.04 to 0.37/d.

The differences in EDBVs for economic milk contents in terms of FP and PP are given in figs. from 2 to 4; illustrated the persistently negative values and descripted inconsistent trends for FP over the 2nd and 3rd lactations. Regarding the 1st lactation, there was no specific trend noticed. Moreover, there were negative and insignificant genetic responses that varied over birth years from -0.01 to 0.05, from -0.32 to -0.05, and from -0.13 to -0.05 for FP in the first three lactations.

Abrif, an inconsistent pattern noticed previously of EDBVs in bulls according to the birth year of their daughter may contribute to the explanation of these results during the studied period. In most cases, buffaloes do not adapt to disturbances in management conditions. However, there were not clear genetic responses in these three lactations. These findings can be caused by low estimates of heritability (h^2), despite the fact that the experimental Egyptian buffalo has not gone through intense genetic selection that could result in eroding the additive genetic variance as indicated by EL-Bramony *et al.* (2017) for these economic traits. The similar h^2 estimate reported by Rosati and Van Vleck (2002) in Italian buffaloes originated from a very small size which caused low genetic variability. Likewise, Meyer *et al.* (1989) reported that low estimates were not only caused comparative small variances between sires, but also result in more short-term environmental variation affecting dairy animals. Consequently, the genetic evaluation based on breeding value estimates of milk yield in most cases is delayed to subsequent lactations. It seems appropriate to evaluate animals for high breeding value estimates through the first three lactations. Even more, alternative schemes that make use of techniques to overcome the problem of spurious genealogy might be required than with ineffective traditional (Rosati and VanVleck, 2002). According to Lazaro *et al.* (2024), the candidate genes identified associated with test-day milk traits contribute to better explaining the genetic background and reinforce the value of integrating genomic information in breeding programs of Murrah breeding.

Moreover, for developing breeding strategies, a framework for implementing a sustained straight-breeding scheme for local populations and/or alternative populations using a systematic strategy to sustainable genetic improvement of native Egyptian buffalo populations was performed by El-Bramony (unpublished, 2023) at the buffalo breeding Research Department- Animal Production Research Institute.

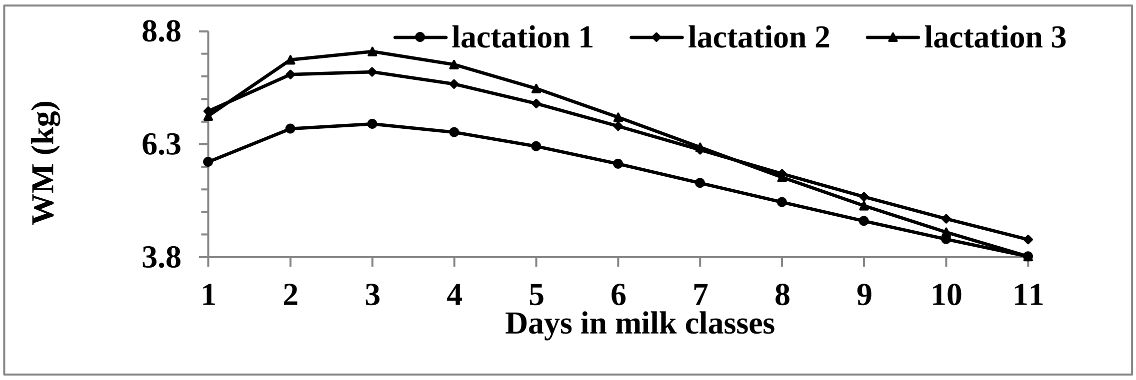

Fig. 1. Pattern of changes in WM at selected DIM in the first three lactations.

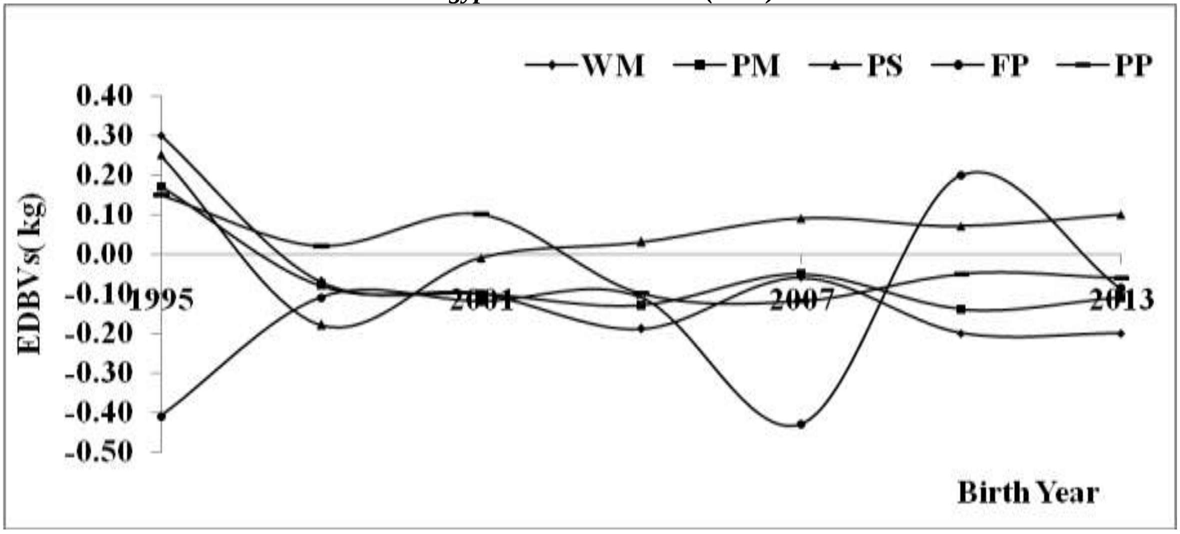

Fig. 2. Genetic changes in bulls over three-generation intervals (GI$_1$: 1995-2001; GI2: 2001-2007; GI$_3$: 2007-2013) for WM, PM, PS, FP, and PP of the 1st lactation.

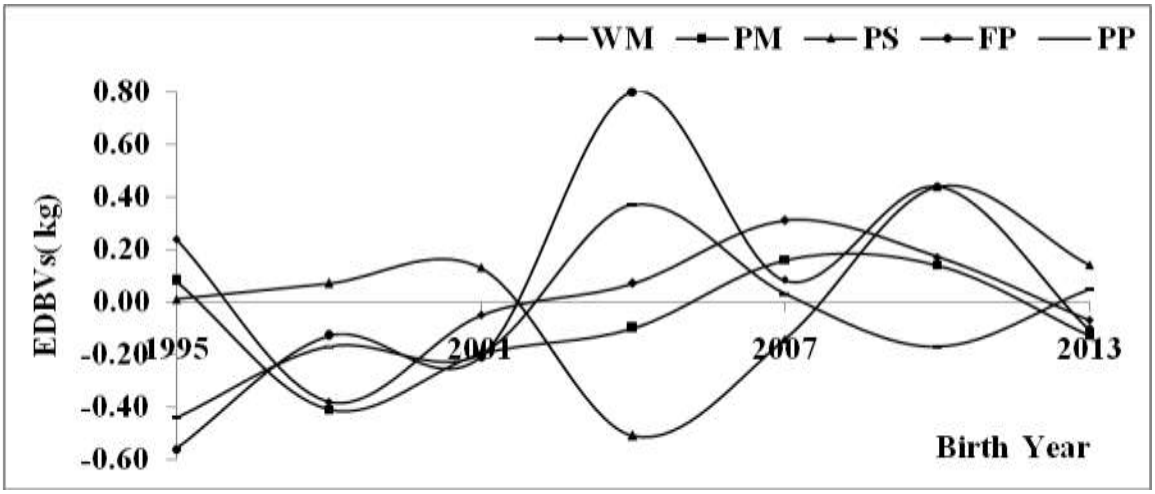

Fig. 3. Genetic changes in bulls over three-generation intervals (GI$_1$: 1995-2001; GI2: 2001-2007; GI$_3$: 2007-2013) for WM, PM, PS, FP, and PP of the 2nd lactation.

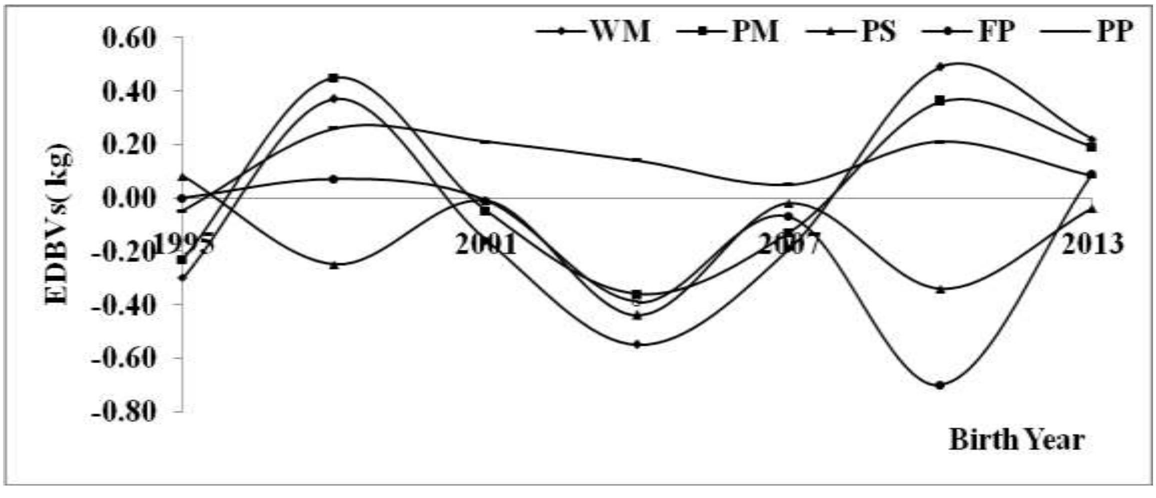

Fig. 4. Genetic changes in bulls over three-generation intervals (GI$_1$: 1995-2001; GI2: 2001-2007; GI$_3$: 2007-2013) for WM, PM, PS, FP, and PP of the 3rd lactation.

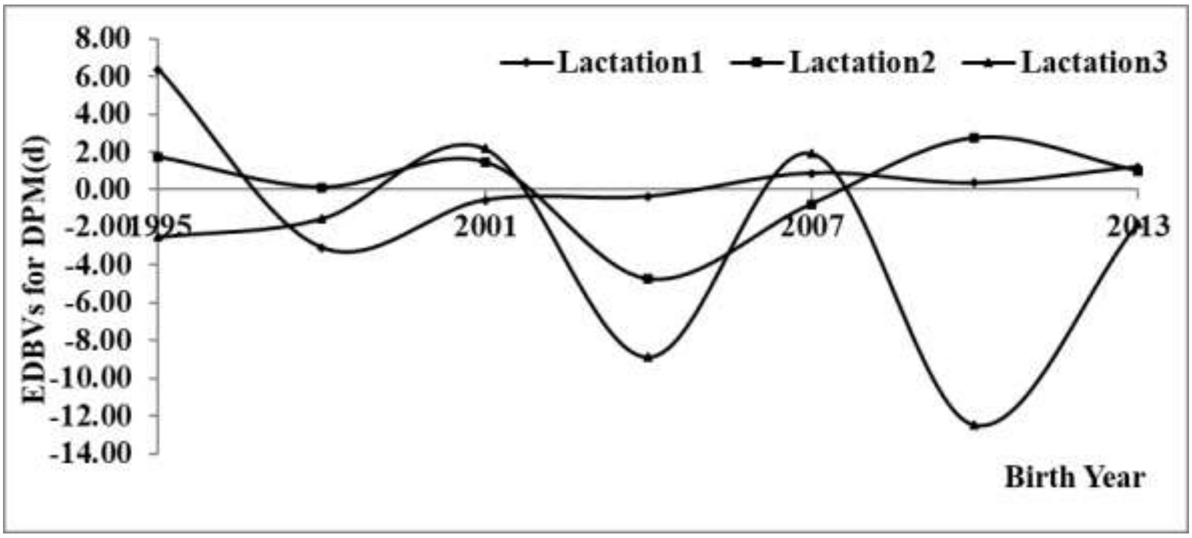

Fig. 5. Genetic changes in bulls over three generation intervals (GI_1: 1995-2001 years; GI2: 2001-2007; GI_3: 2007-2013) for DP of the first three lactations.

CONCLUSION

Wood's model was identified as suitable for fitting common buffalo lactation curves along the DIM of the first three lactation curves. Regressed EDBVs of bulls on the birth year of their daughters, an assumed over-generation interval of 6 years, indicate that small and insignificant genetic gain can be considered negligible over the calving years between 1999 and 2021. These might have been impacted by the commonly utilized bulls that had lower or higher breeding values throughout the study period. As a result, the genetic evaluation based on breeding value estimates for milk yield in most cases is delayed to subsequent lactations. It seems appropriate to evaluate animals for high breeding value estimates through the first three lactations. Up to now, traditional breeding plans focused on the phenotype of local buffalo populations have been ineffective because of the low heritability estimates of economic traits.

As an alternative, an adoption of a strategy that makes use of techniques to overcome the erosion of biodiversity is intended to maintain population structures on a wide scale in order to promote gene flow at the national level. Therefore, a greater focus on severely constrained practices may have an effect on marginal practices. These include health issues and feeding means developed by nutrition researchers to meet the needs of animals without financial support from government sources. Further genetic investigation should consider the use of more detailed data to identify genetic patterns of the lactation curve for milk production and its constituents.

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التغيرات الوراثية لإنتاج اللبن اليومي ومكونات اللبن في طلائق الجاموس المصري

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يُعد التنبؤ بخصائص منحنيات إنتاج لبن الجاموس أمرًا بالغ الأهمية للحفاظ على التنوع الوراثي لعشائر الجاموس الأصيلة. تم استخدام معادلة Wood لملائمة سجلات يوم الاختبار الفردية خلال الولادة، من عام ١٩٩٩ إلى ٢٠٢١، في ثلاثة قطعان تجريبية في معهد بحوث الإنتاج الحيواني، لمركز البحوث الزراعية. تم تقدير إنتاج اللبن اليومي لـWood (WM)، وأقصي إنتاج لبن يومي (PM)، وعدد الأيام حتى أقصى إنتاج اللبن (DP)، والمثابرة (PS)، ونسبة الدهن (FP) ، ونسبة البروتين (PP) باستخدام أفضل طريقة للتنبؤ الخطي غير المتحيز (BLUP) بالقيم التربوية اليومية. تم تقدير التغيرات الوراثية اليومية للصفات المدروسة من خلال معامل انحدار متوسط القيم التربوية اليومية المقدرة (EDBVs) للطلائق تحت الدراسة على سنة الولادة لبناتهم مدى فترة الأجيال بافتراض ٦ سنوات لإجراء تقييم التقدم الوراثي. تم تحديد متوسط القيم التربوية المقدرة للصفات المدروسة على أنها منخفضة وذات تأثيراً غير معنوياً. وقد تراوحت هذه القيم من -٠,٣٠ إلى ٠,٣١ لـصفة WM، ومن -٠,٢٣ إلى ٠,١٩ لصفة PM، ومن -٠,١٤ إلى ٠,٢٥ لصفة PS، ومن -٢,٥ إلى ٦,٦٣ لصفة DP، ومن -٠,٥٦ إلى ٠,٠٩ لصفة FPومن -٠,٤٤ إلى ٠,٢١ لصفة PP، وذلك على مدار مواسم الحليب الثلاثة المنفصلة. كانت الاستجابات الوراثية للطلائق إما إيجابية أو سلبية أظهرت تأثيراً غير معنويا خلال فترة الدراسة. وتشير هذه النتائج إلى ضرورة تنفيذ مخططات تربية ملائمة ومستدامة في عشائر الجاموس المصرية النقية التجريبية.