

## Cattle/ Genetics/ West-Central Africa

■ Title  <i>Titre</i>	<b>Genetic Characterisation of Cattle in West and Central Africa</b>  <i>Caractérisation génétique du bétail en Afrique de l'ouest et en Afrique centrale</i>
■ Contract number <i>Numéro de contrat</i>	<b>TS3-CT91-009</b>
■ Project leader <i>Chef de projet</i>	Daniel G. Bradley
■ Host institution <i>Institution-hôte</i>	University of Dublin Trinity College
■ Address <i>Adresse</i>	Department of Genetics, Trinity College Dublin 2, Ireland
■ Telephone	+353- 1- 6081088
■ Fax	+353 -1 -6798558
■ Associated institutions <i>Institutions associées</i>	- United Kingdom: University of Glasgow - Nigeria: University of Ibadan - Senegal: Institut Sénégalais de Recherches Agricoles
■ Key words  <i>Mots clés</i>	trypanosomiasis; disease resistance; animal breeding; dna; molecular genetics; cattle; genetic conservation; biodiversity; evolution; population genetics; major histocompatibility complex; microsatellites; domestication <i>trypanosomiase; résistance à la maladie; amélioration animale; adn; génétique moléculaire; bovin; conservation génétique; biodiversité; évolution; génétique des populations; complexe majeur d'histocompatibilité; microsatellite; domestication</i>
■ Final report <i>Rapport final</i>	5 p., English

# Genetic Characterisation of Cattle in West and Central Africa

## Objectives

West Africa differs from the rest of the continent in possessing significant populations of both sub-species of domestic cattle, *Bos taurus* (taurine) and *Bos indicus* (zebu). Most of Africa is populated with zebu breeds and varieties of stabilised cross breeds. It is only in regions of West and Central Africa that large numbers of apparently pure taurine remain. These breeds, including N'Dama, Kuri and varieties of West African Shorthorn are the descendants of the original domestic cattle of the continent and represent a genetic resource unique to this portion of the globe.

Thus the earliest cattle in Africa were humpless or taurine in character. They may have had a common domestic origin with European cattle but recent analysis has suggested that a third, separate strain of African wild ox may have been involved. These animals and their herders moved throughout the Western subcontinent, around a much-reduced Sahara, some 7,000 yrs BP. Through natural selection resulting from a long association with the natural challenges of humid guinean zones these cattle have become adapted to certain endemic diseases. In particular, some breeds display trypanotolerance; i. e. varied levels of adaptation to the tsetse fly transmitted disease, trypanosomiasis.

Humped, or zebu, cattle have an Eastern origin and, although first appearing in Egypt in ancient times, only started to spread comprehensively through West Africa along with Arabic influences within the last 1,400 years. This sub-species shows marked adaptation to arid environments and predominates in those areas of the Africa with Sudano-Sahelian ecologies. They possess little or no trypanotolerance and consequently, may be maintained in much of Africa only

through the use of expensive disease prevention measures such as tsetse control or chemical prophylaxis.

At present, taurine herds predominate in the more southern, humid ecological zones of West Africa, inhabiting an almost continuous swathe from The Gambia to Cameroon. However, they are significantly threatened with assimilation or extinction from incursion of the more numerous zebu into these regions. Because of the attraction of pastoralists to the larger indicine bulls and because of migrations largely due to droughts such as that between 1972 and 1983, many taurine populations are currently experiencing introgression on a scale greater than ever before. Between 1970 and 1981 in the four Sahelian countries of Mali, Mauritania, Niger and Senegal, the bovine to human ratios fell by 30-40%, a statistic not paralleled in the more southern countries. The future utilisation of the genetic resource represented by the trypanotolerant taurine to harvest the biomass of much of humid subsaharan Africa depends on their conservation, promotion and improvement (BRADLEY et al. 1992). Genetic characterisation of these breeds and their traits forms one important component in a strategy to conserve invaluable genetic resources and expand food production in the tsetse infested third of the African continent's landmass. It is hoped, through the molecular genetic characterisation of native breeds, to contribute to future conservation, utilisation and novel experimental approaches involving these unique cattle populations.

### Specific Project Objectives

- To determine the genetic relationships among local breeds in West and Central Africa, including the most important trypanotolerant populations.

- Quantify the extent of genetic diversity between and within breeds of the region.
- Contribute to genetic resource management by identifying appropriate populations for resource targeting.
- Through collaboration with national institutes to contribute to technology transfer involving molecular and population genetics.

## Materials and methods

### Sampling

The populations which were selected for analysis are shown in table 1. These were selected on the basis of economic importance, value as unique genetic entities or as culturally important breeds in danger of extinction. The zebu breeds and the N'Dama fall into the former category. The other taurine breeds are threatened to differing extents, particularly the West-African Shorthorn breeds, and Namshi, Kapsiki and Kuri cattle which inhabit small pockets in the zebu-dominated regions.

Field operations which have been undertaken to sample populations were as follows:

- February - March 1992. I.S.R.A., Senegal.

Dr. Racine Sow, in collaboration with Dr. Arouna Gueye, Dr. Adama Faye, the staff of the C.R.Z. Kolda, the F.A.O. Regional project, Banjul and Drs. Bradley and MacHugh of Dublin successfully conducted sampling and DNA extraction from five populations.

- October-December, 1992. University of Ibadan, Nigeria.

Prof. L. O. Ngere, in collaboration with Drs. Stear, Strain and Stott, University of

Glasgow, Drs. Bradley and Loftus, Dublin and Dr. Sauveroché of the F.A.O. Regional Project successfully carried out sampling and DNA extraction from ten populations.

- June-July, 1994. Centre International de Recherche-Développement sur l'Élevage en Zone Subhumide (CRTA/CIRDES), Bobo Dioulasso, Burkina Faso.

A joint endeavour between Dublin and CRTA involved the extraction of DNA and microsatellite analysis of samples

taken from the large collections kept in Bobo Dioulasso.

Glasgow research has concentrated on polymorphisms in defined genetic systems, especially the Major Histocompatibility Complex (MHC). Presently this endeavour is concentrating on PCR-sequencing protocols to uncover useful variation. An important component of this laboratory's participation is the highly effective technology transfer represented by the inclusion of Dr Miessa Ndiaye of ISRA, Senegal, in the team as a full time researcher.

## Molecular Genetic Analyses

Polymerase chain reaction (PCR) approaches were used to amplify informative genetic loci such as microsatellites and MHC regions. These and any other techniques used are fully described in the references given below.

## Results

The most important results of the project are denoted in figure 1. This shows genetic admixture proportions derived

Geographical Origin	Breed	Number sampled	No. Males	No. Females	Sampling locations in countries
Cameroon	Namchi	54	19	35	North-Central region
Chad	Kuri	52	22	30	Lake Chad and environs
Gambia	N'Dama	58	28	30	McCarthy Island, Central Gambia
Guinea	N'Dama	63	41	22	Fouta Djallon and environs
Guinea Bissau	N'Dama	54	22	32	Western and Central regions
Mali	N'Dama	44	1	43	Southeastern region
Nigeria	N'Dama	19	2	17	Southern coastal region
Senegal	N'Dama	48	22	26	Central and Southern region
<b>West African Longhorn</b>	<b>8 populations</b>	<b>392</b>	<b>157</b>	<b>235</b>	
Benin	Lagune	60	29	31	Southern-Coastal region
Benin	Somba	60	30	30	Northwestern region
Burkina Faso (1)	Baoule	56	2	54	Southeastern region
Burkina Faso (2)	Baoule	50	3	47	Southwestern region
Cameroon	Kapsiki	60	24	36	Northern region
Côte d'Ivoire	Baoule	50	?	?	Northeastern region
Nigeria	Muturu	28	?	?	Southeastern region
<b>West African Shorthorn</b>	<b>7 populations</b>	<b>364</b>	<b>88</b>	<b>198</b>	
Burkina Faso	Azawak	29	?	?	Central region
Burkina Faso	Peul	79	?	?	Across entire country
Mauritania	Maure	55	3	52	Northern Senegal
Nigeria	Mbororo	47	10	37	Eastern region
Nigeria	Sokoto Gudali	47	17	30	Northwestern region
Nigeria	White Fulani	30	7	23	North-Central region
Senegal	Gobra	59	31	28	Northern and central region
<b>West African zebu</b>	<b>7 populations</b>	<b>346</b>	<b>68</b>	<b>170</b>	
Benin	Borgou*	60	31	29	Northern region
<b>Total</b>	<b>23 breeds</b>	<b>1162</b>	<b>344</b>	<b>632</b>	

\*Borgou are a recent synthetic crossbred population  
NB. Question marks "?" indicate where the ratio of male to female samples was unknown

Table 1a: Populations collected during current project

Geographical Origin	Breed	Number sampled	No. Males	No. Females	Sampling locations in countries
Nigeria	White Fulani	24	16	8	Central region
Sudan	Butana	24	2	22	Southern region
Sudan	Kenana	38	1	37	Central region
<b>East African zebu</b>	<b>2 populations</b>	<b>62</b>	<b>3</b>	<b>59</b>	
<b>North Indian zebu</b>	<b>3 populations<sup>¥</sup></b>	<b>33</b>	<b>3</b>	<b>30</b>	<b>Northern region</b>

<sup>¥</sup>Indian populations sampled were from the Hariana, Sahiwal and Tharparker breeds

Table 1b: Relevant populations sampled during previous projects

from analysis of 20 microsatellite loci in all of the cattle populations surveyed. The red portion of each chart denotes the proportion of the genome in each population that is derived from Asiatic zebu input and the green section indicates the proportion due to the input of African taurine genes.

### Microsatellite results

The strength of these loci as tools in examination of biological diversity lies in the following properties:

- They are highly variable and the presence of multiple alleles offers more information per locus typed.

- The mutation rate per locus is high, which contributes to the detection of genetic divergence between even closely related populations.

- The mutation of microsatellites follows a step-wise model and accordingly, relationships between alleles may be discerned. This additional level of information which resides in quantitative length differences between PCR products allows families of alleles to be discerned.

- Approximately half of loci tested yield separate allele-length distributions of taurine- and zebu-characteristic alleles.

The results provide a confirmation that the taurine cattle of West Africa are subject to the incursion of *indicus* genes. The extent to which this is true differs in various cases. Only one population was virtually devoid of detectable zebu ancestry. This was the N'Dama from Guinea, the region traditionally recognised as the homeland of that breed. Several populations exhibited only very low levels of introgression (0-5% admixture). These were the N'Dama from Guinea Bissau, one Baoule sampling group from Burkina Faso and Somba sampled in Benin. Four groups showed 5-10% admixture: Senegalese N'Dama from Casamance, Lagune from Benin, Baoule from Cote d'Ivoire

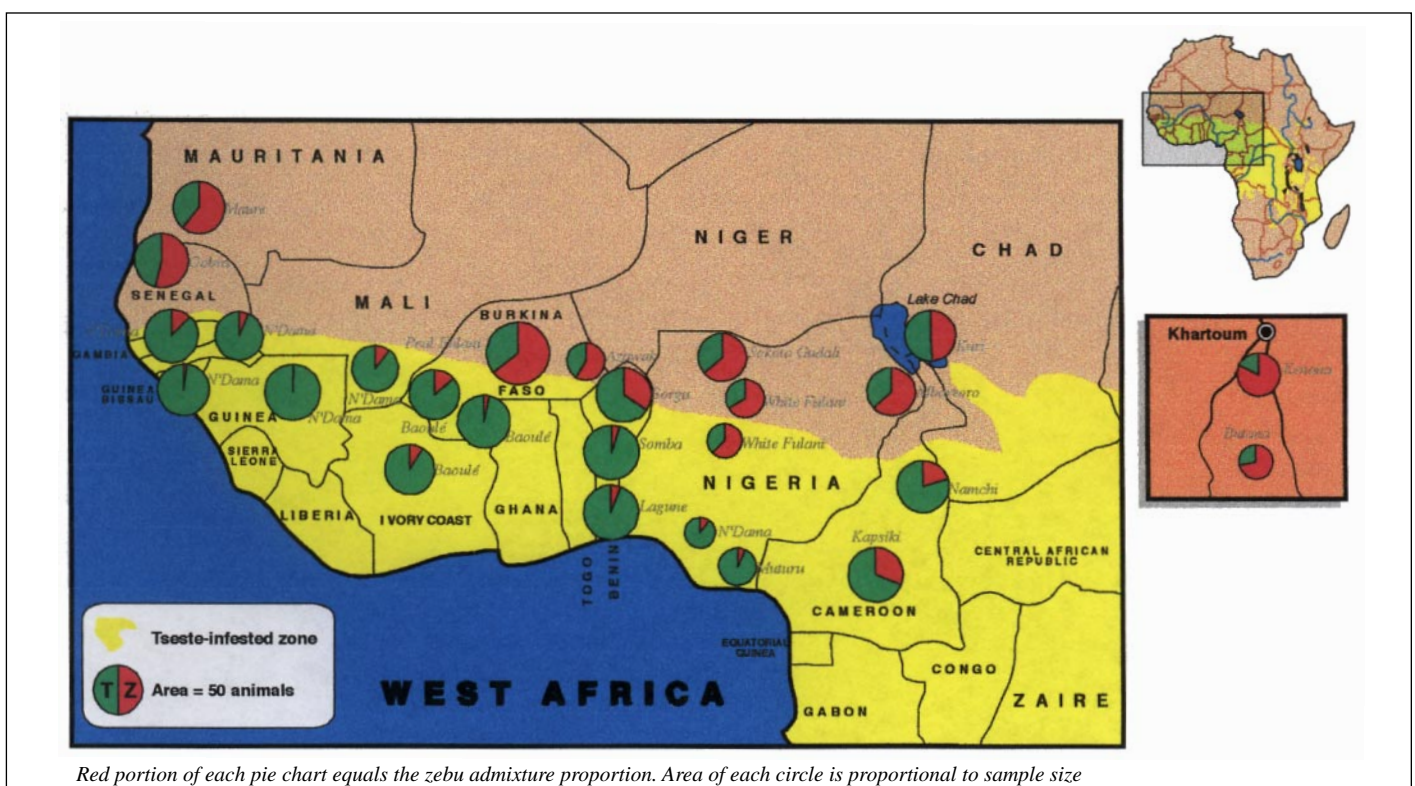


Fig 1: Regression zebu admixture proportion for cattle populations in West and East Africa

and Muturu from Nigeria. The remaining taurine breed samples were taken from more northerly regions close to or within zones in which zebu predominate. Admixture levels in these were between 10 and 20%, with two outlying exceptions. These were the Kapsiki (30.8%) from Northern Cameroon and the Kuri (49.3%) from the islands of Lake Chad. Both of these inhabit geographically isolated regions which are surrounded by zebu herding areas. Interestingly, the levels of zebu admixture in the Kuri decreased as the sample origins moved further from the shore into the Lake, but despite strong efforts to obtain pure animals, never fell below 46%. It is to be noted that a recognised crossbred population, the Borgou from Benin showed admixture of 34.3%.

## Y chromosome and mitochondrial variation

Mitochondrial DNA analysis has been used to elucidate the early history of cattle (Lofrus et al. 1994a, 1994b). A striking feature of its variation is that all African cattle, both taurine and zebu, display mtDNA which is closely related to European variants, implying a more recent common ancestry than that shared with Indian animals. However, a novel indication of the uniqueness and conservation value of the indigenous African cattle breeds is mtDNA sequence evidence that these probably arose from a separate strain of the wild ox. The absence of indicine mtDNA in African samples indicates that the process of immigration of zebu genetics may have been through male-mediated crossbreeding with the indigenous taurines of that continent. (BRADLEY et al. 1996). This hypothesis is strengthened by the distribution of Y chromosome DNA variation in modern cattle and microsatellite-derived estimates. Generally, the introgression of zebu Y chromosomes into taurine herds has progressed more extensively than for other elements of the genome. Detection of zebu Y chromosomes in some taurine herds may be a sensitive indication of crossbreeding and dilution of the trypanotolerance genetic resource (BRADLEY et al. 1994).

## Conclusions and additional comments

The most important conclusions of the body of work described in this report may be summarised under the following points:

- For the first time, convincing evidence has been provided that the indigenous taurine cattle of Africa have emerged from a separate domestic origin from that of European cattle. This is a firm pointer to their biological uniqueness and emphasises the need for their conservation.
- Methods of assessing genetic introgression into these indigenous populations by zebu breeds have been developed, and have provided an accurate assessment of admixture patterns over a comprehensive geographical area.
- Taurine breeds have experienced admixture with zebu to differing extents. Some commercially and culturally important populations have a significant proportion of zebu ancestry. This raises important questions about breed choice for the exploitation, study and conservation of the trypanotolerance trait.
- One collaborative study with scientists in Cameroon has demonstrated a close association between trypanosusceptibility and zebu admixture in three taurine breeds studied.
- The work has directly led to a further DGXII, INCO-DC funded project to study the actual genetic determinants of trypanotolerance.

The significance of admixture levels in taurine animals is borne out by results of a collaborative study involving the Dublin laboratory and the Animal and Veterinary Research Centre, Wakwa, Cameroon. In this, the two indigenous Cameroonian taurine cattle breeds (Namchi and Kapsiki) were evaluated for trypanosusceptibility following inoculation with *Trypanosoma congolense*. Their response to the infection was compared to that of known trypanotolerant (N'Dama) and trypanosusceptible (Ngaoundere Gudali) cattle. There was

no significant difference between the N'Dama and Namchi nor between the Kapsiki and Gudali. Notably, when the experimental herds were assessed to ascertain zebu admixture levels, the Kapsiki showed high levels of zebu ancestry, close to that of the local zebu Gudali, and those in the Namchi were significantly lower, closer to that in the local N'Dama. This is the first study combining these data in the same populations and is a clear indication of the importance of the genetic dilution of the indigenous African taurine breeds.

In a breed such as the N'Dama, where large numbers and populations in several countries exist, there is little immediate threat to the survival of the breed. However, the choices made concerning populations and animals involved in development and expansion programmes should be influenced by results such as those presented here. With the rarer populations of West African Shorthorn breeds, crossbreeding with zebu is often a more serious matter and threatens the continued existence of many as discrete genetic entities. Whereas the several breeds are still relatively intact, it is clear that the trypanotolerance resources embodied in some dwindling cattle populations are seriously threatened with dilution and assimilation by the more numerous *Bos indicus* breeds of the region.

## Publications

The following are publications which have emerged from the project (copies enclosed):

Bradley, D. G., (1992) Genetic characterisation of cattle breeds in West and Central Africa. Trypanotolerant Livestock Newsletter 5:3-8

Bradley, DG, MacHugh, DE, Loftus, RT, Meghen, C, Sharp, PM, Cunningham, EP. (1993) Genetic Characterisation of Indigenous Cattle Breeds: First Results and Implications for Genetic Improvement. FAO Animal Production and Health Paper 110:37-45

Bradley, D.G., MacHugh, D.E., Loftus, R.T., Sow, R.S., Hoste, C.H. and Cunningham, E.P. (1994) Zebu-taurine variation in Y chromosomal DNA: a sensitive assay for genetic introgression in West African trypanotolerant cattle populations. *Animal Genetics*, 25:7-12.

Loftus, R.T., MacHugh, D.E., Bradley, D.G., Sharp, P.M. and Cunningham, E.P. (1994). Evidence for two independent domestications of cattle. *Proc. Natl. Acad. Sci USA* 91, 2757-2761

MacHugh, D. E., R. T. Loftus, D. G. Bradley, P. M. Sharp and E. P. Cunningham. (1994) Microsatellite DNA variation within and among European cattle breeds. *Proc. R. Soc. Lond. Ser. B* 256: 25-31.

Meghen, C., MacHugh, D.E. and Bradley, D.G. (1994). Genetic Characterisation and West African Cattle. *World Animal Review*, FAO, Rome. 78:59-66.

Cunningham, E.P., RT Loftus, DE MacHugh, DG Bradley. (1994) Molecular evolution of African, European and Asian Cattle. *Proceedings of the 5th World Congress on Genetics Applied to Livestock Production*. 21:86-89

Loftus, R.T., D. E. MacHugh, L.O. Ngere, D.S. Balain, A.M. Badi, D. G. Bradley, E. P. Cunningham. (1994) Mitochondrial genetic variation in European, African and Indian cattle populations. *Animal Genetics* 25:265-271

Teale, A.J. J. Wambugul, P.S. Gwakisa, G. Stranzinger, D.G. Bradley, S.J. Kemp. (1995) A polymorphism in randomly amplified DNA which differentiates the Y chromosomes of *Bos indicus* and *B. taurus*. *Animal Genetics* 26: 243-248

Hall, S.J.G. and D.G. Bradley. (1995) Conserving livestock breed diversity. *Trends in Ecology and Evolution* 10:267-270.

Bradley, D.G., David E. MacHugh, Patrick Cunningham and Ronan T. Loftus. (1996) Mitochondrial diversity and the origins of African and European cattle. *Proceedings of the National Academy of Sciences USA*, 93:5131-5135

#### Citations of the project's work:

Science

New Scientist

Libération (Paris)