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Genetic and Phenotypic Aspects and Trends of Longevity and Lifetime Production Traits in Friesian Cattle in Egypt

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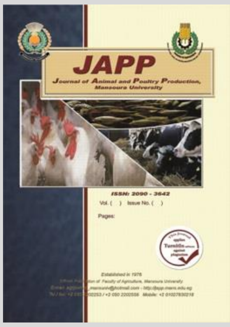

ABSTRACT

A total of 2914 cow records with complete set of all traits, daughters of 66 sires and 427 dams were used. The VCE animal model programs were used to estimate heritability, genetic and phenotypic correlations for longevity and lifetime production traits.Heritability estimates were 0.087, 0.149, 0.159 and 0.101 for LLNO, HL, PL and LLP, respectively, however it were 0.187, 0.176, 0.154, 0.146 and 0.108 for LM305, LTMY, LMYHL, LMYLP and LPHL, respectively. Genetic correlations between longevity traits (LLNO, HL, PL and LLP) were high and ranged from 0.901 between HL and LLP to 0.991 between LLNO and PL. Genetic correlations between lifetime production traits were high and ranged from 0.843 between LMYHL and LPHL to 0.995 between LM305 and LTMY. Phenotypic correlations were less than the corresponding genetic correlations among most traits. Genetic trend over 35 years was favorably positive for lifetime production traits, however it was unfavorably negative for longevity traits. The annual genetic changes were 53.6kg for LM305, 65.5kg for LTMY, 0.031kg for LMYHL, 0.063kg for LMYLP and 0.021% for LLPHL, however the annual genetic changes were -0.080, -0.356d, -4.9d and -4.9d for LLNo., LLP, HL and PL, respectively. Phenotypic trend was unfavorable deteriorating negative for all longevity and lifetime production traits over 35 years, except LMYLP, it was favorably positive.

Keywords: Genetic parameters, trends, longevity and lifetime, Friesian.

INTRODUCTION

Longevity and lifetime yield traits are of major economic importance in dairy cattle (VanRaden and Wiggans, 1995). Longevity affects profitability by reducing replacement costs due to reducing number of replacement heifers needed to be raised with higher selection intensity and increasing the proportion of cow producing at mature level with more opportunities to voluntary culling (Powell and VanRaden, 2003, Sewalem *et al*.,2005, Tsuruta *et al*., 2005). In Egypt, Sadek *et al*., (2009) reported that genetic correlation between first lactation milk yield and longevity traits (number of completed lactations, productive life, culling age, lifetime lactation length, lifetime milk yield) ranged from 0.20 to 0.45. In many countries, functional traits have received increasing attention in breeding programs for dairy cattle (Zavadilova and Stipkova, 2013). Functional longevity reflects fertility, health and overall fitness of cow, not the level of cow's production. The relationship between longevity and animal health and integrity makes longevity a high desirable trait in dairy production. When longevity of dairy cows is analyzed, age at first calving (AFC) is regularly taken into account (Zavadilova and Stipkova, 2013).

The main objective in animal breeding is to increase the economic efficiency of animal production by directional selection (Tarres *et al*., 2006). Functional traits refer to traits that increase the economic efficiency by reducing costs instead of increasing quantity of saleable products. So, domestic animals have to be alive and to reproduce normally to be profitable for the breeder. Functional traits have increased significantly their economical importance, in particular in dairy cattle (Essel, 1998). In general, functional traits exhibit rather low heritabilities, leading to genetic evaluation with low reliabilities for young sires (Ducrocq, 2001). Fortunately, more heritable traits can be used as early predictors of these functional trait e.g., somatic cells count or functional longevity (Weigel *et al*., 1998; Druet *et al*., 1999; Larroque and Ducrocq, 2001; Buenger *et al*., 2001).

The cost of raising weaned calves depends largely on how early cows calve and how long they remain in production. If cows are productive extendedly and raise more progeny, specific cost of raising per calf decrease proportionally. Consideration of life span and, specifically, longevity plays an important role in practical breeding (Dakay, *et al*., 2006). One common way to measure longevity is length of productive life, the time from first calving to culling or death of a cow (Ajili, *et al*., 2007). Increased longevity reduces the direct costs of raising or purchasing replacement females (Rogers *et al*., 2004; Ajili, *et al*., 2007).

Genetic evaluations provide the base for ranking of animals and estimate the magnitude of differences between animals (Hussain, *et al*., 2014). The Best Linear Unbiased Prediction (BLUP) procedure is widely used not only to sire evaluation but also to estimate the genetic trend (Mingfeng *et al*., (1988). The effectiveness of breeding programs is determined through calculation of genetic trend (Ibrahim *et al*., 2009). Genetic trend estimates represent the best tool to follow genetic changes in a livestock population (Falconer and Mackay, 1996).

The objective of this study was to get insights into the genetic and phenotypic parameters and trends of longevity and lifetime production traits of Friesian cattle in Egypt.

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MATERIALS AND METHODS

Data of the present study were collected over the period from 1979 to 2013 from two herds of Friesian cattle raised at Sakha and El-Karada experimental stations, located in the northwest of the Nile Delta in Kafr El-Sheikh governorate, belong to Animal Production Research Institute, Ministry of Agriculture and Land Reclamation, Dokki, Giza, Egypt. Data were 3940 complete lactation records for cows that had been culled by the time data were collected.

All cows whose sires and/or dams had been unknown identification numbers were discarded. Cows whose age at first calving was less than 22 or greater than 42 months were eliminated. Records were deleted if first lactation days in milk were less than 150 days. Data editing left 2914 cows with complete set of all longevity and lifetime production traits, daughters of 66 sires and 427 dams were used. Longevity traits were number of lactations completed (LLNO); length of herd life (HL), i.e., time elapsed between birth and culling/death date in days; length of productive life (PL), time elapsed between first calving date and culling /death date in days, and total days in lactation over all lactation (LLP). Lifetime production traits expressed as: 305-day milk yield (LM305), i.e., accumulation of individual lactation 305-day milk yield in Kg of individual cow; total milk yield (LTMY) , i.e., accumulation of individual lactation total milk yield in Kg of individual cow; average of lifetime milk yield per day of herd life (LMYHL), i.e., LTMY/HL, Kg.; average of lifetime milk yield per day of lactation period (LMTLP), i.e., LTMY/LP, Kg., and longevity index (LLPHL), i.e., (LLP/HL)*100.

Different fixed effects affecting longevity and lifetime traits were accounted (Table 1) using GLM procedure of SAS (2011). Age at first calving (AFC) classes every three months were <23, 23-, 26-, 29-, 32-, 35- and 38-42 mo. Nine first lactation service period classes were zero service period, <21, 22-43, 44-65, 66-87, 88-109, 110-131, 132-153, and >153 day. Nine lactation period of first lactation were 150-180, 181-211, 212-242, 243-273, 274-304, 305-335 336-366, 367-397 and >397 day, and ten lifetime lactation number. Genetic and phenotypic parameters were estimated by using VCE6 program (Groeneveld *et al*., 2010) after incorporating animal, error as random effects as well as fixed effects (Table 1) in the model. Pedigree file was included to estimate EBV by using PEST program (Groeneveld *et al*., 2001), fitting multi-trait animal model. Genetic and phenotypic trends were measured as the regression of the breeding values and least square means on year of first calving.

Table 1. Statistical model summary[a] for Longevity and lifetime production traits

Trait[b]	F	M1c	Y1c	AFCc	SP1c	LP1c	LLNo	Model No.
LLNO	X	X	X	X		X		1
LM305	X	X	X	X		X	X	2
LLP, HL, PL, LTMY, LMYHL, LMYLP, LPHL	X	X	X	X	X	X	X	3

a: F: farm, M1c: month of first calving, Y1c: year of fist calving, FMY1c: farm-month-year of first calving, AFCc: age at first calving classes, SP1c: first lactation service period classes, LP1c: lactation period classes of first lactation, LLNo: lifetime lactation number,
b: LLNo: lifetime lactation number, LM305: lifetime 305-day milk yield, LTMY: lifetime total milk yield, LLP: lifetime lactation period, HL: herd life, PL: productive life, LMYHL: lifetime daily milk yield per day of herd life, LMYLP: lifetime daily milk yield per day of lactation period, and LLPHL: longevity index.

RESULTS AND DISCUSSION

Descriptive statistics

Means of the present study were 3.0, 2094.9d, 1107.4d, 872.3d, 7507.0kg, 8224,6kg, 3.32kg, 8.84kg and 36.35% for LLNO, HL, PL, LLP, LM305, LTMY, LMYHL, LMYLP and LLPHL, respectively (Table 2). Zahed *et al*., (2004) in Holstein cattle of commercial herds in Egypt, found that means of LLNO, HL, PL, LLP and LTMY were 5.6, 106.1 mo., 82.5 mo., 67.8 mo., and 36800 kg, respectively. Sadek *et al* (2009) reported that means of NOL, HL, LPL, LLP and LTMY were 3.34, 76.4 mo., 45.0 mo., 35.8 mo. and 8831 kg, respectively.

Coefficient of variability (CV%) of the present study (Table 2) were 62.5, 9.5, 17.2, 20.8, 32.4, 35.7, 29.8, 20.1 and 16.1% for LLNO HL, PL, LLP, LM305, LTMY, LMYHL, LMYLP and LLPHL, respectively. Values of CV% were 24.4, 21.9, 28.3, 37.9 and 30.3% for LLNO, HL, PL, LTMY and LLP, respectively (Zahed *et al*., 2004). Sadek *et al*., (2009) reported that values of CV% were 62.66, 41.44, 70.19, 68.30 and 83.17% for LLNO, HL, PL, LLP and LTMY, exhibiting high variation.

Table 2. Descriptive statistics for longevity and lifetime productive traits of Friesian cattle.

	Trait	Mean	SD	CV%	R^2%	Min.	Max.
Longevity Traits	LLNO (no.)	3.00	1.88	62.5	41.9	1	10
	HL (d)	2094.9	199.8	9.5	95.9	677.0	5404.0
	PL (d)	1107.4	193.6	17.2	96.1	110.0	4550.0
	LLP (d)	872.3	181.3	20.8	94.8	150.0	3685.0
Lifetime production Traits	LM305 (Kg)	7507.0	2435.7	32.4	90.6	633.0	45835.0
	LTMY (Kg)	8224.6	2933.5	35.7	88.8	633.0	53382.0
	LMYHL (kg)	3.32	0.99	29.7	82.8	1.0	10.0
	LMYLP (kg)	8.84	1.78	20.1	65.4	4.0	17.0
	LPHL (%)	36.35	5.9	16.1	90.5	22.0	177.0

Heritability Estimates

Heritability estimates for LLNO, HL, PL, LLP, LM305, LTMY, LMYHL, LMYLP, and LPHL were 0.087, 0.149, 0.159, 0.101, 0.187, 0.176, 0.154, 0.146 and 0.108, respectively (Table 3). The estimates of the present study for LLNO, HL, PL, LLP and LTMY were lower (0.04, 0.05, 0.06, 0.05 and 0.15) than estimates of the same traits as reported by Zahed *et al*., (2004), and it was also lower than estimates for NOL, PL, HL, LLP and LTMY reported by Sadek *et al*., (2009). The estimates of the present study for NOL, PL, HL, LLP and LTMY were higher than those reported in the literature, which ranged from 0.022 to 0.172 (Hoque and Hodges, 1980, Ashmawy, 1985, VanRaden and

Klaaskate, 1993, Vollema and Groen, 1996, Valencia *et al*., 2002, and Tsuruta *et al*., 2005).

Genetic and Phenotypic Correlations

Genetic correlations between LLNO and each of HL, PL, LLP, LM305, LTMY, LMYHL, LMYLP and LPHL were 0.974, 0.991, 0.924, 0.996, 0.968, 0.913, 0.944 and 0.979, respectively (Table 3). Genetic correlations between HL and each of PL, LLP, LM305, LTMY, LMYHL, LMYLP and LPHL were 0.962, 0.901, 0.963, 0.919, 0.734, 0.860 and -0.914, respectively (Table 3). Genetic correlations between PL and each of LLP, LM305, LTMY, LMYHL, LMYLP and LPHL were 0.912, 0.968, 0.898, 0.732, 0.818 and -0.767, respectively (Table 3). Genetic correlations between LLP and each of LM305, LTMY, LMYHL, LMYLP and LPHL were 0.895, 0.939, 0.847, 0.850 and 0.975, respectively (Table 3). Genetic correlations between LM305 and each of LTMY, LMYHL, LMYLP and LPHL were 0.995, 0.953, 0.898 and 0.903, respectively (Table 3). Genetic correlations between LTMY and each of LMHL, LMLP and LPHL were 0.917, 0.951 and 0.907, respectively (Table 3). Genetic correlations between LMHL and each of LMLP and LPHL were 0.942 and 0.843 (Table 3). Genetic correlation between LMYLP and LPHL was 0.858 (Table 3).

In Egypt, Zahed *et al*., (2004) found that genetic correlation between LLNO and each of HL, PL, LLP and LTMY were 0.98, 0.98, 0.59 and 0.90, respectively. Genetic correlations between HL and each of PL, LLP and LTMY were 1.0, 0.73, and 0.85 respectively (Zahed *et al*., 2004). The same authors reported that genetic correlation between PL and each of LLP and LTMY were 0.74 and 0.85, however genetic correlation between LLP and LTMY was 0.96. Sadek *et al*., (2009) reported that genetic correlations between NOL, LPL, HL and LLP were quit high and ranged from 0.96 to 1.0, indicating that many of the same factors are involved in controlling these traits and further measure the same trait. Sadek *et al*., (2009) reported that genetic correlation between LLNO and each of PL, HL, LLP were 0.99, 0.99 and0.98, respectively, however correlations between PL and each of HL and LLP were 1.0 as well as between HL and LLP (1.00). The same authors added that genetic correlations between LTMY and each of LLNO, PL, HL and LLP were 0.96, 0.99, 0.99 and 0.99, respectively. Sadek *et al*., (2009) concluded that genetic correlations between lifetime traits were quit high indicating that many of the same factors are involved in controlling these traits and further measure the same trait.

Phenotypic correlations were generally lower than genetic correlations. The phenotypic correlations ranged from 0.468 between LPHL and LM305 to 0.939 between LTMY and LM305, (Table 3). In Egypt, Zahed *et al*., (2004) reported that phenotypic correlations between LLNO and each of HL, PL, LLP and LTMY were 0.84, 0.84, 0.48 and 0.53, respectively. Phenotypic correlations between HL and each of PL, LLP and LTMY were1.0, 0.68 and 0.62, respectively (Zahed *et al*., 2004). Phenotypic correlations between HL and each of PL, LLP and LTMY were 1.0, 0.68 and 0.0.62 respectively (Zahed *et al*., 2004). The same authers reported that phenotypic correlation between PL and each of LLP and LTMY were 0.66 and 0.62, however genetic correlation between LLP and LTMY was 0.90. Phenotypic correlations between LLNO, LPL, HL and LLP ranged from 0.91 to 0.98, which were slightly lower than genetic correlations for the same traits (Jairath *et al*., 1995 and Sadek *et al*., 2009). Sadek *et al*., (2009) reported that phenotypic correlation between LLNO and each of PL, HL, LLP were 0.96, 0.96 and0.95, respectively, however correlations between PL and each of HL and LLP were 1.0 and 0.98 as well as between HL and LLP (0.98). The same authors added that phenotypic correlations between LTMY and each of LLNO, PL, HL and LLP were 0.91, 0.95, 0.95 and 0.97, respectively.

Table 3. Heritability, genetic and phenotypic correlations for Longevity and lifetime production traits

Trait	LLNO	HL	PL	LLP	LM305	LTMY	LMYHL	LMYLP	LPHL
LLNO	0.087	0.974	0.991	0.924	0.996	0.968	0.913	0.944	0.979
HL	0.666	0.149	0.962	0.901	0.963	0.919	0.734	0.860	-0.914
PL	0.544	0.913	0.159	0.912	0.968	0.898	0.732	0.818	-0.767
LLP	0.561	0.484	0.502	0.101	0.895	0.939	0.847	0.850	0.975
LM305	0.698	0.498	0.743	0.564	0.187	0.995	0.953	0.898	0.903
LTMY	0.612	0.565	0.684	0.680	0.939	0.176	0.917	0.951	0.907
LMYHL	0.628	0.670	0.544	0.554	0.897	0.603	0.154	0.945	0.843
LMYLP	0.792	0.611	0.520	0.841	0.510	0.524	0.697	0.146	0.858
LPHL	0.500	0.628	0.539	0.823	0.468	0.547	0.605	0.781	0.108

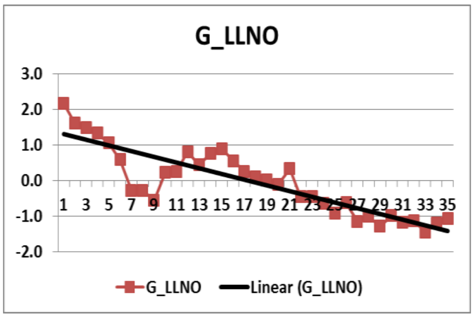
Genetic Trend

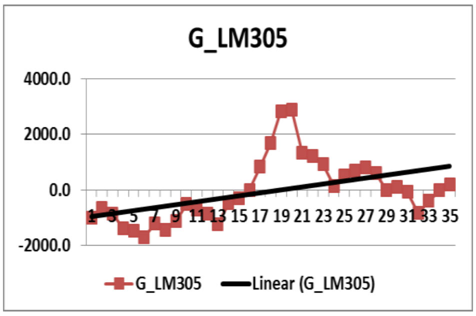
Mean breeding values increased over 35 years for LM305, LTMY, LMYHL, LMYLP and LLPHL (Figure1 b, c, g, h, i). The genetic changes were favorably positive, and a linear regression analysis of BV for these traits on year of first calving resulted in annual genetic changes of 53.6kg (P<0.01) for LM305, 65.5kg (P<0.001) for LTMY, 0.031kg (P<0.001) for LMYHL, 0.063kg (P<0.001) for LMYLP and 0.021% (P<0.001) for LLPHL (Table 4). The genetic trends were unfavorably decreasing over 35 years for LLNo, HL, PL and LLP (Figure 1 a, d, e, f). The annual genetic changes were -0.080 (P<0.001) for LLNo, -4.9d (P<0.001) for HL, -4.9d (P<0.001) for PL and -0.356d (P>0.05) for LLP (Table 4). Positive genetic trends indicate that the selection program performs correctly. Jenko *et al*., (2015) reported that the linear regression coefficient of the genetic trend for LTMY was 0.041, however it was remained stable (0.006) for PL.

Table 4. Linear regression equations of breeding values and phenotypic values for longevity and lifetime production traits on year of birth for Friesian cows.

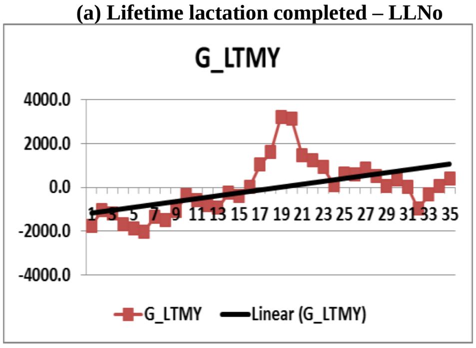
Trait[a]	Genetic Trend	Sig.[b]	Phenotypic Trend	Sig.
LLNo. (no.)	160X – 0.080	***	152X – 0.075	***
HL (d.)	9809X – 4.9	***	64514X – 31.3	***
PL (d.)	9865X – 4.9	***	68017X – 33.5	***
LLP (d.)	709X – 0.356	n.s.	48265X –23.7	***
LM305 (kg)	–107079X + 53.6	**	322099X –157.6	***
LTMY (kg)	–130851X + 65.5	***	330101X – 161.3	***
LMYHL (kg)	- 61.9X + 0.031	***	66.0X – 0.031	*
LMYLP (kg)	-125X+ 0.063	***	-87.1X + 0.048	*
LLPHL (%)	-42.4X + 0.021	***	1197X – 0.582	***

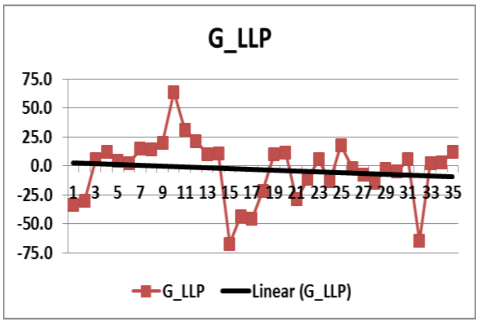
a: the abbreviations as described in Table 1.
b: n.s.= non significant, * = significant at P<0.05, ** = significant at P<0.01,
*****= significant at P<0.001.**



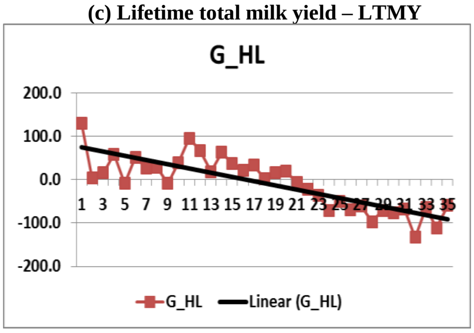


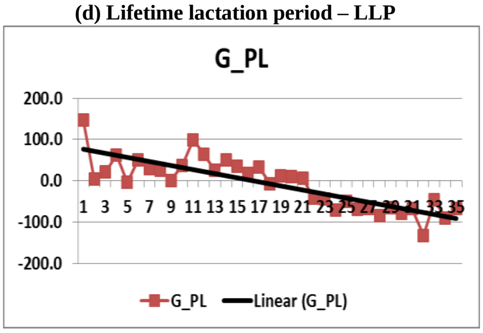
(a) Lifetime lactation completed – LLNo **(b) Lifetime 305-day milk yield - LM305**



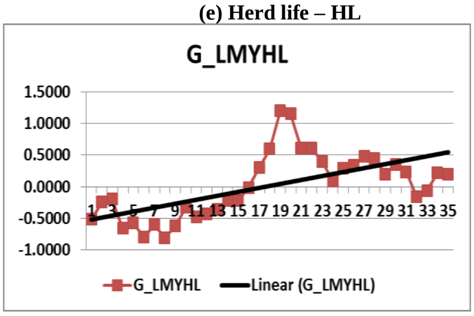


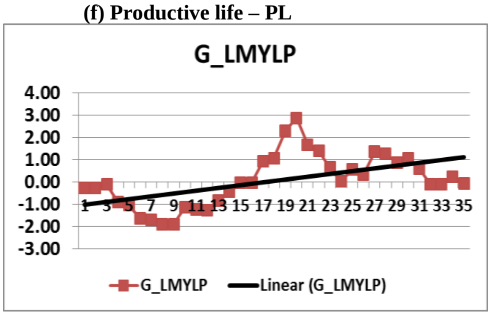
(c) Lifetime total milk yield – LTMY **(d) Lifetime lactation period – LLP**



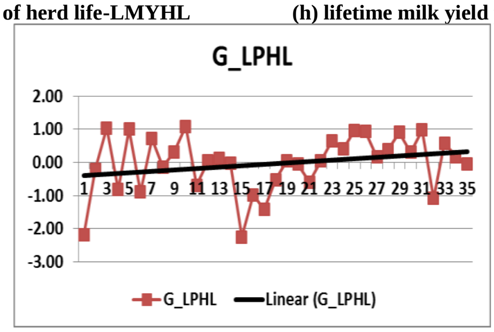


(e) Herd life – HL **(f) Productive life – PL**





(g) lifetime milk yield per day of herd life-LMYHL **(h) lifetime milk yield per day of lactation period-LMYLP**

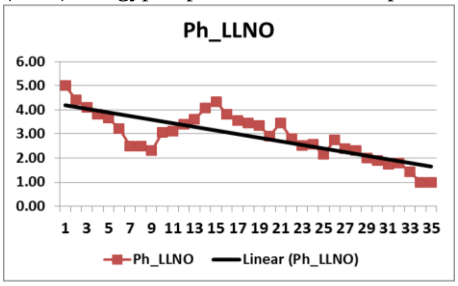


(i) Longevity index - LLPHL

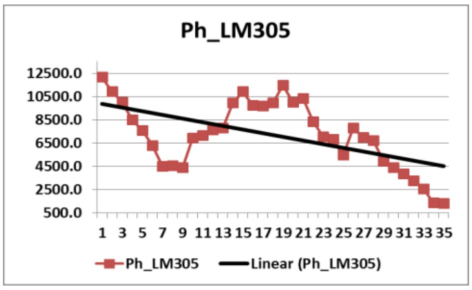
Figure 1. Genetic trend for (a)LLNO, (b) LM305, (c) LTMY, (d) LLP, (e) HL, (f) PL, (g) LMYHL, (h) LMYLP, (I) LLPHL.

Phenotypic Trend

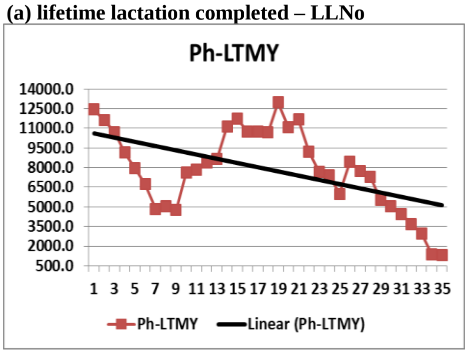
Figure (2 a, b, c, d, e, f, g, i) depicts the unfavorable deteriorating phenotypic trend over 35 year for most of longevity and lifetime production traits except LMYLP (Figure 2 h). The linear regression analysis of phenotypic means of longevity and lifetime traits on year of first calving resulted in negative annual phenotypic changes of -0.075 ($P<0.001$) for LLNo, -31.3d ($P<0.001$) for HL, -33.5d ($P<0.001$) for PL, -23.7d ($P<0.001$) for LLP, -157.6kg ($P<0.001$) for LM305, -161.3kg ($P<0.001$) for LTMY, -0.031kg ($P<0.05$) of LMYHL and -0.582% ($P<0.001$) for LLPHL (Table 4). However, a positive favorable phenotypic trend was observed for LMYLP (Figure 2 h) with a phenotypic change (Table 4) of 0.048kg (P<0.05). The deteriorating phenotypic trends indicate that the presence of some environmental inadequacies. Rizzi *et al*., (2002) reported that Holsteins showed a decrease in phenotypic trend until 1985 and an increase in 1986 for HL, PL and LLNo. Halawa (2007) in Egypt reported that over the period from 1961 to 1994, LTMY shows an increase until its peak in year 1968 after that a steady decrease until 1988 then sudden increase followed by a sharp decrease until reached the lowest level in year 1994. The same author added that both of HL and PL show fluctuation from year to another over the period from 1961 to 1994.



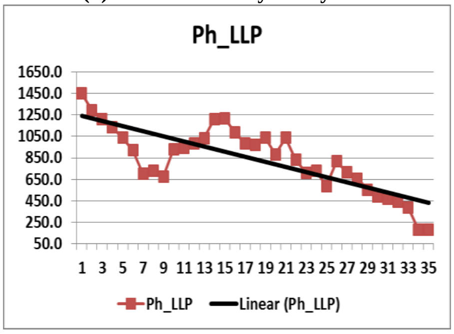
(a) lifetime lactation completed – LLNo



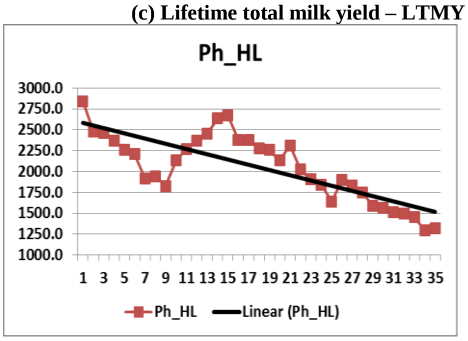
(b) Lifetime 305-day milk yield - LM305



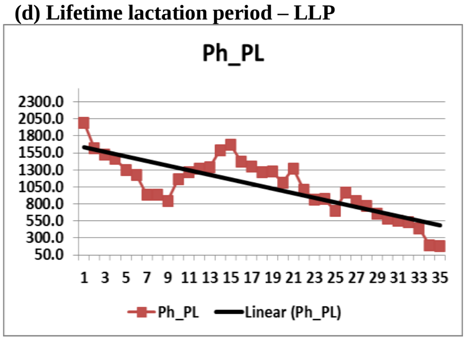
(c) Lifetime total milk yield – LTMY



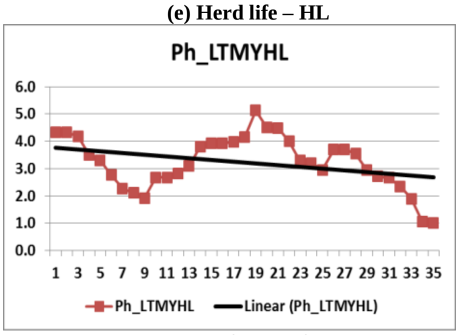
(d) Lifetime lactation period – LLP



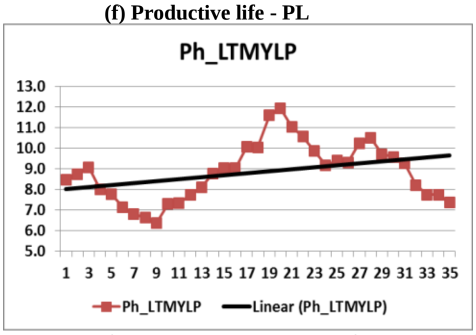
(e) Herd life – HL



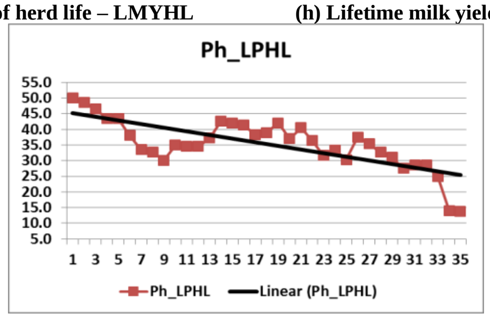
(f) Productive life - PL



(g) Lifetime milk yield per day of herd life – LMYHL



(h) Lifetime milk yield per day of lactation period-LMYLP



(i) Longevity index - LLPHL

Figure 2. Phenotypic trend for (a) LLNO, (b) LM305, (c) LTMY , (d) LLP, (e) HL, (f) PL, (g) LMYHL, (h) LMYLP, (I) LLPHL.

CONCLUSION

High genetic correlations between longevity traits (>0.961) and between LM305 and LTMY (>0.994) indicate that these traits were measuring the same thing and the performance of any of these traits would refer to the level of performance of any of the other traits.

The linear regression coefficient of the genetic trend over 35 year was positive for lifetime production traits (LM305, LTMY, LMTHL, LMYLP and LPHL), however it was negative for longevity traits (LLNo, LLP, HL and PL). Phenotypic trend was negative for all longevity and lifetime production traits except LMYLP, it was positive.

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المفاهيم والإتجاهات الوراثية والمظهرية لصفات طول الحياة وطول الحياة الإنتاجية فى ماشية الفريزيان فى مصر

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الملخص

تم إستخدام سجلات ٢٩١٤ بقرة بنات لـ٦٦ طلوقة و٤٢٧ أم، متضمنة كل الصفات المدروسة. تم إستخدام برنامج VCE لنموذج الحيوان لتقدير المكافئ الوراثى ومعاملات الإرتباط الوراثى والمظهرى لصفات طول الحياة وكذلك صفات طول الحياة الإنتاجية. كانت تقديرات المكافئ الوراثى ٠,٠٨٧، ٠,١٤٨، ٠,١٥٩و٠,١٠١ لصفات LLNO, HL, PL, LLP على التوالى بينما كانت ٠,١٨٧، ٠,١٥٤،٠,١٧٦، ٠,١٤٦ و ٠,١٠٨ لصفاتLM305 LTMY, LMYHL, LMYLP, LPHL , على التوالى. كانت قيم معامل الإرتباط الوراثى بين صفات طول الحياة عالية وتراوحت من ٠,٩٠١ بين صفتى HL و LLP إلى ٠,٩٩١ بين صفتى LLNO و PL. كانت قيم معامل الإرتباط الوراثى بين صفات طول الحياة الإنتاجية مرتفعة وتراوحت من ٠,٨٤٣ بين صفتى LMYHL و LPHL إلى ٠,٩٩٥ بين صفتى LM305 و LTMY. كانت قيم معامل الإرتباط المظهرى أقل من مثيلاتها الوراثية بين معظم الصفات. كان إتجاه التحسين الوراثى خلال فترة ٣٥ عام موجب ومرغوب فيه بالنسبة لصفات طول الحياة الإنتاجية ، بينما كان التحسين الوراثى سالب وغير مرغوب فيه بالنسبة لصفات طول الحياة. كان معدل التحسين الوراثى السنوى ٥٣,٦ كجم لصفة LM305، ٥٦,٥ كجم لـLTMY، ٠,٠٣١ كجم لـLMYHL، ٠,٠٦٣ كجم لـLMYLP و ٠,٠٢١٪ بالنسبة لصفة LLPHL، بينما كان معدل التدهور الوراثى السنوى -٠,٠٨٠، -٠,٣٥٦ يوم، -٤,٩ يوم و -٤,٩ يوم بالنسبة لصفات LLNO, LLP, HL, PL على التوالى. أظهرت الدراسة تدهور مظهرى سنوى غير مرغوب فيه لكل صفات طول الحياة وطول الحياة الإنتاجية خلال ٣٥ عاما فيما عدا صفة LMYLP كان معدل التحسين المظهرى السنوى موجب ومرغوب فيه.