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GENETIC EVALUATION OF MILK YIELD OF BOS TAURUS DAIRY BREEDS IN KENYA

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Abstract

The objective of this study was to quantify the rate of genetic progress in 305-d milk yield (MY) in *Bos taurus* dairy cattle breeds. The *Bos taurus* breeds considered were Holstein Friesian (F), Ayrshire (A), Jersey (J) and Guernsey (G) kept for milk production in small, medium and large scale Kenyan farms. Data were obtained from the Livestock Recording Centre (LRC) which is mandated to analyse data from the Dairy Recording Services of Kenya collected from various farms across the country and make the results available for use in making selection decisions. The best linear unbiased prediction (BLUP) fitting a repeatability animal model was used to estimate breeding values for MY for cows born between 1980 to 2000. Breeding values were 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. The average genetic progress for the F breed was close to zero while the regressions indicated an overall rate of increase of 1.5 kg, 10.8 kg and 9.8 kg 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.

Introduction

Dairy production is one of the leading enterprises in the livestock sub-sector and forms an important livelihood to most small-scale farmers. 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* breeds and their crosses (KDDP, 2001). The main *B. taurus* breeds kept include 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. Improved production can be achieved through appropriate breed improvement programmes. Precise and accurate knowledge of genetic and phenotypic parameters becomes critical in planning and developing appropriate breed improvement strategies (Kahi *et al.,* 2004). Such breed improvement 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). This will also help in designing more appropriate genetic improvement and management strategies aimed at increasing production. However, estimates of genetic and phenotypic trends for various *B. taurus* on small, medium and large scale farms are scarce in literature. The objective of this study was therefore to quantify the rate of genetic progress in 305-d milk yield (MY) in *B. taurus* dairy cattle breeds.

Materials and methods

Data on MY were obtained from the Livestock Recording Centre (LRC) at Naivasha. The data consisted of 305-d MY of F, A, J and G on small, medium and large scale dairy farms located in various parts of the country. 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. Cows calving between 1980 and 2003 were included in the analysis. A cow was to have at least the first lactation record to be included in the analysis. Lactation records arising from abortions and records of cows whose parity could not be determined were excluded. 10040, 2523, 1634 and 441 lactation records for F, A, J and G, respectively, were available for analysis.

Variance components were estimated for each breed using a repeatability animal model based on derivative free restricted likelihood method (Meyer, 2000). A repeatability model was used in this case to account for permanent environmental effects common to the repeated lactation records in the different parities on the same cow. 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.

It was assumed that the covariances of the three random effects were zero and that levels of each were independently distributed with variance σ^2_a for animal, σ^2_{pe} for permanent environmental effects, and σ^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 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

Variance components, heritability and repeatability estimates for the 4 breeds are presented in Table 1. The additive variance was highest for the J breed. Generally, the estimate of additive variance and the resultant heritability estimates for the 4 breeds indicate that there is sufficient genetic variance. Therefore selection efforts to increase 305-d lactation yield is expected to result in substantial progress if appropriate improvement strategies are employed. 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 Kenya farms. For the Jersey, 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– Estimates of heritability (h^2) with standard errors in parenthesis, repeatability (r) and additive (σ_a), permanent environmental (σ_{pe}), residual (σ_e) and phenotypic (σ_p) variances of milk yield

Component	Breed			
	F	A	J	G
σ^2_a	222641	58806	431070	148716
σ^2_{pe}	227815	119379	2867033	110448
σ^2_e	899357	292523	601359	159904
σ^2_p	1349813	470709	3899463	419069
h^2	0.16(0.005)	0.13(0.06)	0.12(0.9)	0.35(0.26)
r^2	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 circumstance. 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.

Figure 1 shows the genetic and environmental trends in 305-d MY for the 4 breeds. Generally, the mean annual breeding value (BV) for all the breeds was 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 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 4 breeds (Table 1), 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.
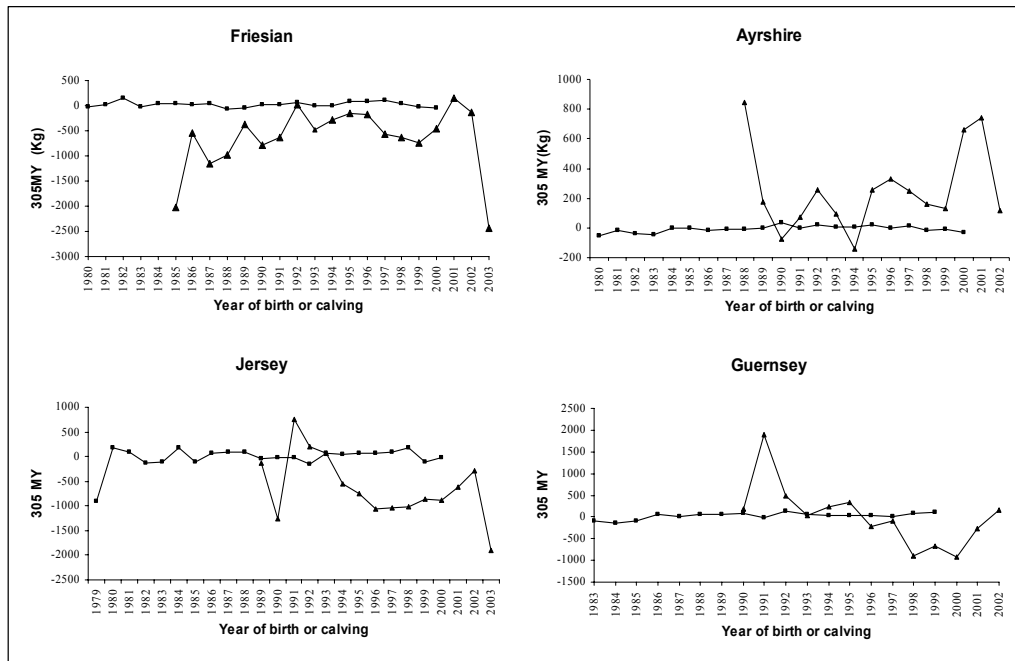

Fig 1. Genetic (■) and environmental (▲) trends for 305-d MY. The genetic and environmental trends are shown by year of birth and calving, respectively. Environmental trends are expressed as deviations from the overall mean.

Large scale F herds have had a stead genetic progress for 305-d MY (Ojango and Pollot, 2001) as a result of continuous use of imported semen of bulls that have been highly selected for increased milk yield in the temperate countries. 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. For the small and medium scale dairy herds, 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. Lack of information on the genetic merit of local AI bulls is a consequence of many physical and socio-economic constraints, poor performance and pedigree field recording and lack of expertise in genetic evaluation of breeding bulls (Kahi et al., 2005).

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 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.

The heavy use of AI is the main reason why sire selection has become the most important and efficient way of disseminating superior genes and obtaining genetic progress. It would be immaterial if pedigree and performance data relating to performance of daughters of such sires is not subjected to analysis using recent statistical approaches for purposes of obtaining breeding values and monitoring the rate of progress in herds that participate in the recording. Genetic evaluation has to be undertaken regularly to ensure that the best animals are given an opportunity to be parents of the next generation based on their genetic merit. Therefore, estimation of unbiased breeding values would be an important component of functional dairy cattle breeding scheme in Kenya (Kahi et al., 2004). Use of animal model BLUP procedures would guarantee accuracy in discriminating superior cows and bulls, while accounting for variations that arise due to systematic environmental effects.

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 was 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. Information pertaining to genetic merit of dairy cows and bulls is now available for herds participating in the recording scheme. These results can be used by herd owners to understand the genetic merit of their animals and use this information to make objective selection decisions.

Conclusion

This study has shown that the additive genetic variance for milk yield of *B. taurus* breeds is sufficient thus offering a great opportunity for genetic progress under a well defined and effective breeding programme. The fluctuations in genetic and environmental trends indicate that selection decision may not have been consistent and appropriate management strategies to reduce on inimical effects of climatic changes have not been sufficient. In order to realise higher genetic progress, the need to redesign the current breeding programme based on well defined breeding objectives and schemes supported by the various stakeholders is necessary. It is important to document genetic parameters estimates for other economically important traits such as butter fat, protein yield and reproductive traits to allow for design of more efficient breeding programmes.

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