Cattle Breeding Strategies using Genetic Markers as a Pathway for Improving Competitiveness of Pastoral Systems in Kenya

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Introduction

Pastoralists in Kenya have become increasingly food insecure and vulnerable to poverty over the last two decades. This is largely a consequence of the increasing frequency of droughts, a rising population and changes in the land tenure system. Livestock, which constitute the foundation of pastoralist livelihoods, are vulnerable to a variety of factors that increase the risk profile of the pastoralist enterprise. Diseases, particularly endemic diseases transmitted by vectors such as ticks and tsetse flies, are a key concern.

Owing to the centrality of livestock to pastoral welfare, any poverty alleviation efforts targeted at pastoral communities will have to focus on strategies to improve livestock productivity by minimizing the incidence, and thus the costs, of disease. According to a study based in the pastoral area of Kitengela, livestock health was shown to account for 45 to 48 percent of the total annual expenditures per year per household. This research is concerned with investigating cattle breeding strategies as a means of minimizing the consequences of cattle diseases, especially trypanosomiasis, which is ranked among the top ten global cattle diseases impacting on the poor in pastoral systems.

Genetic Selection for Breeding Programs

The main objective of this study is to evaluate the potential of conventional and novel genetic breeding methods to improve the genetic merit of African cattle. The authors place an emphasis on studying the generic improvement of cattle traits highly valued by pastoralists, especially trypanotolerance.

The use of genetic markers (DNA information) to guide breeding selection is a relatively new and promising methodology. Traditionally, statistical tools were used to compare animals based on the heritability of the traits desired for selection. However, especially for traits that are difficult to measure and that show low heritability, the use of genetic markers has been shown to improve genetic gain by more than 20% depending on the trait. Nonetheless, no study has thus far investigated the potential of using genetic markers in cattle nucleus breeding programs specific to pastoral conditions.

To assure the relevance of the results for the target population, the authors chose to limit the traits they focused on to those identified as critical among pastoralists. They use the results of a study by Ouma et al. (2006), which ranked cattle traits among a sample of pastoralists using an experimental method aimed at identifying the relative preference pastoralists have for various traits. The study was conducted in the Mara division of Narok district in Kenya and covered 111 pastoralist households. Trypanotolerance, live weight, milk yield and reproduction potential were shown to be the favored traits and define the breeding objective the authors use.

To arrive at the expected economic benefit of breeding schemes that select for certain traits, the rate of genetic transfer of each trait from one generation to the next needs to be predicted and an economic value placed on the trait. Parameters for the heritability of the target traits where drawn from various studies. For trypanotolerance, the trait of main interest in this study, genetic parameters were estimated from a program crossbreeding the N'Dama and Boran cattle breeds. The economic values of different traits were estimated from the Ouma et al. (2006), study on revealed preference where each trait was associated with different levels and valued by participating pastoralists.

Results

Using the heritability parameters for each cattle trait in the breeding objective and their associated economic values, simulations where run based on two different breeding schemes: the conventional statistical method and a combined hybrid of the statistical method conditioned on genetic marker information. Simulations were iterated several times to mirror the effects of multiple generation breeding. As Table 1 below shows, both breeding methods indicate that crossbreeding will result in higher valued animals. The table displays the additional expected value resulting from crossbreeding, as well as the generation-on-generation marginal change in value. The values are the sum total of the value gains from each of the four traits under consideration: typano-tolerance, live weight, milk yield, and reproduction.

Table 1: Estimated value of aggregate genotypes over all animals in each generation and genetic gain of successive generations

	Breeding gains ($)		Marginal gains ($)	
Generation	Conventional Method	Genetic Marker Method	Conventional Method	Genetic Marker Method
2	-0.02	0.69		
3	63.00	62.06	63.01	61.37
4	125.13	119.33	62.13	57.27
5	182.65	171.65	57.53	52.32
6	237.62	149.68	54.97	-21.98
7	291.42	125.63	53.80	-24.04
8	341.22	111.53	49.80	-14.10
9	389.84	123.26	48.61	11.73
10	435.58	131.96	45.75	8.70

As one will note, the conventional method shows a far higher gain from breeding, especially in successive generations of crosses. Given that using genetic markers adds an important source of information to the analysis, and given the unrealistically high gains posted for greater than five generation crosses by the conventional method, the gains derived with the use of genetic markers seem more plausible. The use of genetic markers also suggests a decreasing marginal returns from successive crossings which is consistent with natural laws against unbounded gains from physical traits. Of the individual traits,

the value gain on milking yields were the highest followed by live weight. Modest improvements in trypanotolerance were also recorded.

Conclusion and Policy Implications

Breeding cattle that are more robust to costly diseases and unfavorable climates is a critical component of maintaining the viability of the pastoralist livelihood. The central aim of this study was to estimate the value of a breeding program by predicting the selection response of various cattle traits. The results suggest that crossing the N'Dama and Boran species is likely to result in a hybrid whose production traits and trypanotolerance is superior to those of its parents. As the Boran is particularly susceptible to trypanosomiasis, this is a surprising but encouraging result. Furthermore, the authors show that estimation methods that utilize genetic markers produce results that are significantly different from those generated by conventional methods. This and the fact that detecting markers in the cattle doesn't require the infection of the animals to measure the trait emphasizes the benefits that genetic markers could bring to breeding programs.

The demonstrated potential of targeted breeding programs to improve the productive capacity and the disease resistance of cattle justifies a policy agenda that lays out a concrete breeding and dissemination program. Supporting efforts to extract the genetic markers of various traits across several different cattle species, such as the popular Maasai Zebu, and to parameterize the heritability of the different traits across species would be an important first step.

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