

Genetic Analyses Of Cattle Breeding Schemes Including Genetic Markers for Trypanotolerance

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Introduction

In eastern Africa, cattle play a vital role in securing resource poor farmers' livelihood but productivity is hampered by harsh environmental conditions (e.g. Bebe *et al.* (2003)). Trypanosomosis is a disease which poses a severe threat to livestock production throughout sub-Saharan Africa (Kristjanson *et al.* (1999)). The mapping of quantitative trait loci (QTL) controlling trypanotolerance in a cross of tolerant West African N'Dama and susceptible East African Boran cattle has identified phenotypic traits that are under considerable genetic control (Hanotte *et al.* (2003)). This opens the possibility to include genetic marker information in a breeding scheme which addresses production traits as well as adaptation traits to achieve sustainable livestock production under low input as well as harsh disease prone conditions. The aim of this study is to compare alternative selection strategies for improved productivity and marker-assisted selection for trypanotolerance in a crop-livestock production system in Kenya with information from a field survey.

Material and methods

Genetic, phenotypic and economic parameter estimates. The breeding goal is to increase milk and meat production and adaptation to trypanosomosis. Taking into consideration that sires are only used by natural service under crop-livestock production system, the breeding goal consists of yearling weight (BW12), daily milk yield in first lactation (MY) and trypanotolerance (Tryps). The traits of minimum packed red blood cell volume (PCV), average body weight after trypanosomosis challenge (BWA), and the mean natural log of parasitaemia count (Para) during a 150 day challenge trial (defined in Hanotte *et al.* (2003)) were used to represent Tryps in the selection index. Table 1 summarizes the population parameters and economic values that were used. Specific economic values were derived from results of Ouma *et al.* (2007) who used a choice modeling approach to local livestock keepers' responses for cattle traits in Kenya and Ethiopia to quantify the value farmers attach to cattle with alternate descriptive characteristics of cattle. To convert these results to specific economic values, it was assumed that livestock keepers consider 20 % of cattle to be tolerant and 20 % to be susceptible for the disease which corresponds to a selection intensity of $i = 1.4$ (Falconer and Mackay (1996)). The phenotypic variance for Tryps was set at 1 so that the assigned economic value corresponded to one phenotypic standard deviation change in the trait. The heritability for these traits was from our own genetic parameter estimation of

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14 traits measured on pedigreed cattle used by Hanotte *et al.* (2003) to describe trypanotolerance. Population parameters for BW12, PCV, BWA and Para were likewise estimated from data supplied by Hanotte *et al.* (2003). Genetic correlations with Tryps were assumed to be 0.80 for PCV, because control of PCV level in animals alleviates much of the suffering during infection and as such is a strong indicator for the tolerance level, 0.60 for BWA, since control of average body weight depends on several factors not only trypanotolerance, and -0.90 for Para, because with the control of parasites, the cause of the disease would be eliminated and as such be the most effective tolerance measure. For MY, phenotypic variance was taken from reported average daily milk off-take by crop-livestock farmers in Ethiopia (Ayalew and Rowlands (2004)) because of similar production conditions. Heritability for MY was based on a number of publications for milk production in tropical climates with an average of 0.3 (e.g. Paneto (2008)), and correlation estimates were deduced from parameters used by Bosso *et al.* (2009) for 100-day-milk yield and live weight at 36 months of age from N'Dama cattle in The Gambia.

Assumptions for marker-based estimated breeding values (M-EBV). Following findings of Hanotte *et al.* (2003), it was assumed that marker information explained 30 % or 50 % of genetic variance in each tolerance trait. Genetic and phenotypic correlations between phenotypic traits and M-EBV are presented in table 2. Estimation followed the selection index method for deterministic prediction of the potential benefit of marker-assisted selection on response to selection developed by Dekkers (2007).

Simulation method and selection procedure. The computer program SelAction (Rutten *et al.* (2002)) was used to carry out deterministic simulation of truncation selection schemes with overlapping generations based on selection index theory (Hazel (1943)). The selected proportion in each age class was determined automatically by truncation across age classes with a truncation point such that the number of selected parents equals the desired number of parents (Rutten *et al.* (2002)).

Population structure. The population was simulated on the basis of findings from surveys of the crop-livestock production system (unpublished). A nucleus breeding scheme with overlapping generations and a maximum age of 12 years for cows and 6 years for bulls was simulated. Age at first calving was 36 months, with subsequent calving intervals of 18 months. Every 18 months, 400 females and 10 males were selected as parents and used to produce the new age-class with 280 offspring. Post-weaners were assumed to undergo a trypanosomosis challenge trial at the age of 12 months, which is expected to cause 20 % loss due to disease. In subsequent age-classes, culling among female herd members for reasons of health and survival was expected to be 15, 20, 20, 5, 8, 10 and 15 % which left 432 female selection candidates in the nucleus herd. Assuming equal rates of culling among bulls in age-classes one to three and a maximum use of two breeding seasons, so that only 10 bulls were candidates in age-class four, this left a total of 86 male selection candidates. At the age of 18 months, phenotypic measures for BW12, PCV, BWA and Para were available on both sexes, i.e. on 11.2 male and 11.2 female half-sibs, and at the age of 54 months for MY in cows, i.e. 4.58 half-sibs. No progeny information was available at the time of selection.

Alternative simulation scenarios. Simulation scenarios one to five varied in the traits included in the selection index. Scenario 1 represents the baseline nucleus breeding scheme using phenotypic trait measures for production and adaptation traits. The index included BW12, MY, PCV, BWA and Para. In scenario 2, the index included these phenotypic traits and in addition markers for PCV, BWA, and Para that together explained 30 % of genetic

variation for each trait. Scenario 3 differed from scenario 2 only in the proportion of genetic variance explained by markers being 50 % for each adaptation trait. Scenarios 4 and 5 were based on marker information only for the adaptation traits, so that the index included BW12, MY and M-EBVs explaining 30 % or 50 % of genetic variation for PCV, BWA and Para.

Table 1: Phenotypic variances^a, heritabilities^b, economic values^c, phenotypic (above diagonal) and genetic (below diagonal) correlations for the individual traits

Traits ^δ	Var(P) ^a	h ² ^β	v ^c (\$)	BW12	MY	Tryps	PCV	BWA	Para
BW12	400	0.35	1.05/kg		0.10	0.00	0.11	0.72	- 0.10
MY	0.81	0.30	6.2/l	0.08		0.00	0.00	0.05	0.00
Tryps	1	0.30	10.52/SD	0.05	- 0.10			0.00	0.00
PCV	8.7	0.40	-	0.08	0.00	0.80		0.33	- 0.35
BWA	445	0.20	-	0.70	0.02	0.60	0.34		- 0.16
Para	0.5	0.20	-	0.00	0.00	- 0.90	- 0.05	0.00	

^δBW12: weight at 12 months of age, MY: first lactation daily milk yield, Tryps: trypanotolerance, PCV: minimum PCV after disease challenge, BWA: average body weight after disease challenge, Para: mean of natural logarithm of parasitaemia count.

Table 2: Phenotypic (above diagonal) and genetic (below diagonal) correlations between phenotypic traits and marker-based EBV (M-trait) explaining 30 or 50% of genetic variation per trait. Phenotypic and genetic parameters for marker-based EBV were derived following the method of Dekkers (2007)

Traits ^δ	Var(Q) ^a	PCV	BWA	Para	Tryps	MPCV		MBWA		MPara	
						30%	30%	30%	50%	50%	50%
PCV						0.35	0.12	-0.02	0.45	0.15	-0.02
BWA						0.08	0.24	0.00	0.11	0.32	0.00
Para						-0.01	0.00	0.24	-0.02	0.00	0.32
Tryps						0.00	0.00	0.00	0.00	0.00	0.00
MPCV	1.044	0.55	0.19	-0.03	0.39			0.34	-0.05		
MBWA	26.7	0.19	0.55	0.00	0.26	0.34			0.00		
MPara	0.03	-0.03	0.00	0.55	- 0.47	-0.05	0.00				
MPCV	1.74	0.71	0.24	-0.04	0.51					0.34	-0.05
MBWA	44.5	0.24	0.71	0.00	0.33				0.34		0.00
MPara	0.05	-0.04	0.00	0.71	- 0.60				-0.05	0.00	

Results and discussion

The generation interval was 5.6 years for each scenario. Highest emphasis in the investigated selection schemes was clearly placed on BW12, which presented between 71 to 92 % of total economic response (Table 3). The variation between scenarios was mainly due to differences in response in Tryps per year. Selection for phenotypic traits PCV, BWA and Para appeared to be highly effective (scenario 1). Even when the correlation of each trait with Tryps was divided by two, the decrease in total economic response was less than 7 % (results not shown). However, highest responses were achieved with a combination of phenotypic and marker information (scenario 3) which increased the emphasis on Tryps and yielded highest

accuracies of index. Nevertheless, the advantage was limited because phenotypic information on adaptation traits was already available early in life and marker information had no effect on the generation interval. Still, from an animal welfare point of view, scenario 5 is most interesting because it resulted in superior responses in comparison to the baseline scenario 1 and increased accuracy of selection solely on the basis of marker information for the adaptation traits correlated with Tryps. The advantage of following this selection scheme would be that the number of cattle which need to undergo a challenge experiment with trypanosomiasis to obtain trait measures for PCV, BWA and Para could be reduced.

Table 3: Total economic and genetic response per year for the breeding goal traits^a, correlated genetic response for the selection index traits^a and accuracy of index^b

Scenarios	Genetic response				Correlated genetic response						Accuracy of index ^γ
	Total ^β	BW12	MY	Tryps	PCV	BWA	Para	MPCV	MBWA	MPara	
1	1.37	1.03	0.01	0.02	0.07	0.66	-0.01				0.63
2	1.41	1.01	0.01	0.03	0.08	0.70	-0.01	0.03	0.10	-0.01	0.66
3	1.45	0.99	0.01	0.04	0.08	0.73	-0.01	0.05	0.16	-0.01	0.68
4	1.34	1.05	0.01	0.02	0.05	0.69	-0.01	0.03	0.10	-0.01	0.62
5	1.39	1.01	0.01	0.03	0.06	0.73	-0.01	0.05	0.17	-0.01	0.65

^aSee table 1 and 2 for description of traits; ^βTotal economic response per year; ^γSires in age-class 3.

Conclusion

The results show that breeding schemes with a simple population structure have the potential to successfully increase body weight, milk yield and trypanotolerance in cattle and that marker information explaining 50 % of the genetic variance in adaptation traits may substitute phenotypic measures without the risk to decrease economic response per year.

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