GENETIC AND PHENOTYPIC PARAMETER ESTIMATION OF FIRST LACTATION, LIFE-TIME YIELD AND LONGEVITY TRAITS IN HOLSTEIN CATTLE

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Life-time yield and longevity are of major economic importance in dairy cattle (VanRaden and Wiggans, 1995). Longevity affects profitability by reducing replacement costs because of fewer number of replacement heifers needed to be raised with higher selection intensity and increasing the proportion of cows producing at mature level with more opportunities to voluntary culling (White, 1973; Burnside et al., 1984; Van Arendonk, 1985; Jairath et al., 1994; Boettcher et al., 1998; Pryce and Brotherstone, 1999; Nakano and Terawaki, 2002; Rogers, 2002; Canavesi et al., 2003; Powell and VanRaden, 2003; Sewalem et al., 2005; Tsuruta et al., 2005).

Longevity reflects a cow's ability not to be culled. Culling is a complex issue and many factors are involved. Cows could be culled for one or more reasons that include low production, health problems, low fertility and other reasons. Culling a cow for low production irrespective of her health is usually referred to as voluntary culling while culling for disease and/or low fertility regardless of her performance relative to her herdmates is called involuntary culling (Silva et al., 1986; Ducrocq et al., 1988; Dekkers, 1993; Grohn et al., 1998; Pryce and Brotherstone, 1999; Rogers, 2001).

Longevity can be defined and measured quantitatively in many different ways. It can be defined as the ability of the cow to both produce and reproduce for many years (Hoque and Hodges, 1980). Van Doormaal et al. (1985) and Rogers (2001) defined it as the length of time a cow remains productive in the herd. It can be expressed as age at last calving, number of lactations initiated or completed, length of life from first calving to disposal and survival to various ages (Van Doormaal et al., 1985). Vollema and Groen (1996) reported that lifetime longevity traits can be expressed as number of lactations, total milk production, number of days in lactation, herd life (culling age), and length of productive life.

Two approaches have been suggested to include longevity in a breeding program. The first approach is to include a

direct measure of longevity in the selection index (VanRaden and Wiggans, 1995). The other approach is to select for other traits, which are genetically correlated with longevity but are expressed earlier (Vollema and Groen, 1996).

Genetic improvement of life-time production and longevity by direct or indirect selection requires estimates of genetic parameters of these traits and their relationships with early lactation traits. Jairath *et al.* (1994) stated that knowledge of relationships between lifetime performance traits and early lactation traits is important for prediction of expected correlated response to selection.

The objective of this study was to estimate genetic and phenotypic parameters of first lactation milk yield, life-time yield and longevity traits expressed as: the number of lactation completed, length of productive life, culling age and total lifetime months in lactation.

MATERIALS AND METHODS

Data collection

Data were 4,932 complete lactation records for cows that had a complete longevity record, i.e. had been culled by the time data were collected. Data were collected over the period from 1960 to 1997. Cows born after 1997 were not used to avoid censored records (records for cows still alive in the herd) for lifetime longevity traits. The data were collected from two herds of Holstein cattle raised at Sakha and El-Karada experimental stations, located in the northwest of the Nile Delta in Kafr El-Sheikh governorate. These herds belong to Animal Production Research Institute, Ministry of Agriculture and Land Reclamation, Egypt.

A total of 128 herd-year-seasons (HYS) subclasses were formed by specifying two seasons of first calving, November to April and May to October.

All records for cows whose sires and/or dams had unknown identification numbers were discarded. Records were eliminated if age at first calving was less than 24 or greater than 40 months of age and/or if disposal reason was unknown to avoid censored records. Records were deleted if first lactation days in milk were less than 180 days. HYS was considered only if it had progenies of at least two sires to avoid the complete confounding of sires and HYS's or having disconnected sub sets of data. Therefore, the minimum number of sires per HYS was two sires and the minimum number of daughters per HYS was two daughters. Hudson and Van Vleck (1981) reported that records in herd-year-season subclasses in which only one sire was used would not contribute to the sire's solution.

Data editing left 3,211 cows with complete set of all traits, daughters of 284 sires and 2088 dams, dispersed in 128 herd-year-seasons.

Traits considered were first lactation milk yield (FLMY), life-time production (LTMY) and longevity traits expressed in four different ways as:

number of lactation completed (NLC), length of productive life (LPL), i.e. time between first calving and culling date in months, culling age (CA), i.e. time between birth date and culling date in months and total months in lactation over all lactations (TML).

Culling reason percentages throughout lactations were calculated. Regardless of culling reasons, culling percentage per lactation was calculated based on number of culled cows relative to all present. However, culling percentage due to each reason, regardless of lactations, was calculated based on number of culled cows per reason to all culled.

Data analysis

Data were analyzed by the multivariate Restricted Maximum Likelihood animal model utilizing the DFREML program developed by Meyer (2000) to estimate descriptive statistics and genetic parameters for all traits.

Data of all traits were analyzed according to the following multiple traits animal model:

$$y_{ijkl} = \mu + h_i + age_j + a_k + e_{ijkl}$$

Where: y_{ijkl} = observation of the traits;

μ = the overall mean;

h_i = fixed effect of herd-year-season i;

age_j = fixed effect of age at first calving j;

a_k = additive genetic random effect of the
    animal k; and

e_{ijkl} = random residual term.

The a_k and e_{ijkl} were assumed uncorrelated and distributed randomly and independently with mean zero and variances σ_a^2 and σ_e^2, respectively.

The pedigree file for the animal model contained all known pedigree information (animal, sire, and dam identification numbers).

RESULTS AND DISCUSSION

Descriptive statistics

Table (1) shows the descriptive statistics for different traits. Values of coefficient of variability (from 41.44% for CA to 83.17% for LTMY) revealed that these data exhibit high variations.

Culling reasons

Table (2) shows cows culling reasons and their percentage throughout lactations. The risk of being culled differed between and within lactations. Accumulative across all lactations, the main culling reasons were health problems (40.6%) and reproductive problems (11.5%). However, low production and mastitis represented 7.4% and 3.8%, respectively. Within lactation, the highest rate of culling due to health problems occurred after the second lactation (12.55%) while the highest culling rate for reproductive problems occurred after the first lactation (3.26%). Considering all culling reasons together, the highest culling risk was 26.54% after the second

lactation. Roxstrom (2001) reported that the risk of being culled because of impaired fertility, mastitis, or low production differed between and within lactations. In early lactation, there was a high risk of being culled for mastitis, while fertility problems resulted in culling toward the end of lactation. Roxstrom and Strandberg (2002) reported that the reasons for involuntary culling could range from reproductive and health problems to severe injury and accidents. They reported that about 28% were culled due to fertility problems (reduced fertility or not pregnant) as compared to 11.5% in the present study (Table 2). The other main reasons for culling were udder health and low production, 22% and 10%, respectively.

Heritability estimates

Table (3) shows heritability estimates of the studied traits. Heritability estimate of FLMY was 0.21. In the literature, heritability estimates for FLMY ranged from 0.22 to 0.40 (Hoque and Hodges, 1980; Ashmawy, 1985a; Short and Lawlor, 1992; VanRaden and Klaaskate, 1993; Jairath *et al.*, 1995; Vollema and Groen, 1996; Valencia *et al.*, 2002; Tsuruta *et al.*, 2005). Generally, heritability estimate for FLMY was slightly less than estimates in the literature. The slight difference might be due to different models and type of data used in the analysis.

Heritability estimates for LTMY, NLC, LPL, CA, and TML were higher than those reported in the literature.

Different researchers reported estimates of heritability for these traits ranging from 0.022 to 0.172 (Hoque and Hodges, 1980; Ashmawy, 1985a; Short and Lawlor, 1992; VanRaden and Klaaskate, 1993; Jairath *et al.*, 1994; Jairath *et al.*, 1995; Vollema and Groen, 1996; Valencia *et al.*, 2002; Tsuruta *et al.*, 2005).

Genetic and Phenotypic correlations between FLMY and longevity traits

Table (3) shows estimates of genetic and phenotypic correlations between studied traits. Genetic correlations were generally higher than phenotypic correlations. The genetic correlations ranged from 0.20 to 0.45. The highest genetic correlation was (0.45) between FLMY and LTMY as expected (being partly a part-total correlation) while the lowest one was (0.20) between FLMY and NLC. Phenotypic correlations ranged from 0.10 to 0.30 and showed a pattern similar to the genetic correlations. The highest phenotypic correlation was (0.30) between FLMY and LTMY while the lowest one was (0.10) between FLMY and NLC. Hudson and Van Vleck (1981) and Short and Lawlor (1992) reported that because lowest yielding cows are culled, phenotypic and genetic correlations often are favorable between yield and longevity. Hoque and Hodges (1980) reported that genetic correlations between first lactation milk yield and each of LTMY, NLC, LPL and CA ranged from 0.41 to 0.56. Phenotypic correlations were smaller ranging from 0.26 to 0.36 and showed a pattern similar to the genetic correlations.

Ashmawy (1985a) reported that genetic correlations between first lactation milk yield and NLC until the 5th lactation was 0.42. Short and Lawlor (1992) reported that genetic and phenotypic correlations between first lactation milk yield and true herd life as a measure of LPL were 0.44 and 0.21 for registered cows, respectively. Jairath et al. (1995) reported that genetic correlations between first lactation milk yield and LTMY, NLC, LPL, CA, and TML were high and ranged from 0.79 to 0.86. Phenotypic correlations were smaller and ranged from 0.46 to 0.57, and showed a pattern similar to the genetic correlations. Tsuruta et al. (2005) reported that genetic correlations between first lactation milk yield and lifetime longevity traits PL305 (total number of days in milk up to 84 mo of age with a restriction of 305 days per lactation) and LPL (herd life, total number of days from first calving to culling date) estimated with multivariate REML analysis using sire model were -0.11 and 0.04, respectively. Valencia et al. (2002) estimated genetic correlations between first lactation milk yield and LPL until the third lactation and total lifetime milk production until the third lactation as 0.33 and 0.64, respectively. Phenotypic correlations were smaller, 0.08 and 0.54, respectively.

Selection on first lactation milk yield seems to be most desirable for changing lifetime milk production because of its high positive genetic correlation with total lifetime milk production (Hoque and Hodges, 1980; Jairath et al., 1995). Ashmawy (1985b) concluded that from the highly significant relationship prevailing between stayability trait (NLC until the 5th lactation) and first lactation milk production, selection on the basis of the first lactation milk yield would lead to an increase in the length of herd life and cows would produce more offspring. He added that the early selection is essential for minimum generation interval and subsequently maximum genetic progress. Pryce and Brotherstone (1999) stated that including lifespan (number of lactations a cow completed or expected to complete prior to culling) in the United Kingdom's Profitable Lifetime Index may already be beneficial in terms of slowing down the rate of increase in incidence of health disorders and decline in fertility when selection is for production alone. Rogers (2001) stated that yield traits are economically the most important traits in the breeding goal for most countries, but the economic value of the genetic variability in the traits that impact longevity and culling is substantial. He added that this makes longevity and culling very important to a properly designed breeding program. In addition, selection for yield alone will lead to deterioration in health and reproductive performance and ultimately increase involuntary culling in dairy cattle.

Genetic correlations between NLC, LPL, CA and TML traits were slightly higher than phenotypic correlations (Table 3). Genetic and phenotypic correlations were quite high and showed similar pattern (from 0.98 to 1.00 and 0.95 to 1.00, respectively).

Both genetic and phenotypic correlations between NLC, LPL, CA and TML were high (>0.95). High genetic correlations indicate that older cows were also genetically the high producers and that many of the same factors are involved in controlling these traits and further suggest that they essentially measure of the same trait. Ducrocq *et al.* (1988) reported that use of continuous measures, such as length of productive life or age at disposal (culling age), which don't limit the evaluation to those sires whose daughters have reached a given age threshold (e.g. 84 months) might allow consideration of stability (longevity) in breeding programs without a drastic change in the current generation interval. Van Doormaal *et al.* (1985) reported that length of productive life is free of the variation in age at first calving whereas length of total life (culling age, time from birth to culling) is not.

Finally, the interest in implementing longevity in breeding programs is manly due to the need to have cows with higher efficiency by reducing involuntary culling rate. Actual measurement of longevity is only possible after the cow has been culled. However, most selection decisions are made long before culling. Therefore, there is a need to evaluate longevity for live cows. First lactation milk yield could be used in selection programs as a criterion to improve longevity and total life-time production.

SUMMARY

A total of 3,211 cows with complete set of all traits, daughters of 284 sires and 2088 dams were used. The MTDFREML animal model programs were used to estimate heritability, genetic and phenotypic correlations for first lactation milk yield (FLMY), life-time milk yield (LTMY) and longevity traits expressed as: number of lactations completed (NLC), length of productive life (LPL), culling age (CA) and total number of months in milk over all lactations (TML). The model included herd-year-season and age at first calving as fixed effects and the animal as random effect. Heritability estimates were 0.21, 0.29, 0.25, 0.28, 0.28 and 0.29 for FLMY, LTMY, NLC, LPL, CA and TML, respectively. Genetic correlation between FLMY and other traits (LTMY, NLC, LPL, CA and TML) was 0.45 0.20, 0.32, 0.32 and 0.37, respectively. Phenotypic correlations showed same trend with less magnitude. Genetic and phenotypic correlations between NLC, LPL, CA and TML were very high indicating that these traits were measuring the same thing. This study showed that life-time production and longevity can be improved indirectly by including first lactation milk yield in selection indices.

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Table (1): Descriptive statistics of different traits.

Trait	Minimum	Maximum	Mean	SD	CV%
First lactation milk yield (kg)	392.0	7,755	2,326	0.97	41.71
Life-time milk yield (kg)	392.0	42,135	8,831	7.34	83.17
Number of lactation completed	1.0	13	3.34	2.09	62.66
Length of productive live (mo.)	6.2	160.2	45.0	31.59	70.19
Culling age (months)	31.7	191.7	76.4	31.67	41.44
Total months in lactations	6.1	133.3	35.8	24.45	68.30

Table (2): Culling reasons and their percentages throughout the first six lactations.

Culling reasons	Lactation						All lactations
	1	2	3	4	5	6	%
Reproductive problems	3.26	2.45	1.81	1.27	1.21	0.73	11.5
Health problems	9.61	12.55	7.89	4.14	2.03	1.33	40.6
Mastitis	0.51	0.63	0.79	0.57	0.84	0.27	3.8
Low production	0.63	1.90	2.12	1.18	0.63	0.42	7.4
Sale for dairy purposes	1.03	0.97	0.91	0.21	0.12	0.03	3.3
Improper type traits	0.24	0.21	0.27	0.18	012	0.09	1.4
Death or slaughter[1]	3.30	2.96	1.78	1.54	1.12	0.54	12.2
Unknown reason	5.65	4.87	3.54	2.54	1.30	1.30	19.8
Total %	24.23	26.54	19.11	11.63	7.01	4.44	

[1] Accidental death

Table (3): Heritability estimates (diagonal and underlined), genetic (below diagonal) and phenotypic correlations (above diagonal) for studied traits.

Trait[1]	FLMY	LTMY	NLC	LPL	CA	TML
FLMY	**0.21**	0.30	0.10	0.20	0.20	0.25
LTMY	0.45	**0.29**	0.91	0.95	0.95	0.97
NLC	0.20	0.96	**0.25**	096	0.96	0.95
LPL	0.32	0.99	0.99	**0.28**	1.00	0.98
CA	0.32	0.99	0.99	1.00	**0.28**	0.98
TML	0.37	0.99	0.98	1.00	1.00	**0.29**

[1] FLMY = First lactation milk yield (kg), LTMY = Life-time milk yield, NLC = Number of lactations completed, LPL = Length of productive life (months), CA = Culling age (months), TML = Total months in lactation.