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Genetic and environmental trends in the long-term dairy cattle genetic improvement programmes in the central tropical highlands of Ethiopia

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A total of 1979 lactation records from 550 selected crossbred dairy cows that born between 1974 and 2005 were used to estimate annual genetic and environmental trends in milk production and reproduction traits at Holetta Agricultural Research Center, Ethiopia. Annual genetic and environmental trends were estimated by regressing BLUP estimated breeding value on year of birth. Variance components and genetic parameters were estimated using univariate analysis of individual animal model based on restricted maximum likelihood procedures. Annual genetic trends were -3.384 days, -8.00 kg and -5.96 kg, -0.26 months, -0.29 months and -0.88 days, for lactation length (LL), lactation milk yield (LMY), adjusted 305 milk yield (305-days MY), age at puberty (APU), age at first calving (AFC) and calving interval (CI), respectively. Environmental trends for LMY was positive (6.717 kg) and was in the desired direction. Heritability estimates were 0.14, 0.44, 0.39, 0.38, 0.40 and 0.17 for LL, LMY, 305-d MY, APU, AFC and CI, respectively. Negative genetic trends in all milk production traits reflect ineffective selection program and/or lack of using sires that have positive breeding values. The result from the environmental trends shows substantial improvement in the management practices over time. Contrasting directions in genetic and environmental trends reflect ineffective breeding objectives. This warrants reconsideration of the existing breeding program in the country.

Key words: Genetic trends, environmental trends, genetic parameters, breeding objectives, variance components.

INTRODUCTION

From the very outset, in whatever way we implement it, genetic improvement implies change. For a change to be an improvement, however, the overall effects of the change must bring positive benefits to target stakeholders and respond to the broad national development objectives (FAO, 2007). Therefore, planning national genetic improvement program takes into account careful analysis of the short and long-term objectives, socio-economic and environmental context in which it operates

(FAO, 2007). Under the Ethiopian context, livestock, particularly adapted cattle genetic resources are an important element in the livelihood of many resource-poor farmers living in wide arrays of production systems and contribute more than marketable products that are considered in economic statistics. Their special adaptive traits to harsh climates, disease resistance, heat tolerance, ability to utilize poor quality feeds and the multipurpose role they play in ranges production systems are some of their inherent genetic attributes. However, they are poor milk and meat producers. Consequently the demand for milk and milk products remained lagging behind supply for many years in Ethiopia.

As compared to many countries in Africa, Ethiopians

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consume lesser amount of dairy products (Ahmed et al., 2003), which is currently estimated at 19 L per annum (CSA, 2009). Motivation for popularizing crossbreeding between high-yielding European dairy breeds and cattle breeds adapted to local environments was initiated in the national agricultural research system (NARS) of Ethiopia in the early 1970s. As compared to other dairy cattle genetic improvement strategies, this approach was believed to be the only feasible and quick way of increasing milk production in Ethiopia. The outcome of the crossbreeding programs have been amply reported in several literatures with various outcomes (Beyene, 1992; Beyene et al., 1987; Demeke et al., 2004a, b; Kefena et al., 2006; Haile et al., 2009). The effectiveness of any dairy cattle genetic improvement program is measured by the genetic progress obtained (Hallowell et al., 1998). Bakir and Cilek (2009) also stated that the genetic capacity and its progress in dairy cattle breeding are measured by genetic trend. A standard way of measuring progresses in animal breeding is by regressing estimated annual environmental and breeding value on year of birth (FAO, 2007).

However, the dairy cattle genetic improvement program started in Ethiopia in the early 1970s has never been subjected to periodic evaluation for the genetic and environmental trends. Thus, the effectiveness of this program is not clearly known. Moreover, no information is available on the status of the national dairy cattle genetic improvement program that guide policy makers, development planners and breeders to redesign appropriate breeding programs that respond to the current scenarios in Ethiopia. The purpose of this study was, therefore, to investigate genetic and environmental trends for selected crossbred dairy cows produced at Holetta agricultural Research Center in the past two decades.

MATERIALS AND METHODS

Data source and traits recorded

Data for this study were obtained from long-term dairy cattle crossbreeding programme conducted from 1974 to 2005 at Holetta agricultural research center, central Ethiopia. A total of 550 crossbred cows that belong to two genetic groups, derived from crossing two exotic dairy breeds (Friesian and Jersey) with Ethiopian Boran were used. Details of the traits recorded and the number of records are depicted in Table 1.

Description of the study site and animal management

The Holetta agricultural research centre is located at 35 km west of Addis Ababa at 38.5°E longitude and 9.8° N latitude. It is situated at about 2400 m above sea level and is delineated as one of the areas known as “the Addis Ababa milk shed”. The average annual rainfall is about 1200 mm and the average monthly relative humidity is 60.6% (Haile et al., 2009). All heifers and cows above six months of age were allowed to graze on natural pasture for about 8 h

during daytime. At night, all animals are housed in an open shade and supplemented with natural pasture hay. Except for the lactating cows, which were supplemented with approximately 1 to 2 kg of concentrate at each milking, no other animal received any regular concentrate supplement.

All animals had free access to clean water. All calves were weighed at birth and allowed to suckle their dams for the first 24 h in order to obtain colostrum, after which they were moved to individual calf pens for bucket feeding until weaning at 94 days of age. Each calf was fed a fixed amount of 260 kg of whole milk during the pre-weaning period. Weaned calves were kept indoors until 6 months, during which they were fed ad lib on natural pasture hay and supplemented with approximately 1 kg per day per animal of concentrate composed of 30% wheat bran, 32% wheat middling, 37% noug seedcake (*Guizoita abyssinica*) and 1% salt. There is no partial management option based on genetic groups or level of milk production. All local Boran cows were bred by artificial insemination (AI) while second generation crosses were bred by both natural services and AI as necessary.

Data editing

Data has been collected on both F x Bo and J x Bo crossbred dairy cows that have sufficient information on both milk production and reproduction traits. Animals with limited information, missing pedigree or failed to meet minimum criteria to be parents of next generation were excluded from the final data set. The final data set with complete information consisted of 550 cows (Table 1). Lactation lengths of less than 60 and greater than 1000 days were excluded from the data set following the lactation length truncation points recommended by Kiwuwa et al. (1983) and Sendros (2002), respectively for indigenous and crossbred cows.

Adjusted 305 days milk yield were computed following standard procedures (305 days x total milk yield/actual lactation length). Records of animals with abnormal calving such as abortion and stillbirth were also ignored. Two data sets were prepared and used separately in the analysis. Data set 1 consisted of data structured into six periods (5 years each) from 1974 to 2005 and used to estimate least squares means for milk production and reproduction traits with time. Data set 2 consisted of all data for animals born in each year and was used to compute estimated breeding value (EBV) for yearly genetic and environmental trends.

Statistical analysis

The statistical analysis involved three steps. At the preliminary stage, least squares means analysis was carried out to compare between the genotypes and identify systematic environmental factors that have significant effects on the traits using type III model of the Statistical Analysis System (SAS, 2004). Two genotypes (F x Bo and J x Bo), six periods (1974 to 1980) period 1; (1981 to 1985) period 2; (1986 to 1990) period 3; (1991 to 1995) period 4; (1996 to 2000) period 5 and (2000 to 2005) period 6, and eight parity classes (1, 2, 3, 4, 5, 6, 7 and 8⁺) were identified significant ($p < 0.05$) and retained for the final analysis. For the least squares means analysis in data set 1, all parities greater than 8 were grouped together and analyzed as single parity record denoted as 8⁺. In the second step of statistical analysis, genetic parameters and estimated breeding value for each trait was estimated by running series of univariate analysis using the derivative-free restricted maximum likelihood algorithm fitting individual animal model (Meyer, 1998). Convergence criteria for REML solution were considered to have been reached when the variance function values ($-2\log$ -likelihood) in the simplex was less than 10^{-8} . If the likelihood values changed substantially during the analysis, iterations

Table 1. Traits considered and number of Friesian and Jersey derived genotypes.

Traits	Friesian crosses (n)	Jersey crosses (n)	Total
Lactation length (LL)	1258	721	1979
Lactation milk yield (LMY)	1258	721	1979
Adjusted 305 milk yield (305 LMY)	1258	721	1979
Age at first calving (AFC)	399	151	550
Age at puberty (APU)	399	151	550
Calving interval (CI)	847	559	1406

n= number of records in each genetic group.

were restarted using the final parameter estimates from the previous analysis as starting values. The mixed linear model equation in matrix notation for the analysis of each trait was as follows:

$$y_i = X_i \beta_i + Z_i a_i + e_i \quad (1)$$

where y_i is the vector of observations of the animal for trait i (No. of records \times 1); β_i is the vector of unknown fixed effects including, overall mean, genetic classes and year and parity for trait i (total No. of fixed effect levels); X_i is the known design matrix relating fixed effects to y_i (No. of records \times total No. of fixed effect levels); a_i is the vector of random animal solutions for trait that is, breeding values (total No. of animals \times 1); Z_i is the known design matrix relating animals direct additive genetic effects to y_i (total No. of records \times total No. of animals) and e_i is the vector of unknown random residual effects (total No. of records \times 1). The variance and covariance structure for the model was assumed to be:

$$V(a) = A\sigma_a^2; \quad V(e) = I\sigma_e^2 \quad \text{and} \quad \text{Cov}(a,e) = \text{Cov}(e,a) = 0 \quad (2)$$

where;

I is an identity matrix, A is a numerator relationship matrix, σ_a^2 is additive direct and σ_e^2 is residual variance.

In the third step, genetic and environmental trends were estimated for each trait. Best Linear Unbiased Prediction (BLUP) estimates of breeding values were estimated fitting a univariate individual animal model as described in Equation (1). The yearly mean estimated breeding values (EBV) that used to predict true breeding value were then calculated. Deviations of yearly mean EBV from the base year (year 1) were taken as estimates of genetic progress in each year and used to plot responses. The base animals with unknown pedigree were assumed to have EBV of zero. Genetic trends (average increase in each year in EBV) were estimated by regressing yearly mean EBV on the birth years. To account for environmental trends, the environmental values were described as the difference between the genetic values from phenotypic values for the year of birth (Table 2).

RESULTS

Estimates of genetic and non-genetic effects

No variation was observed in AFC and APU between the two genetic groups, but considerable differences ($p < 0.001$) were observed in LL, LMY, adjusted 305-day

MY and in CI for genetic groups, birth years and parities (Table 3). Overall LMY showed that F \times Bo crossbred cows had longer LL (21 days), produced more milk (376 L), adjusted 305 milk yield (247 L) and had longer CI (20 days) as compared to J \times Bo crossbred cows. Though the trend fluctuates, lactation length for aggregated genotype generally showed a declining trend with time. Similarly, LMY showed a declining trend from period 1 to period 4, slightly improved in period 5 and considerably deteriorated in the last period. Though the pattern was irregular, APU and AFC generally showed a declining trend from period to period. Animals born in period 5 (1996 to 2000) had the lowest AFC and APU while the longest AFC and APU were recorded in period 2 (1981 to 1985) (Table 3). Parity was also a significant sources of variation ($p < 0.001$) for LL, LMY, adjusted 305-day MY and CI. Lactation lengths showed an increasing trend from the first parity through to the fourth parity and starts declining from the fourth parity onwards. Other correlated traits such as LMY and adjusted 305-day MY also showed similar trends (Table 3). However, CI showed a declining trend from the first parity to latter parities. The rate of decline was slight from the first to the fourth parity but rapidly decreasing from the fourth parity onwards. Generally, overall evaluation of least square means for milk production traits showed declining trend over the periods considered.

Estimates of variance components and genetic parameters

Table 4 presents variance components and heritability estimates for milk production and reproduction traits. Heritability estimates were higher for LMY (0.44) and 305-days milk yield (0.39), AFC (0.40) and APU (0.38) and relatively lower for LL (0.14) and CI (0.17).

Genetic and environmental trends

Figures 1, 2, 4 and 5 depict genetic trends (average yearly increases in EBV) as estimated by regressing yearly

Table 2. Characteristics of the data and pedigree structure used for genetic trend evaluation.

	Ψ LL	LMY	305-day MY	APU	AFC	CI
Number of "base" animals	345	345	345	356	356	283
Number of animals with records	550	550	550	550	550	386
With unknown/pruned sire	140	140	140	241	241	116
With unknown/pruned dam	167	167	167	291	291	126
Number of sires with progeny records	90	90	90	60	60	77
Number of dams with progeny records	269	269	269	180	180	207
Number of grand-sire with progeny records	69	69	69	35	35	66
Number of grand-dam with progeny records	130	130	130	30	30	102
Average	346.4	1958	1720.0	29.5	40.3	488.7
Standard deviation	106.5	883.5	613.9	10.4	11.0	156
CV (%)	30	32	32.5	27.3	21.7	31.8

Ψ LL= Lactation length; LMY= Lactation milk yield; 305-days MY= Adjusted 305 milk yield; APU= Age at puberty; AFC=Age at first calving; CI=Calving interval.

Table 3. Least squares means (\pm S.E) for genetic effects, periods and parity for milk production and reproduction traits.

Effect and level	Ψ LL (Days)	LMY (Liter)	305-days MY (Liter)	AFC (Month)	APU (Month)	CI (Days)
Overall mean	333.0 \pm 4.1	1900.3 \pm 32.9	1734.8 \pm 22.0	42.5 \pm 0.7	31.7 \pm 0.6	462.4 \pm 8.7
CV (%)	30.0	42.8	32.7	22.7	28.9	36.2
Genetic groups	***	***	***	NS	NS	*
Frisian crosses	343.8 \pm 3.6 ^a	2088.7 \pm 29.4 ^a	1858.3 \pm 19.7 ^a	43.4 \pm 0.6	32.4 \pm 0.6	472.8 \pm 8.0 ^a
Jersey crosses	322.3 \pm 4.5 ^b	1712.0 \pm 36.4 ^b	1611.3 \pm 24.4 ^b	41.7 \pm 0.8	31.1 \pm 0.7	452.0 \pm 9.4 ^b
Periods	***	***	***	***	***	***
1974-1980	370.1 \pm 5.3 ^a	2012.4 \pm 43.1 ^b	1674.6 \pm 28.9 ^c	43.9 \pm 1.1 ^b	32.5 \pm 1.1 ^c	507.1 \pm 10.3 ^a
1981-1985	366.4 \pm 5.4 ^a	1913.2 \pm 43.4 ^{bc}	1594.2 \pm 29.1 ^d	50.9 \pm 1.1 ^a	39.4 \pm 1.0 ^a	489.3 \pm 10.3 ^{ab}
1986-1990	347.6 \pm 6.2 ^b	1858.5 \pm 50.1 ^c	1658.5 \pm 33.5 ^{cd}	44.7 \pm 1.2 ^b	33.5 \pm 1.1 ^c	465.6 \pm 12.2 ^b
1991-1995	329.8 \pm 8.3 ^b	1996.1 \pm 66.6 ^{bc}	1845.5 \pm 44.6 ^b	46.8 \pm 1.3 ^b	37.1 \pm 1.2 ^a	425.0 \pm 16.8 ^{cd}
1996-2000	309.7 \pm 5.6 ^c	2140.0 \pm 44.8 ^a	2033.1 \pm 30.0 ^a	31.7 \pm 0.8 ^d	21.4 \pm 0.8 ^e	415.8 \pm 11.4 ^d
2000-2005	274.7 \pm 7.8 ^d	1481.8 \pm 63.0 ^d	1602.9 \pm 42.2 ^{cd}	37.3 \pm 0.9 ^c	26.6 \pm 0.8 ^d	471.4 \pm 20.5 ^{ab}
Parity	***	***	***	-	-	***
1	356.3 \pm 4.7 ^a	1749.2 \pm 37.9 ^c	1496.9 \pm 25.4 ^c	-	-	533.8 \pm 9.1 ^a
2	352.0 \pm 5.4 ^{ab}	1882.7 \pm 43.8 ^b	1615.7 \pm 29.4 ^b	-	-	491.7 \pm 10.7 ^b
3	336.2 \pm 6.2 ^b	1944.2 \pm 49.7 ^{ab}	1760.9 \pm 33.3 ^a	-	-	482.3 \pm 12.2 ^b
4	346.5 \pm 7.1 ^b	2052.4 \pm 56.8 ^a	1812.4 \pm 38.1 ^a	-	-	479.1 \pm 13.7 ^{bc}
5	334.9 \pm 7.9 ^{bc}	2034.6 \pm 63.4 ^a	1836.2 \pm 42.5 ^a	-	-	440.7 \pm 15.5 ^{cd}
6	332.2 \pm 8.9 ^{bc}	1934.7 \pm 71.9 ^{ab}	1766.4 \pm 48.2 ^a	-	-	433.6 \pm 18.5 ^d
7	310.0 \pm 10.7 ^{cd}	1833.0 \pm 86.1 ^{bc}	1806.3 \pm 57.7 ^a	-	-	427.7 \pm 24.7 ^d
8 ⁺	296.4 \pm 10.5 ^d	1771.7 \pm 84.7 ^{bc}	1783.5 \pm 56.7 ^a	-	-	410.1 \pm 25.6 ^d

Ψ LL= Lactation length; LMY= Lactation milk yield; 305-d MY=Adjusted 305 milk yield; APU=Age at puberty; AFC=Age at first calving; CI=Calving interval; CV=Coefficient of variation.

mean EBV on birth year of animals for LL, LMY and 305-days MY, AFC and APU and CI, respectively. Figure 3 depicts environmental trend taken as a deviation of phenotypic deviations from additive genetic. Regression coefficients for all aggregated genotypes showed negative annual genetic gains of about -3.348 days, -8.0 L,

-6.0 L and -0.89 days for LL, LMY, 305-days MY and CI, respectively. On the contrary, a trend in the environmental components was positive (6.72 kg) for LMY and was in the desired direction. Trends in early growth traits such as AFC and APU showed negative annual genetic gains of about -0.295 and -0.263 months,

Table 4. Estimates of variance components and genetic parameters for milk production and reproductive traits.

Estimate	LL	LMY	305-Days MY	APU	AFC	CI
$\psi \sigma_g^2$	1508	174093.72	122365.01	24.63	31.10	3993.76
σ_e^2	9342.31	225684.84	190914.06	40.07	45.51	20097.96
σ_p^2	10850.31	399778.56	313279.09	64.70	76.61	24091.72
h^2	0.14	0.44	0.39	0.38	0.40	0.17

$\psi \sigma_g^2$ = additive genetic variance; σ_e^2 =residual variance; σ_p^2 = phenotypic variance; h^2 = heritability.

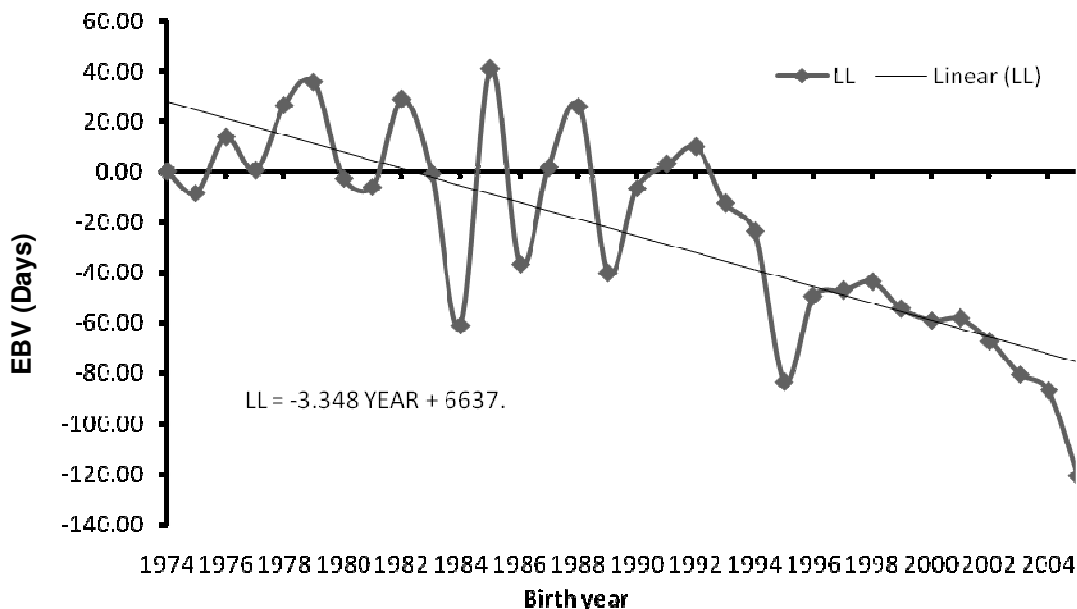


Figure 1. Yearly mean EBV for LL and its trends over birth years.

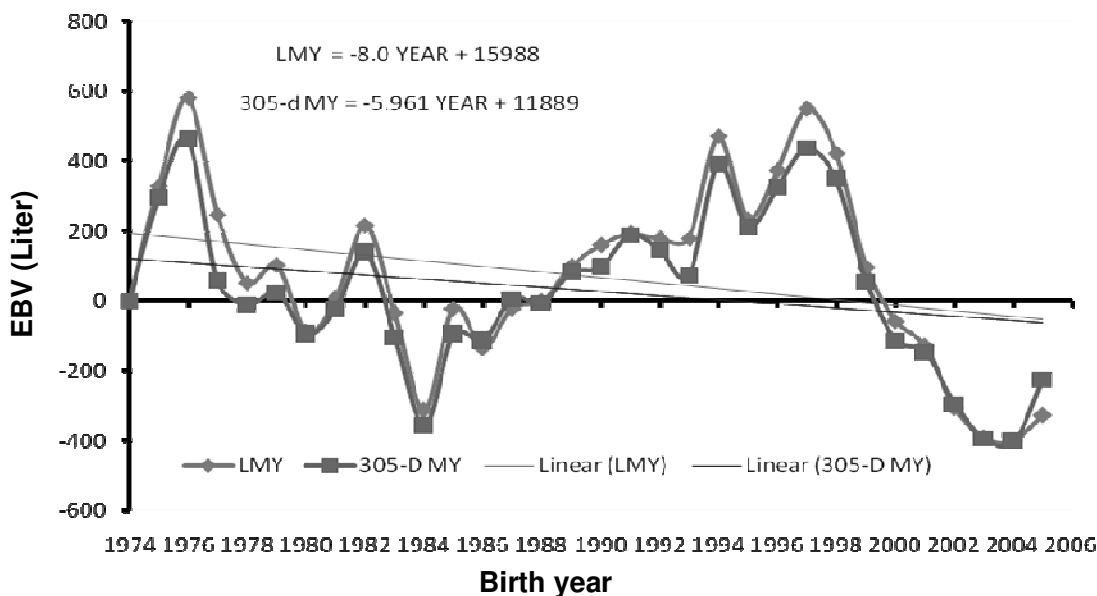


Figure 2. Yearly mean EBV for LMY and 305-MY and their trends over birth years.

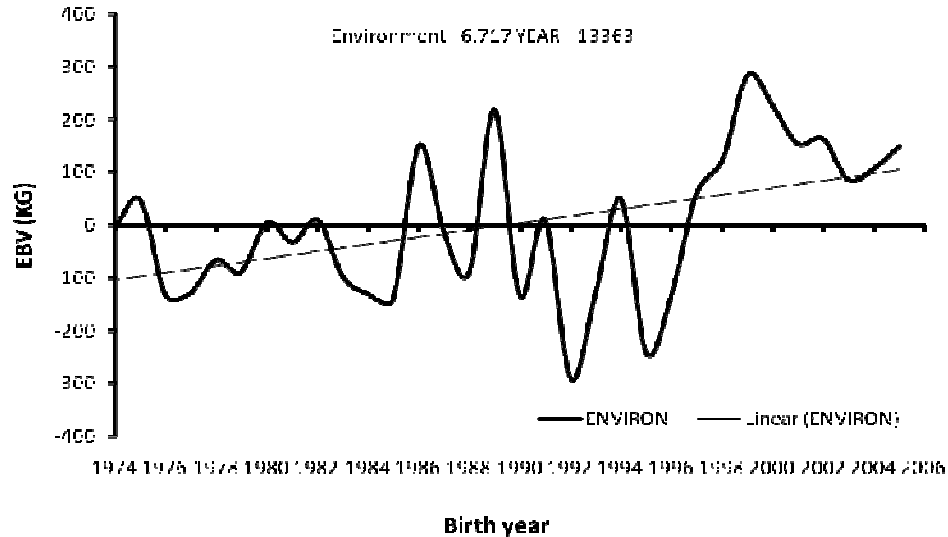


Figure 3. Yearly mean EBV for the environment and its trends over birth years.

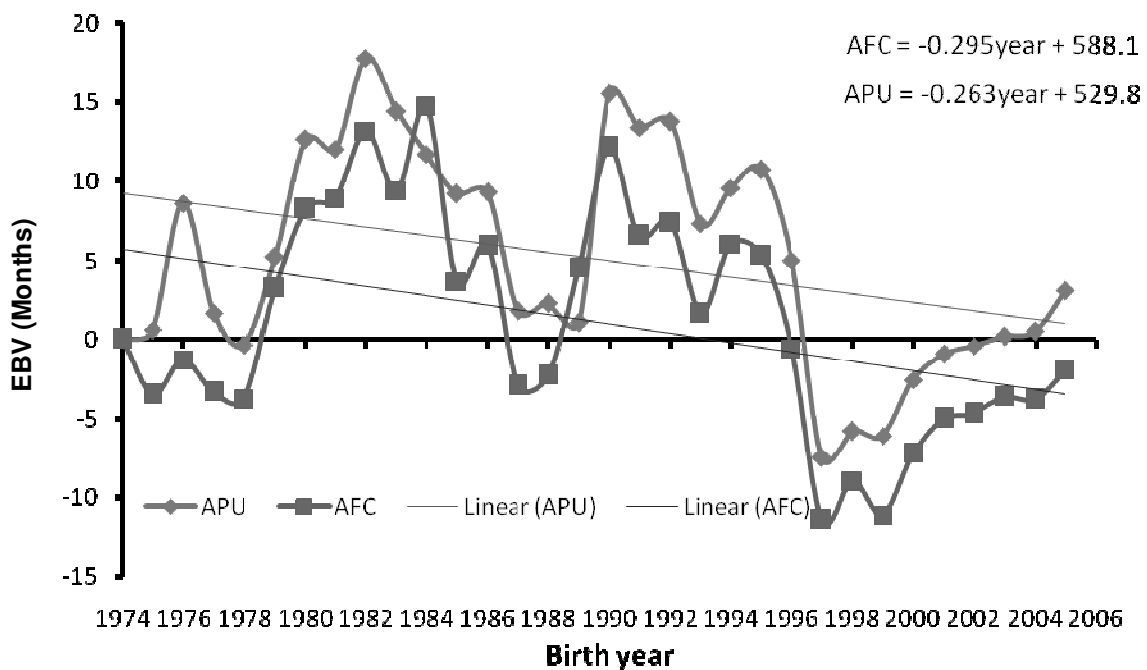


Figure 4. EBV for APU and AFC and their trends over birth years

respectively, and were in the desired direction (Figure 3).

DISCUSSION

Estimates genetic and non-genetic effects

In this study, F x Bo crossbred cows had longer LL (6.8%),

gave more milk (22%), 305-days MY (15.32%) and had longer CI (4.6%) as compared to J x Bo crossbred cows. Superiority of F x Bo crossbred cows in these traits over J x Bo crossbred cows were amply reported in several crossbreeding experiments (Cunningham and Syrstad, 1987; Demeke et al., 2004b; Kefena et al., 2006). Contrary to expectation in dairy cattle genetic improvement programs, results of least squares means showed

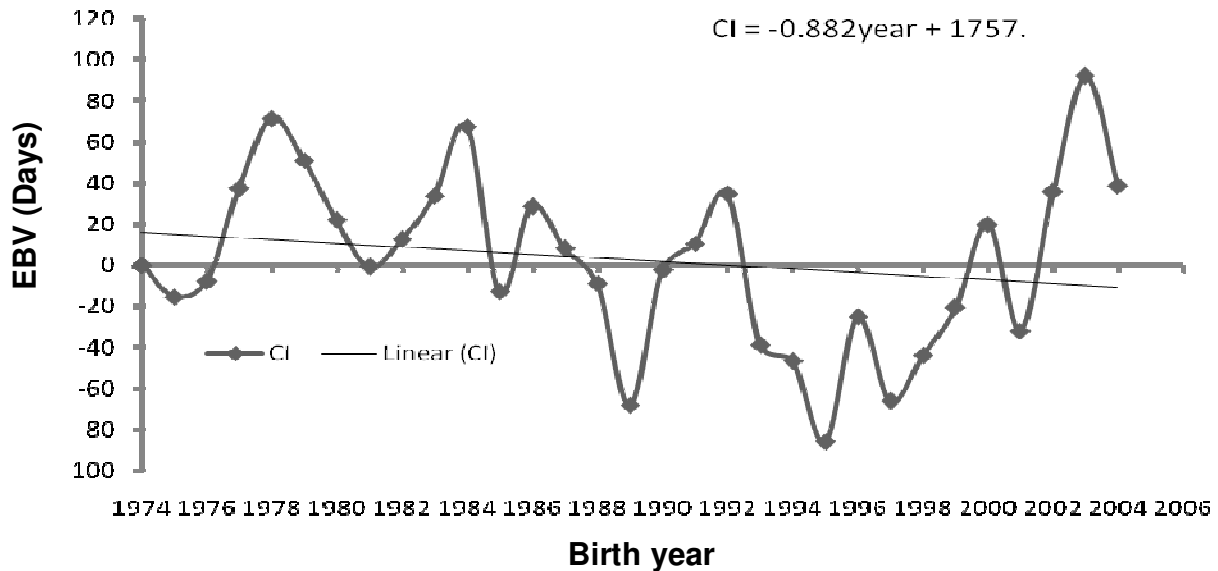


Figure 5. EBV for CI and its trends over birth years

that milk production traits drastically deteriorating in later periods. For instances, the difference in least squares means for LL, LMY and 305-day MY between period 1 and period 6 was to the extent of 95 days (34.7%), 530 L (35.8%) and 71.7 L (4.5%), respectively. On the contrary, reproductive traits substantially improved over the periods. For instances APU, AFC and CI reduced from period 1 to period 6 by about 5.9 months (22.2%), 6.6 months (17.7%) and 36 days (7.6%), respectively.

Improvements in all reproductive traits were in the desired directions and this reflects improvement in herd management practices over the periods. However, declining trends in milk production traits certainly reflect deterioration in the genetic component of the dairy breeding program in the country. Possible explanations for unexpected trends in milk production traits are as follows. Firstly, there are no effective and clearly set selection criteria to identify animals with superior breeding values on the farm. Secondly, most of the semen used in this program has been purchased from the national artificial insemination center (NAIC) of Ethiopia that has virtually no progeny-testing program. Thirdly, there is no clearly established national dairy cattle breeding strategies and breeding goals that are responsive to changing demands and scenarios in Ethiopia. Evidences (Cunningham and Syrstad, 1987; Falconer and Mackay, 1996) indicated that the average performance of a group of animals is determined its inherent genetic makeup, the environment in which it is kept and the interaction between genetic and the environment. Therefore, partial improvement in the environmental components alone may not guarantee improvements in the genetic merits unless all components of the genetic improvement programs are simultaneously considered.

Estimates of genetic parameters

Effective breeding programmes depend on the accuracy of genetic and phenotypic parameter estimates (Demeke et al., 2004a; Ilatsia et al., 2007). Therefore, accurate estimation of these parameters will help to design an efficient breeding programme for goal traits that are to be improved by selection. Table 4 shows estimates of genetic parameters and variance components. The heritability estimate obtained for LL in the current study is similar with the estimate reported in Demeke et al. (2004b) for pure and crossbred dairy herds in Ethiopia.

However, estimates for LMY and CI were higher than that previously reported by Demeke et al. (2004b). This probably attributed to the differences in data size and structure and models used for estimating these traits in the previous study. Heritability estimate for AFC was also similar with that reported by Demeke et al. (2004b) but higher than that reported by Ilatsia et al. (2007) for Sahiwal cows in Kenya. Generally, selection and breeding programs based on traits with higher heritability estimates improves the genetic components of the breeding program and therefore, their performances in the next generation.

Genetic and environmental trends

Estimated breeding value for genetic and environmental trends in this study indicated that the overall objective of the program was not fully achieved (Figures 1, 2, 4 and 5). Decreasing trends observed in LMY, 305-days MY, LL and CI over the periods for least means squares estimates were consistent with the negative annual genetic

trend demonstrated by regressing average annual EBV on years of birth. Negative genetic trend in early growth and fertility traits showed overall improvement in the environmental components the breeding program (Figure 4) implying that reproductive efficiencies were improving with time. The overall trend for positive environmental trends (Figure. 3) shows that emphasis was given to the environmental components of the breeding programme than to the genetic components. Reports for genetic and environmental trends for crossbred dairy cows are scarce in the literature with variable outcomes. Peixoto et al. (2006) reported a positive annual genetic gain ranging from 6.47 to 7.09 in local Brazilian Guzerat herd under selection program.

An annual genetic trend ranged from 9.13 to 183.14 L was also reported for cows born and raised in the multiple ovulation and embryo transfer (MOET) program in the same Brazilian Guzerat herd showing the potential of using MOET for rapid genetic improvement programs. On the other hand, Freitas et al. (1995) reported negative annual genetic trends in 20 crossbred dairy herds in Brazil. Musani and Mayer (1997) reported positive genetic trend of about 0.8 kg per year for milk production in a large commercial Jersey herd in the central Rift Valley of Kenya. Hallowell et al. (1998) also reported a positive genetic trend of about 19 kg per year for first lactation milk yield in Ayrshire dairy herd in South Africa. Variable results in different dairy cattle genetic improvement programs probably showed differences in selection intensity in different farms, type of herd involved and extent of monitoring genetic progress over time in a particular program.

Conclusion

Comparison of milk production and reproduction performances in this study showed that Frisian crossbred dairy cows were more productive than Jersey crosses. However, Jersey crossbred dairy cows have shorter lactation lengths and calving interval than Frisian crossbred dairy cows that reflects better reproduction efficiencies in Jersey crosses. Continuous decline in the milk production traits over time accompanied by substantial improvements in reproduction traits showed gradual deterioration in the genetic components of the breeding programmes. From this viewpoint, improvement in the environmental components of the breeding program alone would not guarantee improvements in milk productions.

Moreover, non-uniform and generally negative genetic trends in milk production traits followed by positive trend in the environmental components provide additional evidences of gradual deterioration of the genetic components of the dairy cattle genetic improvement programme. It generally reflects the lack of efficient selection program, absence of periodic monitoring of the genetic progresses attained

and use of sires with low breeding value. Therefore, the dairy cattle genetic improvement programmes need to be subjected to national evaluations to redesign appropriate strategies that would be more responsive to the currently changing scenarios in the country.

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