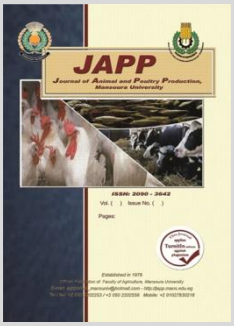
Journal of Animal and Poultry Production

Journal homepage & Available online at: www.jappmu.journals.ekb.eg

Genetic and Phenotypic Changes For Female Fertility and First Lactation Production Traits in Friesian Cattle in Egypt

Anas A. A. Badr* and S. M. Zahed

Animal Production Research Institute, Ministry of Agriculture and Land Reclamation, Nadi El-Said, Dokki, Giza, Egypt.



Article Information
Received 27/ 8 /2025
Accepted 1/ 10 /2025

ABSTRACT

This study aimed to evaluate the genetic and phenotypic trends of heifer and first-lactation cow traits using a multi-trait animal model. Data were obtained from 2,914 performance and pedigree records of Friesian heifers and first-lactation cows collected between 1979 and 2013 at the Saka and El-Karada experimental stations, Kafr El-Sheikh Governorate, under the Animal Production Research Institute, Ministry of Agriculture, Egypt. Linear regression of breeding values on year of first breeding revealed unfavorable genetic trends for age-related reproductive traits, with annual increases of 2.51, 0.18, and 0.09 days/year for age at first breeding (AFB), age at successful service (ASB), and age at first calving (AFC), respectively. In contrast, favorable improvements were observed for heifer fertility traits, including number of services per conception (NSC0; –0.01 unit/year), conception rate (CR0; +0.16%/year), and service period (SP0; –0.34 days/year). For cows, desirable genetic changes were detected for NSC1 (–0.09 unit/year), CR1 (+0.19%/year), and SP1 (–0.69 days/year), whereas unfavorable trends were noted for calving to first service interval (CFS1; +0.49 days/year) and days open (DO1; +0.44 days/year). Milk yield traits demonstrated consistent positive genetic progress, with annual increases of 2.41 kg, 14.9 kg, and 1.71 kg for 305-day milk yield (M3051), total milk yield (TMY1), and daily milk yield (DMY1), respectively. However, an unfavorable decline of –1.7 days/year was recorded for lactation period (LP1). Phenotypic trends closely paralleled the genetic results, confirming the observed patterns of change across the study period.

Keywords: Genetic, phenotypic, trends, heifer, first lactation.

INTRODUCTION

The estimation of genetic trends represents a fundamental approach to monitoring genetic improvement in dairy cattle populations (Potocnikl et al., 2007). A genetic trend, defined as the change in breeding values of traits over time, provides an effective measure of the efficiency of selection programs (Falconer and Mackay, 1996). However, achieving genetic progress in dairy cattle is often constrained by several factors, including low reproductive performance, extended generation intervals, and the high costs and time demands associated with large-scale selection programs. Consequently, the evaluation of genetic improvement should encompass multiple traits simultaneously, as this provides a more powerful and comprehensive assessment of selection efficiency (Yaeghoobi et al., 2011).

Previous studies have reported estimates of genetic trends over relatively short time spans, typically less than 20 years (Lee et al., 1985; Van Vleck et al., 1986; Meinert and Pearson, 1992). It has been established that extending the study period enhances the precision of genetic trend estimates (Burnside and Legates, 1967).

In this context, the present study was undertaken to estimate the genetic and phenotypic trends of heifer and first-lactation cow traits in Friesian cattle, using long-term data spanning more than three decades.

MATERIALS AND METHODS

Data for this study were obtained from Friesian cows maintained between 1979 and 2013 at the Sakha and El-Karada Experimental Stations, Kafr El-Sheikh Governorate, under the Animal Production Research Institute (APRI), Ministry of Agriculture, Dokki, Giza, Egypt. Historical records were extracted from herd files and used for genetic and phenotypic analyses.

Traits Considered

Heifer traits included:

- **Age at first breeding (AFB):** the interval from birth to first breeding (days).
- **Age at successful breeding (ASB):** the interval from birth to conception (days).
- **Age at first calving (AFC):** the interval from birth to first calving (days).
- **Number of services per conception (NSC0).**
- **Conception rate (CR0):** calculated as 1/NSC0.
- **Service period (SP0):** the interval from first service to conception (days).

First-lactation cow traits included:

- **Number of services per conception (NSC1).**
- **Conception rate (CR1):** calculated as 1/NSC1.
- **Calving to first service interval (CFS1):** interval from calving to first service (days).
- **Service period (SP1):** interval from first service to conception (days).
- **Days open (DO1):** interval from calving to conception (days).
- **305-day milk yield (M3051, kg).**
- **Total milk yield (TMY1, kg).**
- **Lactation period (LP1):** interval from calving to drying off (days).

* **Corresponding author.**
E-mail address: enas_emad22@yahoo.com
DOI: 10.21608/jappmu.2025.408261.1156

• **Daily milk yield (DMY1, kg):** calculated as TMY1 ÷ LP1.

To minimize selection bias, heifer records were matched with their corresponding first-lactation records.

Statistical Analysis

Preliminary statistical analyses were conducted using the GLM procedure of SAS (2011) to identify the most appropriate fixed models for genetic evaluation (Table 1). Heifers were classified into age-at-first-breeding (AFB) groups at three-month intervals: 12, 15, 18, 21, 24, 27, and 30–32 months. Similarly, age-at-first-calving (AFC) was classified into seven categories: <23, 23, 26, 29, 32, 35, and >37 months.

Genetic parameters were estimated using VCE6 software (Groeneveld et al., 2010), fitting a multivariate animal model with animal and residual effects considered random, and the fixed effects specified in Table 1. Pedigree information was incorporated to estimate breeding values (BV) using PEST software (Groeneveld et al., 2001).

Genetic and phenotypic trends were derived as the regression of breeding values and least square means on year, respectively.

Table 1. Model[a] summary for multivariate analysis of heifer and cow traits.

Heifer Trait[b]	F	M1s	Y1s	FMY1s	AFBc	NSC0			Model	No.
AFB	X	X	X	X					1	
NSC0, CR0, ASB, AFC	X	X	X	X	X				2	
SP0	X	X	X	X	X	X			3	
Cow Trait[b]	F	M1c	Y1c	FMY1c	AFCc	NSC1	DO1	LP1	Model	No.
NSC1, CR1, CFS1	X	X	X	X	X				4	
SP1, DO1	X	X	X	X	X	X			5	
LP1, DMY1	X	X	X	X	X		X		6	
M3051, TMY1	X	X	X	X	X		X	X	7	

a: F: farm, M1s: month of first breeding, Y1s: year of fist breeding, FMY1s: farm-month-year of first breeding, AFBc: age at first breeding classes, NSC0: heifer number of service per conception, M1c : month of first calving, Y1c: year of fist calving, FMY1c: farm-month-year of first calving, AFCc: age at first calving classes, NSC1: first lactation number of service per conception, DO1: first lactation days open as a covariate, LP1: lactation period of first lactation as a covariate.

b: AFB: age at first breeding, ASB: age at successful breeding, AFC: age at first calving, NSC0: heifer number of service per conception, CR0: heifer conception rate, SP0: heifer service period, NSC1: first lactation number of service per conception, CR1: first lactation conception rate, SP1: first lactation service period, DO1: first lactation days open, M3051: first lactation 305-day milk yield, TMY1: first lactation total milk yield, LP1: lactation period of first lactation, DMY1: first lactation daily milk yield.

RESULTS AND DISCUSION

Genetic Trends

The mean breeding values (BV) of heifers for age-related reproductive traits (AFB, ASB, and AFC) increased between 1979 and 2013 (Figure 1a–c). These increases correspond to unfavorable annual genetic changes of +2.51 days (P<0.005) for AFB, +0.18 days (P>0.05) for ASB, and +0.09 days (P>0.05) for AFC (Table 2). In contrast, favorable genetic improvements were observed for fertility traits, as indicated by the reductions in NSC0 (–0.01 services/year, P<0.05) and SP0 (–0.34 days/year, P<0.01) (Figure 1d, f). Similarly, CR0 showed a favorable annual increase of +0.16% units (P>0.05) (Figure 1e). These findings are consistent with Andersen-Ranberg et al. (2005), who reported an annual increase of 0.14% units in CR0 (P<0.01) between 1980 and 1998. Conversely, Fogh et al. (2003) found that SP0 increased by three days during 1980–1996, while Zahed and Anas (2020) reported overall genetic improvements in heifer fertility traits, with annual reductions of –0.01, –0.01, and –0.002 months/year for AFB, ASB, and AFC, respectively, as well as declines of –0.01 services/year in NSC0 and –0.21 days/year in SP0.

For first-lactation cows, mean BV for NSC1 declined favorably over the study period (Figure 2a), with an annual genetic improvement of –0.09 services (P<0.02) (Table 2). CR1 increased significantly (+0.19% units/year, P<0.001) (Figure 2b). In contrast, CFS1 and DO1 exhibited unfavorable increases of +0.49 days/year (P<0.01) and +0.44 days/year (P<0.001), respectively (Figure 2c, e). Favorable improvement was observed for SP1, which decreased by –0.69 days/year (P<0.001) (Figure 2d). These findings corroborate Andersen-Ranberg et al. (2005), who reported genetic improvement in CR1 but unfavorable lengthening of CFS1. Similarly, Fogh et al. (2003) observed increases in SP1 (+12 days) and CFS1 (+8–9 days) during 1980–1996, while CR1 decreased by 3–4%. In the United States, VanRaden (2003) documented an unfavorable genetic increase of 17 days in DO. Liu et al. (2007) also reported unfavorable genetic trends in Holsteins between 1990 and 2001, including reductions in CR1 (–2.77%), increases in SP1 (+4.53 days), and increases in DO1 (+7.4 days).

Table 2. Genetic and phenotypic trends for heifer and cow fertility traits and first lactation production traits.

Traits[b]	Genetic Trend	Sig.	Phenotypic Trend	Significant[a]
		Heifer Traits		
AFB (d)	-5005X + 2.51	***	-2768.5X + 1.72	*
ASB (d)	-366.0 X + 0.18	n.s.	-2391.3X + 1.55	*
AFC (d)	-181.3X + 0.09	n.s.	-2196.7X + 1.59	*
NSC0 (No.)	17.2X -0.01	*	27.5X – 0.01	**
CR0 (%)	-314.4X +0.16	n.s.	-320.3X + 0.20	*
SP0 (d)	683.8X – 0.34	***	2158.6X – 1.06	***
		First lactation cow Traits		
NSC1 (No.)	22.6X – 0.09	*	30.5X – 0.04	*
CR1 (%)	72.5X + 0.19	***	78.8X + 0.12	***
CFS1 (d)	-986.3X +0.49	**	-1016.7X + 0.54	*
SP1 (d)	-1382.9X - 0.69	***	-1294.7X - 0.49	**
DO1 (d)	2881.4X + 0.44	***	983.1X + 0.45	n.s.
M3051 (Kg)	-4808.7X + 2.41	***	-368.6X + 0.27	n.s.
TMY1 (Kg)	-29904.4X + 14.9	*	-13403.3X + 7.8	n.s.
DMY1 (Kg)	3418.3X + 1.71	***	2781.4X + 1.24	*
LP1 (d)	-49298.4X - 1.7	***	-20717.4X - 1.6	n.s.

a: n.s.= non significant, * = significant at P<0.05, ** = significant at P<0.01, * = significant at P<0.001.**

b: abbreviations as described in table 1.

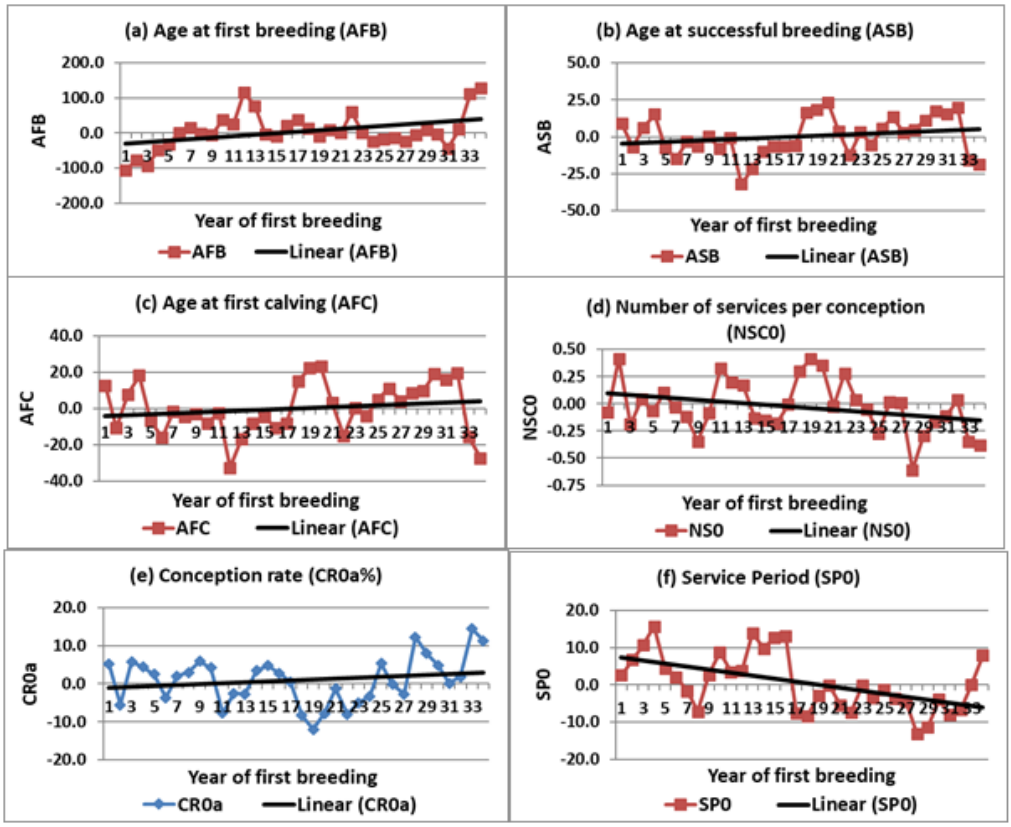


Figure 1. Genetic trend for (a) AFB, (b) ASB, (c) AFC, (d) NSC0, (e) CR0, (f) SP0.

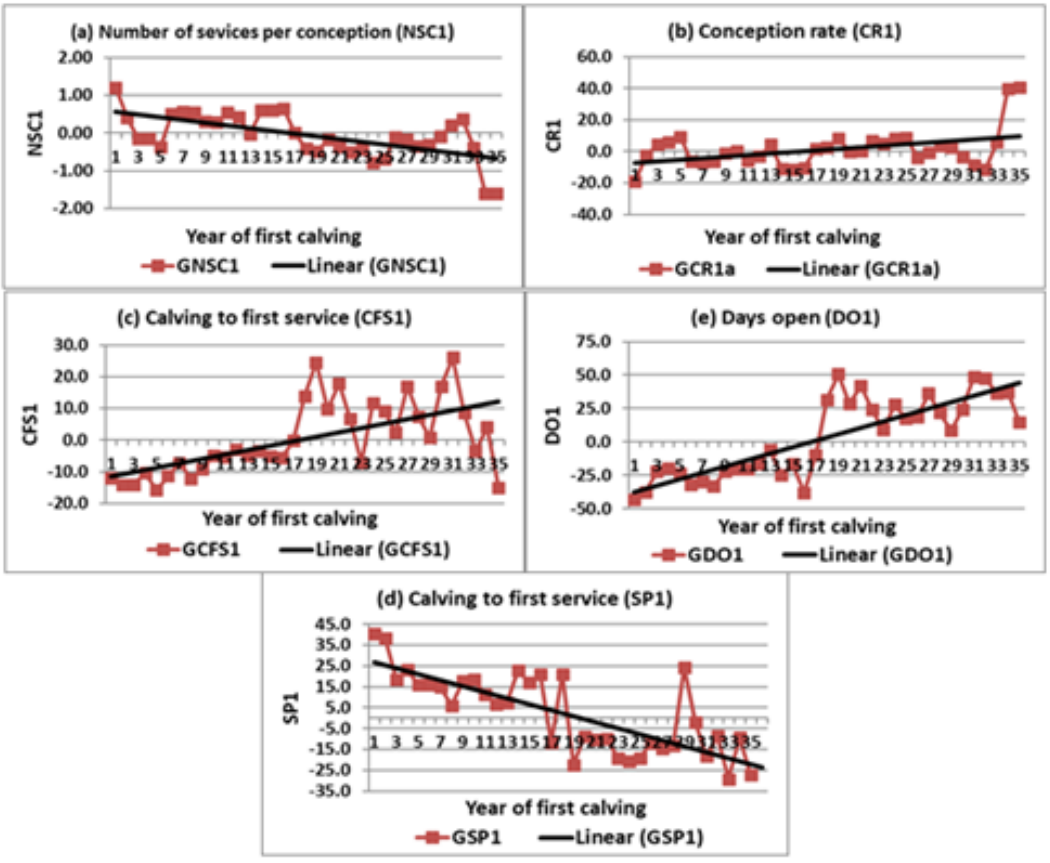


Figure 2. Genetic trend for (a) NSC1, (b) CR1, (c) CFS1, (d) SP1, (e) DO1.

Milk production traits demonstrated clear favorable genetic progress. Annual improvements were +2.41 kg (P<0.001) for M3051, +14.9 kg (P<0.02) for TMY1, and +1.71 kg (P<0.001) for DMY1 (Figure 3a, b, d; Table 2).

However, LP1 showed an unfavorable decline of –1.7 days/year (P<0.001) (Figure 3c). Similar positive changes were reported by Andersen-Ranberg et al. (2005), who found an annual increase of 0.63 kg in PY1 (P<0.01).

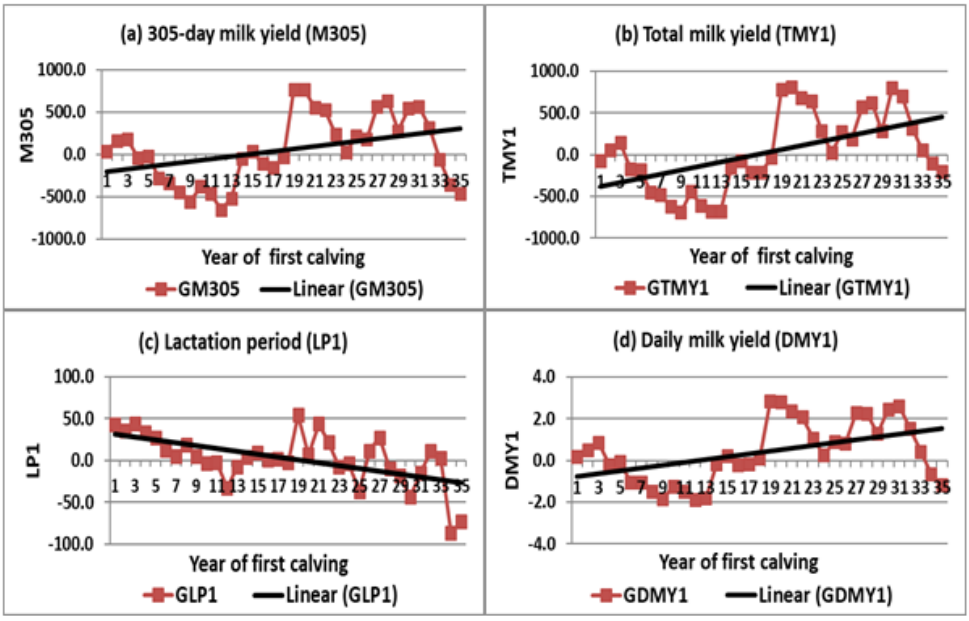


Figure 3. Genetic trend for (a) M3051, (b) TMY1, (c) LP1, (d) DMY1.

Phenotypic Trends

Phenotypic means for AFB, ASB, and AFC increased unfavorably over the study period, with annual changes of +1.72 days (P<0.05), +1.55 days (P<0.05), and +1.59 days (P<0.05), respectively (Figure 4a–c; Table 2). In contrast, NSC0 and SP0 showed favorable decreases of –0.01 services/year (P<0.01) and –1.06 days/year (P<0.001) (Figure 4d, f). CR0 exhibited a favorable increase of +0.20% units/year (P<0.05) (Figure 4e). These findings are in line with Van Doormaal et al. (2004), who reported little phenotypic change for AFB and CR0 in Canadian Holsteins, and with Zahed and Anas (2020), who observed positive phenotypic trends for AFB, ASB, and AFC but negative trends for NSC0 and SP0.

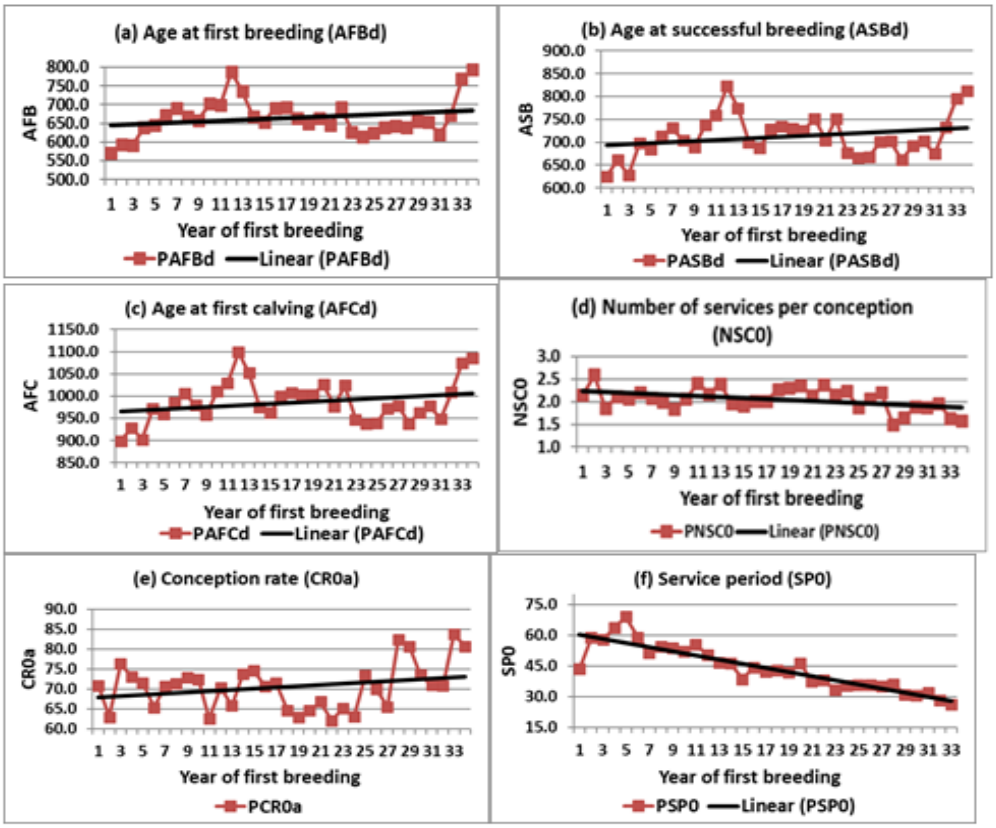


Figure 4. Phenotypic trend for (a) AFB, (b) ASB, (c) AFC, (d) NSC0, (e) CR0, (f) SP0.

For first-lactation cow traits, NSC1 declined favorably (–0.04 services/year, P<0.05) (Figure 5a; Table 2), while CR1 increased (+0.12% units/year, P<0.001) (Figure 5b). In contrast, CFS1 and DO1 showed unfavorable

phenotypic increases of +0.54 days/year (P<0.01) and +0.45 days/year (P>0.05), respectively (Figure 5c, e). SP1 decreased favorably (–0.49 days/year, P<0.001) (Figure 5d). Van Doormaal et al. (2004) similarly reported a phenotypic decline in CR1 (–0.23%/year) and an increase in CFS1 (+0.77 days/year) in Canadian Holsteins.

For milk yield traits, phenotypic means increased favorably by +0.27 kg/year (P>0.05) for M3051, +7.8 kg/year (P>0.05) for TMY1, and +1.24 kg/year (P<0.04) for DMY1 (Figure 6a, b, d; Table 2). LP1, however, declined unfavorably by –1.6 days/year (P>0.05) (Figure 6c).

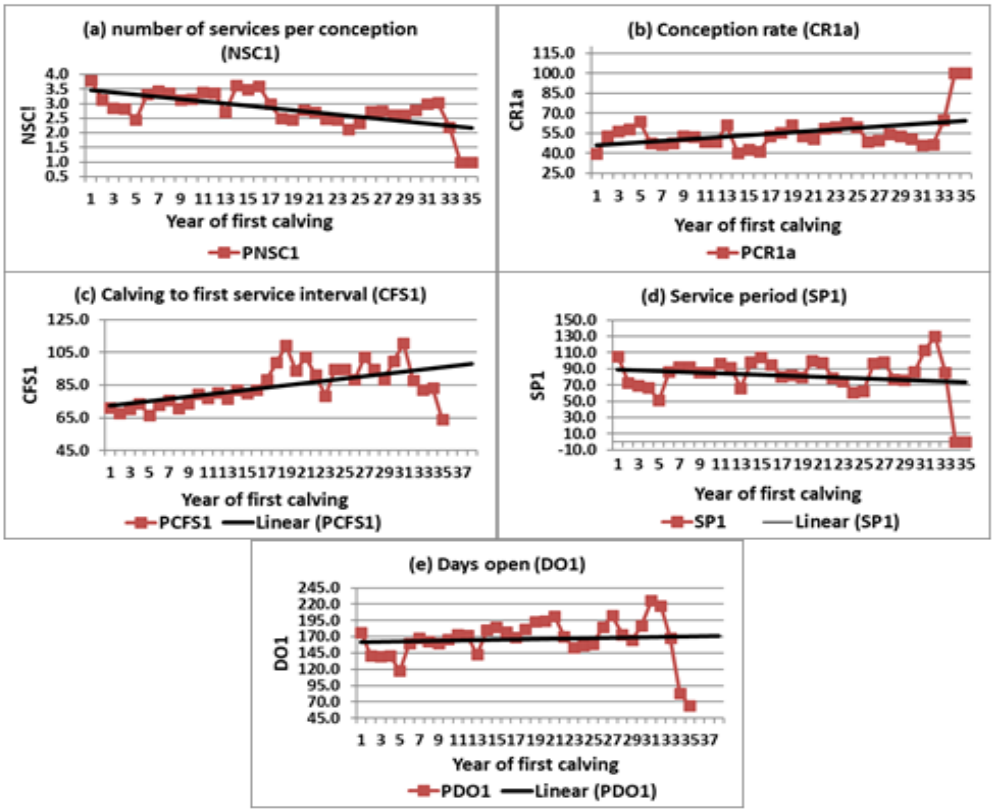


Figure 5. Phenotypic trend for (a) NSC1, (b) CR1, (c) CFS1,(d) SP1, (e) DO1.

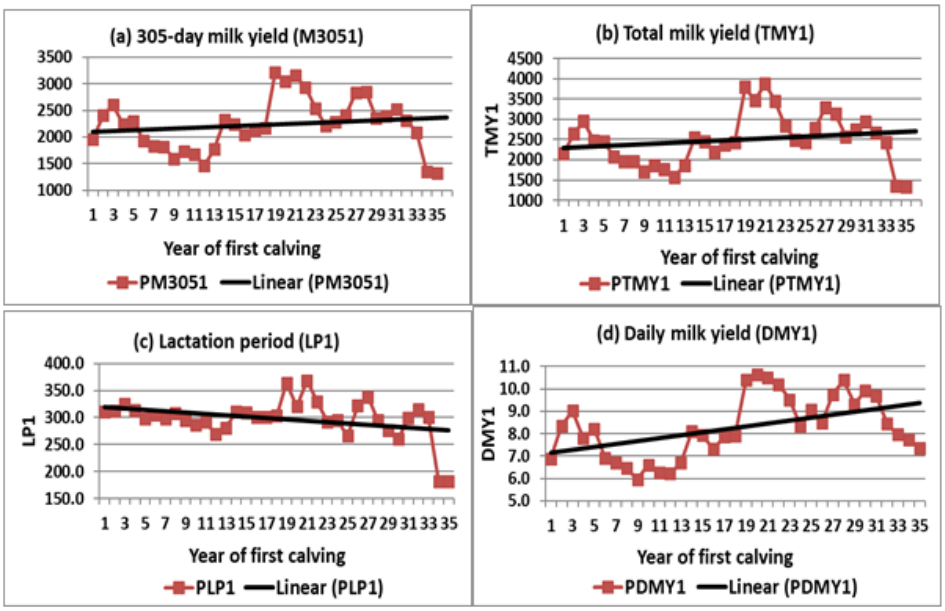


Figure 6. Phenotypic trend for (a) M305, (b) TMY1, (c) LP1, (d) DMY1.

CONCLUSION

The analysis of genetic and phenotypic trends from 1979 to 2013 demonstrated consistent improvements in fertility efficiency—specifically, reduced services per conception, improved conception rates, and shorter service periods—in both heifers and first-lactation cows. Substantial genetic and phenotypic progress was also observed in first-lactation milk yield traits, including 305-day milk yield, total milk yield, and daily milk yield, highlighting the effectiveness of the selection program.

Nonetheless, unfavorable trends were evident for age-related reproductive traits in heifers (AFB, ASB, AFC),

as well as for postpartum fertility indicators in cows (CFS1, DO1) and lactation length (LP1). These results suggest that while genetic selection was successful in enhancing productivity, environmental and management factors—such as inadequate culling policies, suboptimal nutrition, and limitations in reproductive management—likely contributed to the observed unfavorable changes.

The findings underscore the importance of incorporating both reproductive and production traits into a comprehensive selection index to achieve sustainable genetic improvement in Friesian cattle populations.

REFERENCES

Andersen-Rangerg, I.M., Klemetsdal, G., Heringstad, B., and Steine, T. (2005). Heritabilities, genetic correlations and genetic change for female fertility and protein yield in Norwegian dairy cattle. J. Dairy Sci., 88:348-355.

Burnside, E.B. and J.E. Legates, (1967). Estimation of genetic trends in dairy populations. J. Dairy Sci., 50: 1448-1457.

Falconer, D.S. and T,F.C. Mackay, (1996).Introduction to quantitative genetics. 4th Edn., Longman, England.

Fogh, A., Roth, A., Pedersen, O.M., Eriksson, J.A., Juga, J., Toivonen, M., Ranberg, I.M.A., Steine, T., Nielsen, U.S. and Aamand, G.P. (2003) A joint Nordic model for fertility traits.

Groeneveld, E., Kovac, M. and Mielenz,N. (2010). VCE6 User's Guide and Reference Manual, Version 6.0.2.

Groeneveld, E., Kovac, M. and Wang, T. (2001). PEST User's Guide and Reference Manual, Version 4.2.3.

Lee, K.L., Freeman, A.E. and L.P. Johnson (1985). Estimation of genetic change in registered Holstein cattle population. J. Dairy Sci., 68: 2629-2638.

Liu, Z., Jaitner, J., Pasman, E., Rensing, S, Reinhardt, F. and Reents, R. (2007). Genetic evaluation of fertility traits of dairy cattle using a multiple trait model. Interbull Bull., 37: 134-139.

Meinert, T.R. and R.E. Pearson (1992). Estimates of genetic trend in an artificial insemination progeny test program and their association with herd characteristics. J. Dairy Sci., 75: 2254-2264.

Potocnikl, K., Stepec, M. and J. Krsnik (2007). Genetic trends for production and non-production traits in Simmental breed in Slovenia. Biotecnol. Anim. Husbandry, 23: 47-53.

SAS (2011). SAS/STAT User's guide, Release 9.3. SAS institute Inc., Cary, North Carolina, USA.

Van Doormaal, B.J., Kistemaker, G., Fateh, J., Miglior, F., Jamrozik, J. and Schaeffer, L.R. (2004). Genetic evaluation of female fertility in Canadian dairy breeds. Interbull Bull., 32:86-89.

Van Raden P.M. (2003). Presentation. NDHIA Annual Meeting. March 2003.

Van Vleck, L., Westell, D.R.A. and J.C. Schneider (1986). Genetic change in milk yield estimated from simultaneous genetic evaluation of bulls and cows. J. Dairy Sci., 69: 2963-2965.

Yaeghoobi, R. , Doosti, A., Noorian, A.M. and A.M. Bahrami (2011). Genetic parameters and trends of milk and fat yield in Holstein's dairy cattle of west provinces of Iran. International J. of Dairy Sci., 6: 142-149.

Zahed, S.M. and Anas, A.A. Badr (2020). Characterization of Friesian heifer fertility under Egyptian conditions. J. Anim. and Poultry Prod., Mansura Univ., 11(3): 89-93.

التغيرات الوراثية والمظهرية لصفات الخصوبة في الإناث والصفات الإنتاجية للموسم الأول في ماشية الفريزيان في مصر

أناس عبدالسلام أبو العنين بدر .وسميح محمد زاهد.

معهد بحوث الإنتاج الحيواني، وزارة الزراعة واستصلاح الأراضي، الدقي، جيزة، مصر .

الملخص

هدفت هذه الدراسة إلى تقدير الاتجاهات الوراثية والمظهرية لصفات العجلات وأبقار الموسم الأول باستخدام نموذج الحيوان متعدد الصفات. اشتملت البيانات على ٢٩١٤ سجلًا لعجلات وأبقار الفريزيان في الموسم الأول خلال الفترة من ١٩٧٩ إلى ٢٠١٣، وذلك بمحطتي التجارب بسخا والقرضا – محافظة كفر الشيخ، التابعة لمعهد بحوث الإنتاج الحيواني، وزارة الزراعة. أظهرت نتائج تحليل الانحدار الخطي للقيم التربوية على سنة أول تلقيحة للعجلات اتجاهًا وراثيًا موجبًا غير مرغوب فيه (تدهور وراثي) في صفات AFB، ASB، AFC، حيث بلغ معدل التدهور السنوي ٢,٥١، ٠,١٨، و٠,٠٩ يوم/سنة على التوالي. في المقابل، لوحظ تحسن وراثي مرغوب فيه في صفات NSC0، CR0، SP0بمعدلات بلغت - ٠,٠١ وحدة/سنة، ٠,١٦%/سنة، و-٠,٣٤ يوم/سنة على التوالي. أما بالنسبة لأبقار الموسم الأول، فقد تحقق تحسن وراثي مرغوب فيه في صفات NSC1، CR1، SP1بمعدلات - ٠,٠٩ وحدة/سنة، ٠,١٩%/سنة، و-٠,٦٩ يوم/سنة على التوالي، بينما ظهر تدهور وراثي في صفتَي CFS1، DO1بمعدلات ٠,٤٩ و٠,٤٤ يوم/سنة على التوالي. وعلى صعيد الصفات الإنتاجية في الموسم الأول، سُجل تحسن وراثي في صفات M3051، TMY1، DMY1بمعدلات ٢,٤١، ١٤,٩، و١,٧١ كجم/سنة على التوالي، في حين أظهرت صفة LP1تراجعًا وراثيًا بمعدل -١,٧ يوم/سنة. وبشكل عام، أظهرت الاتجاهات المظهرية للصفات محل الدراسة نمطًا مشابهًا للاتجاهات الوراثية، مع وجود اختلاف في حجم مقدار التغير.