

# The Mahibere-Silassie composite: a new cattle breed type in north-western Ethiopia

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## Abstract

Despite the significant contribution of cattle to the country, little attention has been given to identify, characterize and conserve the diversity of cattle breeds. This paper presents a unique cattle population found in a monastery in the northwest of Ethiopia referred to as Mahibere-Silassie composite breed. With the view to investigate to what extent the breed in question is different from the rest of the cattle population of the study area a survey work that included focus group discussions, administration of semi-structured and measurement of variations using quantitative and qualitative traits was conducted in 2003. Findings of the study showed that the breed is reported as closed and geographically isolated within the territories of the Mahibere-Silassie Monastery. Also some descriptive data on general husbandry practices, population size, and phenotypic features categorized as primary and secondary features were documented and which further confirmed that the Mahibere-Silassie herd is distinct. Series of different but interlinked statistical tests have confirmed that the breed is basically different from the rest of cattle population of the study area. Particularly, the generated Mahalanobis' distance matrix of the canonical discriminate analysis from twelve quantitative variables which was used to construct the phenograms or classification trees for the female and male populations, singled out the monastery cattle population far from the rest of the group. Apart from its distinct breed characteristics, the fact that the population has been maintained within the territories of the Monastery in isolation for over three centuries may have particular relevance in the study of evolutionary relationships of cattle breed types in this part of eastern Africa. Therefore, without doubt, the Mahibere-Silassie herd is a unique cattle breed type. However, the effective population size ( $N_e$ ) of the herd was calculated to be around 94; this low value can cause inbreeding at a rate of about 0.5% per generation. Thus, this herd is vulnerable to sudden or persisting threats that cause loss of genetic diversity and lead to gradual extinction unless urgent genetic conservation measures are taken.

Key words: Mahibere-Silassie cattle, characterization, phenotypic distance

## Introduction

The ideal procedure in genetic improvement of livestock involves identification of the breeds and their environment, characterization of their adaptive as well as productive capabilities, and determination of the extent to which variations in performance are due to additive and non-additive genetic effects. Based on these appropriate strategies can be outlined for combining the superior traits of different breeds, or possibly for exploiting outstanding abilities in the purebred (ILCA, 1992; Falconer and Mackay, 1996). The initial step for long-term genetic improvement of indigenous livestock is, therefore, identification of the breed types, estimation of their population size, and documentation of their common uses and description of the management system in which they are maintained (Hall, 1992). Traditional animal breeding efforts and techniques are important for any breed improvement work, but more information is needed regarding the breeding population that exists in the system. This background information should precede any major interventions. Indigenous genotypes may well be adequate and able to respond sufficiently to reasonable economic improvements in the system (Workneh et al., 2003). Over many generations they have evolved to perform various functions under local conditions. Unfortunately, inadequate attention has been given to evaluating these resources or to setting up realistic and optimum breeding goals for their improvement. As a result some of the animal genetic resources of Africa are endangered and, unless urgent concerted efforts are made to characterize and conserve, these may be lost even before they are described and documented. The classical description of breeds is based upon phenotype on the basis that an organism's phenotype is principally a manifestation of its genotype, and that it lends itself to direct measurement on the organism. As such, phenotypic characterization is therefore complementary to the powerful biotechnological techniques for measuring genetic diversity on the genome. Given its diversified ecology, its huge livestock size and cattle types which have evolved over time in the various production systems, and its geographic location on the route to major livestock migrations across Africa, Ethiopia can be considered a centre of diversity for animal genetic resources. It is also home to most important cattle breeds for eastern and southern Africa (Beyene and Bruke, 1992; Workneh et al., 2004). The indigenous breeds as explained by Epstein (1957, 1971) and Hanotte et al. (2002) originated from the migration of Hamitic Longhorn and Shorthorn from Egypt along the Nile Valley and the humped Zebu from India through the horn of Africa.

The present day Ethiopian cattle are classified into four main breed groups: the Humpless, Zebu, Sanga and Zebu-Sanga (intermediate) (Beyene and Bruke, 1992; Workneh et al., 2004). Besides, the Red Bororo or Fellata are also confirmed for their presence (Zewdu, 2004). Sometimes the Humpless cattle are divided into Shorthorn Humpless and

Longhorn Humpless (Alberro and Hailemariam 1982a, b; Beyene and Bruke, 1992). With similar classification, 17 Ethiopian cattle breeds are registered in Mason's (1988) dictionary of livestock breeds of the World. Rege et al. (2001) identified two more breeds, the Simada and Adwa. The Domestic Animal Genetic Resources Information System (DAGRIS) being developed by ILRI shows a total of 23 Ethiopian indigenous cattle breed types (DAGRIS, 2004). Generally other than such broad classifications, very little effort has been made to describe each of the indigenous cattle populations of the nation. Alberro and Hailemariam (1982a; b) attempted to identify and classify some of the cattle types by compiling available literature and gathering information from field reports of the Ministry of Agriculture (MOA) provincial offices, and in so doing they have contributed an eye-opener work for this field. Later, Sisay (1996) had also worked on characterization of some of the most known cattle types using protein polymorphism. Recent study made by Zewdu (2004) on characterization of indigenous cattle genetic resources in North-western Ethiopia identified a new cattle breed located in Metema district. The breed is owned by an Orthodox Church Monastery and is referred to as "Mahibere-Silassie composite" (Zewdu, 2004).

The objective of this paper is to confirm how the breed type in question is different from the rest of the indigenous cattle breeds found in the area.

## **Materials and methods**

### **The study area**

The study area, North Gondar and some part of South Gondar, is located in northwestern part of Ethiopia. It has 2.654 million cattle, 1.12 million sheep, 0.657 million goats, 0.312 million equines and 2.445 million poultry (DOA, 2003). The altitude ranges from 4620 meters in the Semein Mountain in the North to 550 meters in the western parts of the study area and rainfall varies from 880 mm to 1772 mm from a monomodal distribution with the maximum temperature of 44.5°C in the West and minimum temperature of -10°C in the highland. The area is also characterized by two seasons, the wet season, from June to September and the dry season from October to May. The farming system of the study area is largely characterized by crop-livestock production system, which in turn grossly divides into two: the crop-livestock production system in the lowland and crop-livestock production system in the highland. So, the term mixed crop-livestock farming is preferred to denote farming system that exists in the high and mid highland areas. Trans-humance, from the highlands to western lowlands, is practiced as one of the most important strategies to secure grazing resources for the highland livestock during lean seasons of the year.

### Sampling frame work and data collection procedures

The study covered the majority of North Gondar Zone and partly South Gondar. Initially rapid field survey was conducted with the specific objective of exploring available knowledge on the type, distribution, movement and utility of cattle genotypes in North Gondar and parts of South Gondar on the eastern flanks of Lake Tana. Based on the outcomes of this survey, six study sites were selected representing home areas of the six cattle types identified. These were;

Semein (1) = site representing cattle population found >3200 m.a.s.l Wegera

(2) = site representing cattle population found at 2200 -3200 m.a.s.l

Dembia (3) = site representing cattle population found at 1500 – 2200 m.a.s.l Fogera

(4) = site representing Fogera cattle breed found at 1700 – 1800 m.a.s.l Lowland (5)

= site representing cattle population found at 500 - 1500 m.a.s.l Monastery(6) = site

representing cattle population found at 500 – 700 m.a.s.l

The actual survey work consisted of linear body measurements on adult male and female animals, administration of semi-structured questionnaires on husbandry practices and farmer perceptions on cattle breed types and breeding preferences, and focus group discussions on the identity, origin and characteristics of the local cattle types of the area.

Table 1. Details of data sources and sites.

Sites	Sample size	Measured for quantitative traits			Individual interviews	Focus group discussions
		Male	Female	Total		
1	301	24	122	146	29	2
2	347	23	134	137	29	2
3	329	47	144	191	22	2
4	283	19	129	148	24	2
5	172	27	118	145	35	2
6	184	6	61	67	1	1
Total	1616	146	708	854	140	11

### Data management and statistical technique

The importance of each quantitative variable in explaining phenotypic differences between sample cattle populations of the six sites was examined using the Generalized Linear Model (GLM) procedures of SAS (1999). When the analysis showed significant differences between sites (all the 12 quantitative variables were found significant), the generated **site** least squares means of each of the variable were then compared using Tukey's test of multiple comparison (Klockars *et al.*, 1995). Because of known biological differences between males and females in the measured quantitative variables, and hence to avoid confounding effects of sex, data for the male and female populations were analysed separately. The following model was used for the female sample by taking site and birth class as fixed main effects:

$Y_{ijk} = \mu + S_i + B_j + e_{ij}$  where:  $Y_{ijk}$  = observed value of the trait of interest,  $\mu$  = overall mean  $S_i$  = fixed effect of site  $i$ , ( $i = 1 \dots 6$ );  $B_j$  = fixed effect of birth class  $j$ , ( $j = 0 \dots 6$ );  $e_{ij}$  = residual random error

The interaction of site and birth class was not found significant, and hence it was dropped from the model. Similarly, taking site and age class as fixed main effects, the following model was fit for males, after eliminating non-significant interaction effects:

$Y_{ij} = \mu + S_i + A_j + e_{ij}$  where:  $Y_{ijk}$  = observed value of the trait of interest,  $S_i$  = fixed effect of site  $i$ , ( $i = 1 \dots 6$ );  $A_j$  = fixed effect of age class  $j$ , ( $j = 1 \dots 3$ ); where age was categorized as 3-5, 5-7 and >7 years,  $e_{ij}$  = residual random error.

For the categorical variables, chi-square tests were employed to test for the independence between the two factors of interest (Petrie and Watson, 1999; SAS, 1999). In this case unlike the quantitative variables, both male and female populations of each sample site were treated as one population. Since the statistics produced by the chi square tests for most of the variables are highly significant ( $p < .0001$ ), other statistics derived from the Pearson chi square were used to measure the levels of association. Furthermore, multiple mean comparisons were also made for categorical variables using Bonferroni's correction (Petrie and Watson, 1999).

Furthermore, to evaluate differences between the Monastery populations with that of other breed groups on multivariate basis, taking into account quantitative traits, canonical discriminant analysis was conducted for males and females separately.

## Results

### Description of the breed

Results from the questionnaires and group discussions indicated that Mahibere-Silassie composite is a hitherto undocumented indigenous breed type that has been maintained within the territories of the Monastery in isolation for over three centuries. The Monastery rests on a mountainous landscape in the middle of a large lowland area with altitudes as low as 550 m.a.s.l. near the border with the Sudan. Inhabitants of the Monastery raise them with very little or no technical support from the extension services and that is limited to veterinary services. For quite a long time, no breeding animals were introduced into the herd, but culled and other animals have been disposed via local cattle markets. At present the herd is estimated to be as large as 3000 heads. Based on the information of age and sex structure of the population, effective population size ( $N_e$ ) of the herd was calculated to be around 94; this low value can cause inbreeding at a rate of about 0.5% per generation. Thus, this herd is vulnerable to sudden or persisting threats that cause loss of genetic diversity and lead to gradual extinction unless urgent genetic conservation measures are taken. Information gathered from key informants

both from within and outside the Monastery, confirmed that the herd was established at the initiation of the Monastery in the middle of the 17th century (about 1630), from religious donations of breeding cattle from the area as well as far off places. According to the key informants it is believed that at least three breed types from the vicinity were involved in the creation of this herd: the Dembia, the Barca (Rutana) and the Felata (Red Bororo). The resultant breeding population interbred since then without additional introduction of breeding stock. It can therefore be considered a composite breed type.

The major characteristic features of this cattle type are larger frame of body and more aggressive temperament than all breed types in the area, loose drooping horns and sometimes polledness, light coat colour ranging from white to brown and dairy type body conformation, including wide hind quarters, large udder and teats. This cattle type is different in many respects from the rest of other cattle populations of the vicinity. Their coat colour pattern is predominately plain. Most common coat colour types are white, brown, and red. Patchy and spotted coat colour patterns account for less than 10%. The hair is always shiny. The facial profile is always concave. The majorities have droopy rumps. Hump size is moderate and purely cervico-thoracic in its position.. Ear is big in size. Cows have the largest naval lengths (an average width of 10.08 cm) of all the breed types in the north-western Ethiopia. The majority have medium to large teat and udder size, but they are not used mainly for milk as income generation and traction appear to be more important functions of the herd. The surrounding communities also consider this herd distinctly different from other breed types in the area

There has never been systematic recording of pedigree or performance, but dedicated herdsman have been in charge of the day-to-day management of the herd. Cows are closely monitored for good milking ability, regular calving and cool temperament. The herd size is steadily declining due to shrinking land holdings of the Monastery under pressure from expanding cultivation in the lowlands. The herdsman from the Monastery reported that contagious diseases transmitted from trans-humant cattle herds that often trespass grazing territories of the Monastery have been increasingly affecting the herd. Breeding of this herd has been closed for a long time, and mating is normally random. Breeding bulls are kept separately as are breeding females and young stock, and the herdsman say there is no shortage of bulls. Because there is no pedigree recording, it is possible that closely related animals can be mated. Breeding animals are selected by way of selection for good phenotypic performance as well as culling of undesirable animals. Breeding males are selected based on body size (height and body length) and family performance mainly on milk yield, whereas breeding females are selected mainly based on good milk yield and mothering ability. In both cases large sized animals are preferred. Culling is also practiced occasionally against cows that are poor in milk yield and for undesirable temperament. Culled animals, often oxen and old cows, are sold

in a livestock market in Metema. Essentially this composite cattle type is maintained very much like an extensive ranching system (Jahnke, 1982), but without systematic recording of performance and genetic selection.

## Quantitative variation

### *Female populations:*

The analysis of variance showed that in all cases site, which represents cattle population types, and birth class, a proxy variable for age, were highly significant ( $p < .0001$ ) in the model for all the twelve quantitative variables. Table 2 shows the level of significance of main effects. The respective  $R^2$  value ranged from 34.7% in the case of horn length to 56.1% for mouth circumference. Subsequent pair-wise means comparisons also showed highly significant ( $P < 0.0001$ ) or significant ( $p < 0.01$ ) differences between the sites for all twelve measured quantitative traits (Table 17).

Table 2. Level of significance of main effects for each of the variables and their associated  $R^2$  values for the female sample population.

Variable	Site	Birth class	$R^2$
Body length	$p < .0001$	$p < .0001$	42.8
Cannon bone circumference	$p < .0001$	0.0028	56.0
Chest depth	$p < .0001$	$p < .0001$	45.2
Dewlap width	$p < .0001$	$p < .0001$	42.2
Ear length	$p < .0001$	Excluded	47.5
Heart girth	$p < .0001$	$p < .0001$	52.5
Horn length	$p < .0001$	$p < .0001$	34.7
Hump length	$p < .0001$	0.0019	34.9
Mouth circumference	$p < .0001$	$p < .0001$	56.1
Naval length	$p < .0001$	excluded	55.7
Pelvic width	$p < .0001$	$p < .0001$	37.9
Wither height	$p < .0001$	$p < .0001$	55.0

Considering only the four important linear measurements, namely body length, chest depth, pelvic width and height at wither, the sample cattle population in the monastery have the largest of the measurements and those of the Semien mountains have the smallest of the measurements of all sites (Table 3).

Pair wise comparison of least squares means of these variables between sites shows significant differences for many of the traits (Table 3). In many instances Semien stands alone, where as monastery are highly significantly different from other study sites.

Table 3. Least squares means and pair wise comparisons of body measurements for females by site (cm)

Traits	Semien	Wegera	Dembia	Fogera	lowland	Monastery	RMSE
Body length	111.49a	115.60b	117.35bc	119.77c	114.72b	127.33d	5.61
Wither height	102.39a	109.37b	108.57b	111.78c	109.69b	120.82d	4.66
Pelvic width	35.81a	37.60b	37.28b	37.77b	38.37b	41.07c	2.39
Chest depth	53.59a	56.13b	55.98b	56.81b	56.73b	60.77c	2.74
Heart girth	129.15a	139.88b	132.76a	143.59c	147.95d	146.93cd	8.06
Dewlap width	16.79a	18.06ab	18.77b	20.58c	21.84c	24.08d	3.19
3Cannon bone circumference	12.39a	13.73b	12.98c	13.91b	15.04d	14.86d	0.89
Mouth circumference	33.41a	36.80b	32.64a	34.95c	37.73d	33.80a	1.97
Hump length	18.17a	22.27b	17.83a	20.55c	-	17.70a	3.61
Horn length	21.08ab	20.96ac	15.6d	16.98d	21.24a	17.95bcd	6.13
Ear length	17.73a	20.29b	18.41a	20.68bc	22.52d	21.68cd	2.02
Naval width	1.77a	3.94b	7.09c	8.30c	5.68d	10.08e	2.51

3 forelimb

a.b.c.d.e.f. means with different superscripts within the same row are significantly ( $p < 0.01$ ) different.

-- no data collected for that particular variable

*Male populations:*

Similar to the female sample populations, the overall F test was highly significant ( $P < .0001$ ) for all dependent variables considered, indicating that the sample populations indeed differed between sites and age classes. Site was highly significant ( $p < .0001$ ) for all traits, but age class was significant only for some of the traits. This might be due to the narrow age range (4-7 years) of the sample populations. However, in most cases the  $R^2$  value of each of the dependent variable was slightly higher in the male than it was for the female population. Similar to those of the female population, population of cattle from Semien Mountains (site 1) is the shortest and narrowest, and the sample population from the monastery (site 6) is longest and widest.

Table 4. Least square means and pair wise comparisons of body measurements for males by site (cm)

Traits 2	Semien	Wegera	Dembia	Fogera	Lowland	Monastery	RMSE
body length	111.45e	119.15bd	119.23bc	124.39b	118.16cd	138.00a	6.80
wither height	102.43c	111.65b	110.77b	114.59b	113.62b	131.76a	5.39
pelvic width	34.11de	39.10ba	36.03ce	36.75bde	37.52bc	42.54a	3.30
chest depth	53.03d	59.13b	55.63c	57.47bc	58.19b	67.08a	3.41
heart girth	128.41c	146.90b	133.56c	148.21b	152.24b	170.48a	9.82
dewlap width	19.42a	22.69b	20.67ac	23.01cb	25.44b	25.50bc	3.87
3cannonbone circu	13.13e	15.61ac	13.77e	15.43bcd	16.11dba	17.11a	1.06
mouth circumference	34.18de	39.60ba	34.14e	37.60cb	40.28a	37.52acd	2.23
hump length	22.90a	35.71b	26.32a	32.18b	41.13c	34.70bcd	6.54
horn length	17.14a	19.84a	12.87b	13.10b	18.92a	17.30ab	5.16
ear length	17.50c	20.87b	17.75c	19.80b	23.06a	21.56ab	1.95
sheath width	8.86b	12.23a	13.70a	13.32a	13.60a	12.01ab	3.31

3 cannon bone circumference (forelimb)

a.b.c.d.e.f. means with different superscripts within the same row are significantly ( $p < 0.01$ ) different.

### Qualitative variation

The chi-square test was highly significant ( $P < .0001$ ) for all variables with an association ranging from the lowest of 0.33 for coat pattern to the highest of 0.73 for horn orientation using phi coefficients, from 0.31 for coat pattern to 0.59 for horn shape using contingency coefficients and from 0.17 for coat pattern to 0.71 for hump position using Cramer's V. Generally, in all three measures of associations the level of correlation for most factors was medium, with a few exceptional cases of high levels. Pair wise comparisons between sites on categorical data was made after the general chi square test of independence was performed and found significant. Table 5 presents the pair-wise comparisons made for each of the categorical variables across sites based on p-value derived from Bonferroni's correction (Petrie and Watson, 1999).

Table 5. Pair wise comparisons using the Bonferroni's correction\*

Trait/variable	Semien	Wegera	Dembia	Fogera	Lowland	Monastery
Coat color pattern	a	b	b	c	dc	e
Body score	a	b	c	d	e	f
Hair type	a	a	b	b	b	b
Facial profile	a	b	a	c	d	e
Rump slope	a	a	a	b	b	c
Hump position	a	b	b	c	b	d
Tail length	a	b	c	c	c	d
Horn shape	a	b	c	d	e	f
Horn orientation	a	b	c	d	e	f
Udder size	a	b	c	d	e	f
Teat size	a	b	c	d	e	f
Coat color	a	b	c	d	e	f
Birth class	a	b	a	ab	c	d

\* sites with different letters in the same row are significantly different

The result based on pair-wise Mahalanobis' distances for females (Table 6) and males (Table 7) populations showed that the Monastery herd is distinctly different from all other sample populations.

Table 6. Mahalanobis distance between sites for the female sample populations

Sites	Semein	Wegera	Dembia	Fogera	lowland	Monastery
Semein	0	5.57	5.67	11.27	15.54	28.29
Wegera	5.57	0	6.80	5.38	4.57	18.88
Dembia	5.67	6.80	0	3.28	14.95	11.93
Fogera	11.27	5.38	3.28	0	7.64	7.38
Lowland	15.54	4.58	14.95	7.64	0	18.80
Monastery	28.30	18.88	11.93	7.38	18.80	0

Table 7. Mahalanobis distances between sites for the male sample populations

Sites	Semein	Wegera	Dembia	Fogera	Lowland	Monastery
Semein	0	12.97	5.90	13.57	24.73	48.83
Wegera	12.98	0	13.39	9.02	5.34	32.58
Dembia	5.90	13.39	0	5.92	21.47	32.58
Fogera	13.57	9.02	5.92	0	9.80	20.73
lowland	24.73	5.34	21.47	9.80	0	30.94
Momastery	48.83	32.58	32.58	20.73	30.94	0

Finally the phenograms or classification trees were constructed separately for the female and male populations, using only the twelve quantitative variables. The Mahalanobis' distance matrix was used to calculate arithmetic averages using the Unweighted Pair-Group Method (UPGMA) (Sneath and Sokal, 1973). The tree topology as well as the branch length differs between the sexes. However, in both cases the Monastery cattle type, cluster 1, came out distinctly singled out far from the rest of the group (Figures 1 and 2). Therefore, without doubt, the Mahibere-Silasie herd is a unique cattle breed type. Apart from its distinct breed characteristics, the fact that the population has been maintained within the territories of the Monastery in isolation for over three centuries may have particular relevance in the study of evolutionary relationships of cattle breed types in this part of eastern Africa.

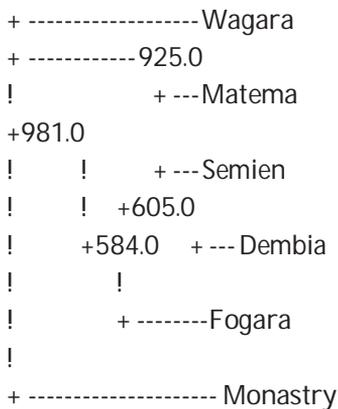


Figure 1. Consensus tree: male population:

the numbers at the forks indicate the number of times the group consisting of the species which are to the right of that fork occurred among the trees, out of 1000.00 trees

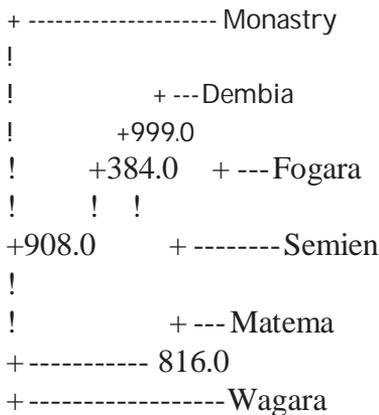


Figure 2. Consensus tree: female population\*

\*the numbers at the forks indicate the number of times the group consisting of the species which are to the right of that fork occurred among the trees, out of 1000.00 trees

### Conclusions and recommendations

The outcomes of key informant interviews, multivariate analysis of quantitative as well as categorical variables and the phenograms constructed from the Maha-lanobis' distance matrix strongly supported the hypothesis that the Monastery cattle population is distinctly different from other cattle breed types in the area and has some unique phenotypic features. It can therefore be considered as a breed type in its own right. Because of its effective isolation from breeding with neighbouring cattle populations for over three centuries, this cattle population may have relevance in the study of evolution of cattle breed types in the eastern Africa in general.

The breed is referred to as Mahibere-Silassie Composite since it is constituted from different breeds that existed in the surrounding three centuries ago. Preliminary data on its performance showed that the breed is potentially rich in milk yield, reproductive performance and known to have good adaptation to the harsh environmental conditions of the area. Despite this, support from livestock extension services has been minimal. The Monastery particularly needs animal health service, and possibly advice on improved breeding, feeding and marketing of products. Furthermore, as the breed is closed and isolated for more than 300 years, it has a paramount importance for evolutionary studies. However, the effective population size of the breed in question is 94, which makes the population vulnerable to rapid build up of inbreeding at a rate of 0.5% per annum. Thus, unless urgent conservation measures are taken, the breed is feared to be in danger of genetic erosion and eventually gradual extinction. Unfavourable environmental effects

and cattle diseases could speed up the loss of genetic diversity. Mention should be made here that as the findings reported in this study are only preliminary, and detailed studies on selected key traits is urgently needed.

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