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Genetic Parameters of Female Fertility and First Lactation Production Traits of Friesian Dairy Cattle in Egypt

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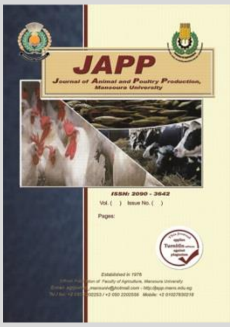

ABSTRACT

This study aimed to estimate genetic parameters for fertility traits in Friesian heifers and traits associated with their first lactation. Data from animals that calved between 1979 and 2013 at Saka and El-Karada stations were analyzed using a multi-trait linear animal model.The heritabilities (h^2) of fertility traits in both heifers and cows were generally low. For virgin heifers, the heritabilities of age-related traits (AFB, ASB, and AFC) were slightly higher (0.152, 0.161, and 0.163, respectively) compared to other fertility traits such as NSC0, CR0, and SP0 (0.027, 0.019, and 0.022, respectively). In cows, heritability estimates for NSC1 and SP1 (0.044 and 0.035, respectively) were higher than those for heifers. Genetic correlations among traits were notably high, including correlations between NSC0 and CR0 (-0.903) and SP0 (0.951), and between AFB, ASB, and AFC (0.994–0.997) in heifers. Similarly, strong correlations were observed among cow traits, such as NSC1 with SP1 (0.925) and DO1 (0.980), CR1 with SP1 (-0.994) and DO1 (-0.918), and SP1 with DO1 (0.976). These results suggest that fertility traits in both heifers and cows can be included in genetic selection. Notably, selecting heifers based on age-related traits (AFB, ASB, and AFC) may encourage earlier maturation in cows.

Keywords: Friesian; Female fertility; Genetic parameters; First lactation.

INTRODUCTION

Holstein-Friesian cows have long been recognized for declining reproductive performance as a consequence of intensified genetic selection for milk yield (Shook, 2006). The antagonistic genetic relationship between reproductive efficiency and milk production is well-documented (Pryce et al., 2002). However, less attention has been given to the fertility of virgin heifers, and limited information is available regarding the relationship between reproductive performance in virgin heifers and production traits during the first lactation (Veerkamp et al., 2001; Pryce et al., 2002). Fertility data from virgin heifers, collected earlier in life, provide an unbiased evaluation of reproductive performance, unaffected by milk production. Conversely, the fertility of lactating cows has declined significantly, largely due to the negative impact of milk production on reproductive physiology (Andersen-Ranberg et al., 2005; Tiezzi et al., 2012).

Virgin heifers generally exhibit better fertility performance than lactating cows. Since their traits can be measured early in life, incorporating virgin heifer fertility traits into dairy cattle selection programs could enhance reproductive efficiency (Buaban et al., 2015). Including these traits in genetic evaluation programs may improve both fertility and production traits in cows (Mokhtari et al., 2015). The availability of early fertility data, higher heritabilities for heifer fertility compared to cows, and favorable genetic correlations with cow reproductive traits make virgin heifer fertility traits valuable for dairy breeding programs (Mokhtari et al., 2015; Muuttoranta et al., 2019). Hahn (1969) also suggested that selection for heifer fertility may yield greater benefits than focusing solely on cow fertility.

Genetic correlations between virgin heifer fertility traits and those of cows, including yield traits, are generally favorable. This indicates that selecting for heifer fertility traits could enhance lifetime fertility performance without compromising genetic progress in milk production (Abe et al., 2009). However, as heifer fertility traits are closely linked to early productive maturity, their relationship with long-term productivity must be examined before incorporating these traits into a comprehensive selection index (Abe et al., 2009).

This study aims to estimate the genetic parameters of fertility traits in virgin heifers and first lactation Friesian cows, as well as their production traits, within the context of Egyptian dairy farming.

MATERIALS AND METHODS

Data

The dataset included 2,914 records from Friesian heifers, representing 66 sires and 427 dams, spanning the period from 1979 to 2013 which collected from Saka and El-Karada Stations, belonging to Animal Production Research Institute, Ministry of Agriculture, Dokki, Giza, Egypt. Measures of fertility and production traits for heifers and first-lactation cows, along with their respective ranges, are presented in Table 1. Records falling outside these ranges were excluded. To minimize selection bias, animals included in the genetic evaluation were required to have data either as a heifer or during their first lactation. For instance, heifer records were matched with corresponding first-lactation records.

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Table 1. Abbreviations and ranges for measures of fertility and production traits

Abbreviation	Definition	Min	Max
	Heifer Fertility Traits		
AFB	Age at first breeding (day): age in days from birth date to first breeding date	357	989
ASB	Age at successful breeding (day): age in days from birth date to successful breeding date	357	991
AFC	Age at first calving (day): age in days from birth date to first calving date	635	1296
NSC0	Number of service per conception	1	5
CR0	Conception rate = (1/NSC0)*100	20	100
SP0	Service period (day): number of days between first service date to conception date	0	200
	First Lactation Cow Traits		
NSC1	Number of service per conception	1	5
CR1	Conception rate (%)= (1/NSC1)* 100	20	100
SP1	Service period (day): number of days between first service date to conception date	0	200
CFS1	Calving to first service interval (day): number of days between calving date to first service date	20	200
DO1	Days open (day): number of days between calving date to conception date	20	400
M305	305-day milk yield (kg): milk yield in 305-day of lactation	900	6232
LP1	Lactation period (day): interval in days from 3-day after calving date to dry date	150	600
TMY1	Total milk yield (kg): milk yield through lactation period	900	9999
DMY1	Daily milk yield (kg):TMY1/LP1	4	17

A preliminary statistical analysis was conducted using the MIXED procedure in SAS software (2011) to identify non-significant fixed effects. The final fixed effects used in the analysis are detailed in Table 2. Genetic parameters, including heritability, genetic, residual, and phenotypic variances, as well as genetic, residual, and phenotypic correlations, were estimated using the VCE6 program (Groeneveld et al., 2010), incorporating animal and error as random effects. Pedigree data was included to estimate estimated breeding values (EBVs) using the PEST program (Groeneveld et al., 2001), applying a multivariate animal model with genetic parameters derived from the VCE program.

Table 2. Model summary for multivariate analysis of heifer and cow traits.

Traits [b]	F	$M1_B$	$Y1_B$	$FMY1_B$	AFBc	NSC			Model No.
					Heifer traits				
AFB	X	X	X	X					1
NSC0, ASB, AFC	X	X	X	X	X				2
CR0, SP0	X	X	X	X	X	X			3
					Cow traits				
Trait[a]	F	M1c	Y1c	FMY1c	AFC	NSC	DO	LP	Model No.
NSC1, CFS1	X	X	X	X	X				4
CR1, SP1, DO1	X	X	X	X	X	X			5
LP1,DMY1	X	X	X	X	X		X		6
M305, TMY1	X	X	X	X	X		X	X	7

b: F: farm, $M1_B$: month of first breeding, $Y1_B$: year of fist breeding, $FMY1_B$: farm-month-year of first breeding, AFBc: age at first breeding classes, NSC: 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, DO: days open as a covariate, LP: lactation period as a covariate.

RESULTS AND DISCUSSION

Descriptive Statistics

The means, standard deviations (SD), and coefficients of variation (CV%) for various measures of heifer fertility, cow fertility, and first lactation production traits are summarized in Table 3. The mean age at first breeding (AFB) for heifers was 661.2 days, higher than the values reported by Abe et al. (2009), de Haer et al. (2013), and Guo et al. (2014) at 594.8, 518.6, and 519.8 days, respectively. This estimate is comparable to the 21.7 months reported by Zahed and Anas (2020) but lower than the 698.5 days documented by Buaban et al. (2015). The CV% for AFB was 14.39%, aligning with the 14.0% reported by Jagusiak (2006) and Jagusiak and Zarnecki (2007), but smaller than the 25.9% and 17.3% reported by Raheja et al. (1989) and Abe et al. (2009), respectively. However, it exceeded the 8.5% and 9.8% documented by de Haer et al. (2013) and Guo et al. (2014).

The mean age at successful breeding (ASB) for heifers was 709.6 days, higher than the estimates of 556.8 days reported by Jagusiak (2006), Jagusiak and Zarnecki (2007), and Abe et al. (2009). This value was comparable to the 23.3 months reported by Zahed and Anas (2020). The CV% for ASB (7.22%) was lower than the values of 18.18%, 14.2%, and 18.8% reported by Zahed and Anas (2020), Jagusiak and Zarnecki (2007), and Abe et al. (2009), respectively. The mean age at first calving (AFC) was 983.1 days, smaller than the 1003.5 days reported by Buaban et al. (2015) but larger than the 835.8 days documented by Jagusiak and Zarnecki (2007). This estimate was close to the 32.2 months reported by Zahed and Anas (2020). The CV% for AFC (5.71%) was lower than the estimates of 13.57% and 9.9% reported by Zahed and Anas (2020) and Jagusiak and Zarnecki (2007), respectively.

The mean number of services per conception for heifers (NSC0) was 2.09, exceeding the values of 1.57, 1.31, and 1.56 reported by Buaban et al. (2015), Mokhtari et al. (2015), and Tiezzi et al. (2012), respectively, but close to the 2.07 reported by Zahed and Anas (2020). The CV% for NSC0 was 65.07%, larger than the 52.9%, 51.9%, and 58.9% documented by Raheja et al. (1989), Mokhtari et al. (2015), and Tiezzi et al. (2012), respectively.

The phenotypic mean for heifer conception rate (CR0) was 69.64%, consistent with the 69.0% reported by Jagusiak (2006), Jagusiak and Zarnecki (2007), and Abe et al. (2009), but smaller than the 70.6%, 77.0%, and 78.0% reported by Pasman et al. (2007), de Haer et al. (2013), and Mokhtari et al. (2015), respectively. The CV% for CR0 was 45.98%, smaller than the estimates of 52.6%, 69.2%, and 73.8% reported by Mokhtari et al. (2015), Tiezzi et al. (2012), and Muuttoranta et al. (2019), respectively, but larger than the 39.5% reported by de Haer et al. (2013).

Table 3. Mean, Standard deviation (SD), Coefficient of variability (CV) and model type used for analyzing heifer and first lactation cow traits of Friesian dairy cattle.

Traits[a]	Mean	SD	C.V.	Model
		Heifer Traits		
AFB (d)	661.24	95.15	14.39	1
ASB (d)	709.56	51.22	7.22	2
AFC (d)	983.08	56.11	5.71	2
NSC0 (no.)	2.09	1.36	65.07	2
CR0 (%)	69.64	32.02	45.98	3
SP0 (d)	44.09	29.32	66.50	3
		1st Lactation Traits		
NSC1 (no.)	2.89	1.59	55.02	4
CR1 (%)	53.19	33.51	63.00	5
CFS1 (d)	84.31	35.65	42.28	4
SP1 (d)	83.87	41.21	49.14	5
DO1 (d)	168.73	53.26	31.57	5
LP1 (d)	305.46	79.57	26.05	6
DMY1 (kg)	8.23	1.75	21.26	6
M305 (kg)	2271.56	662.96	29.19	7
TMY1 (kg)	2539.72	605.77	23.85	7

a: Abbreviations as described in table 1.

The mean estimate of heifer service period (SP0) was 44.09 days, larger than the 26.8, 35.6, and 18.1 days reported by Buaban et al. (2015), Tiezzi et al. (2012), and Muuttoranta et al. (2019), respectively, but smaller than the 48.0 days reported by Hansen et al. (1983). The CV% for SP0 was 66.5%, smaller than the estimates of 177.8%, 200.8%, and 197.2% reported by de Haer et al. (2013), Tiezzi et al. (2012), and Muuttoranta et al. (2019), but slightly higher than the 65.97% reported by Zahed and Anas (2020).

Heritability of Heifer Traits

Estimates of heritability (h^2), genetic correlations (r_g), and phenotypic correlations (r_p) for heifer fertility traits are summarized in Table 4. The heritability estimate for heifer NSC0 in this study was 0.027 (Table 4), closely aligning with the estimate of 0.026 reported by Tiezzi et al. (2012), lower than the 0.04 reported by Raheja et al. (1989), but higher than 0.012 and 0.015 reported by Mokhtari et al. (2015) and Zahed and Anas (2020), respectively. Similarly, the heritability estimate for heifer CR0 was 0.019 (Table 4), which was comparable to 0.01 reported by Mokhtari et al. (2015) and Buaban et al. (2015), lower than 0.04 and 0.027 as reported by Kuhn et al. (2006) and Abe et al. (2009), respectively, but higher than 0.008 noted by Fogh et al. (2003) and Muuttoranta et al. (2019). The heritability estimate of heifer SP0 (0.022, Table 4) was higher than values reported by Zahed and Anas (2020), Muuttoranta et al. (2019), and Tiezzi et al. (2012) at 0.011, 0.012, and 0.017, respectively, but lower than the 0.03 reported by Hansen et al. (1983).

The heritability estimate for heifer AFB (0.152, Table 4) was nearly identical to 0.159 reported by Berry et al. (2007), lower than 0.324, 0.227, and 0.26 as reported by Jagusiak and Zarnecki (2007), de Haer et al. (2013), and Buaban et al. (2015), respectively, but higher than 0.100, 0.128, and 0.146 as reported by Guo et al. (2014), Abe et al. (2009), and Zahed and Anas (2020), respectively. Similarly, the heritability estimate for heifer ASB (0.161, Table 4) was comparable to 0.16 reported by Hansen et al. (1983), lower than 0.312 reported by Jagusiak and Zarnecki (2007), but higher than 0.10, 0.115, and 0.12 as reported by Raheja et al. (1989), Zahed and Anas (2020), and Abe et al. (2009), respectively. The heritability estimate for heifer AFC (0.163, Table 4) was lower than 0.24, 0.25, and 0.296 reported by Berry et al. (2007), Buaban et al. (2015), and Jagusiak and Zarnecki (2007), respectively, but higher than 0.111 noted by Zahed and Anas (2020). These estimates (0.152–0.163) for AFB, ASB, and AFC suggest that a reasonable response to selection can be anticipated.

Table 4. Heritability (on diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations of heifer fertility traits

Traits[a]	NSC0	CR0	SP0	AFB	ASB	AFC
NSC0	0.027	-0.903	0.951	-0.199	0.195	0.197
CR0	-0.932	0.019	-0.936	0.020	-0.328	-0.324
SP0	0.879	-0.833	0.022	0.075	0.463	0.468
AFB	-0.033	0.017	-0.044	0.152	0.994	0.997
ASB	0.479	-0..453	0.553	0.777	0.161	0.996
AFC	0.471	-0.446	0.549	0.765	0.985	0.163

a: Abbreviations as described in table 1.

Heritability of Cow Traits

Heritability estimates for fertility traits during the first lactation are presented in Table 5. The estimate for cow NSC1 (0.044, Table 5) was similar to 0.04 and 0.046 reported by Guo et al. (2014) and Tiezzi et al. (2012), respectively, and higher than 0.03 and 0.029 reported by Buaban et al. (2015) and Mokhtari et al. (2015). The heritability estimate for cow CR1 during the first lactation (0.035, Table 5) was smaller than 0.051 reported by Abe et al. (2009) but higher than 0.02, 0.03, and 0.025 reported by Buaban et al. (2015), Tiezzi et al. (2012), and Muuttoranta et al. (2019), respectively.

Table 5. Heritability (on diagonal), genetic (above diagonal),and phenotypic (below diagonal) correlations of first lactation cow fertility traits.

Traits[a]	NSC1	CR1	CFS1	SP1	DO1
NSC1	0.044	-0.753	0.726	0.925	0.980
CR1	-0.939	0.035	-0.860	-0.994	-0.918
CFS1	0.159	-0.161	0.033	0.975	0.965
SP1	0.786	-0.764	0.512	0.034	0.976
DO1	0.841	-0.810	0.106	0.906	0.029

a: Abbreviations as described in table 1.

The heritability estimate for first lactation CFS1 (0.033, Table 5) was consistent with the 0.034 reported by Guo et al. (2014), smaller than 0.040, 0.061, and 0.082 reported by Fogh et al. (2003), Jagusiak and Zarnecki (2007), and de Haer et al. (2013), respectively, and larger than 0.019 reported by Berry et al. (2007). Similarly, the heritability estimate for first lactation SP1 (0.034, Table 5) was smaller than 0.092 and 0.039 reported by Jagusiak and Zarnecki (2007) and Tiezzi et al. (2012), respectively, but larger than 0.020 reported by Fogh et al. (2003) and Buaban et al. (2015). The heritability estimate for first lactation DO1 (0.029, Table 5) was lower than 0.053, 0.04, and 0.049 reported by Guo et al. (2014), Buaban et al. (2015), and Mokhtari et al. (2015), respectively, but higher than 0.008

and 0.026 reported by Berry et al. (2007) and Pasman et al. (2007), respectively.

The heritability estimates for interval traits during the first lactation (CFS1, SP1, and DO1) ranged from 0.029 to 0.034, which were lower than estimates for CR1 and NSC1 (0.035–0.044). A similar pattern was observed for heifer traits (e.g., SP0 at 0.022 compared to NSC0 at 0.019). Comparing the heritability estimates of the same traits between heifers and cows (e.g., 0.027 vs. 0.044 for NSC0 and NSC1; 0.019 vs. 0.035 for CR0 and CR1, Tables 4 and 5) indicates that fertility in cows is generally more heritable than in heifers.

Heritability of Production Traits

Heritability estimates for first lactation production traits were 0.101, 0.214, 0.227, and 0.219 for LP1, DMY1, M3051, and TMY1, respectively (Table 6). The heritability estimate for M3051 (0.227) was lower than 0.285, 0.386, and 0.252 reported by Abe et al. (2009), de Haer et al. (2013), and Mokhtari et al. (2015), respectively.

Table 6. Heritability (on diagonal), genetic (above diagonal)and phenotypic(below diagonal) correlations of first lactation production cow traits.

Traits[a]	LP1	DMY1	M305	TMY1
LP1	0.101	-0.767	0.825	0.915
DMY1	0.055	0.214	0.787	0.746
M305	0.611	0.717	0.227	0.948
TMY1	0.771	0.609	0.927	0.219

a: Abbreviations as described in table 1.

Genetic and phenotypic correlation

Heifer fertility traits

Genetic correlation

Genetic (rg) and phenotypic (rp) correlations among heifer fertility traits (NSC0, CR0, SP0, AFB, ASB and AFC) are presented in Table (4). Genetic correlation between NSC0 with CR0 (-0.903, table 4), was lower (-0.97 and -1.0) than estimates of Abe et al., (2009) and Buaban et al., (2015), and was nearly the same (-0.93) as reported by Mokhtari et al., (2015). Genetic correlation between NSC0 with SP0 (0.951) was higher (0.85) than those reported by Buaban et al., (2015). Correlation of NSC0 with AFB, ASB and AFC were -0.199, 0.195 and 0.197, respectively (Table 4), was lower than -0.123, 0.119 and 0.160, respectively (Zahed and Anas, 2020).

Genetic correlation between CR0 and SP0 was negatively high (-0.936) as (-0.901 and -0.95) reported by de Haer at al., (2013) and Muuttoranta et al., (2019), respectively. Genetic correlations between CR0 with each of AFB, ASB and AFC were small (0.02, -0.328 and -0.324, respectively, table 4). Genetic correlations between SP0 with the same traits (0.075, 0.463 and 0.468, respectively, table 4) were smaller than the estimates (0.580, 0.768 and 0.795, respectively) reported by Zahed and Anas (2020).

Genetic correlations between AFB with ASB and AFC were high and positive (0.994 and 0.997), which was similar (0.97, 0.96 and 0.99, between AFB and ASB) to those of Hansen et al., (1983), Jagusiak and Zarnecki (2007) and Abe et al., (2009). Correlation between ASB and AFC (0.996) was similar to 0.98 as reported by Jagusiak and Zarnecki (1989).

For virgin heifers there is a strong positive r_g between NSC0 and SP0 (0.951, table 4) suggesting that increasing NSC0 will increase SP0, however increasing NSC0 will decrease CR0 (-0.903). The same trend was observed for CR0 and SP0 (-0.936) i.e., increasing CR0 will decrease SP0 (de Haer et al., 2013).

Negative genetic correlation between AFB and NSC0 (-0.199), may indicate that fertility was reduced when heifer breeding was initiated at young ages. A slight r_g between AFB or AFC with each of NSC0, CR0 and SP0 indicate that selection for lower AFB or AFC had little correlated responses to NSC0, CR0 and SP0 in heifers. This may be due to that AFB and AFC often reflect body growth of the heifer rather than its fertility. Therefore, body size of heifers is mainly considered by farmers when deciding on the right time for inseminations.

Phenotypic correlation

Phenotypic correlations between NSC0 and both CR0 and SP0 were -0.931 and 0.879 (Table 4). The same negative correlations between NSC0 with CR0 (-0.851 and -1.0) were reported by Mokhtari et al., (2015) and Buaban et al., (2015). Correlation between CR0 and SP0 was -0.833 (table 4), quit similar to -0.49 and -0.73 (Liu et al., 2007 and Buaban et al., 2015).

Phenotypic correlations between AFB and both NSC0, CR0 and SP0 were low (-0.033, 0.017 and -0.044, respectively, table 4), as -0.02 between AFB and CR0 (Jagusiak and Zarnecki, 2007). Correlation between ASB and the same traits were 0.479, -0.453 and 0.553, respectively and those between AFC with the same traits were 0.471, -0.446 and 0.549, respectively (Table 4). Zahed and Anas (2020) found that phenotypic correlation between AFB with each of NSC0 and SP0 were -0.044 and 0.014, respectively, between ASB and the same traits were 0.458 and 0.561 and between AFC and each of NSC0 and SP0 were 0.451 and 0.561, respectively.

Phenotypic correlations were medium to high between AFB and both ASB and AFC (0.777 and 0.765) as estimates of 0.81, 0.78 and 0.82 between AFB and ASB (Raheja et al., 1989, Jagusiak and Zarnecki, 2007 and Abe et al., 2009). Phenotypic correlation between ASB and AFC was 0.985 (table 4), as 0.94 and 0.98 found in the literature (Buaban et al., 2015 and Jagusiak and Zarnecki, 2007). Zahed and Anas (2020) reported that phenotypic correlations between AFB and both ASB and AFC were 0.791 and 0.780, respectively, and those between ASB and AFC was 0.985.

AFB was closely related genetically to ASB and AFC (0.994 and 0.997) and phenotypically (0.777 and 0.765), and also ASB with AFC (0.996 and 0.985), however CR0 was negatively genetically correlated to each of ASB and AFC (-0.328 and -0.324, respectively). These results indicate that earlier service without loss in CR0 would be possible with optimum timing of insemination.

Cow Fertility Traits

Genetic Correlations

The genetic (rg) and phenotypic (rp) correlations between cow fertility traits—NSC1, CR1, CFS1, SP1, and DO1—are summarized in Table 5. The genetic correlations between NSC1 and CR1, CFS1, SP1, and DO1 were medium to high, with values of -0.753, 0.726, 0.925, and 0.980, respectively (Table 5). These findings align with previous studies. For instance, Buaban et al. (2015) reported genetic correlations between NSC1 and these traits as -1.0, 1.0, 0.58, and 0.87, respectively. In this study, negative genetic correlations of medium to high magnitude were observed between CR1 and CFS1, SP1, and DO1, ranging from -0.860 to -0.994 and -0.918 (Table 5), consistent with Buaban et al. (2015), who found values of -0.70, -0.95, and -1.0. These results suggest that selecting cows with higher CR1 may lead to reductions in CFS1, SP1, and DO1 durations.

High and positive genetic correlations were found between first-lactation interval fertility traits (CFS1, SP1, and DO1), ranging from 0.965 to 0.976 (Table 5). Specifically, correlations between CFS1 and SP1 and DO1 were 0.975 and 0.965, respectively, while the correlation between SP1 and DO1 was 0.976 (Table 5). These values are higher than the 0.86 (CFS1 and DO1) and 0.78 (SP1 and DO1) reported by Liu et al. (2007). These findings suggest that CFS1 reflects the ability to return to estrus, CR1 reflects conception performance, and DO1 reflects both return to service and conception performance. Therefore, simultaneous evaluation of CR1 and CFS1 might be more beneficial than evaluating CFS1 alone.

The negative and high genetic correlations between heifer SP0 and CR0 (-0.936, Table 4) and between cow SP1 and CR1 (-0.994, Table 5) are biologically advantageous, as shorter SP values are associated with higher CR. Similarly, the strong positive correlation between SP1 and CFS1 (0.975) indicates that cows with shorter CFS1 tend to exhibit better SP1 values. While both SP and CR reflect the ability of cows to conceive and for embryos to survive, they differ in estrus detection. Prolonged SP can result from unnoticed estrus but does not affect CR observation.

Phenotypic Correlations

Phenotypic correlations among cow fertility traits were generally lower than their genetic counterparts, except for NSC1 and CR1, which showed a correlation of -0.939 (Table 5). The phenotypic correlations of NSC1 with CFS1, DO1, and SP1 were 0.159, 0.841, and 0.786, respectively (Table 5). Buaban et al. (2015) reported phenotypic correlations of NSC1 with CR1, CFS1, DO1, and SP1 as -0.99, -0.09, 0.69, and 0.81, respectively. In this study, phenotypic correlations of CR1 with CFS1, DO1, and SP1 were -0.161, -0.810, and -0.761, respectively (Table 5), which were higher than the values reported by Buaban et al. (2015) of 0.07, -0.75, and -0.70.

The phenotypic correlations between interval traits (CFS1, DO1, and SP1) were 0.106 (CFS1 and DO1), 0.512 (CFS1 and SP1), and 0.906 (DO1 and SP1) (Table 5). Buaban et al. (2015) found a slightly lower correlation of 0.83 between DO1 and SP1. Strong negative phenotypic correlations between CR1 and CFS1, SP1, and DO1 (-0.860, -0.994, and -0.918, respectively, Table 5) were favorable, while positive correlations between NSC1 and CFS1, SP1, and DO1 (0.726, 0.925, and 0.980, respectively), as well as between CFS1 and SP1 (0.975), CFS1 and DO1 (0.965), and SP1 and DO1 (0.976), indicate that any of these traits can be used as a substitute when data on others are incomplete due to reasons such as cow culling or abortion (Guo et al., 2014).

Cow Production Traits

Genetic Correlation

The genetic and phenotypic correlations among first lactation production traits are summarized in Table 6. The genetic correlations between LP1 and DMY1, M305, and TMY1 were -0.767, 0.825, and 0.915, respectively. The genetic correlations between DMY1 and M305, as well as DMY1 and TMY1, were 0.787 and 0.746, respectively. Furthermore, the genetic correlation between M305 and TMY1 was found to be 0.948. These medium-to-high positive genetic correlations suggest that selecting for traits like M305 or TMY1 could simultaneously result in genetic gains in LP1, DMY1, and other related traits.

Phenotypic Correlation

Phenotypic correlations between first lactation production traits were generally lower than the corresponding genetic correlations (Table 6). The correlations between LP1 and DMY1, M305, and TMY1 were 0.055, 0.611, and 0.771, respectively. Similarly, DMY1 exhibited phenotypic correlations of 0.717 with M305 and 0.609 with TMY1. The phenotypic correlation between M305 and TMY1 was notably high at 0.927.

Cow Fertility and Production Traits

Genetic Correlation

Table 7 outlines unfavorable genetic correlations between production traits and most fertility traits. For example, NSC1 showed negative genetic correlations with LP1 (-0.451) and M305 (-0.069), while CR1 had unfavorable correlations with DMY1 (-0.657) and TMY1 (-0.184). Similarly, negative correlations were observed between CFS1 and LP1 (-0.554), SP1 and LP1 (-0.578), and SP1 and DMY1 (-0.078). The genetic correlation between DO1 and LP1 was highly negative (-0.930). These findings indicate that fertility tends to decline as the genetic merit for milk yield increases.

Table 7. Genetic and phenotypic correlations of first lactation reproductive and productive cow traits

Traits[a]	LP1	DMY1	M305	TMY1
	Genetic Correlation			
NSC1	-0.451	0.837	-0.069	0.188
CR1	0.677	-0.657	0.067	-0.184
CFS1	-0.554	0.767	0.038	0.219
SP1	-0.578	-0.078	0.049	0.046
DO1	-0.930	0.480	0.145	0.946
	Phenotypic Correlation			
NSC1	0.375	-0.094	-0.022	0.050
CR1	-0.374	0.095	0.003	-0.060
CFS1	0.206	-0.039	0.020	0.940
SP1	0.282	-0.013	-0.006	0.014
DO1	0.333	-0.028	-0.002	0.030

a: Abbreviations as described in table 1.

Positive genetic correlations were also observed, such as between NSC1 and DMY1 (0.837) or TMY1 (0.188), and between CR1 with LP1 (0.677) or M305 (0.067). Positive correlations were further noted between CFS1 and DMY1 (0.767), M305 (0.038), and TMY1 (0.219), as well as between DO1 and the same production traits. These patterns may be influenced by management decisions, such as earlier insemination for lower-yielding cows.

A positive relationship between production and fertility traits might reflect underfeeding during early lactation. Underfeeding during this critical period could suppress genetic production potential while negatively affecting fertility (Buckley et al., 2003). Negative energy balance (NEB) during early lactation, often due to high milk production, can impair reproductive functions such as follicular development, ovulation, and embryo implantation (Britt, 1992; Veerkamp et al., 2003).

Genetic correlations between lactation length and fertility traits (CFS1, SP1, DO1, NSC1, CR1) were high and unfavorable, indicating that extended lactation primarily results from reduced fertility. For instance, lactation milk yield has been shown to correlate moderately yet unfavorably with fertility interval traits (Tiezzi et al., 2012). This underscores the importance of balancing selection for production and reproductive traits to optimize genetic gains.

Phenotypic Correlation

Phenotypic correlations between fertility and production traits of the first lactation were generally lower than their genetic counterparts (Table 7). Correlations between NSC1 and production traits (LP1, DMY1, M305, TMY1) ranged from -0.094 to 0.375. Relationships between CR1 and production traits were similarly variable, ranging from -0.374 to 0.095. Other fertility traits, such as CFS1 and SP1, exhibited lower correlations with production traits, with values typically near zero, except for DO1, which showed slightly higher associations with certain traits.

These results highlight the complex interplay between milk production and fertility traits, emphasizing the need for an optimal balance in selection strategies to improve both production efficiency and reproductive performance.

CONCLUSION

The findings of this study emphasize the importance of including the effect of service number in conception rate and service period models to account for the declining likelihood of successful artificial insemination (AI) with an increasing number of services.

Heritability estimates for all fertility traits in heifers and cows were generally low, ranging from 0.019 for CR0 to 0.044 for NSC1. However, higher heritability estimates were observed for heifer traits such as AFB, ASB, and AFC, ranging from 0.152 to 0.163, respectively. The low estimates for interval traits (SP1, CFS1, DO1) are consistent with the substantial influence of environmental factors on these traits.

In virgin heifers, NSC0, CR0, and SP0 showed strong and favorable genetic relationships, with CR0 also being favorably correlated with SP0.

The moderate to high genetic correlations observed among heifer fertility traits and among cow fertility traits suggest that including both in selection indices could improve dairy cattle reproductive performance. Incorporating heifer fertility traits into genetic evaluation programs may prove beneficial for enhancing reproductive efficiency and milk production in Egyptian Friesian cows. Early access to data on heifer fertility traits presents an opportunity to integrate these traits into genetic evaluation programs in Egypt.

However, the unfavorable genetic relationships between first-lactation reproductive traits and milk production traits must be carefully considered. Therefore, it is recommended to include heifer fertility traits in selection indices to achieve a balanced improvement in reproductive and productive performance.

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المقاييس الوراثية لصفات الخصوبة فى الإناث والصفات الإنتاجية للموسم الأول لماشية الفريزيان فى مصر

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الملخص

الهدف من هذه الدراسة هو تقدير المقاييس الوراثية والمظهرية للصفات التناسلية للعجلات وصفات أبقار الموسم الأول. تم التحصل على بيانات الأبقار التى ولدت خلال الفترة من عام 1979 وحتى عام 2013 من محطتى سخا والقرضا. تم إستخدام نموذج الحيوان متعدد الصفات فى تحليل هذه الصفات.كان المكافئ الوراثى لصفات الخصوبة فى كلا من العجلات والأبقار منخفض. كانت قيم المكافئ الوراثى للعجلات البكر بالنسبة لصفاتAFB, ASB, AFCمرتفعة بعض الشئ (0.152، 0.161 ، 0.163) بالمقارنة بباقى صفات الخصوبة (0.027، 0.019، 0.022 ، لصفات NSC0, CR0, SP0على التوالى). كانت قيم المكافئ الوراثى للصفات NSC1 و SP1 فى الأبقار مرتفعة (0.044، 0.035) بالمقارنة بمثيلاتها فى العجلات.كان معامل الإرتباط الوراثى بين NSC0 وكل من CR0 و SP0 (-0.903، 0.951) وبين CR0 و SP0 (-0.936) وبين AFB وكلا من ASB و AFC (0.994 و 0.997) وبين ASB و AFC (0.996) وذلك فى الصفات التناسلية للعجلات. وكانت قيم معامل الإرتباط الوراثى بين صفة NSC1 مع كل من SP1 و DO1 (0.925، 0.980)، وبين CR1 مع نفس الصفتين(-0.994 ، -0.918)، وبين CFS1 مع نفس الصفتين (0.975، 0.965) وبين SP1 و DO1 (0.976) وذلك فى الصفات التناسلية للأبقار. إرتفاع قيم معاملات الإرتباط الوراثى فى صفات الخصوبة للعجلات والأبقار تأكد على أن هذه الصفات على نفس الدرجة من الأهمية فى الإنتخاب ويمكن إستخدام إى منها بديلا للآخرين فى كلا من العجلات والأبقار. بناءا على قيم المكافئ الوراثى وكذلك قيم معاملات الإرتباط الوراثى فى صفات العجلات والتى تم التحصل عليها من هذه الدراسة تأكد على أن صفات AFB, ASB, AFC يمكن الإعتماد عليها فى الإنتخاب المبكر للأبقار التامة النضج .