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Genetic and Phenotypic Association between Productive and Reproductive Traits in Friesian Cows In Egypt

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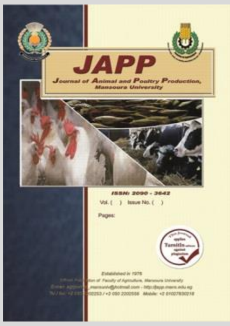

ABSTRACT

Genetic parameters for Friesian cows were estimated from 9155 lactation records for 3625 cows sired by 182 bulls covered 34 years (1982-2015) in two herds (Sakha and El-Karada), belongs to the Animal Production Research Institute, Ministry of Agriculture, Egypt. Multi-trait repeated animal model was employed using the REML procedure to estimate (co)variance components of productive (305-day milk yield-M305 and lactation period-LP) and reproductive traits (number of services per conception-NSC, calving to first service interval-CFS and days open-DO), There is sufficient genetic variation in productive (from 9.5 to 17.1%) and reproductive traits (from 3.9 to 10.3 %). Heritability estimates for M305 and LP traits were 0.204 and 0.110, however, reproduction traits were ranged from 0.010 to 0.044. Genetic correlation between M305 and LP was high (>0.94). Among reproductive traits, absolute genetic correlations were also high (>0.85). Genetic correlations between reproductive and productive traits were high (>0.99). The annual genetic changes were positive for M305, LP, CFS and DO (9.07 kg/yr., 0.30, 0.07 and 0.24 d/yr., respectively), however it was -0.003 number/yr for NSC. The annual phenotypic changes were positive for M305, CFS and DO (12.4 kg/yr., 0.029 and 0.829d/yr., respectively), however it were negative for LP and NSC (-0.265 d/yr. and -0.002 number /yr.).

Keywords: Genetic, Phenotypic trend, Reproduction, Production.

INTRODUCTION

Selection for a long period for high milk production has led to reduced reproductive performance, especially in Holstein herds (Castillo-Juarez *et al*., 2000 and Zink *et al*., 2012). This situation caused a decline in the reproductive efficiency, increased susceptibility to several diseases as will as the risk of culling due to reproductive or health disorders (Rogers *et al*., 1999 and Lassen *et al*., 2003). Consequently, profitability of high-yield dairy herds has reduced (Zink, *et al*., 2012). Therefore, interest in including fertility and functional traits in the breeding goal for dairy cattle population has increased.

It is difficult to determine which traits to include in genetic evaluation for fertility. Calving intervals or days open could be computed from availability of calving dates, assuming a standard gestation length (Jamrozik, *et al*., 2005). Availability of insemination data has allowed the calculation of calving to first service interval, service period, calving to conception interval, as well as number of services till conception. So, reproductive performance of a cow is therefore an array of several traits. They are observed around each pregnancy so that a cow may have repeated measurements as she ages.

A lot of environmental factors as fertility of service sire, frozen semen characteristics, AI technician, feeding, heat detection, etc. were found to have very large effect on fertility traits. Therefore, the heritability of most of reproductive traits was generally below 0.10 (Kadarmideen *et al*., 2003, Wall *et al*., 2003). Reproductive traits are genetically correlated with traits that are either well recorded or more heritable as milk yield (Pryce and Veerkamp, 2001). As a result, direct measures of fertility and records on correlated traits, can be used to supplement predictions of genetic merit for fertility. Genetic correlation between milk yield and fertility in not unity, therefore a favorable selection response can be achieved in fertility while still achieving gains in milk production.

Due to economic value, milk yield has traditionally been the single most important trait of dairy cattle selection programs in most countries (Canmpos *et al*. 1994), therefore, milk yield is expected to show positive (favorable) genetic trend (Musani 1995). In general, improving environmental and breeding management, favorable phenotypic and genetic trends can be achieved. Continuous evaluation of genetic, phenotypic and environmental parameters and trends in dairy cattle, are needed to monitor whether the parameters and trends are desirable for each trait.

The objectives of the present study were (1) estimate genetic parameters, and (2) estimate genetic and phenotypic trends of productive and reproductive traits in the Friesian population in order to investigate genetic improvement possibilities for both.

MATERIALS AND METHODS

Data of the present study covered 34 year (1982-2015), obtained from the history sheets of Friesian research herds raised at Sakha and El-Karada experimental farms-Animal Production Research Institute, Ministry of Agriculture and Land Reclamation, Egypt. A total of 9155 multiparous records were collected for 3625 cows, sired by 182 bulls. During December to May, animals were grazed on Egyptian clover (*Trifolium alexandrinum*) berseem,

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however, during the rest of the year animals were fed on concentrate mixture along with rice straw and limited amount of hay when available. Cows producing milk more than 10 kg/d and those that are pregnant in the last two months of pregnancy were supplemented with extra concentrate mixture ration. Cows were artificially inseminated and machine milked twice a day.

Traits studied are productive traits (305-day milk yield-M305 and lactation period-LP) and reproductive traits (number of services per conception -NSC, calving to first services interval-CFS and calving to conception interval- DO).

Repeatability animal model was used with the REML procedure to estimate (co)variance components by VCE6 program (Groeneveld *et al*., 2010). A linear model included the fixed effects of farm (2), year of calving (34), season of calving (4) and age at calving as a covariate to analyze M305, LP, NSC, CFS and DO. A linear model was also included additive genetic, permanent environmental and error as random effects. Covariances between additive, permanent environmental and residual effects were assumed to be zero. Multivariate EBV were estimated by PEST program (Groeneveld *et al*., 2001).

The genetic trend was estimated by regressing means of estimated breeding values on year of birth for all traits. Phenotypic trend was estimated by regressing phenotypic values on year of birth (SAS, 2011).

RESULTS AND DISCUSSION

Descriptive Statistics

Mean, standard deviations (SD), phenotypic coefficient of variability (CV_p%), genetic standard deviation (SD_g) and genetic coefficient of variability (CV_g%) of productive and reproductive traits are presented in Table 1. Mean estimate ± SD for M305, 2680±1015 Kg (Table 1) was lower than the range of 6384±1237 to 10847±2206 Kg (Faid Allah, 2015, Salem *et al*., 2006 and Abou-Bakr *et al*., 2006) for Holstein commercial herds in Egypt. Mean estimate of LP (302±86 d) was lower than the range of 327±49 to 470±27 d (Abou-Bakr *et al*., 2006, Salem *et al*., 2006, El-Shalmani, 2011, Faid Allah, 2015, Salem and Hammoud, 2016 and Abosaq *et al*., 2017).

Mean estimate of NSC, 3.1±1.6 (Table 1) was greater than the range of 1.7±1.0 to 2.14±1.5 reported by Wall *et al*., (2003), Berry *et al*., (2003), Kadarmideen *et al*., (2003) , Jamrozik *et al*., (2005) and Salem and Hammoud (2016). Estimate of CFS (76.2±29.3 d), Table (1) was lower than the range of 81.6±30.0 to 97±57 (Wall *et al*., 2003, Jamrozik *et al*., 2005 and Toghiani 2012), however it was greater than 73±27 and 72.8 d (Kadarmideen *et al*., 2003 and Berry *et al*., 2003, respectively). Mean estimate of DO, 159.0±77.8 d was nearly the same as 154±88, 157.9±35.7 and 144.49d, (Abou-Bakr *et al*., 2006, Faid Allah, 2015 and Abosaq *et al*., 2017, respectively), however it was greater than the range of 103±54 to 127±77 d reported by Kadramideen *et al*., (2003), Zink *et al*., (2012), Toghiani (2012), Zambrano and Echeverri (2014) and Salem and Hammoud (2016).

The coefficients of genetic variation (CV_g), Table 1, showed a considerable genetic variation existed (>17%) for M305, however, reproductive traits (NSC and CFS) showed CV_g <6%, except DO (10.3%). These estimates were in agreement with Berry *et al*., (2003) for CFS (2.4%), however, the estimate of CV_g for NSC (5.5%, Table 1) was lower than (8.7%) obtained by the same author. These results indicate that there is sufficient genetic variation in reproductive traits which can be used for selecting superior animals for breeding.

Table 1. Mean, phenotypic standard deviation (SD_p), phenotypic coefficient of variation (CV_p%), genetic standard deviation (SD_g) and coefficient of genetic variation (CV_g%) for productive and reproductive traits.

Trait[a]	Mean	SD_p	CV_p%	SD_g	CV_g%
M305 (Kg)	2680	1015	37.9	459	17.1
LP (day)	302	86	28.4	29	9.5
NSC (count)	3.1	1.6	51.9	0.2	5.5
CFS (day)	76.2	29.3	38.4	3.0	3.9
DO (day)	159.0	77.8	48.9	16.4	10.3

a: M305 = 305-day milk yield, LP = lactation period, NSC = number of services till conception, CFS = calving to first service interval and , DO= days open.

Variance Components

Estimates of phenotypic variance, heritability and standard error (h^2±SE), permanent environmental variance ratio and standard error (c^2±SE) and repeatability (t) for productive and reproductive traits are shown in Table (2). h^2 estimates for productive (M305 and LP) traits were generally higher (range 0.110 - 0.204) than reproductive (NSC, CFS and DO) traits (range 0.010 - 0.044). Estimate of h^2 for M305 was 0.204±0.007 which was lower than (0.27±0.014 and 0.33±0.02) reported by Salem *et al*., (2006), Radwan *et al*., (2015), Rushdi (2015) and Abosaq *et al*., ((2017). However, it was greater than (0.130±0.040 and 0.189±0.030) reported by Abou-Bakr *et al*., (2006), Faid Allah (2015) and Salem and Hammoud (2016), in Egypt. Estimate of h^2 for LP (0.110±0.004), was nearly the same as (0.112±0.025 and 0.10±0.018) found by Faid Allah (2015) and Radwan *et al*., (2015), respectively, however it was greater than (0.030±0.020, 0.029+0.038 and 0.07±0.002) reported by Abou-Bakr *et al*., (2006), Salem *et al*., (2006) and Salem and Hammoud (2016), respectively.

Estimate of h^2 for NSC (0.010±0.003) in the present study was nearly the same as (0.016±0.005 and .01) reported by Kadarmideen *et al*., (2003) and De Haas *et al*., (2007), however, it was lower than the range of 0.02±0.01 to 0.04±0.025 obtained by Berry *et al*., (2003), Wall *et al*., (2003), Zambrano and Echeverri (2014) and Salem and Hamouud (2016). Estimate of h^2 for CFS (Table 2), 0.010±0.001 was lower than the range of 0.02±0.008 to 0.04±0.01 (Berry *et al*., 2003, Kadarmideen *et al*., 2003, Wall *et al*., 2003, Toghiani 2012 and Zink *et al*., 2012). h^2 estimate for DO in the present study (0.044±0.001) was greater than the range of 0.014±0.025 to 0.03±0.004 (Abou-Bakr *et al*., 2006, Kadarmideen *et al*., 2003, Zink *et al*., 2012 and Salem and Hammoud, 2016), however, it was smaller (0.06±0.008 and 0.08±0.037) than those obtained by Toghiani (2012) and Zambrano and Echeverri (2014), respectively. Low h^2 estimates for reproductive traits in the present study indicate that improving management practices (intensive feeding, heat detection, semen quality and insemination technique, time of insemination and health programs) would be efficient for improving all reproductive performance of the cow.

Relative permanent environmental variance (c^2) were moderate (Table 2) for M305 and LP (17.3 and 10.5%, respectively), however, it was low for NSC, CFS and DO (1.2, 1.7 and 4.3%, respectively). Berry *et al*., (2003) reported that no permanent environmental variance existed for CFS, however it was 0.2% for NSC. Kadarmideen *et al*., (2003) reported that estimates of c^2, for M305 was 11.5%, however it was 5.4, 2.4 and 2.4% for NSC, CFS and DO, respectively. Ojango and Pollot (2001) reported that c^2 for M305 and LP were 5 and 2.5%, respectively.

Table 2. Phenotypic variance, ratios with respect to phenotypic variance for additive genetic[b] (h^2), permanent environmental[c] effect (c^2) and repeatability (t) estimates for productive and reproductive traits.

Trait[a]	M305	LP	NSC	CFS	DO
σ^2(p)	1031026.0	7382.0	2.69	856.0	6051.8
h^2	0.204	0.110	0.010	0.010	0.044
c^2	0.173	0.105	0.012	0.017	0.043
t	0.377	0.215	0.022	0.027	0.087

a: M305= 305-day milk yield, LP=lactation period, NSC= number of services till conception, CFS =calving to first service interval and DO = days open. b: Standard error for h^2 ranged from 0.001-0.007, c: Standard error for c^2 ranged from 0.001 to 0.009.

Repeatability estimates (t) of M305 and LP (Table 2) were 0.377 and 0.215, which were lower than 0.50 and 0.31 (Salem *et al.,* 2006) and 0.79 and 0.62, respectively (Abou-Bakr *et al*., 2006), in Egypt. Rushdi (2015) with another herd of Holstein Friesian found that t estimates of M305 was 0.39±0.001.In Kenya, Ojango and Pollot (2001) reported that **t** estimates of M305 and LP were 0.34 and 0.11, respectively. In the present study t estimates for NSC, CFS and DO were low (0.022, 0.027 and 0.087, respectively). Kadarmideen *et al*., (2003) in UK, reported that **t** estimates of M305 were 0.398, however it were 0.049, 0.047 and 0.050 for NSC, CFS and DO, respectively. Toghiani (2012) reported that t estimates of CFS and DO were 0.06 and 0.10, respectively. Rushdi (2015) found that t estimate of DO was 0.05±0.047. Low repeatability estimates for reproductive traits indicate that reproductive performance is of little use in predicting later performance, which are strongly influenced by a lot of temporary environmental factors and decision policies of dairy producer with regard to when rebreed a cow, difficulties in detection of estrus and other nutritional factors in the dairy herds.

Genetic correlations

Genetic (r_g±SE), and phenotypic (r_p) correlations are given in Table (3). The genetic correlation of M305 and LP were high, as would be expected (0.941±0.015). In Egyptian studies, the r_g estimates were 0.43, 0.24 and 0.83 between M305 and LP (Salem *et al*., 2006, Abou-Bakr *et al*., 2006 and Abosaq *et al*., 2017, respectively).

Absolute r_g among all reproductive traits (NSC, CFS and DO) were high, as would be expected, the highest value was 0.996+0.006 between CFS and DO, while the lowest value was 0.854+0.093 between NSC and DO. The high negative r_g estimates were found between NSC and CFS (-0.994+0.050) and between CFS and DO (-0.996+0.006) indicated that there is no length of the voluntary waiting period after calving to inseminated cows in these herds and consequently, inseminating early luteal activity cows lead to non successful conception (i.e., more inseminations to conceive), leading to longer service period and consequently longer DO. Kadarmideen *et al*., (2003) also, found that r_g between CFS and DO was 0.70. Genetic correlation between CFS and DO was 0.83 (Zink *et al*., 2012). Strong genetic correlations among reproductive traits suggested that improving one fertility trait would result in a similar parallel improvement in the highly correlated traits and also indicated that animals ranked for one trait would rank similarly in the other correlated traits (Wall *et al.,* 2003 and Kadarmideen *et al*., 2003).

Table 3. Genetic ±SE (above diagonal) and phenotypic (below diagonal) correlations for productive and reproductive traits.

Trait[a]	M305	LP	NSC	CFS	DO
M305		0.941±0.015	0.990±0.001	0.997±0.006	0.993±0.001
LP	0.520		0.995±0.009	0.995±0.002	0.998±0.002
NSC	0.064	0.245		-0.994±0.050	0.854±0.093
CFS	0.070	0.237	0.153		-0.996±0.006
DO	0.145	0.472	0.741	0.332	

a: M305= 305-day milk yield, LP = lactation period, NSC= number of services till conception, CFS = calving to first service interval and DO = days open.

Estimates of genetic correlations between productive and reproductive traits were high (>0.990), indicating a large deleterious impact of production on female fertility. Wall *et al*., (2003) reported that estimates of r_g between milk yield and CFS was 0.49 while it was not significantly differ from zero (0.06) between milk yield and NSC, indicating that increasing milk yield is associated with delay ovarian activity and longer calving interval. Zink *et al*., (2012) found unfavorable genetic correlations between milk yield and each of CFS and DO (0.30 and 0.39). Toghiani (2012) reported that genetic correlations of milk yield with DO was unfavorable (0.355), indicating that increased milk production is associated with increased days to successful conception and consequently longer calving interval. Increasing calving intervals can lead to reduce the number of calves born during the economic period of cows in the herds. Inadequate herd reproductive performance, manifested in prolonged time to conception, and longer calving interval, increased forced culling, less directional culling, fewer calves per cow per year and therefore increased replacement cost and lower net returns (Toghiani, 2012). Reproductive traits exhibit low heritability, but are genetically correlated with traits that are more heritable and can be recorded with greater reliability such as production traits. Hence, these traits are natural candidates as indirect traits for improving fertility of dairy cattle and to support the prediction of genetic merit for fertility (Dal Zotto *et al*., 2007).

Phenotypic correlations

Estimates of phenotypic correlations (r_p) are shown in Table (3). The estimate of r_p between M305 and LP was high (0.520), similar to value reported by Absosaq *et al*., (2017) and contradicted with estimate of Salem *et al*., (2006), -0.21, however it was greater than 0.294 findings of Radwan *et al*., (2015) on Holstein cows raised in commercial dairy herds in Egypt. The discrepancies found between the present study and others may be attributed to differences in statistical models, breeds involved, number of available records per animal, and data editing procedures (Dal Zotto *et al*., 2007).

Among reproductive traits, estimates of r_P between NSC and DO was high (0.741), and consistent with estimates of 0.76 (Kadarmideen *et al*., 2003). High r_P estimates between NSC and DO (0.988) was found by Zambrano and Echeverri (2014). In the present study, estimate of r_P between CFS and DO was 0.332, consistent with estimate 0.39 (Kadarmideen *et al*., 2003) .

Estimates of r_P between M305 and all reproductive traits (Table 3) were low and ranged between 0.064 and 0.145. Estimates of r_P between LP and all reproductive traits were ranged from 0.237 to 0.472. In Egypt, Faid Allah (2015) and Radwan *et al*., (2015) found that r_p between LP and DO were 0.894 and 0.642, respectively in Holstein commercial dairy herd. Kadarmideen *et al*., (2003) found that r_P between milk yield and DO was 0.22.

Genetic and Phenotypic Trends

Figures 1a&b shows that, after an initial decrease in mean breeding values for M305 and LP, there has been a steady increase for cows born between 2004 and 2012. Over 34-yr period, the average annual increase in mean breeding values were 9.07$\pm$0.61 Kg/yr for M305 and 0.30$\pm$0.05 d/yr for LP. These results indicated that there is success in choosing better sires to improve production traits with improved management and nutrition. Genetic change for NSC decreased by -0.003$\pm$0.001 number/yr, however, there is an unfavorable positive genetic trend in CFS and DO traits (Figures 1c, d, e).

The interval traits increased over the last years, resulting in longer CFS and DO. The annual genetic change in interval traits were positive (0.07$\pm$0.02 and 0.24$\pm$0.04 for CFS and DO, respectively) indicating that more attention should be given to reproductive traits to avoid losses related to these traits in the future. As the trait is mainly governed by non-genetic factors, managemental practices should be improved for lowering the interval traits (Singh *et al.*, 2002). Atil and Khattab (2005) found that genetic trend for 305 d milk yield to be 44.85 kg/yr and concluded that selection objective focused on choosing the best sires and cows to be the next generation parents would lead to increase in milk traits and decrease in reproductive traits simultaneously. In Egypt also, Osman *et al*., (2013) found that the annual genetic trend for milk yield in the first and second lactations are positive and being 18.9 kg/yr and 5.99 kg/yr, respectively. Selection for milk production with little or no emphasis on reproduction has led to a decline in reproduction performance in dairy population (Weller and Ezra, 2004; Gonzales-Recio and Alenda, 2005, Berry and Cromic, 2009 and El-Shalmani, 2011). De Jong (2005) reported undesirable genetic trends for CFS from 1982 to 1998 in Netherlands Holstein cows. Andersen-Ranberg *et al*., (2005) reported that the genetic change for CFS was toward a longer interval from calving to first service, i.e., unfavorable. The estimated annual genetic change of CFS was 0.11 d /yr. in the period from 1980 to 1998. Ghiasi and Honarvar (2016) reported that genetic trend in fertility traits was as desired and the annual genetic trends for NSC, CFS, SP and DO were -0.0029 number /yr, -0.062, -0.041 and -0.24 d/yr, respectively.

The estimated annual phenotypic change increased by 12.4 $\pm$7.06 kg/yr, for M305, however LP decreased by -0.265$\pm$0.337 d/yr (Fig. 2a & b). The phenotypic changes were -0.002+0.005, 0.029$\pm$0.117 and 0.829$\pm$0.277 for NSC, CFS and DO, respectively (Fig. 2c, d, e). The negative value for NSC was favorable decrease the number of service per conception, however positive values for CFS and DO were unfavorable long interval traits. In USA Holstein cows NSC were increased from 1.76 to 3.0 over a period of 20 years (Lucy, 2001).

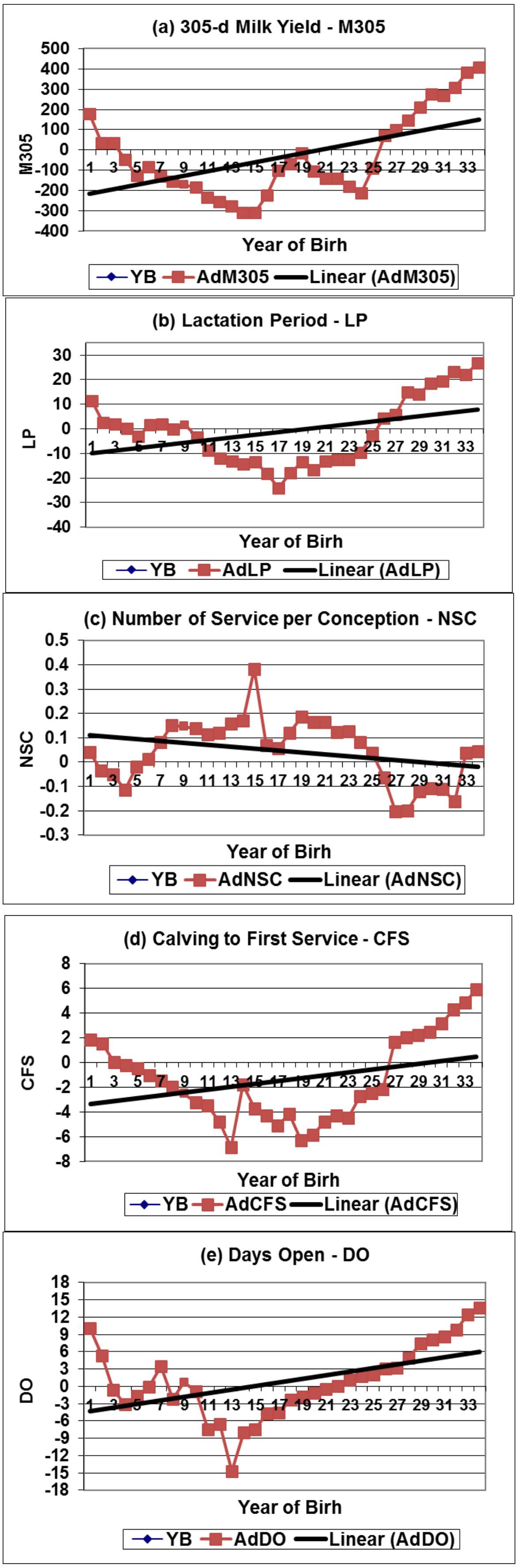

Figure 1. Genetic Trends for (a) M305, (b) LP, (c) NSC,(d) CFS, (e) DO.

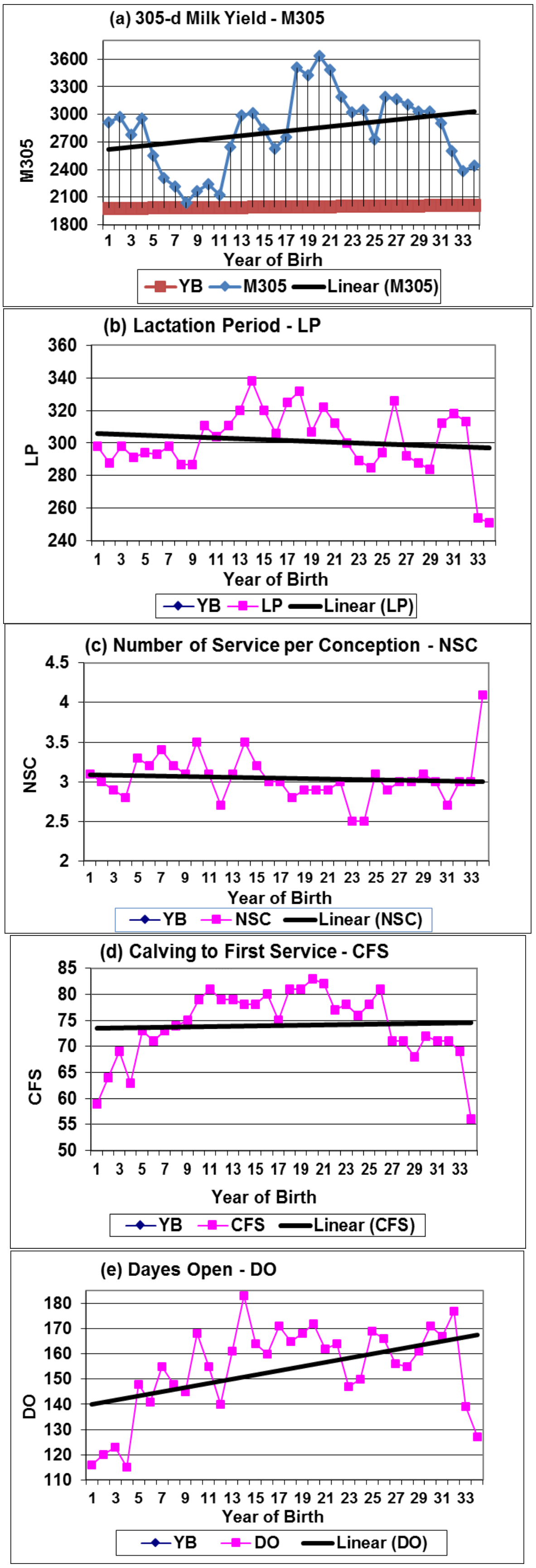

Figure 2. Phenotypic Trends for (a) M305, (b) LP, (c) NSC, (d) CFS, (e) DO. (d) CFS, (e) DO.

In Ireland, NSC increased from 1.54 to 1.75 between 1990 to 2000 (Mee *et al.*, 2004). De Vries and Risco (2005) found that the CFS for Holstein cows increased from 84 in 1983 to 104 d in 2001. Vanraden *et al.*, (2004) reported a decline in fertility shown by phenotypic trends for DO. In United States, Washburn *et al.*, (2002) reported that DO increased from 126 d in 1976 to 169 d in 1999 . El-Shalmani (2011) reported that the annual phenotypic changes of M305, LP and Do were 42 kg/yr, 2.64 d/yr and 1.03 d/yr, respectively. Ghiasi and Honarvar (2016) reported that phenotypic trend for CFS decrease by -1.6 d/yr, this shows that ability of cow to recycle after calving is improved overtime, however NSC showed undesirable positive trend and increased by 0.04 number/yr.

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العلاقات الوراثية والمظهرية بين الصفات الإنتاجية والتناسلية لأبقار الفريزيان في مصر

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تم تقدير المعالم الوراثية لأبقار الفريزيان من ٩١٥٥ سجل حليب لـ٣٦٢٥بقرة بنات لـ١٨٢طلوقة على مدى ٣٤سنة (من ١٩٨٢ وحتى ٢٠١٥) فى مزرعتين (سخا والقرضا) التابعتين لمعهد بحوث الإنتاج الحيوانى - وزارة الزراعة – مصر . تم عمل التحليل الإحصائى باستخدم نموذج الحيوان المتكرر للصفات المتعددة بطريقة الإحتمالات العظمى المحددة (REML)، وذلك لتقدير مكونات التباين والتغاير للصفات الإنتاجية (إنتاج اللبن فى ٣٠٥ يوم حليب - M305، وطول موسم الحليب - LP) والصفات التناسلية (عدد التلقيحات اللازمة للإخصاب -NSC ، الفترة من الولادة وحتي أول تلقيحة - CFS وفترة الأيام المفتوحة - DO). كان هناك اختلاف وراثى واضح (CVg) فى الصفات الإنتاجة (من ٩,٥% إلى ١٧,١%) وتراوح فى صفات الأداء التناسلى بين ٣,٩% إلى ١٠,٣% . كانت تقديرات المكافئ الوراثى (h2) لصفتى M305، LP هى ٠,٢٠٤ و٠,١١٠ على التوالى، بينما فى الصفات التناسلية تراوحت قيم المكافئ الوراثى بين ٠,٠١٠ إلى ٠,٠٤٤ . كان الإرتباط الوراثي بين M305 و LPعالى (اكبر من ٠,٩٤) ، كما كانت الإرتباطات الوراثية المطلقة بين الصفات التناسلية أيضا عالية (اكبر من ٠,٨٥) . كانت الإرتباطات الوراثية بين الصفات الإنتاجية والتناسلية عالية وغير مستحبة (أكبر من ٠,٩٩). كانت قيم التحسين الوراثى السنوى موجبه لصفات DO, CFS, LP, M305 (٩,٠٧ كجم / سنة و٠,٣٠، ٠,٠٠٧, ٠,٢٤ يوم / سنة ، على التوالى) ، ببينما كانت سالبه (- ٠,٠٠٣ تلقيحة / سنة) لصفة NSC. كانت قيم التحسين المظهرى السنوى موجبه لصفات M305، CFS و DO (12,4كجم / سنة ، ٠,٠٢٩ و ٠,٨٢٩ يوم / سنة ، على التوالي) ، بينما كانت القيم سالبة لكل من LP و NSC (-٠,٢٦٥ يوم / سنة و – ٠,٠٠٢ تلقيحة / سنة ، على التوالى).