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2007

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The effects of non-genetic factors and estimation of genetic and phenotypic parameters and trends for milk yield in Ayrshire cattle in Kenya

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Abstract

Dairy cattle production in Kenya has been growing into an important agricultural sector, but it still faces numerous difficulties in environmental constraints. The purpose of this study was to identify significant non-genetic effects on milk production to give advices for farm management and estimate genetic and phenotypic parameters for milk traits. Data consisting of 4475 lactation records from 10 large-scale Ayrshire herds collected from 1980 to 2005 were used to evaluate effects of non-genetic factors and determine genetic and phenotypic parameters and trends of 305 d milk yield (305d MY).

The data analyses using least square techniques of Proc GLM of SAS identified significant sources of variation by herd, parity and year of calving on 305d MY. The overall mean for 305d MY was 3009.8 ± 1098 kg, with the corresponding heritability and repeatability estimates of 0.12 ± 0.05 and 0.35 ± 0.01 respectively. Genetic trend for 305d MY was -2.1 kg/yr and statistically significant ($P < 0.01$) indicating annual decrease in breeding values over the study period. The high variation as indicated by both large standard errors and low heritabilities of the milk trait indicate that much improvement in this trait could be achieved through improved management. The negative annual genetic changes in milk yield observed could largely be due to ineffective breeding strategies both at herd and national level.

Key words: genetic parameters and trends, milk yield, non-genetic effects

Introduction

The European *exotic* cattle population and their crosses with indigenous cattle estimated at 3.3 million (MoA and RD 2001) are the main genotypes for commercial milk production in Kenya. The poor performance is not only due to the direct effect of climate but more importantly the poor quality of roughage, low concentrate feed inputs and the high incidence of diseases and parasites and poor economic environment and infrastructure. Improvements targeted towards any of these areas have realized substantial improvement in dairy performance (Njubi et al 1992). Ojango and Pollot (2001) observed that despite the existence of major problems in the tropics, moderate levels of milk production could be obtained. The prerequisite for effective management of production is the accurate quantitative knowledge of the factors affecting production performance (Mukasa- Mugerwa et al 1992). Therefore, adjusting records for non-genetic effects is essential to define appropriate models for estimation of variance components and improving selection procedures.

Generally production traits have been reported to have a medium to high repeatability and low to medium heritability hence there exists opportunity for improvement through selection. Phenotypic, genetic and environmental trends in performance traits are important in that they allow for the evaluation of the efficacy of selection and management schemes. The estimates of trends in the performance traits of dairy cattle in Kenya seem to vary from breed to breed and from herd to herd due to differences in locality, management and selection objectives. The trends are indicative of the progress or decline that

has been attained using the breeding strategy in place (Rege and Mosi 1989; Njubi et al 1992; Ojango and Pollot 2001).

Due to economic value of milk, milk yield has traditionally been the single most important trait of dairy cattle selection programs in most countries (Mosi 1984; Campos et al 1994), therefore, milk yield is expected to show positive (favourable) genetic trend (Njubi 1990; Rege 1991; Musani 1995). In general, favourable phenotypic and genetic trends can be achieved if the environment and breeding management are improved. There is therefore, a need to continuously evaluate the genetic, environmental and phenotypic parameters and trends in dairy cattle, to monitor whether the parameters and trends are desirable for each trait. The purpose of this study was to evaluate the effects of non-genetic factors limiting milk traits in Kenyan Ayrshire herds and estimate genetic and phenotypic parameters and trends for 305-d milk yield.

Materials and methods

Data source and processing

Data for this study were obtained from 10 large-scale Ayrshire farms covered by the official dairy record Scheme (DRSK). The management system of the herds varied but generally animals were grouped and managed according to their ages into three basic age groups; calves, weaners and mature stock. From the age of 14 months heifers coming on oestrus regularly were served through artificial Insemination. Most of the farms served their heifers for the first time at about 18 months of age.

Rainfall data for different study areas were obtained from the Meteorological Department in Nairobi. Monthly rainfall totals over study period (1986-2005) were used to determine the rainfall pattern to define the three seasons. The seasons in the country were generally classified into three based on rainfall pattern (Rege ad Mosi 1989): Long rains, (March to May), Short rains (October to November) and Dry seasons (June -September and December-February).

A total of 8301 lactation records were sourced from DRSK covering the years 1980 to 2005 from Kenyan Ayrshire herds. Records of animals without birth and calving dates and cows without pedigree information were excluded. All cows that had less than 23 months age at first calving were also edited out and cow with lactation length less than 60 days were omitted. After editing 4475 records were available from 1955 cows sired by 211 bulls (Table 1).

Table 1. Data structure and means and standard deviations for milk yield and lactation length traits

Data structure	Number	
Number of records	4475	
Cows	1955	
Sires with progeny	211	
Traits	Mean	SD
TLMY	3592.08	2191.02
305m-d MY, kg	3009.8	1098.0
305l-d MY, kg	3048.7	1091.2

TLMY = Total unadjusted lactation milk yield
305l-d MY= milk yield adjusted by regressing actual milk yield on lactation length
305m-d MY = milk yield adjusted using multiplicative factors.

Milk yield were standardized to 305-day lactation length, the records were adjusted using multiplicative

extension factors developed from the records that remained after editing and also adjustment by regressing actual MY on lactation length. The lactation length classes of 7 days intervals were fitted as fixed effect to get the least square means which was used in derivation of multiplicative extension factors (model 1)

$$Y_{ijklmn} = m + p_i + h_j + y_k + s_l + lc_m + e_{ijklm} \quad (1)$$

Where

- Y_{ijklm} = the observations on milk yield
- m = the underlying constant,
- p_i = the fixed effect of the i^{th} parity ($i=1,2,\dots,7$),
- h_j = the fixed effect of j^{th} herd ($j=1, 2, \dots, 10$),
- y_k = the fixed effect of k^{th} year of calving ($k=1986, 1987,\dots,2005$),
- s_l = the fixed effect of l^{th} season of calving ($l=1,2, 3$)
- lc_m is the fixed effect of m^{th} lactation length sub-class ($m=1,2,3,\dots,36$).
- e_{ijklm} = the random residual error NID ($0, s^2_e$)

Multiplicative extension factors for uncompleted lactation yields were computed using the least square means of the lactation subclasses according to according to formular of Chauhan (1988)

$$MEF_i = LSM_b / LSM_i \quad (1)$$

Where

- MEF_i is the multiplicative extension factor or the i^{th} lactation length subclass
- LSM_b is the least square means of reference subclass (305 day) to which all subclasses were adjusted.
- LSM_i is the least square mean of the i^{th} subclass of lactation length.

The mean 305day milk yields derived from MEF were compared with the 305d MY calculated by regressing actual lactation MY on lactation length a method commonly used. The comparison was done to assess the effectiveness of the correction methods (Table 2).

Table 2. Estimated genetic (above diagonal) and phenotypic (below diagonal) correlations between TLMY, 305l-d MY and 305m-d MY

	TLMY	305l-d MY	305m-d MY
TLMY	1	0.88	0.83
305l-d MY	0.48	1	0.96
305m-d MY	0.37	0.96	1

TLMY, 305l-d MY and 305m-d MY = as described in Table 1

In the regression of milk yield on lactation length, the increases and decreases in milk production due to the effect of environmental factors were assumed to be of the same magnitude for all cows (Chauhan 1988). However, effects of environmental factors were accounted for by use of multiplicative extension

factors. Therefore, in this study we found that adjusting lactation milk yield using multiplicative extension factors was more effective than regression of lactation yield on lactation length as indicated by their phenotypic and genetic correlations with unadjusted lactation yield (Table 2). Extending records of cows culled before 305 days in lactation has been recommended because it decreases the effects of differential culling, allows earlier and more accurate evaluation of young animals and permits comparisons among cows in all stages of lactation for herd management. Therefore, in this study records of cows culled before reaching 305 days were included.

Statistical data analyses for genetic parameters

Analyses for fixed effects were carried out using the least squares techniques of the General Linear Models procedure of SAS (SAS[®] 1989). The least squares analyses showed that all interaction among fixed effects were not significant ($P>0.05$) and therefore interactions were not included in the final mixed model. The genetic and phenotypic parameters were estimated using Derivative Free Restricted Maximum Likelihood (DFREML) method (Meyer 1989). The general mixed model equation used in the analysis, in matrix notation was:

$$Y = Xb + Zu + e, \quad (2)$$

where,

Y = vector of observations;

X = known incidence matrix of fixed effects;

Z = known incidence matrix of random effects;

b = Unknown vector of fixed effects;

u = Unknown vector of random effects $IND(0, \sigma_a^2)$;

e = vector of residuals, $IND(0, \sigma_e^2)$, where $\sigma_e^2 = \sigma^2_E$, the random environmental variance.

For the analyses of trends, the overall additive genetic trend in a trait was estimated by regressing the mean predicted breeding values on the respective year of birth in that trait. Similarly, for phenotypic trends, the adjusted performance records were averaged within year of birth and then regressed on years of birth (Wahungu 1988; Rege and Mosi 1989). This was done only for the records that were adjusted using multiplicative extension factors.

Results and discussion

Means and variation

The overall means for 305m-d and 305l-d milk yield were 3009.8 Kg and 3048kg (Table 1). The milk yield had a moderate variation with coefficients of variation (CV) of 26.6% and 27.8% for 305l-d MY (305d milk yield adjusted by regressing actual lactation yield on lactation length) and 305m-d MY (305d milk yield adjusted using multiplicative extension factors) respectively, these CVs were higher than the range reported in temperate regions of 18 %- 20 % (Abubakar et al 1986; Bondoc et al 1989), but were within the range reported in the tropics (Bondoc et al 1989; Njubi 1990; Muasya 2005). Milk yield of exotic dairy breeds in the tropics have been reported to have high standard deviations and hence large CVs, some over 40 % (Bondoc et al 1989). The high CVs may partly indicate potential for improvement through selection. However the high CVs reported for exotic dairy breeds in the tropics have been generally attributed to differences in management rather than genetic differences (Abubakar et al 1986; Wahungu 1988; Rege and Mosi 1989).

Non-genetic factors affecting milk yield

Year of calving ($P < 0.01$), herd ($P < 0.001$) and parity ($P < 0.01$) significantly influenced milk yield, while the season of calving did not significantly influence all MY.

Year of calving significantly influenced MY ($p < 0.01$), this was consistent with reports in the literature (Wakhungu 1988; Rege and Mosi 1989; Ojango 2000; Olukoye and Mosi 2002). The variation in milk yield from one year to other could be attributed to changes in herd size, age of the animals and good management practices introduced from year to another, e.g. fluctuations in feed availability and quality and herd genetic levels. Rege (1991), Kaya (1996) and Atil et al (2001) also came to the same conclusion.

Herd significantly ($P < 0.001$) influenced both MY, similar significant effects of herds have been reported in the tropics (Rege 1991; Kaya 1996; Ojango 2000; Olukoye and Mosi 2002). All herds were located in the high potential zones of the country; therefore, variations from one herd to another could be due to differences in management practices.

Parity significantly ($P < 0.001$) affected milk yield, the results of this study were similar to findings in other studies made in tropics (Rege 1991; Njubi et al 1992; Olukoye and Mosi 2002). The peak milk yield was attained during the 4th parity (figure 1), this was due to the increase in body weight combined with advancing age at full development of secretory tissues of the udder.

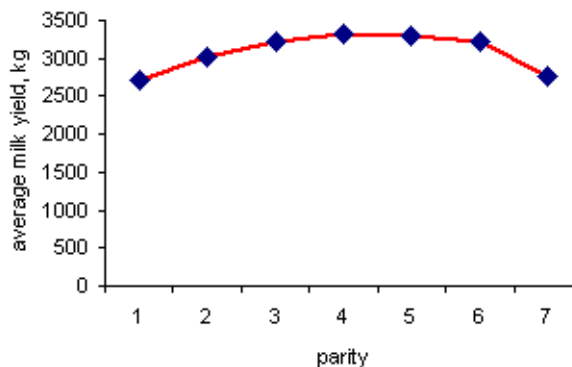


Figure 1. Relationship between 305-d milk yield and parity

The decline in milk yield after 4th parity was because the physiological activities of all body systems start to decrease and the secretory tissues of mammary gland is partially degenerated leading to gradual decrease in milk production with advancing age.

Phenotypic and genetic parameters

The estimated phenotypic, additive genetic, permanent environmental, and error variances as well as heritability and repeatability are presented in Table 3. The heritability estimate found in this study for MY was lower than those reported by other authors for other breeds in Kenya (Mosi 1984 (Fresian); Njubi 1990 (Jersey); Musani 1995 (Jersey); Ojango 2000 (Fresian)). The phenotypic variance of milk yield obtained (Table 3) was smaller than those reported by Ojango and Pollot (2001) for Fresians, but larger than those reported by Muasya (2005) for Kenyan Ayrshire breed.

Table 3. Additive genetic, phenotypic and relative permanent

environmental variances and heritabilities and repeatabilities of milk yield

Parameter	305l-d MY	305m-d MY
Additive-genetic variance	79104	88480
Variance due to permanent cow effect	154347	159514
Error variance	425066	452435
Phenotypic variance	658516	700430
Phenotypic coefficient of variation, %	26.6	27.8
Heritability	0.12 ± 0.05	0.13 ± 0.05
C ²	0.26 ± 0.05	0.23 ± 0.05
Repeatability	0.35 ± 0.01	0.36 ± 0.01

305l-d MY and 305m-d MY = as described in Table 1,

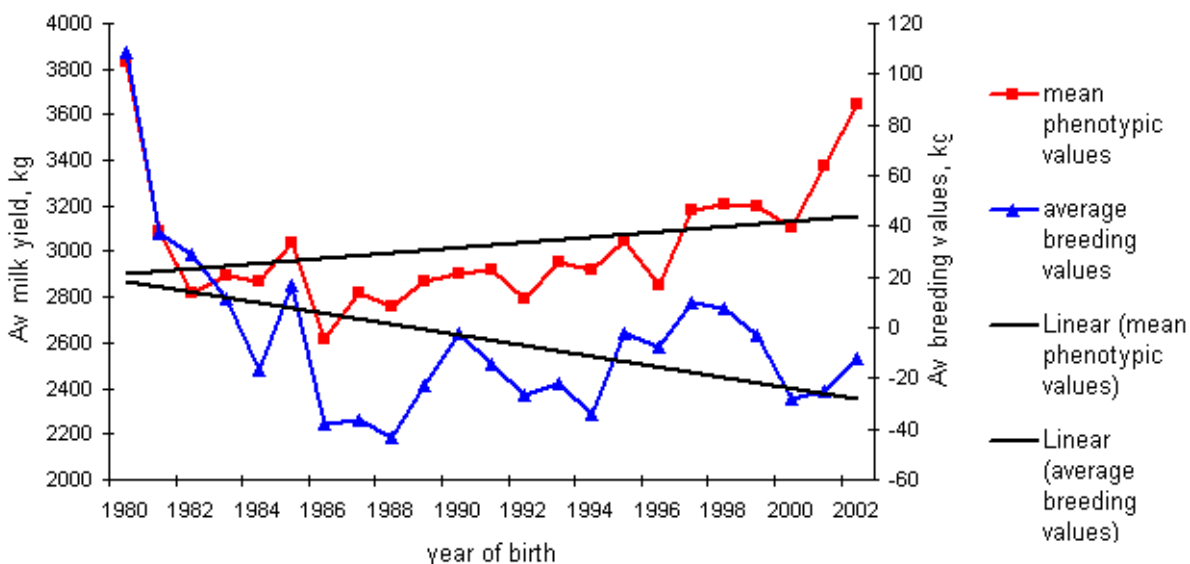
C² = Permanent environmental variance

The low heritability estimate for 305-d MY reported in this study could be attributed to the low additive genetic variance obtained against large phenotypic variance (Table 3), this could be because the population of Ayrshire cattle under the study has been highly selected for milk yield leading to a reduction of the genetic variation (and also since many farmers milk record only superior cows within their herds) and also effect of inbreeding could not be ignored since from the data analysed seven cows were inbred with average inbreeding coefficient of 0.23. However, the effect of inbreeding on MY was not analysed in this study since the overall inbreeding coefficient was negligible (0.0004) and is considered acceptable (Falconer 1989). In addition the use of genetically similar sires from the same source over longer period could lead to low additive genetic variance, since most of the studied herds used same bulls while few bulls were used exclusively by one herd.

Due to the low heritability estimate for MY it could be concluded that the genetic improvement in milk yield cannot be achieved through selective breeding programme within the studied Ayrshire herds. Therefore, genetic improvement in the studied herds could be achieved through efficient choice and use of Ayrshire germ plasm from different origin. Controlling the temporary causes of variation e.g. fluctuations in feed availability and quality and herd management levels could also lead to considerable improvement.

Genetic, phenotypic and environmental trends

The mean 305m-d MY and mean breeding values by year of birth were plotted against time to give phenotypic and genetic trends of milk yield (figure 2). There was a positive though non-significant ($P > 0.05$) phenotypic and environmental trends in MY with an overall rate of increase of 11.7 and 13.8 kg per year respectively.



Regression equation: Phenotypic trend is $y = 11.658x + 2890.8$; Genetic trend: $y = -2.14x + 20$

Figure 2. Genetic and phenotypic trends for 305m-d milk yield (kg).

Similar trends have been reported by other workers (Ojango 2000; Muasya 2005, Damatawewa and Berger 1998) for different breeds. There was a negative significant ($p < 0.01$) trend in mean breeding value for milk yield over time (figure 2). The regression coefficient of mean breeding values on year of birth was significant ($P < 0.05$) indicating an overall decrease of 2.1 kg per year over the study period. These results were consistent with those reported by Njubi et al (1992) for jersey cattle, but not with the findings of Ojango and Pollot (2001) who reported a positive genetic trend in Kenyan Fresian cattle.

The negative annual genetic changes in milk yield observed could largely be due to ineffective breeding strategies both at herd and national level. Therefore, the present result shows that the Kenyan breeding program still does not have the expected impact on milk yield in Ayrshire dairy herds. This fact can be attributed to the small number of recorded Ayrshire cows, continuous entry of new sires and cows in the recording program, a more advanced age at first calving and long calving interval. Other aspects are related to dairy operations such as fulfilment of nutritional needs and diet formulation and milking management.

Conclusion

- Highly significant effects ($P < 0.001$) on milk yield was found for several environmental variables including herd, parity and year of calving. Therefore, the effects of environmental variables must be taken into consideration when developing and comparing models to be used in adjusting data to provide the best estimates of genetic values and parameters in the dairy cattle evaluation.
- The genetic parameter estimates for 305-d MY obtained for Kenyan Ayrshire population in this study were lower than those obtained for other breeds in literature.
- The negative genetic trend of MY obtained in this study was undesirable. This suggested low efficiency of animal evaluation procedures used in the herds studied. Hence, the breeding and

management strategies in the studied herds were working against their breeding objectives. Therefore, the nature of these trends calls for national economic feasibility analysis of dairy enterprises improvement.

- Knowledge of genetic relationships between basic functions of milk yield and fertility and the computation of the index weights to be applied to fertility and milk yield traits in order to maximize the response on the breeding objective should be the next step in the development of the genetic evaluation for production and fertility in Kenyan Ayrshire cattle.

Acknowledgements

Appreciation is expressed to the Kenya Livestock Breeders Organization for providing data. This study would not have been possible without the support of the Ayrshire commercial dairy farmers. The authors acknowledge their cooperation in relation to access to their dairy herds and to their farm records.

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Received 11 October 2006; Accepted 18 November 2006; Published 1 January 2007

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