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

Ulrike Janssen-Tapken<sup>1</sup>, Haja N. Kadarmideen and Peter von Rohr

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<sup>&</sup>lt;sup>1</sup> Institute of Animal Sciences, Statistical Animal Genetics Group, Swiss Federal Institute of Technology, Universitatstrasse 65, CH-8092, Zurich, Switzerland. Email: <u>Ulrike.janssen@inw.agrl.ethz.ch</u>

#### Introduction

Pastoralists in Kenya have increasingly become less food secure and vulnerable to poverty over the last two decades. This is due to increasing human population and changes in land tenure system as well as the harsh agro-climatic conditions associated with their environments. (Rushton, et al., 2002, Wollny, 2003) Livestock keeping is the mainstay of the pastoral systems and 15 million livestock keepers in rangeland-based systems in Sub-Saharan Africa are poor according to the national poverty rate (Thornton, et al., 2003). The enterprise is beset by several constraints, one of the most important of which is livestock diseases, particularly endemic diseases transmitted by vectors such as ticks and tsetse flies (Rushton, et al., 2002). Resistance against trypanocides for controlling tsetse-transmitted trypanosomiasis becomes increasingly a problem (Geerts, et al., 2001, Sinyangwe, et al., 2004). Owing to the strong attachment to livestock by the pastoral communities, any poverty alleviation goal targeted at pastoral communities will have to focus on strategies to improve livestock productivity by minimizing some of the livestock enterprise constraints. One of the issues that this paper focuses on is the breeding strategies as a pathway to minimize cattle disease constraints, especially trypanosomosis, which is ranked among the top ten global cattle diseases impacting on the poor in pastoral systems (Thornton, et al., 2002) As will be shown, our strategy is to develop cattle breeding schemes to ensure genetic gain through selection programs that utilize identified trypanotolerant genotypes, using conventional genetic evaluation techniques with or without the use of genetic (DNA) markers for trypanotolerance.

Livestock breeds kept by the pastoralists are mainly indigenous zebu types, adaptable to some degree to the harsh environmental conditions but susceptible to most cattle diseases. According to a study in the Kitengela pastoral area, livestock health accounts for 45 to 48 percent of the total annual expenditures per year per household (Kristjanson, et al., 2002). Generally, there is poor delivery of animal health services in pastoral areas. Conventional veterinary centers are very few, under-equipped, costly and inaccessible due to long distances and poor road infrastructure. Pastoralists mainly rely on livestock drugs purchased from vendors without any quality assurance or proper information on application procedures and dosage requirements which can cause failure of drug treatment (Geerts, et al., 2001). Tolerant cattle breeds could lead to more independence from veterinarian service.

Some of the indigenous livestock in developing countries are well adapted to local environments, exhibiting notable levels of disease tolerance. However, some of these breeds are at risk of becoming extinct. In Africa, 22 percent of African cattle breeds have become extinct in the last 100 years while 27 percent are at varying degrees of risk (Drucker, et al., 2001). The causes of this often stem from development policies in developing countries which have largely ignored the breeds adapted to the low input systems such as those found in pastoral systems. The focus instead has been on the introduction of higher-yielding exotic breeds that were developed for high-input systems and substituting the indigenous breeds with exotic ones (ILRI, 1999). Such programs can threaten the conservation and maintenance of indigenous breeds which have

superior adaptation traits suitable for most low-input systems. One potential way to promote conservation and use of indigenous cattle breeds is through some organized form of breeding. As noted by Wollny (2003), different communities may have different needs, preferences for cattle traits, beliefs and culture by which they make decisions regarding cattle breeding practices.

Disease resistance is one adaptation trait with high relevance in low-input systems (Gibson and Bishop, 2005). Statistical technology such as best linear unbiased prediction (BLUP) can be used to compare animals and select the best. Meuwissen and Goddard (1996) reported that for traits that are difficult to improve by conventional breeding and selection (e.g. low heritability, trait not recorded or recorded late in life etc.), use of genetic (DNA) markers can improve genetic gain by more than 20% depending on traits. Furthermore, the risks to select for disease resistance on the basis of phenotypic information make it an interesting area for the application of breeding with the use of genome information such as genetic markers (Bishop and Woolliams, 2004). The detection of quantitative trait loci (QTL) or a major gene for disease resistance co-segregating or linked with genetic markers open the possibility to select animals on the basis of estimated breeding values of marker QTL information in combination with traditional BLUP (MA-BLUP) or with marker QTL information only (MAS).

Although several developmental projects in Africa investigated the use of nucleus cattle breeding programs (progeny testing with BLUP and reproductive technologies), no study has thus far investigated the possibility of using (DNA)

genetic markers in nucleus breeding programs specific to African conditions. In fact, substantial amount of time and money has been invested in genomics program (e.g. via International Livestock Research Institute or ILRI) in detecting marker-QTL for trypanotolerance. It makes it worthwhile to investigate the use and application of marker-QTL information obtained from these genomic studies in practical breeding. The main objective of this study is to examine the possible impact conventional genetic evaluation breeding values (BLUP), including marker information in BLUP (Marker Assisted BLUP or MA-BLUP) and use of marker information only (Marker Assisted selection or MAS) in improving genetic merit of African cattle, with particular emphasis on the use of detected major genes or QTL from the QTL mapping experiment for trypanotolerance traits conducted by the ILRI in Kenya (Hanotte, et al., 2003).

We investigate these issues via computer simulation in a nucleus breeding scheme using experimental data obtained from N'Dama x Boran F2 crossbreds as explained in Hanotte, et al. (2003). We define a breeding objective using socio-economic values for preferred traits in a pastoral production system. For this, we present some results from a socio-economic survey of 111 households. Additionally, potential sources of the foundation stock that utilize preferred traits are discussed. Based on this discussion, possible dissemination scenarios for the transfer of genetic gain from the breeding stock to the field population with respect to the pastoral socio-economic and environmental situation are suggested.

#### **Methods and Data**

## Socio-economic surveys for farmer preference traits

In order to understand the breeding practices and preferences for cattle traits by pastoralists a household level survey was conducted in Mara division of Narok district covering 111 households. The preferred traits by pastoralists were identified and their economic values presented in a separate study by Ouma, et al. (2006). On the basis of choice experiments conducted with members of the participating households their socio-economic validation was included. The preference traits used in this study were Trypanotolerance (Tryps), live weight (LW), milk yield (MY) and reproduction potential of cows which was represented by the trait calving interval (CI).

## Evaluation of nucleus breeding programs

#### **Simulations**

The purpose of the simulations was to investigate the expected genetic gains, using BLUP, MABLUP and MAS, based on actual results of ILRI crossbreeding as well as QTL mapping experiment, with respect to approximate breeding program design and number, size and location of QTLs, published by Hanotte, et al. (2003), such that, if one would implement a breeding program with the chosen design, we could predict the future genetic response and returns in practical nucleus breeding program. Although information about the cattle genome and traits related to trypanosomosis tolerance was based on the results of national study (Hanotte, et al., 2003), the genetic and phenotypic parameters for the

remaining traits of the selection criteria was based on international studies (Demeke, et al., 2004, Kahi, et al., 2004, Pryce, et al., 2000, Pryce, et al., 2002, Veerkamp, et al., 2001).

Details of the simulations are given below:

**i Population.** The base population of the closed nucleus in the simulation program consisted of N = 400 unrelated F2 crossbreed individuals from two breeds with fixed alleles in the desired traits. The number of selected candidates was kept constant at 10 sires and 50 dams across 10 discrete generations of selection. The selected animals were randomly mated and modern reproduction techniques like AI and MOET were assumed to generate 8 offspring per dam with 100% survival rate.

ii Genetic model. The two breeds to produce the F2 base population were assumed to have fixed alleles in the desired traits. The genotype of each individual was modeled using 10 unlinked loci with two flanking markers each (QTL effects) and a finite locus model with 100 unlinked loci without marker information for the polygenic effects. The assignment of additive genetic effects from variances followed the theoretical approach described in Falconer and Mackay (1996). The phenotypic values were generated for each trait by adding of a residual effect to the genotype.

**iii Scenarios – input data.** The QTL and marker information from the QTL mapping experiment conducted by the International Livestock Research Institute (ILRI) in Kenya (Hanotte, et al., 2003) was assumed to be known without error in the simulation study. The estimates for three of the described traits related to

Trypanotolerance and one for live weight (LW) are summarized in table 1. The values for genetic and phenotypic parameters for the simulated traits should ideally come from estimates of an experiment with the particular populations in the breeding system including all important traits. This is only partially the case and mainly refers to the traits for trypanotolerance and LW at the age of 12 months. Following the example by Kahi, et al. (2004) the additionally required estimates for this study were derived from literature, adopting the assumed values from Kahi, et al. (2004) and expanding them for estimates on phenotypic correlations between LW and milk yield (MY) as well as calving interval (CI). Due to lack of estimates from Kenyan or even tropical studies, results from exotic breeds in developed countries had to be taken into consideration (Pryce, et al., 2000, Pryce, et al., 2002, Veerkamp, et al., 2001). Genetic and genotypic variance-covariance matrices were checked to be positive definite.

The results for socio-economic values had to be transformed in the following way: (1-3) Trypanotolerance was valued at a price of 75.7 US \$ for bulls and 10.6 US \$ for cows. Assuming the average to be true for breeding with both sexes and this to be equal to 18 treatments, the value for one treatment would be 2.4 US \$. Since PCVD (percentage decrease in PCV up to day 150 after challenge) BWD (percentage decrease in body weight up to day 150 after challenge) and PAR (natural logarithm of the mean number of parasites after challenge) all refer to trypanotolerance, the economic value for each is only the fraction of 0.799 US \$. (4) Live weight was valued with 3.5 and 1.2 US \$ for bulls and cows per kilogram respectively forming the average of 2.35 US \$ per

kilogram for both sexes. (5) The economic value for milk yield refers to a difference of 1.5 l per day. Extrapolated to a whole lactation with length 277 days (Das, et al., 1999), the economic value is 0.0166 US \$ per kg milk per lactation, assuming the weight of one liter of milk to approximate 1 kg. (6) The estimated economic value for reproduction potential for cows amounted to 8.7 US \$ referring to the discrepancy of one calf in two years or one calf each year which results in a difference of 365 days for the calving interval (CI). The value for reducing the CI by a single day is therefore 0.0238 US \$. The summary of the trait values and economic values are presented in table 2. A complete set of input parameters can be requested from the author.

Table 1
Recombination rates between flanking markers and QTL and additive QTL-effects on live weight at 12 months and trypanotolerance traits (PCVD, BWD and PAR)<sup>a</sup>

QTL	Chr.	recombination rate Marker1-QTL r1	recombination rate QTL-Marker2 r2	Effect on PCVD	Effect on BWD	Effect on PAR	Effect on LW <sup>b</sup>
1	2	0.0005	0.019605	1.389602	0.122854	-	16.18765
2	7	0.019605	0.05654	-	0.002108	0.116995	-
3	8	0.020565	0.018644	-	-	0.074719	-
4	16	0.019605	0.066189	-	0.001494	-	-
5	17	0.000999	0.039364	1.283746	-	-	-
6	20	0.070506	0.009901	0.908438	0.00185	0.093497	-
7	24	0.107864	0.105504	1.137472	-	-	-
8	26	0.086934	0.075204	1.256801	0.001801	-	-
9	27	0.015747	0.01768	1.150945	-	-	-
10	28	0.024385	0.05654	-	-	-	15.19909

<sup>&</sup>lt;sup>a</sup> PCVD, percentage decrease in PCV up to day 150 after challenge; BWD, percentage decrease in body weight up to day 150 after challenge; PAR, natural logarithm of the mean number of parasites after challenge.

<sup>&</sup>lt;sup>b</sup> LW, body weight before challenge at age of 12 months.

Table 2 Assumed phenotypic standard deviation  $(\sigma_p)$ , economic values (v), heritabilities  $(h^2)$  on diagonal for the traits in the breeding objective and genetic (below diagonal) and phenotypic correlations (above diagonal) among traits.

Trait <sup>a</sup>	$\sigma_{p}$	$v^b$	h <sup>2</sup> , genetic and phenotypic correlations						
			PCVD	BWD	PAR	LW	MY	CI	
PCVD	9.36	-0.7991°	0.1	0.493	0.117	-0.028	0.000	0.000	
BWD	0.45	-0.7991 <sup>c</sup>	0.493	0.1	0.029	0.068	0.000	0.000	
PAR	0.75	-0.7991 <sup>c</sup>	0.117	0.029	0.1	0.112	0.000	0.000	
LW (kg)	90.35	2.3500	0.028	0.068	0.112	0.2	0.130	-0.070	
MY (I)	1208.46	0.0166 <sup>d</sup>	0.000	0.000	0.000	0.230	0.23	0.110	
Cl (days)	75.34	-0.0238	0.000	0.000	0.000	-0.530	0.170	0.06	

<sup>&</sup>lt;sup>a</sup> PCVD, percentage decrease in PCV up to day 150 after challenge; BWD, percentage decrease in body weight up to day 150 after challenge; PAR, natural logarithm of the mean number of parasites after challenge; LW, body weight before challenge at age of 12 months; MY, milk yield; CI, calving interval.

#### Genetic evaluations

The input parameters were evaluated by an extended version of the stochastic simulation program called MABLUP (Fernando and Kachman, 2005).

i Conventional BLUP animal model. Best linear unbiased prediction (BLUP) is applied to a mixed linear animal model

$$y_i = x_i'\beta + a_i + e_i$$

where  $y_i$  is the phenotypic value for animal i,  $x_i^{'}$  is a vector of known constants,  $\beta$  is a vector of unknown fixed effects,  $a_i$  is the additive effect for individual i and  $e_i$  is a random error. The breeding value for each trait and each individual i corresponds to the additive effect  $(a_i)$ .

<sup>&</sup>lt;sup>b</sup> US \$ per unit.

<sup>&</sup>lt;sup>c</sup> Referring to one treatment of trypanosomosis with an assumed mean of 18 treatments per year.

d Referring to a lactation length of 227 days according to (Das, et al., 1999)

**ii MABLUP evaluation model.** The estimation of best linear unbiased predictors (BLUP) for breeding values with phenotypic and marker information (MABLUP) follows the mixed linear animal model suggested by Fernando and Grossman (1989):

$$y_i = x_i \beta + v_i^p + v_i^m + u_i + e_i,$$

where  $y_i$  is the phenotypic value for animal i,  $x_i\beta$  is the fixed part of the model,  $v_i^p$  and  $v_i^m$  are the random additive values for the paternal and maternal alleles at a marked QTL,  $u_i$  is the random additive genotypic value for the remaining polygene effects, and  $e_i$  is the residual. The total breeding value for each trait is the sum of the estimates for its QTL  $(v_i^p + v_i^m)$  and the breeding value for the polygene  $(u_i)$ . The estimated breeding value for an animal i  $(v_i^p + v_i^m + u_i)$  maximizes the response from the current to the next generation.

**iii Marker evaluation model (MA).** Estimation of marker breeding value follows the evaluation described by Fernando and Grossman (1989) with the MABLUP model ignoring the remaining polygene effects and just fitting the QTL allele effects:

$$y_i = x_i \beta + v_i^p + v_i^m + e_i$$

where  $y_i$  is the phenotypic value for animal i,  $x_i\beta$  is the fixed part of the model,  $v_i^p$  and  $v_i^m$  are the random additive values for the paternal and maternal alleles at

a marked QTL and  $e_i$  is the residual. The breeding value for each trait is the sum of the estimates for its QTL  $(v_i^p + v_i^m)$ .

## **Results and Discussion**

## Socio-economic surveys

i Pastoral production system. *Preferred cattle traits*. Pastoralists named the traits which they use to choose cattle for buying and keeping. The number of times a trait for decision making was named for bulls and for cows separately is shown in figures 1 and 2.

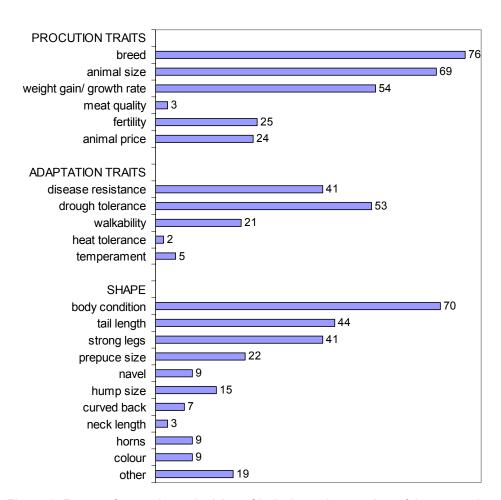


Figure 1: Reason for purchase decision of bulls (counting number of times mentioned).

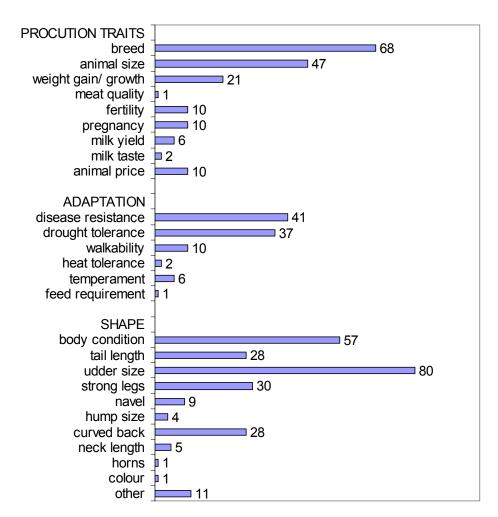


Figure 2: Reason for purchase decision of cows (counting number of times mentioned).

These choice-reasons suggest that animal selection in the pastoral community is not only based on animal's production performance but also on adaptation and cultural practices. Additional information from group discussions and communication with participants show that the choice of breed is linked to the experience with local Maasai Zebu in comparison to Sahiwal, Boran or their crossbreds. The Maasai Zebu is hence better adapted to the harsh environmental conditions and disease constraints. The necessity for drought tolerance and disease resistance accordingly results in the breed choice. Within the breed, bulls are mainly valued by their body size and related traits. Coat color

is an important trait because during traditional ceremonies such as age set graduation, bulls with specific colors are slaughtered for the graduates. Other important phenotypic traits include presence and shape of horns, which are considered when selecting an animal for dowry payment during marriage. The tail length of an animal is associated with its milk production. Since milk yield and fertility of cows are not obvious in a market place, a frequent decision criterion is udder size. Drought tolerance and walkability are necessary requirements for the production system. Only 6 percent of farmers report to keep their cattle sedentary, while 64 and 30 percent follow a transhumance (changing pasture) and nomadic lifestyle respectively. In addition, the distance to the water points during the dry season is 3.6 (± 5) km which requires a high mobility.

After ranking by importance and choice experiments, trypanotolerance, reproductive potential, live weight, coat color and drought tolerance were revealed to be of highest value (Ouma, et al., 2006). In the simulation process for this study, we could take into account trypanotolerance in form of measurements of red packed blood cell volume (PCV), body weight after infection (BW) and parasite count in the blood smear (PAR), reproductive potential with calving interval (CI) and live weight (LW) as it is.

**ii Pastoral production system.** *Disease prevalence*. Considering the disease prevalence in the last three years, pastoralists reported trypanosomosis to be the source in 60 percent of all cases (Figure 3) and 70 percent of respondents state that neglect of treatment will result in death of the affected animal and 27 percent report a loss of live weight. Furthermore trypanosomosis is reported to be

endemic with a high prevalence during the entire year which requires frequent prevention measurements and treatment after infection. The development of a tolerant breed which needs less or no treatment at all is therefore likely to have a measurable impact on the economy of a household.

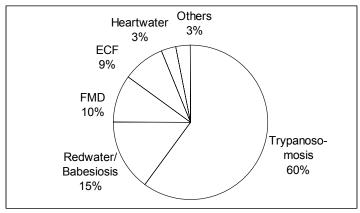


Figure 3: Cattle disease prevalence in the past three years.

Without tolerant breeds, prevention measures against trypanosomosis are essential and the available drugs need to be applied depending on cattle breed and tsetse fly density approximately every 2 to 4 weeks (Kristjanson, et al., 1999, Munga and Ndung'u, 2002). The most common use for prevention and cure of trypanosomiasis in the field is the use of Veriben®Sanofi or Berenil®Hoechst in double dose to clear infection at a price of 1.58 US \$ per animal and Decatix®Coopers as pour-on against tsetse flies and other ectoparasites at costs of 83.69 US \$ per liter for 440 animals (Mwai, 2005). Assuming this practice for the participating households in addition to their information on trypanosomiasis incidents per year, the direct costs for prevention measurements (every 3 weeks) of 9443 cattle and treatment of 90 cattle amount to 32'438 US \$ per year which causes high pressure on household expenses.

iii Pastoral production system. Herd structures and breeding practice. In comparison to other livestock, cattle form the major part of herds in pastoral systems. (Figure 4) The individual cattle herd size is large, averaging 85 cattle in total with 50 cows and heifers as well as 4 bulls per household. The average number and the large standard deviation imply that breeding within the bigger herds can be an option. The details on the cattle inventory and herd structure are listed in table 3.

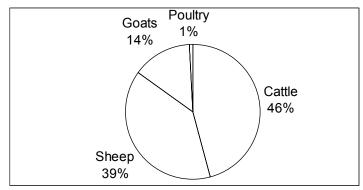


Figure 4: Composition of the average pastoral livestock herds.

Table 3: Number of cattle category per herd (average and standard deviation)

Category	Bulls	Oxen	Cows	Heifer	Immature	Preweaner	Total
Average (s.d)	4 (4.8)	12 (20.7)	32 (51.7)	18 (24.0)	9 (16.4)	10 (11.9)	85 (110.76)

Natural uncontrolled mating using bull service is the common mating method, with 73 percent of the respondents indicating practice of this form of mating while the remaining practice controlled mating. The breeding bulls are in 85 percent of the cases from the owner's or neighbor's herd since communal herded grazing is practiced. With 95 percent of all households using their own bred animals as replacement stock and only 38 percent additionally buying animals from the market the local herds are in danger of inbreeding. This becomes even more

obvious since artificial insemination is not practiced partly because of infrastructural constraints, lack of awareness or faith in the technique and the communities' preference for bull service. (Table 4)

#### Table 4:

#### Reasons for preference of bull service

- Natural
- Cheap
- Available
- Well known and predictable
- Capacity (one bull can mate several cows)
- Practical (bull knows when to mate the cows)
- No trust in possibility of artificial insemination

## Evaluation of nucleus breeding programs

## i Experimental data.

The estimates for aggregate genotypes per generation and genetic gain of the simulation study for BLUP and MABLUP evaluation are presented in table 5. Due to intensive computational time (1 day per replicate for MABLUP), results for MABLUP scheme refer to 10 replicates in comparison to 50 replications for BLUP scheme, resulting in larger standard deviations for estimates, furthermore results from simulation data on MAS were not yet available at the time of submission.

Table 5: Estimated aggregate genotypes per generation and genetic gain presented as averages  $\bar{x}$  across replicates (no. reps.) and corresponding standard deviations in parenthesis (sd).

Generation	,	eding values $\bar{x}$		Average genetic gain, $\Delta G \ \overline{x}$ , (sd)		
	BLUP	MABLUP	MA	BLUP	MABLUP	MA
no. reps.	50	10		50	10	
F2	-0.02 (0.22)	0.69 (0.12)				
F3	63.00 (4.98)	62.06 (4.51)	-	63.01 (5.00)	61.37 (4.51)	-
F4	125.13 (8.53)	119.33 (8.01)	-	62.13 (9.88)	57.27 (6.62)	-
F5	182.65 (10.17)	171.65 (12.23)	-	57.53 (13.27)	52.32 (9.24)	-
F6	237.62 (11.919)	149.68 (104.00)	-	54.97 (15.66)	-21.98 (103.28)	-
F7	291.42 (14.70)	125.63 (133.59)	-	53.80 (18.92)	-24.04 (83.85)	-
F8	341.22 (15.26)	111.53 (144.89)	-	49.80 (21.19)	-14.10 (56.09)	-
F9	389.84 (15.80)	123.26 (160.28)	-	48.61 (21.97)	11.73 (68.53)	-
F10	435.58 (16.39)	131.96 (171.69)	-	45.75 (22.76)	8.70 (61.56)	-
F11	480.45 (16.71)	106.85 (173.21)	-	44.87 (23.40)	-25.11 (22.90)	-

The aggregate genotypes per generation with 400 individuals represent the additional hypothetical value from the last to the current generation that an average animal would present as consequence of the achieved genetic gain in each trait which is multiplied with its economic weight. This monetary value would be the true possible additional price in US\$ under the condition that each economic value is completely explained by market prices and a unit gain in one trait would fetch that exact amount of money. This, however, is not true in the described system because a market only exists for live weight and every other trait is valued on a socio-economic basis from the farmer's point of view taking

production system and environment into account. Therefore, the numbers should rather be interpreted as a direction of breeding. It can clearly be seen that both evaluation and selection strategies have a positive effect and would result into higher valued animals. To get a clearer picture on the change in each trait, the following tables present the results for BLUP and MABLUP estimates for Trypanotolerance and production traits separately.

Table 6:
Average breeding value per generation for trypanotolerance traits

Generation		eeding values		MABLUP breeding values ( $\bar{x} \pm sd$ )			
	PCVD	BWD	PAR	PCVD	BWD	PAR	
no. reps.	50	50	50	10	10	10	
F2	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	
F3	0.11 (0.20)	-0.00 (0.01)	-0.01 (0.02)	0.08 (0.15)	0.06 (0.07)	0.06 (0.07)	
F4	0.12 (0.45)	0.01 (0.02)	-0.02 (0.04)	0.14 (0.29)	0.09 (0.08)	0.09 (0.09)	
F5	0.21 (0.56)	0.01 (0.02)	-0.01 (0.05)	0.22 (0.38)	0.10 (0.07)	0.08 (0.07)	
F6	0.28 (0.69)	0.01 (0.03)	-0.02 (0.06)	0.18 (0.37)	0.07 (0.09)	0.07 (0.08)	
F7	0.35 (0.86)	0.01 (0.03)	-0.03 (0.06)	0.08 (0.47)	0.06 (0.09)	0.05 (0.09)	
F8	0.41 (0.93)	0.01 (0.03)	-0.04 (0.07)	0.06 (0.46)	0.03 (0.08)	0.03 (0.09)	
F9	0.39 (0.98)	0.01 (0.04)	-0.05 (0.08)	-0.02 (0.47)	0.04 (0.10)	0.03 (0.11)	
F10	0.48 (1.09)	0.01 (0.04)	-0.05 (0.08)	-0.02 (0.46)	0.04 (0.11)	0.04 (0.13)	
F11	0.46 (1.09)	0.01 (0.04)	-0.06 (0.09)	-0.02 (0.46)	0.03 (0.11)	0.03 (0.14)	

Due to the high standard deviations for all numbers, the results have to be interpreted with caution. Nevertheless, the comparison of the development of trypanotolerance traits over generations shows a steady increase in PCVD when animals are selected according to BLUP estimates while PCVD decreases with MABLUP scheme. The changes in BWD and PAR are minimal. An increase in either trait is not desired but since PCVD and LW are negatively correlated in the phenotype and the economic weight puts a strong emphasis on LW, the

estimates for PCVD with BLUP scheme are not surprising. The direct selection on markers for the genotype with MABLUP seems to be an option to stop this drive.

Table 7: Average breeding value per generation for production traits

Generation	BLUP br	eeding values (	$\overline{x} \pm sd$ )	MABLUP breeding values ( $\bar{x} \pm sd$ )			
	LW	MY	CI	LW	MY	CI	
no. reps.	50	50	50	10	10	10	
F2	-0.03	2.06	0.01	0.11	14.49	0.00	
	(0.05)	(3.53)	(0.01)	(0.03)	(2.88)	(0.00)	
F3	25.95	68.55	-0.39	24.77	131.47	-0.59	
	(2.06)	(39.32)	(0.81)	(2.15)	(36.06)	(1.06)	
F4	51.61	128.73	-0.38	48.14	212.23	-0.65	
	(3.52)	(58.40)	(2.19)	(3.43)	(62.77)	(2.47)	
F5	75.51	176.31	-0.31	69.68	270.22	-1.00	
	(4.12)	(70.25)	(3.06)	(4.90)	(50.79)	(3.18)	
F6	98.33	222.16	-0.71	61.06	211.73	-0.13	
	(4.90)	(72.51)	(3.89)	(42.40)	(151.28)	(3.79)	
F7	120.45	282.44	-1.17	51.41	164.17	0.74	
	(6.04)	(90.33)	(3.90)	(54.63)	(184.16)	(2.59)	
F8	140.94	339.11	-0.92	45.64	144.87	0.85	
	(6.21)	(101.87)	(4.11)	(59.23)	(198.61)	(2.55)	
F9	160.90	394.16	-1.13	50.37	163.17	1.13	
	(6.40)	(115.08)	(3.98)	(65.42)	(223.22)	(2.32)	
F10	179.73	445.40	-1.22	54.05	164.62	0.73	
	(6.48)	(130.47)	(4.33)	(70.26)	(225.45)	(2.22)	
F11	198.13	497.93	-1.59	43.91	121.62	0.47	
	(6.76)	(143.00)	(4.82)	(71.13)	(203.26)	(2.22)	

LW is valued high by pastoralists and could be increased through selection according to the predictions of the simulation study for both evaluation schemes. The estimates for MY show a considerable genetic gain and even if it would be less in case the assumptions for its variance are overestimated the direction remains clear and promises a positive development through selection. The

changes in CI are minimal and standard deviation is high which doesn't allow for a clear interpretation.

#### ii Foundation stock.

Potential sources of foundation stock for a nucleus breeding scheme include (1) indigenous animals from the cattle keepers' herds that show high levels of trypanotolerance combined with targeted performance in the other desired traits for on-station breeding or community based management with controlled mating, (2) indigenous animals and trypanotolerant exotic breeds from other countries for on-station comparison and crossbreeding and (3) improved Kenyan Boran and trypanotolerant N'Dama for the development of a synthetic breed through marker assisted selection (MAS or MABLUP) according to the ongoing experiment at the Kenya Agricultural Research Institute (KARI) in collaboration with the International Livestock Research Institute (ILRI). The basic aim of that study was to detect quantitative trait loci (QTL) which made it necessary to use breeds that show an opposite phenotype in the targeted trait, trypanotolerance (Hanotte, et al., 2003). The demonstrated results from our simulation study with the input parameters from the experiment show the potential in developing a synthetic breed from Kenyan Boran and N'Dama exceeding the level of trypanotolerance of either breed due to the unexpected finding of additional trypanotolerance QTL that are present in the supposedly susceptible species, Kenyan Boran. Therefore forming a synthetic breed from N'Dama and Orma Boran which is also trypanotolerant (Dolan, 1997) and possesses a greater potential in the favorable production traits than the local Maasai Zebu could be an even more promising variety of the described study. Maasai Zebu or Orma Boran can be integrated into current breeding schemes, as parents to produce the next generation but with the caution on retaining good adaptability and disease resistance traits of N'Dama. If QTL are detected in either zebu, it would accelerate the genetic gain; this however, requires the start of a QTL mapping study. Since the acceptance of a synthetic breed (from N'Dama x Boran) by the farmers is the requirement for the success of such a breeding program, this possibility should be considered. A small study comprising of group discussions and household surveys involving farmers that have been in contact with the experimental animals from ILRI-KARI herds reveal reservations against the crossbreed mainly due to its lower tolerance level against trypanosomosis (Ouma, 2005). In comparison to Orma Boran, only growth rate was considered to be similar or exceed the performance of the purebred, but color and other adaptation traits are preferred in Orma Boran and Maasai Zebu. An introduction of a synthetic breed therefore can only be successful when the improvement in trypanotolerance in connection with improved weight gain and body weight presents an obvious advantage over the present animals. Otherwise, bulls from a potential synthetic breed might only be used for terminal crossbreeding to produce offspring for slaughter. With this practice pastoralists would keep the breeding stock of Maasai Zebu purebred and exclude their cattle population from the crossbreeding process that is dependent on their participation to prohibit inbreeding and achieving higher genetic gain per generation through larger population size and increased selection intensity.

This strong emphasis on bull service shows, that introduction of a new cattle breed into pastoral production system is dependent on its adaptation ability to the harsh environmental conditions with emphasis on trypanotolerance. Pastoralists in this study report negative experience with purebred bulls from cattle breeds with higher production potential that they intended to use for crossbreeding. According to their observation, breeds that are not as disease resistant as local Maasai Zebu cannot survive.

#### iii Dissemination scenario.

Dissemination of breeding gain to the pastoral community would heavily rely on transfer of proven bulls under current practices. As has been shown in the report about pastoralist's experiences with N'Dama x Boran crossbreds by Ouma (2005), this is a highly sensitive matter when the number of distributed animals is still scarce and needs to take social ties and political relationships between members of the community into consideration to avoid conflicts and negative reputation of the involved breeding organization. A distribution scheme has to give equal chance for purchasing breeding bulls to each farmer in the addressed community. A suggested solution by farmers was to provide adequate time for financial preparation to enable farmers with fewer assets to concurrently purchase animals.

Communal management of breeding bulls in pastoral society seems highly unlikely due to reservations against collaborative work. According to the report by Ouma (2005), 84% of respondents would not be willing to participate in a

communal management group because of potential for quarrels and group management difficulties.

The use of artificial insemination (AI) requires comparatively more input into the infrastructure and education since firstly pastoralist's experiences with the technique are very little and they consequently don't put much confidence into it; secondly, the availability is practically zero and needs an organization structure that targets livestock under current management with intensive herd movement and far distances between herds; thirdly labor for farmers would increase because AI service relies on observation of the farmer and separation of cows on heat. On the other hand, benefits for farmers would be independency of bull service on farm and purchase of breeding animals which could be especially valuable for pastoralists with smaller herd-sizes and lesser assets. Assuming proper recording of pedigree, danger of inbreeding could also be addressed more easily and sexually transmitted diseases could be prevented.

The high infrastructural requirements on an AI system make governmental involvement necessary and are the most serious barrier to overcome. Where AI service with frozen sperm is not possible due to constraints with supply of liquid nitrogen, proven bulls from nucleus breeding could be used for AI with fresh semen with a minimum mating ratio of 300 cows per bull assuming proper use of the technique in comparison to an average mating ratio of 25-40 cows per bull with the traditional method of herding (Sprott, et al., 2005, Webb, 2003) which would also ensure a faster and more wide spread genetic gain in the field population. In this case envisioned, bulls proven based on BLUP or MABLUP

estimated breeding values would be used and put through a process of MAS before supplying them for natural mating. A possible scenario could be the location of bulls on different stations that are spread out in the field to overcome the distances between herds and rotation of breeding bulls between stations to prevent inbreeding and ensure consistent dissemination of average genetic gain.

More sophisticated technologies for faster spread of genetic gain especially on the female pathway like multiple ovulation and embryo transfer (MOET) are not likely to be feasible under the infrastructural and technical constraints in pastoral systems. However, it may be possible to select superior dams proven based on MOET in a nucleus program in governmental studs or university farms which can than be disseminated to pastoralists, much like bulls.

The sources of breeding stock need to be organized nucleus breeding herds with testing schemes for phenotypic and/or genetic values of desired traits to implement BLUP, MABLUP or MA evaluation to identify bulls of high genetic merit in the desired traits and ensure genetic gain through efficient management and breeding methods. Record taking on all desirable traits would be essential and although measurements of traits indicating trypanotolerance are possible in the field, they require skilled personal and laboratory equipment (Sinyangwe, et al., 2004). Government institutions such as KARI or any other national breeding institution would need to be involved in providing the infrastructure for the evaluation of breeding bulls and cows in the nucleus herds which favorably need to be maintained under similar conditions. Possible breeders are necessarily governmental farms or NGOs with a development mission because the financial

risk is high when the expectations cannot be met and the marketing of live animals and semen is not sure.

## **Implications**

Control of trypanosomosis by utilizing resistant breeds that also have other preferred traits by pastoralists is an important poverty reduction strategy as it has the potential of increasing competitiveness of pastoral production systems, through reduction of production costs resulting from control and treatment of trypanosomosis and simultaneously increase productivity through improvement of production traits. Animals with a higher level of tolerance will cause less treatment costs throughout their lifetime and additionally have the potential to spread the causative genes in the herd.

In addition, encouraging the use of indigenous African cattle breeds with superior adaptation qualities is an important contribution to conservation of these livestock species in low-input pastoral systems. Conservation of indigenous livestock species is in tandem with the Convention on Biological Diversity (CBD, 2000) to which many national and international public agencies are committed. As outlined by Wollny (2003), the CBD provides a framework for integrating conservation and sustainable use of biological diversity including animal genetic resources into relevant sectoral plans and policies. As far as the penetration of new genetic technology such as the use of genetic markers, the appreciation of benefits that it could bring to genetic improvement has to be realized by funding bodies and integrated into progeny testing / nucleus breeding programs.

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