Joint genetic analysis of Jersey dairy cows performing in two countries in Sub Saharan Africa

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Application Currently, there are a few countries that carry out genetic evaluation for dairy cattle in Sub Saharan Africa. Where this is done, it is at individual country level. Results from a joint genetic evaluation may provide robust and accurate genetic parameters.

Introduction Genetic improvement of farmed livestock has had a major impact on productivity and its effects being permanent, cumulative and usually highly cost effective. However, genetic improvement has not been carried out systematically in most Sub Saharan Africa countries because of lack of performance recording and pedigree information. However, some data has been collected in some countries which are currently used for national evaluation. A joint across-country analysis may result in more accurate evaluations in cases where common foreign sires have been used. Using a case study approach with data from Jersey cattle performing in Kenya and South Africa, the hypothesis was that joint genetic evaluation would result in robust and accurate genetic parameters and hence, improve genetic progress.

Material and methods Test interval method (ICAR 2003) was used to determine 305-day milk yield from test day records for Jersey cattle (n=46,242) obtained from the Kenya Livestock Breeders Organisation. In South Africa, 305-day milk yield records (n=1,858,021) were obtained from Agricultural Research Council. Data were from cows between first and fifth lactation from 1988 to 2012. A total of 400 sires with an average of 14 daughters per sire from Kenya and 9,962 sires with an average of 34 daughters per sire from South Africa were used. There were 31 sires that had daughters in both Kenya and South Africa from several foreign countries. The common sires were from USA (18), New Zealand (7), Denmark (1), Canada (1), Great Britain (1) and Australia (1). Variance component estimation was performed fitting a bivariate mixed linear model using ASReml (Gilmour *et al*., 2009). The model was y_{ijkl} = lac_i (age) + HYS_k + $animal_l$ + pe_m + e_{ijkl}, where lac_i was the effect of the j^{th} lactation, HYS_k was the herd-year-season, $animal_l$ and pe_m were the random l^{th} animal and m^{th} pe effect. e_{ijkl} was the error term. In the joint evaluation, country of performance was included in the model to account for the production system.

Results Descriptive statistics for production and fertility traits for Jersey cattle performing in Kenya and South Africa are presented in Table 1.

Table 1 Means and standard deviations of Jersey cow performance traits in Kenya and South Africa between 1988 and 2012.

Trait	Kenya	South Africa	Joint data
Age at first calving (months)	31.0 ±7.21	28.0±4.10	29.0±4.50
Calving interval (days)	493.0±152.01	404.0±89.30	405.2± 91.30
305-day milk yield (litres)	4181.0±1428.1	5563.0 ±1417.3	5520.4± 1437.5

Cows in Kenya calved for the first time at a slightly older age than in South Africa. However, cows in Kenya had relatively lower milk yield than cows in South Africa with more variation in milk yield in Kenya (CV% = 34%) than in South Africa (CV% = 25%). Genetic parameters for individual and joint evaluations are presented in Table 2.

Table 2 Estimation of genetic parameters and standard errors for Kenyan and South African Jersey cattle.

Genetic parameters	Kenya	South Africa	Joint genetic evaluation
Heritability of 305-day milk yield (MY)	0.13 (0.10)	0.18 (0.01)	0.21 (0.01)
Heritability of age at first calving (AFC)	0.15 (0.05)	0.44 (0.05)	0.58 (0.05)
Heritability of calving interval (CI)	Non estimable	0.04 (0.01)	0.05 (0.01)
Repeatability of 305-day MY	0.13 (0.10)	0.43 (0.03)	0.43 (0.01)
Genetic correlation of 305-day MY and AFC	-0.53 (0.24)	-0.12 (0.10)	-0.20 (0.10)
Genetic correlation of 305-day MY and CI	Non estimable	0.60 (0.05)	0.58 (0.04)

Joint genetic evaluation increased the value of the genetic parameter estimates and accuracy as reflected in low standard errors associated with the estimates.

Conclusion A joint genetic evaluation between Jersey cattle from Kenya and South Africa is feasible and more appropriate than individual country evaluation. This would generally increase the value of genetic parameter estimates and accuracy of selection especially where there are insufficient data available in individual countries for a robust analysis.

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References

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