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GENETIC PARAMETERS AND ANNUAL TRENDS FOR 305-DAY MILK YIELD OF *BOS TAURUS* DAIRY CATTLE BREEDS IN KENYA

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ABSTRACT

The objective of this study was to estimate genetic parameters and annual trends in 305-d milk yield (MY) of *Bos taurus* dairy cattle breeds in Kenya. The *B. taurus* breeds considered were Holstein Friesian (F), Ayrshire (A), Jersey (J) and Guernsey (G) kept for milk production on various farms. Data were obtained from various farms across the country which is usually stored at the Livestock Recording Centre (LRC). Genetic parameters were estimated by fitting a repeatability animal model and the best linear unbiased prediction (BLUP) procedure was used to estimate breeding values for MY for cows born between 1979 to 2000. All the analyses were conducted using the DFREML computer programme. Breeding values were averaged by year of birth to give the annual genetic trends. Annual environmental trends were obtained by averaging herd-year-season of calving least square solutions within year of calving. Heritability estimates for F, A, J and G breeds were 0.16, 0.13, 0.12 and 0.35, respectively. Repeatability estimates were 0.33, 0.38, 0.84 and 0.61 for F, A, J and G breeds respectively. The average genetic progress for the F breed was close to zero while the regressions indicated an overall rate of increase of 1.5kg, 10.8kg and 9.8kg for A, J and G, respectively. Environmental trends were generally undesirable for all the breeds suggesting fluctuation in feed availability and other management related practises. There is the potential to realise steady genetic progress if sound genetic improvement strategies are adopted.

Keywords: Annual trends, *Bos taurus* breeds, Genetic parameters, Kenya, 305-d milk yield

INTRODUCTION

Dairy production is one of the leading enterprises in the livestock sub-sector and supports livelihoods of many small-scale farmers in developing countries. In Kenya, the total annual milk production is estimated at 2.6 billion litres out of which more than 70% is produced by pure bred *Bos taurus* European breeds and their crosses with local Zebus (KDDP, 2001). The main *B. taurus* breeds kept includes Holstein Friesian (F), Ayrshire (A), Jersey (J) and Guernsey (G). The ever increasing human population and concurrent urbanisation will require that efforts be geared towards increasing production to offset any resultant deficits. One way of achieving this is by setting up appropriate breed improvement programmes. Precise and accurate knowledge of genetic and phenotypic parameters becomes critical in planning and developing such strategies (Ojango and Pollot, 2001; Kahi *et al*., 2004). Furthermore these breeding programmes should undergo regular appraisal to identify optimum efficiency and predict possible rates of progress. Thus, bifurcation of the phenotypic trend into genetic and environmental trends will enable assessment of the effectiveness of the selection programme and management conditions over time (Musani and Meyer, 1997; Ojango and Pollot, 2001). However, estimates of genetic parameters and annual trends for *B. taurus* dairy breeds on various Kenyan farms are scarce in literature. The objectives of this study were to estimate genetic parameters and quantify the rate of progress in 305-d milk yield (MY) in *B. taurus* dairy cattle breeds. Implications of the results for future genetic improvement of these breeds in Kenya are also discussed.

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MATERIALS AND METHODS

Data source and edits

Data on MY were obtained from the various farms across the country and stored at the Livestock Recording

Centre (LRC) at Naivasha. The LRC is located approximately 70 km North West of Nairobi city. The LRC is mandated to analyse data from the Dairy Recording Services of Kenya (DRSK) collected from various farms across the country and make the results available for making selection decisions in participating herds. The data consisted of MY of F, A, J and G. Performance records were obtained from cows calving between 1985 and 2003 (the pedigree consisted of cows born between 1979 and 2000). A cow was to have at least the first lactation record to be included in the analysis. Lactation records that were terminated by death or sale of a cow were not considered for analysis. Furthermore lactation records initiated as a result of abortions and of cows whose parity could not be established were excluded. Animals with missing pedigree information were also excluded from the analysis. A maximum of five lactations were allowed for each cow with at least the first lactation known. The data structure and characteristics of the MY used in the final analysis is presented in Table 1.

Statistical analysis

Variance components and genetic parameter were estimated for each breed using a repeatability animal model based on derivative free restricted likelihood methodology (Meyer, 2000). In this case the animal model allowed for repeated records per cow by fitting an additional random effect that represented the permanent environment. The covariances of the three random effects were zero and levels of each were independently distributed with variances s_a^2 for animal, s_{pe}^2 for permanent environmental effects, and s_e^2 residuals. The mixed model fitted in matrix form was:

$$y = Xb + Za + Wc + e$$

where y is the 305-d MY, b represents the fixed effects of herd-year-season of calving and lactation number, a and c stands for random additive genetic and environmental effect for each animal, respectively and e is the error term. X, Z and W are incidence matrices relating individual cow records to the fixed, random additive genetic and permanent environmental effects, respectively. The year of calving were from 1985 to 2003 each with four seasons: January to March for the primary dry season; April to June for the main wet season; July to September and October to December as the secondary dry and wet seasons, respectively.

It was assumed that the covariances of the three random effects were zero and that levels of each were independently distributed with variance s^2_a for animal, s^2_{pe} for permanent environmental effects, and s^2_e residuals. The genetic level of a herd in a year is the average breeding value of the animals born in that year. Breeding values were obtained for all animals in the pedigree by back solutions and averaged by year of birth to give the genetic trends. Environmental trends were obtained by averaging herd-year-season of calving least square solutions within year of calving.

RESULTS AND DISCUSSION

Estimates of variance components and genetic parameters

Variance components, heritability and repeatability estimates for the four breeds are presented in Table 2. The additive variance was highest for the J breed. Generally, the estimate of additive variance and the resultant heritability estimates for the four breeds indicate that there is sufficient genetic variance. Therefore selection efforts to increase MY is expected to result in substantial progress if appropriate breeding strategies are put in place. Milk yield was moderately heritable in all the breeds. Heritability estimates were generally lower than reported for the same breeds on large scale farms. For example, Ojango and Pollot (2001) obtained a heritability of 0.29 for F on large scale Kenyan farms. For the J breed, Njubi *et al*. (1992) and Musani and Mayer (1997) reported heritability estimates of 0.28 and 0.20, respectively. A comparable heritability estimate of 0.10 has been reported for A breed in the Kenya highlands (Muasya, 2005). Although, the heritability estimate was highest in the G breed, this should be treated with caution because few records were available for analysis. Nevertheless, heritability estimates for G breed in Kenya are scarce in literature.

Table 1: Number of records, overall means and coefficient of variation for MY in the four breeds

	Breed			
	F	A	J	G
No. records	10040	2523	1634	441
Mean	4487	2787	3931	2975
CV	25.4	27.2	30.0	20.0

Table 2: Estimates of heritability (h^2) with standard, repeatability (r) and additive (s^2_a), permanent environmental (s^2_{pe}), residual (s^2_e) and phenotypic (s^2_p) variances of milk yield

Component	Breed			
	F	A	J	G
s^2_a	222641	58806	431070	148716
s^2_{pe}	227815	119379	2867033	110448
s^2_e	899357	292523	601359	159904
s^2_p	1349813	470709	3899463	419069
h^2	0.16±0.005	0.13±0.06	0.12±0.09	0.35±0.26
r	0.33	0.38	0.84	0.61

The repeatability estimates for all the breeds were moderate to high indicating that the records could provide a basis for accurate prediction of the producing abilities of cows. Therefore, under good management, culling decisions to eliminate low producers in early lactations could be done with reasonable degree of accuracy. However, management in F and A herds has to be improved and the environment stabilised for culling decisions to be based on performance records in earlier lactations. The repeatability estimate for J breeds (0.84) was higher than reported for the same breed (Njubi et al., 1992; Musani and Mayer, 1997). Differences between parameter estimates reported in this study and those reported in literature arise probably due to the use of different models with different definition of fixed and random effects, and other unidentified environmental factors whose effects are more pronounced under different production circumstances. Other factors such as data sets belonging to different periods, large variations in phenotypic performance and effects of heterogeneity of variances could also contribute to differences in parameters estimates.

Annual genetic and environmental trends

Fig. 1 shows the annual genetic trends for MY for the four breeds. Generally, the mean annual genetic trends for all the breeds were not steady over the years. The average genetic progress for the F breeds was close to zero while the regressions indicated an overall rate of increase of 1.5kg, 10.8kg and 9.8kg for A, J and G, respectively. The annual genetic trend for J was in the same direction as reported by Musani and Mayer (1997). However, Rege (1991) and Njubi *et al*. (1992) reported non-significant genetic improvement of the F and J breed, respectively. Negative genetic trends have been reported for A breed in the Kenyan highlands (Muasya, 2005). Despite the observed additive genetic variance for the four breeds (Table 2), and the continued use of AI sires from temperate countries (Ojango and Pollot, 2001), the observed progress in all the breeds is slow and below expectations. A steady genetic progress has been reported on large scale F herds (Ojango and Pollot, 2001). This has largely been attributed to use of superior semen of imported bulls. In most cases the cost of semen from such bulls is high and the desire to use it to increase production has been on the increase. However, for the small and medium scale dairy herds (which constitute a large proportion of the data used in this study), the cost of procuring imported semen might be overwhelming and therefore the management opt to use affordable semen from local bulls whose genetic merit is not always available.

Fig. 2 shows annual environmental trends in MY in the four breeds. Generally there were large fluctuations in environmental trends for all the breeds. These unstable environmental trends indicate inefficiencies in the existing management policies on individual herds to initiate feeding strategies aimed at countering the unprecedented effects of climatic changes. Most of the dairy herds are located in areas classified as medium to high potential for

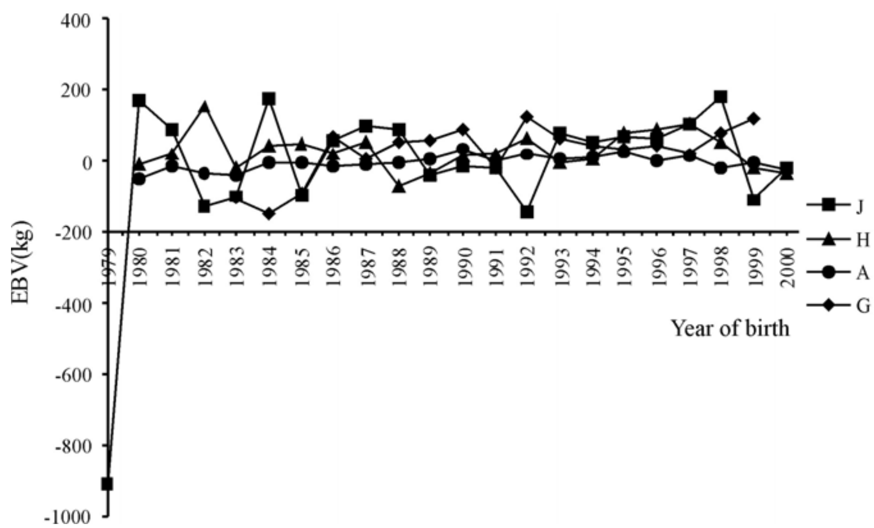

Fig. 1: Annual genetic trends MY for J,F,A and G dairy breeds.

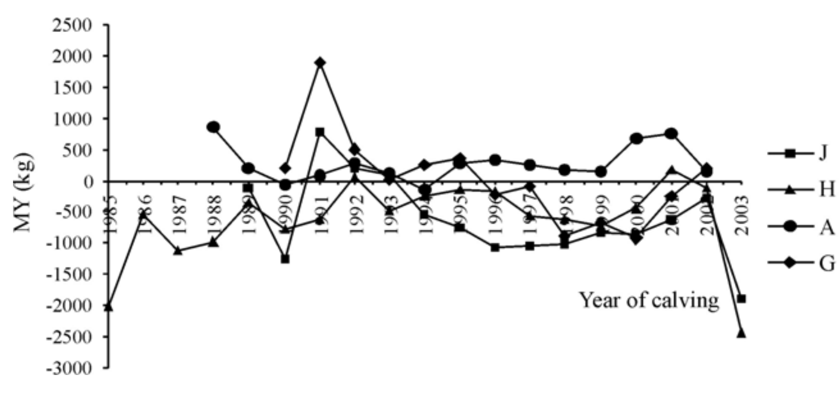

Fig. 2: Annual environmental trends for MY for J, F, A and G dairy breeds. Environmental trends are expressed as deviation from the overall mean for each breed.

agricultural production. In such areas, pastures could be established during favourable seasons and used for supplementary feeding during drought. Profits accrued from sale of milk and culled animals could also be used to finance supplementary feeding strategies aimed at reducing the impact of adverse weather conditions.

Breeding objective and breeding schemes for genetic improvement of local dairy cattle populations have been developed (Kahi and Nitter, 2004; Kahi *et al*., 2004). Based on results from those studies, it has been shown that use of an open nucleus breeding scheme where young bulls are used for mating would result in more genetic progress and reduced operational costs. Since the objective of most of these herds that submit performance data to LRC is to make profits, it has to be demonstrated to them how their involvement in the breeding programme will influence their production objectives. One way of doing this is by providing a quick feedback of the result of genetic evaluation to the participating herds. This study has provided some information pertaining to the rate of progress of the various *B. taurus* dairy breeds for herds participating in the recording scheme. These results can be used by herd owners for appraisal of their management and selection strategies aimed at improving on the overall herd productivity.

It is important to note that the data used in this study were from several farms that varied in terms of herd sizes, operational scale and production circumstances. Variances of milk yield vary with the level of management and environment due to genotype by environment correlation and differences in feeding regimes (Brotherstone and Hill 1986). Bias may therefore arise in genetic evaluations from differences in variation within herds, and may become more severe as intensity of selection increases. In such cases, herds can be grouped according to management, climatic and genetic information to increase the precision of genetic parameter estimates (Weigel and Rekaya 2000). This can lead to borderless evaluation and even specific to each production system (Lohuis and Dekkers 1998; Weigel and Rekaya 2000). There is the need to characterise dairy cattle production systems for the *B. taurus* population in Kenya in terms of production level and some management factors and to determine if evidence exists for heterogeneity of variance for MY as influenced by production environment.

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