Contributed paper

PROPOSED GENETIC IMPROVEMENT STRATEGIES FOR DAIRY CATTLE IN KENYA

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SUMMARY

Genotype by environment interactions and heterogeneity of variance may influence the effectiveness of breeding programs in developing countries. This study investigated optimization of dairy cattle breeding programs within Kenya for low, medium and high input and output production systems in the presence of genotype by environment interactions. Multi-trait selection index theory was applied using the SelAction software package to determine the optimum strategy that would maximise genetic gain across the three production systems. The breeding goal was to maximise overall gain for a breeding objective containing three traits: lactation milk yield; lactation fat yield and calving interval. Three selection strategies based on: 1) sire evaluation and selection within the high production systems only (*single*); 2) independent sire evaluation and selection within each production system (*independent*) and 3) sire evaluation across all production systems (*joint*), were evaluated under scenarios using progeny test information and genomic information. The joint strategy maximised the overall economic gain (1583 Kes) while the single strategy generated the least overall gain (1311 Kes). The dairy industry in Kenya would therefore benefit from implementing production system specific breeding strategies for bull evaluation and selection. In addition, implementing genomic selection could speed up the rate of genetic gain compared to progeny testing due to reductions in generation interval and higher selection accuracy with a moderately large reference population.

INTRODUCTION

Breeding programs are designed to generate and disseminate genetic improvement. The classical approach starts with definition of breeding objectives, followed by development of selection criteria, implementation of genetic evaluation allowing for the selection of superior animals, design of sustainable mating systems, and strategies to disseminate genetic superiority to commercial producers. Selection is however, challenging in developing countries where dairy cattle production systems are highly variable in terms of inputs and outputs (Wahinya *et al*. 2020). When sires are selected from a different environment, for example, from high input and output production systems or via the importation of semen, genotype by environment interactions can result in genotypes re-ranking and reduce selection efficiency. This is likely to affect the accuracy of selection and the rate of genetic progress. In developing countries, genetic improvement programs are more likely to be successful if they are developed as an integrated livestock-production package and not in isolation (Kahi *et al*. 2005). This paper will evaluate different strategies to maximise overall genetic gain across three dairy production systems.

MATERIALS AND METHODS

Definition of environment and simulation of population structure. Definition of the target production system(s) is required for effective implementation of selection strategies. Multiple variables can be used to define production systems. Clustering of herds based on milk production

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* A joint venture of NSW Department of Primary Industries and the University of New England

level has been applied as a classifier to quantify the influence environment has on performance (Ojango *et al.* 2019; Wahinya *et al.* 2020). Low, medium and high production systems were defined by Wahinya *et al.* (2020) using K-means cluster analysis of herd means for 305 days milk yield and applied in this study. Production parameters identified in that analysis were used to simulate three nucleus populations comprising a total of 5000 dams in each. A total of 219 sires were assumed across the three production systems. Sires and dams were spread across 8 age-classes. Every year 10 bulls and 300 cows were selected for each production system. Dams were assumed to produce their first offspring in their third year while progeny information for the bulls was available at six years of age. The sex ratio was assumed to be 0.50 while calving and annual survival rates were 0.67, 0.74 and 0.77, and 0.90, 0.93 and 0.94 for the low, medium and high production systems, respectively.

Breeding strategies. Truncation selection was simulated using multi-trait index selection. Genetic gains were predicted for a dairy cattle breeding objective containing lactation milk yield (LMY in kg), fat yield (FY in kg) and calving interval (CI in days) under three production systems in Kenya. Animals were available for selection when all the information needed for selection was available. Male candidates were evaluated based on their half-sib sisters, daughters and dam's information while females were evaluated on their performance records, half-sib sisters and parent's information. An animal model was assumed for genetic evaluation considering all genetic relationships to estimate the breeding values for selection. Three selection strategies were evaluated based on the groups of test-bulls: 1) a breeding program for a single production system with bull evaluation and selection in the high production system (single); 2) production system specific breeding programs, each with bull evaluation and selection within each environment (independent) and 3) a joint breeding program with bull evaluation and selection in all three production systems (joint). These strategies were simulated under two scenarios using progeny testing and using both phenotypes and genotypes for selection. Genomic selection was simulated by adding an extra trait to represent the marker information as described in Dekkers (2007). Marker information was modelled using a trait correlated to the original trait with a heritability close to 1 (0.999). The accuracy of the estimated genomic breeding values was represented by the correlation between the original trait and the trait specified by marker information. The accuracy of genomic information is dependent on the reference population, the correlation between the true breeding value of a genotyped animal and phenotype as well as the effective population size and was calculated as shown in Dekkers (2007). Six strategies were therefore evaluated in total. The breeding program aimed to maximise genetic gain in the overall objective as follows:

$$\Delta \mathrm{G} = \Delta \mathrm{G}_{\mathrm{L}} + \Delta \mathrm{G}_{\mathrm{M}} + \Delta \mathrm{G}_{\mathrm{H}}$$

where $\Delta \mathrm{G}_{\mathrm{L}}$, $\Delta \mathrm{G}_{\mathrm{M}}$ and $\Delta \mathrm{G}_{\mathrm{H}}$ are the genetic gains in the low, medium and high production systems, respectively. The SelAction software package (Rutten *et al.* 2002) was used to predict genetic gains using a multi-trait selection index. The genetic and phenotypic standard deviations, economic values, heritabilities, genetic and phenotypic correlations used for the traits under the low, medium and high production systems are shown in Tables 1 and 2.

Table 1: Genetic (σ_a) and phenotypic standard deviations (σ_p), and economic weights (EW) for lactation milk yield (LMY; kg), fat yield (FY; kg) and calving interval (CI; days) under low, medium and high production systems

Trait	Low			Medium			High		
	LMY	FY	CI	LMY	FY	CI	LMY	FY	CI
σ_a	285.94	9.94	33.30	467.32	26.97	15.81	613.03	28.66	13.72
σ_p	626.1	29.7	130.85	923.12	60.47	97.56	1226.38	56.84	68.01
EW	22.63	51.3	-114.69	21.45	56.91	-180.42	22.28	61.54	-296.71

Source: (Wahinya 2020)

Table 2: Heritabilities (diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations for lactation milk yield (LMY; kg), fat yield (FY; kg) and calving interval (CI; days) under low, medium and high production systems

System	Trait	Low			Medium			High		
		LMY	FY	CI	LMY	FY	CI	LMY	FY	CI
Low	LMY	0.21	0.65	-0.11	0.42	0.56	-0.46	0.64	0.62	0.00
	FY	0.83	0.11	0.02	0.56	0.33	-0.01	0.66	0.84	0.15
	CI	-0.01	0.08	0.06	-0.53	0.03	0.05	-0.07	0.06	0.08
Medium	LMY	0	0	0	0.26	0.54	0.34	0.75	0.61	0.51
	FY	0	0	0	0.84	0.20	-0.04	0.65	0.58	0.15
	CI	0	0	0	0.02	0.08	0.03	0.14	0.03	0.62
High	LMY	0	0	0	0	0	0	0.25	0.73	0.43
	FY	0	0	0	0	0	0	0.81	0.25	0.14
	CI	0	0	0	0	0	0	0.04	0.08	0.04

Source: (Wahinya 2020); bending was used to make the correlation matrix positive definite

Genetic gain was predicted using equilibrium parameters to account for the accumulation of pedigree information and reduction in genetic variance due to selection. The proportion of cows in the low (0.30), medium (0.33) and high (0.37) production systems in Wahinya *et al.* (2020) were used to weight the gains in the respective production systems to estimate the overall genetic gain.

RESULTS AND DISCUSSION

Animal breeders are faced with a challenge to implement selection in the presence of genotype by environment interactions which can be the case when ranking animals based on breeding values across environments. This has implications for the implementation of optimal design in breeding programs across environments (Mulder and Bijma 2006). Genetic improvement of dairy cattle in Kenya is currently based on genetic evaluation using pedigree information and selection implemented under high input and output production systems. However, due to the heterogeneity of variance across production systems, sires are re-ranked between the production systems (Wahinya *et al.* 2020). Animals from herds with more variability are therefore, likely to be selected, which can lead to bias if the higher variability is as a result of a better environment and not higher genetic variance. Table 3 shows the overall economic response of an index containing lactation milk yield, lactation fat yield and calving interval from the single, independent and joint breeding strategies using progeny testing and genomic information. Milk yield and CI have been reported to have the highest relative economic value under all three production systems while FY has an influence on the revenue from milk and on the energy requirements and hence feed requirements (Wahinya 2020). These results show that a joint selection strategy with genetic evaluation and selection occurring in all three production systems, would generate the highest overall economic response in the scenarios using progeny and genomic information. Using the single breeding strategy with genetic evaluation and selection of candidate bulls only occurring in the high production systems would result in lower economic response (-18% and -30%) for the overall breeding objective compared to the joint strategy in all scenarios. System-specific breeding programs each with an independent genetic evaluation and selection of bulls within each environment would also generate lower response compared to the joint strategy but higher than the single strategy.

A joint selection strategy is also more desirable because genetic evaluation of sires within production systems is likely to lead to selection of more robust animals which also helps to maintain diversity without necessarily developing specialised lines. Sires also benefit from the information in all environments leading to a higher index accuracy. Use of genomic information in addition to phenotypic information is important to reduce generation interval and improve accuracy of selection leading to higher responses (Wahinya 2020). A strategy using genomic selection only could reduce the generation interval further but at a cost of lower accuracies of selection. Genomic information could also be applied for parentage assignment to enhance the pedigree for genetic evaluation where pedigree information is not available and to determine breed composition (Marshall *et al.* 2019). This has been applied for the small-holder dairy cattle in Kenya where pedigree records were unavailable or not reliable (Ojango *et al.* 2019).

Table 3: Comparison of the economic response in Kenyan shillings (Kes) using three selection strategies when either phenotypic or genomic selection is practised

Scenario	Strategy	Economic response (Kes)
Progeny test	Single	1,311.37
	Independent	1,530.99
	Joint	1,583.06
Genomic selection	Single	1,425.85
	Independent	1,816.24
	Joint	2,030.31

A national breeding program involving genetic evaluation and progeny testing of sires, should be implemented across relevant production systems in Kenya since genomic information is still not available partly due to the cost and logistics of establishing a reference population. This would incentivize farmers to select their breeding animals and produce replacement animals through a genetic evaluation conducted within their own production system, minimising the impact of genotype by environment interaction between production systems. The program can work as a two-tiered closed nucleus with performance recording herds under different production systems forming the nucleus. The non-recording herds can then form the commercial tier and then source their semen and replacement cows from the nucleus herds within similar production systems.

CONCLUSION

To maximise genetic gain for the dairy cattle population in Kenya, selection strategies should be based on a genetic evaluation across production systems to account for genotype by environment. Any selection index used should also account for the re-ranking of the breeding objective traits across the production systems. Introduction of genomic information in the current breeding program with a moderately large reference population is likely speed up the rate of genetic improvement.

ACKNOWLEDGMENT

PKW acknowledges the financial support from the University of New England to pursue PhD studies at the Animal Genetics and Breeding Unit and the Livestock Recording Centre for the data.

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