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## Research Article

# Diversity and Genetic Structure of Senegalese Local Cattle Breeds

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## Abstract

**Background and Objective:** Improvement and conservation strategies of animal genetic resources require first of all, a full knowledge of breeds' diversity and genetic structure. In order to disclose the current genetic structure of Senegalese local cattle breeds, this study has used the population genetics approaches. **Materials and Methods:** The DNA samples were taken from 120 unrelated cattle animals sampled from the main livestock breeding areas in Senegal. Genotyping was carried out using 11 microsatellite loci selected within the panel recommended by ISAG-FAO for cattle breeds' genetic characterization. Genetic differentiation and structure analysis were performed using bioinformatics' softwares. **Results:** The  $F_{ST}$ , measure of population differentiation indicated a mean value of  $0.047 \pm 0.011$ , ( $p < 0.05$ ), followed with a mean gene flow ( $Nm$ ) of 5.06. The Bayesian analysis indicated three clusters. The first one grouped mainly the N'Dama cattle, the second the majority of Djakore "hybrid" population and the last one clustered the zebu's populations. **Conclusion:** Population structure analysis has revealed at present that Senegalese local cattle breeds were not running towards genetic erosion, nevertheless they deserve to be closely monitored to avoid the disappearance of important adaptive traits.

**Key words:** Breed's genetic structure, microsatellite genotyping, improvement and conservation strategies

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**Data Availability:** All relevant data are within the paper and its supporting information files.

## INTRODUCTION

Animal genetic resources are playing a vital role in livestock production and are essential to a sustainable agriculture and food security<sup>1,2</sup>. The efforts of conservation of animal genetic resources in developing countries are minimal. The conservation programs that had been launched were running without a full spectrum of conservation strategies<sup>1</sup>. With the advent and development of artificial insemination during the last 50 years, the replacement of locally adapted breeds by a narrow range of high-yielding international trans-boundary breeds, is becoming an area of concern affecting animal genetic diversity in developing countries<sup>3,4</sup>. This development has led to mounting concerns about the genetic erosion<sup>5</sup>. Consequently, livestock breeds are threatened by the devastating effects of genetic erosion, the most significant of which are the dilution of genetic pool and the disappearance of important adaptive traits<sup>1</sup>.

In Africa, several studies have been conducted on cattle breeds for improvement and conservation purposes<sup>6-9</sup>. From these studies, all management strategies are elaborated on the basis of genetic diversity maintaining for better livestock productivity. Gobra zebu, Maure zebu and N'Dama cattle have been the subject of population genetics analysis among studies conducted at a continental scale to retrace indicine and taurine migration across Africa<sup>10-12</sup>. Ndiaye *et al.*<sup>13</sup> reevaluated the genetic diversity and the phylogenetic relationships of Senegalese local cattle breeds including the Djakore cattle which have not been characterized up to now at molecular level. Importantly, the levels of genetic diversity of these cattle breeds have considerably increased under indiscriminate crossbreeding factors and changes in livestock breeding systems<sup>13</sup>. This might be attributed to inbreeding among the populations or the occurrence of population substructure. Following these facts, it appears that Senegalese local cattle have undergone significant modifications in their genetic pool. Therefore, it was crucial to know the changes occurred in the genetic structure of these populations regarding their breeding production environments whose factors influenced directly their fitness traits. In the context of breed improvement and conservation purposes, this study aimed at determining the current genetic structure of Senegalese local cattle by using population genetics approaches.

## MATERIALS AND METHODS

**Sample collection:** The survey was carried out from October-December, 2013 in three agro-pastoral regions of Senegal: Saint-Louis, Kaolack and Kolda. These regions

represent the main livestock breeding areas of Gobra zebu, Maure zebu, Djakore and N'Dama cattle. The sampled population consisted of 120 unrelated cattle animals selected from 15 different localities and the Zootechnical Research Center of Kolda. As no parentage records were available, so to ensure that animals were unrelated and held standard characters of the targeted population, it used the knowledge and experience of farmers and shepherds via questionnaire and interviews whenever possible.

Blood samples were collected from jugular vein into 4 mL vacutainer tubes containing the disodium salt of ethylene diamine tetra-acetate (EDTA) as anti-coagulant and stored  $\pm 4^{\circ}\text{C}$  until DNA extraction. During the blood sampling, adequate measures were taken to minimize pain and discomfort in animals. The Ethics Committee of Cheikh Anta Diop University of Dakar approved this study. Participants' approval was obtained after the study was fully explained.

**Microsatellite loci genotyping:** Genomic DNA was isolated from whole blood using Gentra Puregene Blood kit standard protocol developed by QIAGEN® group. The simplex PCR amplifications of 11 ISAG/FAO microsatellite loci were carried out in a 15  $\mu\text{L}$  reaction volume. The PCR products were labelled with fluorescent dyes and genotyped using Li-Cor® automated sequencer (DNA Analyzer Model 4300) following the manufacturer's procedures in genotyping lab of CIRDES ([www.cirdes.org](http://www.cirdes.org)). After the migration profiles analysis by using SAGA<sup>GT</sup> GENERATION 2.0 software, a data set of 1320 genotypes was generated to perform genetic analysis (Table S1).

**Genetic analysis:** The distribution of genetic diversity among the four cattle populations was assessed by analyzing the F-statistics of Weir and Cockerham<sup>14</sup> ( $F_{ST}$  ( $\theta$ ) and  $F_{IT}$  (F)) and the gene flow (Nm) of Wright<sup>15</sup>, by using<sup>16</sup> GENETIX ver. 4.05.2 and<sup>17</sup> FSTAT ver. 2.9.3.2. Pairwise  $F_{ST}$  values between populations were computed using GENETIX by permutation method.

The factorial correspondence analysis from allele frequencies was performed using GENETIX to decipher the population structure. The genetic assignment tests were done using "simulation-exclusion" approach implemented<sup>18</sup> in GENECLASS program ver. 2.0 and proposed by Cornuet *et al.*<sup>19</sup>. The "exclusion-simulation" tests were carried out using the allele frequencies method of Paetkau *et al.*<sup>20</sup> among all cattle populations (mean  $F_{ST}$  = 0.047) between the most differentiated pair of populations (Djakore and N'Dama:  $F_{ST}$  = 0.107) and between the least differentiated pair of populations (Gobra zebu and Maure zebu:  $F_{ST}$  = 0.003).

To search the occurrence of independent genetic clusters (K) and to assign correctly individuals to

Table S1: Microsatellite genotypes of four Senegalese local cattle populations

Variables	BM1818	BM2113	ETH10	ETH152	ETH225	HEL1	INRA063	INRA37	MM12	TGLA53	HEL9
<b>POP 1</b>											
djkb27	282282	148158	233233	210210	174174	123127	202202	148148	143157	178202	184184
djkb28	284286	154160	229241	210220	158164	123131	202202	142148	125139	184198	182186
djkb29	280286	148154	237239	214224	174174	123127	204204	000000	135151	178202	172188
djkb30	000000	154154	227229	210216	164174	129131	202202	150150	119157	200202	172190
djkb31	276280	148158	229241	210210	174174	121129	196202	000000	119125	184202	168178
djko01	280290	148154	227233	000000	174174	123127	196202	142148	145157	178184	174186
djko02	282288	000000	227237	000000	166166	129129	000000	000000	137149	000000	176186
djko03	280282	000000	000000	000000	166166	121129	196202	148150	133137	000000	182184
djko04	280290	000000	225229	198198	164164	123131	202202	144150	125139	000000	182186
djko05	290290	154158	225239	198202	170174	123129	202202	144150	133139	178192	186186
djko06	280286	146158	227237	198202	158174	123129	202202	148150	139141	172172	174182
djko07	286290	146146	225235	198202	166174	127127	202202	144148	137139	000000	174186
djko08	278282	152158	233237	210216	162164	129131	196196	144150	137139	180202	172182
djko09	286290	148154	000000	210216	164174	125129	202202	144148	000000	190190	176182
djko10	280290	148158	225237	198202	158166	123129	202202	144148	137145	178178	176182
djko11	278280	158158	229237	198202	164174	125129	196202	148148	137157	000000	172182
djko12	286292	148152	225237	198202	164164	127131	202202	144148	119157	178178	182186
djko13	278290	152158	225227	198202	158164	123139	202202	144148	137137	178200	174182
djko14	274290	140148	000000	198202	158174	121129	196202	000000	137151	178200	172172
djko15	000000	000000	000000	000000	000000	000000	000000	000000	000000	000000	172186
djko16	276280	158158	225237	210220	170174	121125	202202	144148	139139	190190	176184
djko17	276280	148158	225225	210214	170174	121131	202202	000000	139139	184202	176176
djko18	280282	000000	225227	202214	164174	121125	202202	144144	137137	000000	176182
djko19	276282	158158	227237	202214	174174	123127	202204	144148	137137	178184	176184
djko21	000000	146156	000000	204216	174174	127127	202202	140148	139157	000000	184184
djnf22	278280	140156	225227	210214	164170	127129	202202	144148	137139	178194	182188
djnf23	280290	156156	237237	202214	164174	127129	202202	144148	151157	200202	174186
djnf24	276286	148158	225241	210216	164174	125129	202202	000000	137139	000000	174174
djsb25	278290	148158	233237	214220	000000	127131	196202	148148	139143	178178	182184
djsb26	282286	148156	237237	210214	166174	121127	196196	138144	135143	178178	164172
<b>POP 2</b>											
godp41	278290	148160	225229	216216	166170	125141	200202	000000	139157	178186	164174
godp42	284290	148158	225225	000000	164174	129141	196196	000000	125139	200202	166174
godp43	286290	152160	235237	216216	170174	123123	200202	152154	137137	178190	166166
godp44	282282	158158	227237	210216	174174	125129	000000	000000	133157	178178	174182
godp45	282286	154154	225241	210216	158164	127131	202204	000000	139139	190198	168172
goko19	280280	140152	225227	210216	164174	123131	196196	142148	137141	192200	166186
goko20	000000	000000	000000	000000	000000	000000	000000	000000	000000	000000	174180
goko21	282290	000000	227227	000000	000000	123127	000000	148148	000000	000000	186188
goko23	000000	148154	000000	210220	158170	123129	204204	000000	139157	178190	000000
goko25	000000	148164	225225	210220	000000	000000	206206	142142	000000	000000	166182
goko27	278280	148148	229229	210210	164174	121123	196202	144150	137139	000000	172180
goko28	280290	152156	237237	210214	164170	121129	204204	000000	125135	000000	176176
goko30	000000	158158	000000	210216	164164	123131	202202	000000	000000	000000	000000
gomm40	282282	158158	227227	210210	158174	129131	202202	000000	139139	178194	168174
gonb01	280286	000000	225237	210214	000000	123131	202204	144144	000000	178200	182184
gonb02	280286	000000	225225	210214	000000	121125	000000	148148	000000	180200	174186
gonb03	274278	152158	225237	202214	158170	125127	000000	144146	139143	000000	174184
gonb04	280290	156156	233237	198198	174174	121121	000000	144148	133139	186202	172174
gopd31	278286	000000	233237	198210	174174	127131	000000	148150	141151	000000	174174
gopd32	000000	154154	000000	198210	174174	129139	196202	000000	137139	000000	000000
gopd34	274280	148152	000000	214216	170174	123123	196202	148150	135143	202202	174186
gopd35	280290	140140	227235	198210	158174	129131	202202	144148	125139	000000	174176
gopd37	280290	158158	000000	210216	164174	121131	202202	000000	137153	178178	000000
gopd38	276282	148154	227235	214216	174174	131133	202204	146150	137139	200202	166172
gopd39	280286	140154	225237	210210	158162	125129	196204	146150	135139	178180	174176
gowd05	000000	148152	000000	198202	000000	127137	000000	000000	139139	000000	000000
gowd06	282286	148158	225227	210214	164174	123133	202202	148148	137139	178192	174186
gowd07	280280	160160	225225	210214	000000	000000	000000	144150	137137	178188	172184
gowd08	276280	000000	000000	000000	000000	000000	000000	000000	000000	000000	172186
gowd14	278290	160160	225225	210216	174174	000000	000000	142148	000000	000000	176176

Table S1: Continue

Variables	BM1818	BM2113	ETH10	ETH152	ETH225	HEL1	INRA063	INRA37	MM12	TGLA53	HEL9
<b>POP 3</b>											
mako02	280290	140148	225233	210214	174174	121131	000000	142150	137139	196204	176182
manf03	000000	154156	000000	210214	000000	123127	202202	000000	137149	000000	000000
manf04	286286	148164	225225	210214	174174	123125	202204	148150	000000	000000	174176
mang19	274274	152154	225227	198210	174174	121129	202202	142150	119133	000000	170172
mang20	278280	000000	237237	000000	174174	123131	000000	000000	137137	000000	000000
mang21	282286	000000	237237	202214	164164	131131	000000	144146	137139	000000	172186
mang22	290290	000000	227239	000000	000000	000000	000000	148148	000000	000000	174186
mang23	280290	158158	225227	000000	162174	121127	196202	136148	125139	000000	182184
mang24	274278	148152	225227	000000	158164	121125	202202	144146	137141	000000	170172
mapd27	278290	154154	227227	000000	158166	125125	200204	144148	137141	178194	172184
mapd28	280290	148160	229233	214220	164164	125125	202204	148152	137139	182188	174184
mapd29	286290	154154	233237	210222	158162	129139	196204	148148	137143	188188	166174
mapd30	284290	154156	225225	210210	164174	123129	202202	144148	143145	182202	172186
mapd32	000000	158158	227237	210210	174174	129129	202202	000000	137137	202202	172186
mapd33	000000	152152	237237	214214	158174	127127	202202	000000	139139	000000	182182
mapd34	000000	148154	233237	210210	174174	123125	196202	142146	137139	178202	166174
mapd35	280286	140154	225237	210210	164174	123127	202202	150152	137139	190202	166176
mapd36	280286	148154	225237	000000	174174	121127	196202	000000	137139	000000	176182
mats06	278280	000000	237237	198210	000000	121121	000000	000000	000000	000000	174176
mats07	000000	000000	000000	210214	158166	129129	000000	144146	137139	178188	000000
mats08	000000	000000	000000	210214	166174	129139	200204	144146	000000	000000	174176
mats09	000000	148158	000000	210214	000000	000000	000000	000000	119137	184184	000000
mats11	286290	000000	233237	210214	000000	123125	200202	000000	000000	000000	178186
mats12	000000	000000	229229	210216	158174	121125	000000	000000	119137	000000	172182
mats13	280286	148154	225237	210210	158174	129129	196202	144148	000000	178190	172172
mats14	280282	154154	229229	198210	158174	123127	202202	150150	137139	000000	182184
mats15	282286	146156	225237	198210	158174	125129	196202	144150	139151	178178	172172
mats16	280282	154156	225237	198210	158174	123123	202202	144144	133137	000000	182186
mats17	280282	152154	225229	198210	174174	125129	196202	144150	119137	000000	172182
mawd01	282290	148156	225235	210214	164164	123123	196204	148148	000000	000000	174186
<b>POP 4</b>											
ndck20	000000	000000	000000	000000	000000	000000	000000	000000	000000	000000	000000
ndck21	284286	152158	235235	216216	164176	123129	196196	134134	137157	000000	176186
ndck23	280286	000000	235235	214214	000000	123125	196202	142142	000000	000000	000000
ndck24	284284	156156	227237	214214	162162	123131	196200	142146	133157	000000	000000
ndck28	000000	148158	235237	000000	000000	000000	000000	000000	000000	000000	172182
ndck29	280286	000000	235237	202214	000000	123131	202202	132142	139157	000000	172184
ndck30	280280	000000	229235	214214	000000	000000	000000	142146	000000	000000	184186
ndck31	278286	156156	237237	214214	164164	123123	196196	142146	133137	000000	184184
ndck32	276286	156156	235237	214214	164174	125131	202202	142142	137157	000000	182182
ndcr15	000000	000000	000000	000000	000000	000000	000000	000000	000000	000000	000000
ndcr17	000000	000000	000000	000000	000000	000000	000000	142146	000000	000000	174188
ndcr18	280284	000000	235235	214214	000000	125131	196196	000000	000000	000000	186186
ndgp02	278284	140140	237237	202214	162166	123133	196196	134144	137139	000000	174184
ndgp03	000000	000000	235235	000000	000000	000000	000000	000000	000000	000000	170176
ndgp05	278280	000000	229237	000000	000000	000000	196200	000000	137137	000000	172172
ndgp06	000000	000000	000000	202202	000000	123127	196200	000000	137137	000000	000000
ndgp07	278290	000000	235237	210214	000000	000000	196202	142150	000000	000000	186186
ndgp08	280284	000000	233233	000000	000000	123123	196200	000000	000000	180192	182186
ndgp09	278280	000000	237237	202214	158170	125131	202202	142142	000000	000000	176186
ndgp11	278280	000000	225237	202214	000000	000000	202202	000000	000000	000000	186186
ndmb34	274278	000000	000000	000000	158164	125131	194200	142142	137139	000000	182188
ndmb35	000000	000000	000000	216216	000000	125131	202202	000000	139139	000000	000000
ndmb37	000000	152160	000000	214216	158158	123131	196196	000000	137139	184184	174186
ndmb38	278282	140158	225235	214214	162164	121123	196202	000000	137137	174184	174186
ndmb39	000000	140158	225235	214214	164164	125125	196202	000000	137137	182182	000000
ndvd40	000000	158158	237237	000000	162164	123125	196196	000000	137137	000000	182186
ndvd41	000000	140148	000000	000000	000000	000000	000000	000000	000000	182186	000000
ndvd42	000000	140148	233237	214214	162164	123135	196200	000000	137137	182186	184186
ndvd43	000000	152156	000000	214214	158164	123131	200202	000000	137139	184192	000000
ndvd44	000000	156158	235239	210214	166174	127129	196204	148148	139157	184192	186186

Each population constituted of 30 individuals corresponding to a total of 1320 genotypes, dj: Djakore, go: Gobra zebu, ma: Maure zebu, nd: N'Dama, Pop: Population

populations where their genotype had the greatest belonging likelihood according to the ancestry proportion (Q), an alternative Bayesian clustering procedure implemented<sup>21</sup> in STRUCTURE ver. 2.3.4. was used. Simulations were performed using a burn-in period of 10,000 iterations followed by 1,000,000 iterations of the Markov chain Monte Carlo algorithm. Independent runs of K were performed from 1-8 clusters and were repeated 20 times to check the reliability of results. To determine the most appropriate number of clusters (K) that best fit the data, the results generated by STRUCTURE have been submitted to STRUCTURE HARVESTER web site program<sup>22</sup>, which implemented the mean esteemed log-likelihood of K, L (K) and the Evanno method<sup>23</sup>.

**RESULTS**

**Population differentiation analysis:** Results of F-statistics measures were presented in Table 1. Considering all cattle populations, a global deficit of heterozygotes ( $F_{IT}$ ) of 11.7% ( $p < 0.05$ ) was observed. The multi-locus  $F_{ST}$  measure of differentiation indicated that 4.7% ( $p < 0.05$ ) of the total genetic diversity were due to unique allelic differences among populations. The mean gene flow (Nm) between populations was valued to 5.06 (Table 1).

The pairwise  $F_{ST}$  values between populations indicated that Gobra zebu and Maure zebu were the least differentiated populations (0.003), even so the highest pairwise  $F_{ST}$  value was observed between Djakore and N'Dama cattle (0.107)

( $p < 0.05$ ) (Table 2). Considering the esteemed Nm, the highest value was obtained between zebu's populations (68.81), whereas the lowest value was found between N'Dama and Djakore (2.08) (Table 2).

**Population structure analysis:** Factorial Correspondence Analysis (FCA) revealed that the first axis with 59.03% of the total genetic variability separated properly N'Dama from the other populations (Fig. 1). Whereas, the second axis that contributed to 21.56% of the total variability showed that Djakore population was genetically closer to zebu's populations and more especially to Gobra zebu.

The assignment tests based on allele frequencies method revealed that 50% of the cattle individuals were correctly

Table 1: Global F-statistics measured from the 11 microsatellite loci considering four cattle populations

Locus	$F_{IT}$	$F_{ST}$	Nm
BM1818	-0.042	0.006	41.41
BM2113	0.215	0.026*	9.36
ETH10	0.181	0.047*	5.06
ETH152	0.116*	0.133	1.62
ETH225	0.145*	0.047*	5.06
HEL1	0.041	0.018	13.63
HEL9	0.081	0.019	12.90
INRA063	0.285	0.092	2.46
INRA037	0.126*	0.082	2.79
MM12	0.011	0.024*	10.16
TGLA53	0.175	0.045*	5.30
Mean ± SE	0.117 ± 0.027*	0.047 ± 0.011*	5.06

\* $p < 0.05$  = significant

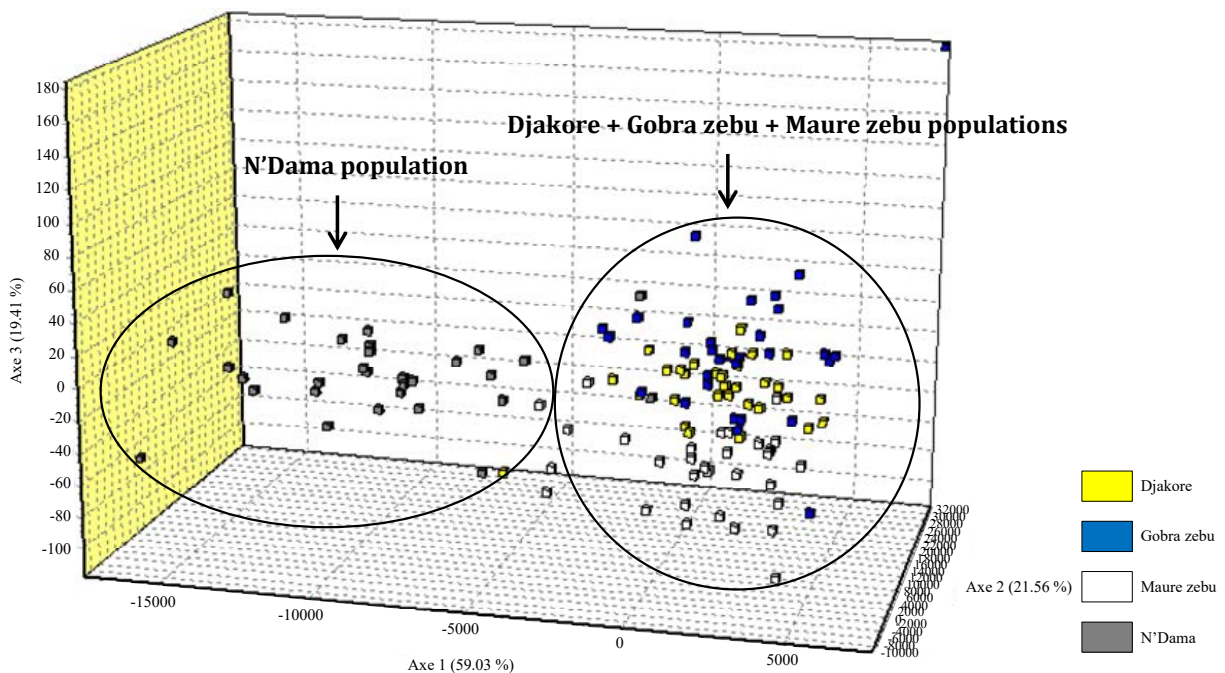


Fig. 1: Factorial correspondence analysis of cattle individuals' genotypes

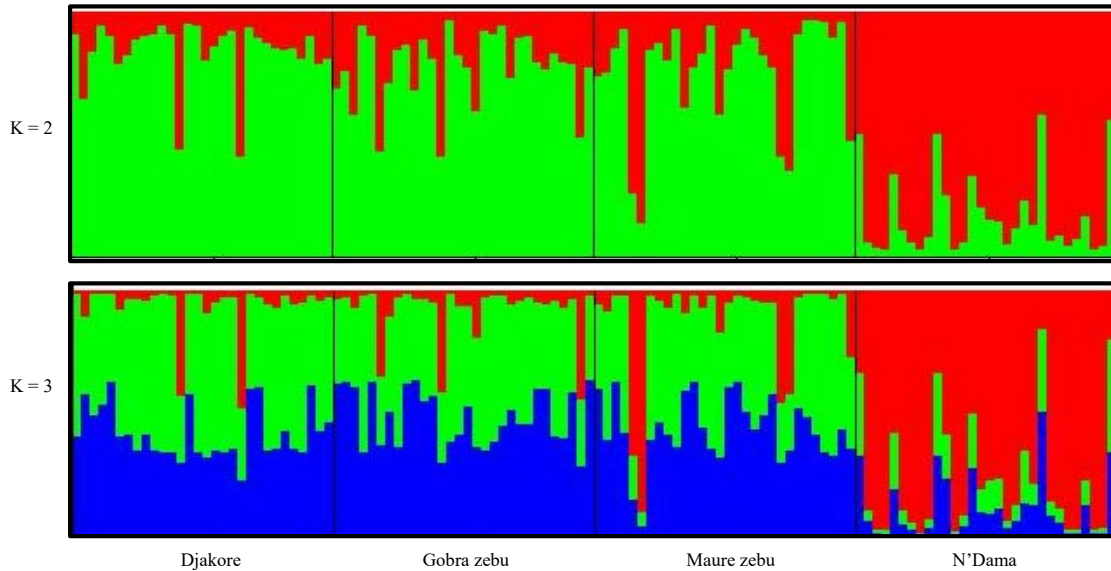


Fig. 2: Genetic structure of four Senegalese local cattle populations

Each cattle individual is represented by a thin vertical bar, often partitioned into colored segments with the length of each segment representing the proportion of individuals' genotypes from K = 2, 3. Thin black lines separated cattle populations

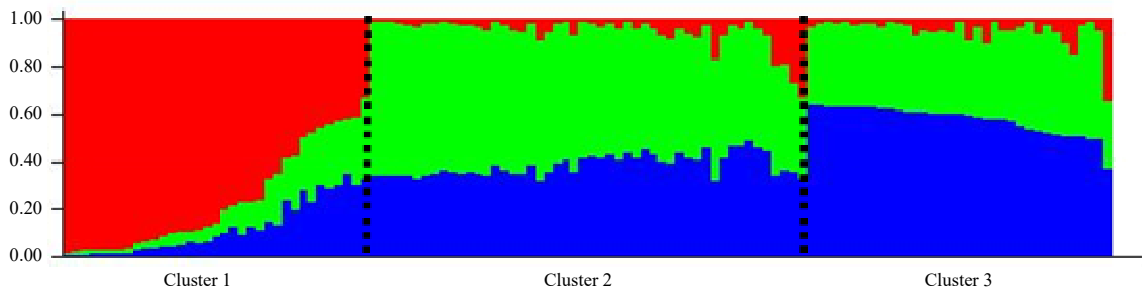


Fig. 3: Assignment of cattle individuals to 3 different genetic clusters inferred from the genotype membership coefficient (Q)

The dashed lines delimited the genetic clusters

Table 2: Pairwise  $F_{ST}$  and  $N_m$  estimates between pair of populations

Cattle populations	Djakore	Gobra zebu	Maure zebu	N'Dama
Djakore	-	0.007	0.010*	0.107*
Gobra zebu	34.71	-	0.003	0.097*
Maure zebu	24.69	68.81	-	0.098*
N'Dama	2.08	2.32	2.28	-

The  $F_{ST}$  values are above the diagonal and those of the  $N_m$  below. \*Values corresponded to significant tests (the repeating percentages of  $F_{ST}$  values lower than those observed, i.e., >95%)

assigned to the population they belong to with the exclusion probabilities of 1 and 0.1% (Table 3). Djakore and N'Dama cattle appeared as the most homogeneous populations because of 53.3 and 71.4% of their individuals were correctly assigned to the most critical threshold ( $p < 0.001$ ), respectively. Among zebu's populations, the percentage of individuals

correctly assigned was 43.3 and 16.6%, respectively. These percentages remained significantly lower than 50%.

The results given by the Bayesian clustering approach, indicated that the likeliest number of clusters considering all cattle populations was obtained for  $K = 3$  (Fig. 2). Only the N'Dama individuals were grouped in their own cluster. However, the zebu's populations and Djakore were assigned into two clusters (Fig. 3). Esteemed membership percentage of N'Dama individuals to cluster 1 was 76.8% (Table 4) and therefore, it was widely constituted of the N'Dama genotype. In the genetic clusters 2 and 3, Djakore and Gobra zebu cattle were mainly assigned with significant percentages of 51.3 and 49%, respectively. Maure zebu individuals were found unevenly distributed amongst the three genetic clusters with 12.3, 44.1 and 43%, respectively.

Table 3: Genetic assignment of individuals to their original population using the “exclusion-simulation” approach

Assignment probabilities	Individuals correctly assigned (%)		
	Exclusion-simulation (reject population probability)*		
	p<0.05	p<0.01	p<0.001
<b>Assignment among 4 populations</b>			
Djakore	40.0	43.3	53.3
Gobra zebu	43.3	43.3	43.3
Maure zebu	16.6	16.6	16.6
N'Dama	50.0	67.8	71.4
Over all	49.2	50.0	50.0
<b>Assignment between 2 populations</b>			
Maure zebu-Gobra zebu ( $F_{ST} = 0.003$ )	60.0	56.7	56.7
N'Dama-Djakore ( $F_{ST} = 0.107$ )	82.2	87.9	86.2

\*With the “exclusion-simulation” approach, an individual is considered as correctly assigned to a population when it is excluded from all excepting his original population (probability of belong to a population under the threshold  $p<0.05$ ,  $0.01$  or  $0.001$ )

Table 4: Percentages of individuals correctly assigned to the three inferred clusters

Reference populations	Inferred clusters			Number of individuals
	1	2	3	
Djakore	6.2 <sup>a</sup>	51.3 <sup>a</sup>	42.5 <sup>a</sup>	30
Gobra zebu	7.9 <sup>a</sup>	43.1 <sup>b</sup>	49.0 <sup>b</sup>	30
Maure zebu	12.3 <sup>b</sup>	44.1 <sup>bc</sup>	43.0 <sup>c</sup>	30
N'Dama	76.8 <sup>c</sup>	11.3 <sup>d</sup>	11.9 <sup>d</sup>	30

<sup>a,b,c,d</sup>Percentages of assignment within a column with no common superscripts differed significantly ( $p<0.001$ )

## DISCUSSION

The mean  $F_{ST}$  value has shown a moderate and significant genetic differentiation among populations that could be attributed to population origin<sup>24</sup> and geographic distribution<sup>25</sup>. Compared to these results, the same mean  $F_{ST}$  value (0.047) was obtained among Mozambican cattle breeds<sup>7</sup>. In contrast with this study, several reports on Cameroonian cattle breeds ( $F_{ST} = 0.061$ )<sup>8</sup>, seven European cattle breeds ( $F_{ST} = 0.112$ )<sup>26</sup> and five Asian cattle breeds ( $F_{ST} = 0.117$ )<sup>27</sup> showed higher genetic differentiation. According to Wright<sup>28</sup>, the differentiation was not negligible if the  $F_{ST}$  was smaller than 0.05 or even less. Following this interpretation, the cattle populations surveyed were moderately differentiated and structured.

The estimations of pairwise  $F_{ST}$  values between populations showed that N'Dama population was genetically differentiated from zebu's populations and more particularly from the Djakore population. The divergence observed between N'Dama and the other cattle populations was supported by genetic distances, phylogenetic relationships and PCA analysis<sup>13</sup>. The genetic differentiation found between zebu's populations were very low and suggesting at molecular level, Gobra and Maure might become one

breed. In most cases, African zebu's populations were characterized by low  $F_{ST}$  values and high levels of genetic diversity relative to a large effective population size and a high migration rate in a usual breeding transhumant system<sup>12,29</sup>. The relatively low gene flow observed between N'Dama and the other cattle populations could be explained by the farming system and a high reproductive isolation that might imply the mechanisms of speciation<sup>30</sup>. In contrast, the values of gene flow appraised between zebu's populations and Djakore showed substantial allelic flow exchanges. This could be confirmed between these three populations that the reproduction occurred without none control during the transhumance period<sup>13</sup>.

The Bayesian approach revealed that Senegalese local cattle populations were grouped into 3 genetic clusters. The cluster 1, where 76.8% of the N'Dama individuals were properly assigned was represented mainly by the N'Dama genotype. At molecular level, N'Dama is a “genetic breed”. As the N'Dama breed was affected by genetic introgression of zebu (Gobra and Maure) with percentages of 7.9 and 12.3%, respectively, therefore it was not a “purebred taurine”. In comparison with the previous studies, MacHugh *et al.*<sup>10</sup> reported that 5.1% of zebu specific-alleles and 12.4% of genetic admixture proportion were found in the N'Dama breed of Senegal. These findings were confirmed by those of Hanotte *et al.*<sup>11</sup>. Accordingly, the current genotypic structure observed in most trypanotolerant breeds and more particularly in the N'Dama breed of Senegal was similar to that described in previous studies following the same context<sup>12</sup>.

Djakore cattle were mainly assigned in the genetic cluster 2. However, 43.1 and 44.1% of Gobra and Maure cattle individuals were assigned in this cluster, respectively. The measures of zebu admixture coefficient ( $q_i$ ) resulted from the



studies of Freeman *et al.*<sup>12</sup> supported these results and confirmed the significant presence of zebu alleles in “hybrid” populations from west Africa. According to these findings, Djakore is genetically a stable “hybrid” population and not a “genetic breed”. This confirmed the theory of Broutin *et al.*<sup>31</sup>, according to which: Djakore was considered as a “hybrid” population because of its phenotypic characters and geographical distribution. The current genotypic structure of Djakore revealed that zebu introgression was the upshot of the high levels of genetic diversity found in this population.

In the genetic cluster 3, the zebu genotype was predominant with 49 and 43% of Gobra and Maure cattle individuals properly assigned. Compared to the results obtained by MacHugh *et al.*<sup>10</sup>, 39.7 and 36.4% of zebu alleles were found, respectively in Maure and Gobra cattle sampled from Senegal. This implies that the increasing of zebu alleles’ proportion followed up significantly the rate of gene flow and the zebu gradient introgression. Since zebu cattle have shared the same genotype, it was inferred that these two populations might become one breed at molecular level. These results contradicted the phenotypic classification that considered them as two distinct breeds<sup>32</sup>. To sum up, at molecular level, Senegalese local cattle populations are consisted of 3 genotypes: N’Dama genotype, Djakore genotype and zebu genotype.

### CONCLUSION

This study was the first to provide, at molecular level, a complete understanding of the diversity and genetic structure of local cattle breeds in Senegal. So, it was imperative to report that Senegalese local cattle populations were characterized by high levels of diversity and a moderate genetic structure. Based on these results, it has been recommended to apply the separate conservation of zebu’s populations (Gobra and Maure) as the highest priority to avoid loss of genetic diversity. N’Dama and Djakore populations should be conserved together to reduce costs and preserve adaptive traits that are valuable for improving cattle breeds’ productivity and conservation.

### SIGNIFICANCE STATEMENT

This study has discovered high levels of diversity and a moderate genetic structure in Senegalese cattle populations underlining a wide range of adaptive traits that can be beneficial for breed improvement and conservation strategies. This study has helped the researcher to uncover the critical areas of animal breeding and conservation genetics that many

researchers were not able to explore. Thus a new theory on cattle breeds’ diversity and genetic structure may have been reached.

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