

GENETIC CHARACTERIZATION OF INDIGENOUS EAST AFRICAN CATTLE BREEDS USING MICROSATELLITE DNA MARKERS

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SUMMARY

Seven cattle populations indigenous to East Africa and three reference breeds (Sahiwal, N'Dama and Friesian) were characterized with 18 autosomal microsatellite loci. Within-breed diversity was high in all breeds with observed heterozygosities ranging from 0.511 ± 0.214 (N'Dama) to 0.660 ± 0.128 (Friesian). All populations, except the Kenya Boran were at Hardy-Weinberg equilibrium. Nei's standard genetic distance (D_S) ranged from 0.023 ± 0.009 (Danakil and Abigar) to 0.868 ± 0.200 (N'Dama and Sahiwal). An UPGMA tree built up from D_S genetic distances revealed the following clusters: the Friesian and N'Dama breeds (*Bos taurus* from Europe and Africa, respectively) were clustered together but they were clearly separate populations, while the Sahiwal breed (*Bos indicus*) native to Asia was more closely related to the East African breeds than to the N'Dama and Friesian. No clear genetic distinction was evident between the East African humped (zebu and sanga) and the humpless (Sheko) breeds. Allele specific analysis suggested taurine influence in the East African zebu breeds, and an indicine influence in the East African taurine (Sheko). The results indicated that all East African cattle studied, while genetically separate, contained both indicine and taurine backgrounds. Their unique genetic identity calls for their conservation and utilisation.

Keywords: Microsatellite, genetic diversity, genetic characterization, African cattle.

INTRODUCTION

A large proportion of indigenous sub-Saharan African cattle breeds are at risk of extinction from indiscriminate crossbreeding, replacement of indigenous cattle with exotic breeds in an effort to improve productivity, neglect and the absence of programs for their development. These cattle are endowed with unique qualities which enable them to survive and produce in the stressful environments in which they live. Therefore, immediate steps need to be taken to conserve these breeds (FAO/UNEP 1995). However, their current classification based on historical, anthropological and morphological evidence is not satisfactory for purposes of conservation and utilisation. The objective of this study was to genetically characterize cattle breeds indigenous to eastern Africa in order to facilitate their rational development, utilisation and conservation.

MATERIALS & METHODS

Blood samples were collected from 35 to 40 unrelated animals of each breed. Seven cattle breeds indigenous to East Africa were studied: Two sanga (Abigar and Danakil) and one East African taurine (Sheko) from Ethiopia, one zebu x sanga intermediate from Eritrea (Arado), two zebu from Kenya (Kenya Boran, Kavirondo Zebu) and one zebu from Tanzania (Kilimanjaro Zebu). Three breeds (one *Bos indicus* - Sahiwal, and two *Bos taurus* - N'Dama and Friesian) were included in the study to serve as reference breeds. DNA amplification was

performed as described by Okomo (1997). Genotyping was performed on an ABI Prism™ 377 automated DNA sequencer (Applied Biosystem).

Allele frequencies and observed heterozygosity (H_0 , number of heterozygous animals) were calculated manually. Standard genetic distance (D_S) (Nei 1972) and UPGMA dendrogram with bootstrapping of 1000 replications were calculated by the DISPAN program (1993). Tests for deviation from Hardy-Weinberg equilibrium (HWE) were done using the GENEPOP (Version 2) program (Raymond & Rousset 1995). Relative frequencies of specific alleles (characteristic of *Bos taurus* as represented by the N'Dama and the Friesian; or *Bos indicus* as represented by the Sahiwal) at four diagnostic loci ILST36, ILST28, TGLA122 and TGLA227 were used to determine the level of indicine and taurine introgression in East African breeds.

RESULTS

Genetic diversity. A total of 208 alleles were detected across the 18 autosomal microsatellite loci studied. Average number of alleles, observed heterozygosities and tests for HWE are summarised in Table 1. Mean number of alleles ranged from 4.3 in the N'Dama to 7.7 in the Kenya Boran. No significant difference was found between the number of alleles in the two sanga breeds (Danakil and Abigar) and the African zebu. Allele frequencies of 8 out of 18 loci in the Kenya Boran deviated from HWE.

Table 1. Mean heterozygosity, mean number of alleles and number of loci showing deviations from HWE

Breed	Mean observed heterozygosity, H_0 (s.e.)	Mean number of alleles	Number of loci showing deviations from HWE
N'Dama	0.511 (0.214)	4.3	2
Sahiwal	0.555 (0.211)	6.4	1
Danakil	0.657 (0.224)	6.9	1
Kilimanjaro Zebu	0.620 (0.199)	6.8	1
Friesian	0.660 (0.128)	6.6	1
Kavirondo Zebu	0.617 (0.146)	6.6	4
Arado	0.641 (0.175)	6.9	0
Abigar	0.614 (0.184)	6.9	2
Sheko	0.655 (0.219)	7.2	3
Kenya Boran	0.620 (0.168)	7.7	8

Genetic composition. A total of 26 taurine- and 13 indicine-specific alleles were identified and their mean frequencies relative to the reference breeds calculated (Table 2). The results suggested substantial indicine influence in the taurine breed (Sheko) and taurine background in the zebu breeds studied.

Table 2. Mean frequencies of indicine- and taurine-specific alleles

Class	Breed	Mean frequencies (s.e.)
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		indicine alleles	taurine alleles
<i>B. indicus</i>	Kavirondo Zebu	0.56 (0.33)	0.32 (0.20)
	Kenya Boran	0.32 (0.28)	0.67 (0.37)
	Kilimanjaro Zebu	0.74 (0.26)	0.29 (0.14)
<i>B. Taurus</i>	Sheko	0.55 (0.24)	0.38 (0.21)
Sanga	Abigar	0.56 (0.10)	0.32 (0.20)
	Danakil	0.66 (0.09)	0.41 (0.09)
Zebu x sanga	Arado	0.66 (0.14)	0.22 (0.08)

Genetic distance. The standard genetic distance (D_S) ranged from 0.023 between the Danakil and Abigar to 0.868 between the N'Dama and Sahiwal (Okomo 1997). Genetic distances between East African breeds were small (0.173 ± 0.185) (Okomo 1997). An UPGMA tree (Figure 1) constructed from genetic distance (D_S) shows that Friesian and N'Dama are closely related and are separated from the Sahiwal which is itself quite close to the East African breeds, obviously through the common zebu genes. Relationships among East African breeds did not take a clear pattern as indicated by the low bootstrap values.

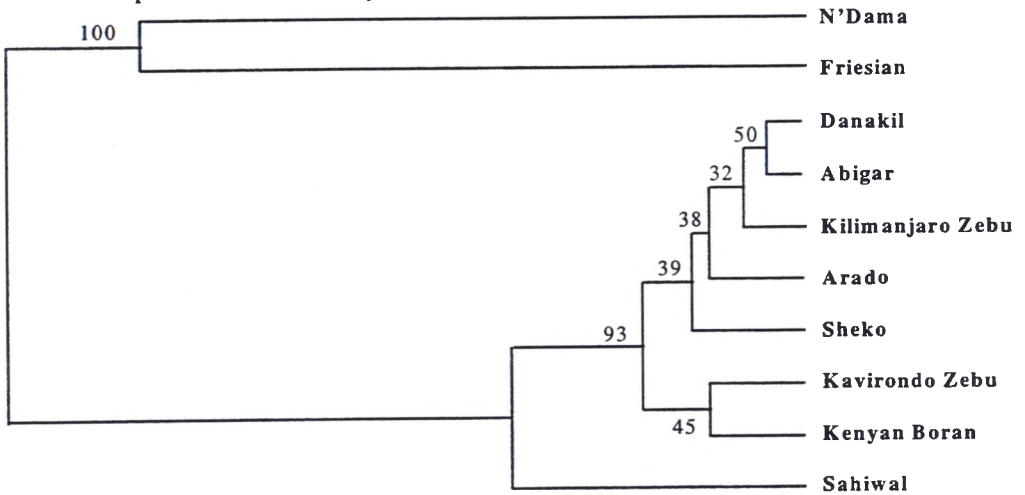


Figure 1. Unrooted UPGMA tree built up from Nei's standard genetic distances. Numbers indicate bootstrap values in percentage (1000 replicates).

DISCUSSION

The East African breeds studied showed a considerable amount of within-breed variation based on allele numbers and heterozygosity values, suggesting that the populations studied were fairly outbred. Only the allele frequencies in the Kenya Boran showed a significant deviation from the HWE. Artificial selection is the major genetic influence on modern domestic cattle population and it is known that the Kenya Boran has undergone strong artificial selection since the 1920s (Maule 1990).

The terms "zebu-specific" and "taurine -specific" alleles used in this study to denote alleles of indicine and taurine origin, are not completely satisfactory given the small number of reference breeds examined. Nevertheless, an analysis of these autosomal diagnostic alleles produced interesting results, and suggest that the East African zebu breeds in this study are not genetically pure *Bos indicus*, as they all exhibit a significant proportion of taurine backgrounds. The taurine alleles are possibly the result of recent crossbreeding (with European breeds) to improve production, though there is no reason to dismiss the possibility that the presence of taurine alleles in the East African zebu breeds may be the result of historical selection and crossbreeding with indigenous East African taurine populations. These results also showed strong zebu introgression in the Sheko, the only cattle breed in Eastern Africa currently classified as taurine (Rege *et al.* 1996). As expected, the sanga sample contained both taurine and indicine backgrounds. The zebu x sanga intermediate (the Arado) exhibited very strong indicine influence.

Based on genetic distance estimates and phylogenetic tree analysis, the indigenous East African cattle studied were found to be very closely related, forming a relatively homogenous and genetically unique group of populations, that was distinct from the pure *B. indicus* and *B. taurus* breeds, but more closely related to the former than the latter. The unique genetic background of East African cattle and their known adaptation to local environmental conditions support the need for their conservation and utilization in local farming systems.

ACKNOWLEDGMENTS

The authors would like to thank Dr. Dan Bradley of Trinity College, Dublin for kindly providing the N'Dama and Friesian DNA samples; Drs. Reuben Mosi and Okeyo Mwai of University of Nairobi for their part in the Kenyan breeds sampling, and Prof. Paul Gwakisa of Sokoine Agricultural University for the Tanzanian breeds sampling. The assistance of Ethiopian and Eritrean scientists in sampling of the Abigar, Danakil and Arado breeds is also acknowledged, as well as the technical assistance of Mr. J. Ochieng (ILRI) in DNA extraction.

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