On-farm Phenotypic Characterization of Cattle Genetic Resources in South and North Wollo Zones of Amhara Region, North Eastern Ethiopia

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Abstract

This study was conducted to identify and describe the cattle genetic resources in South and North Wollo zones of Amhara Region, North Eastern Ethiopia based on their descriptive morphological characteristics. A total of seven sampling sites were selected based on the information obtained about the distributions of cattle types in the area. Quantitative and qualitative characters were taken from 1,321 mature animals and subjected to multivariate analysis of variance. The results showed significant ($p<0.0001$) differences in quantitative traits between sites for both female and male populations. Chi-square tests also showed very strong ($p<0.0001$) associations between qualitative variables and sites. Horn length and navel flap were the best discriminating variables from quantitative and qualitative variables, respectively. The canonical discriminant analysis applied to calculate the Mahalanobis' distances between sites using quantitative variables showed significant ($p<0.0001$) distances between the sites. The maximum and minimum distances were obtained between Were-Ilu and Afar sites (46.96) and Gimba and Kutaber sites (0.49) for female populations. The validity of discriminant analysis was assessed by reclassification statistics putting equal a priori probability levels for all sample populations and the results showed the overall classification rate (hit rate) was 55.2% and 60.1% for female and male populations, respectively. Sample populations from Kobo and Afar were highly divergent from other cattle populations in the other sites. Based on results of cluster analysis, it is concluded that, morphologically, at least three distinct cattle types are found in the area, namely the Wollo Highland Zebu (comprising of cattle from Gimba, Were-Ilu and Kutaber sites), the Raya Sanga (Raya/Kobo site) and the Afar Sanga (Afar site). The fourth cluster is considered as intermediate cattle that are found in the adjacent areas of Sanga and highland zebu cattle types. The Wollo highland zebu cattle type comprises compact animals with short legs, ears and horns with coat color being dominantly black. On the other hand, the Raya and Afar Sanga cattle types found in lower altitude areas have longer legs, ears and horns reaching to maximum measurements for the Afar cattle.

Keywords: indigenous breeds, phenotypic characterization, Wollo Highland Zebu, Raya Sanga, Afar Sanga, cattle, Ethiopia.

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Introduction

Given its diversified topographic and climatic conditions, and its strategic location along the known routes of cattle introduction from Asia into Africa, and from northern Africa to southern and western Africa, Ethiopia has become a major centre of cattle genetic diversity in Africa (Epstein, 1971; Rege, 1999). To date, at least 27 recognized indigenous cattle breeds are known to exist in Ethiopia, dispersed over a diverse range of ecological zones (DAGRIS, 2007). The current cattle population of Ethiopia is estimated at 40 million of which the indigenous breeds constitute over 99% (CSA, 2003).

Despite the long evolutionary history and vital livelihood services that cattle provide to their keepers in the country, very little effort has been made to comprehensively describe the indigenous cattle genetic diversity in Ethiopia. The first comprehensive attempt was made by Alberro and Haile-Mariam (1982a; b), who tried to identify and classify the common Ethiopian cattle breed types based on published literature. Only six of the breed types were fairly described in terms of their physical appearance; only seven of the breeds have at least one estimate of their population and even these were either outdated or based on crude assessments (Workneh Ayalew *et al.,* 2004).

Except the Sheko breed, none of the major cattle breeds of Ethiopia are said to be in serious danger of disappearance (DAGRIS, 2007). However, some of the indigenous cattle are threatened with genetic dilution from a number of factors, including market related cattle movements, restocking following recurrent droughts, cattle keepers' choices for more adapted and preferred breeding animals and neglect. For instance, the Ethiopian Borana cattle are gradually disappearing from their natural habitat (Workneh Ayalew, 1992; Nigatu Alemayehu *et al*., 2003). Rapid survey reports made by Workneh Ayalew *et al*. (2002) also indicated that the Fogera cattle are undergoing serious genetic erosion. The situation of other cattle types of Ethiopia is not known at this time due to lack of information, but it is believed that genetic erosion may be in motion in other breeds too.

There is an increasing awareness of the need for genetic conservation of indigenous livestock genetic resources all over the world (Cunningham, 1992). In a workshop held in 1992 at the International Livestock Centre for Africa (ILCA) in Addis Ababa on characterization, conservation and utilization of African animal genetic resources, it was recommended that macro-level exploratory surveys for identification of indigenous breed types be carried out in countries like Ethiopia where there is a clear lack of information on indigenous livestock genetic resources. Breed identification, estimation of their population size, documentation of their common uses and description of the management systems in which they are maintained are needed before improvement and conservation measures can be planned (Rege and Lippner, 1992).

This paper reports the results of a cattle breed survey initiated to characterize and document cattle genetic resources in the Amhara Region of Ethiopia, and is part of an earlier work (Dereje Tadesse, 2005). The specific objective was to identify and phenotypically characterize indigenous cattle genetic resources in the North and South Wollo Administrative Zones of the Amhara Region, northeastern Ethiopia.

Materials and methods

Study Area

The survey was carried out in the North and South Wollo Administrative Zones of Amhara Regional State from October 2003 to January 2004. The area is situated approximately between 10º 10' N and 12º 25' N latitude and 38º 28' E and 40º 5' E longitude. The two zones have a total surface area of about 30,908 square kilometers, comprising the highland masses in the west and the lowlands in the east (SIDA, 1996).

The topography of the area is characterized by flat to undulating and hilly landscapes, with contrasting tropical, sub-tropical and temperate climates. The minimum and maximum average annual temperatures of the zones are about 15 and 20 ºC, respectively, and average annual rainfall is between 300 and 1200 mm, with 70% of the rains falling during the main rainy season between July and September (SIDA, 1996).

Livestock production in these areas is characterized by minimal management input in terms of feeding, breeding and disease control, and is mainly traditional and subsistence-oriented. Cattle are principally kept to provide draught power, cash and milk for subsistence. Oxen are the main source of traction in the area but in major barely growing highlands of Wollo, equines are also used for traction. Poor nutrition and diseases are major challenges to livestock production in the area. Natural pasture is the source of feed throughout the year. Grazing lands especially in South Wollo Zone are limited and even certain areas with potential for grazing cannot be utilized due to seasonal water logging. Mating is natural and uncontrolled.

Sampling and data collection

The survey purposively included the main indigenous cattle types identified locally by the farmers, with the view to ascertain whether this local classification is in line with the phenotypic classification results. For this reason a rapid appraisal was conducted before the main survey in order to identify and sketch the distribution of main cattle types in the area and to establish sampling framework. Discussions were held with zonal and Wereda agricultural experts and farmers about the distribution of cattle genotypes. Out of 15 Weredas explored, 7 Weredas representing all the three agro-climatic zones were selected based on locally identified cattle types and from these 7 Weredas, again a total of 18 peasant associations used as sampling units were selected based on their accessibility and proximity to each other. The survey included only one visit to the sampling units at which whole herds of cattle were sampled until enough qualitative and quantitative measurements were taken from a minimum of 100 mature females along with about 20 males. However, for site 7 (Afar), only 23 female animals were sampled due to aggressive behavior of the cattle and unwillingness of cattle owners fearing that their cows will develop vice against milking.

Linear measurements were taken using plastic tape and age of animals was estimated from dentition, as demonstrated by Workneh Ayalew (1992) and later applied by Zewdu Wuletaw (2004), to compare with the age information given by the farmers. Morphological variables recorded in this study were adopted from the standard breed descriptor lists developed by the Food and Agricultural Organization of the United Nations (FAO, 1986). Each animal was enumerated by sex, dentition and the location. A total of 21 characters (15 qualitative and 6 quantitative) were recorded from all adult animals.

Linear measurements were taken from 1,315 animals as well as notes on their color and body conformation. Only mature animals were sampled to minimize the effect of age on the classification. Analysis was done separately for female (680) and male (129) sample populations to see whether the results are consistent for the sex categories.

Data analysis

The General Linear Model (GLM) procedures of the SAS (Statistical Analysis Systems) software (SAS, 1999) were employed to analyze the quantitative data and to detect statistically significant quantitative variation in body size between the sample cattle populations. The analysis was done separately for the female and male populations as the breed characterization needs to be sex specific. Taking site and dentition class as main fixed effects, the following model was used to analyze the data. Since none of the interaction components was significant, they were dropped from the final model. The model used was $Y_{ijk} = \mu + S_i + B_j + e_{ijk}$, where; Y_{ijk} is the observed value of trait of interest, μ is the overall mean, S_i is the effect of i^{th} site (i= 1,2, 3...7), B_j is the effect of j^{th} dentition class (j=1,2,3,....14), and e_{ijk} is the residual random error. The Frequency procedure of SAS (1999) was also employed to evaluate categorical variables for both sexes.

The quantitative variables taken from female and male animals were separately subjected to discriminant analysis procedures (SAS, 1999) to ascertain the existence of population level phenotypic differences among the sample cattle populations. The analysis was done taking the individual animal as the unit of classification. Discriminant analysis was also used to build a predictive model of group membership based on observed discriminant scores of each case that have the general form of $Y = A_i + \beta_i x_1 + \beta_i x_2 + \ldots + \beta_i x_p$, where: Y is the classification score (i.e. linear combination of a set of variables), A is the constant for i^{th} group, β is the weights of corresponding variable for i^{th} group, x is the discriminator variable score, and p is the number of discriminator variables.

Pair-wise distance between sample populations and spatial distribution of cattle population on plot of the first two canonical variates (CAN1 and CAN2) were obtained by running canonical discriminant analysis. The stepwise discriminant analysis procedure (SAS, 1999) was run to rank the variables by their discriminating power.

Results and Discussions

Quantitative variation for the female population

Least squares means of all the six variables were significantly different (P<0.0001) between sites (Table 1). Between dentition categories, significant differences (P<0.05) were also detected for all the traits except for two variables - height at withers and ear length.

The respective R^2 values and coefficients of variation (CV) ranged from 13.5 for heart girth to 78.6 for horn length and from 4.6 for height at withers to 23.9 for horn length, respectively. The coefficient of variation for horn length was the highest followed by ear length and pelvic width, indicating the existence of high variations in the populations for these traits. The highly significant (P<0.0001) differences between the sites indicated that these variables are important in explaining variations between sample populations.

Table 1. Level of significance of each quantitative variable for the female sample populations (n = 680)

Variables	P-value for site	P-value for dentition	R2	C.V.
Body length	< 0.0001	0.0095	13.8	5.8
Height at withers	< 0.0001	0.8095	16.4	4.6
Heart girth	< 0.0001	0.0076	13.5	4.9
Pelvic width	< 0.0001	0.0018	17.4	7.2
Ear length	< 0.0001	0.8831	10.9	11.0
Horn length	< 0.0001	0.0361	78.6	23.9

Pair-wise comparisons of least squares means of variables between sites also showed significant differences (P<0.05). In all the six linear measurements, the female population sampled from site 7 (Afar type) had significantly largest value when compared to other populations (Table 2), and those from site 6 (Raya type) had the second larger value in all variables though no significant differences were observed for two of the measurements (heart girth and ear length). This indicates that the two sample populations are more distinct or divergent than the other populations (Table 2).

Body length, height at withers, heart girth and pelvic width measurements of female sample populations from the three sites (Kutaber, Tehuledere and Habru) were not significantly different from each other and had generally smaller measurements when compared to the other sites. Sample populations of sites 1 (Gimba) and 2 (Were-Ilu) had intermediate values for these variables. The female population of site 3 (Kutaber) had body length, height at withers and heart girth measurements with intermediate values between Gimba and Were-Ilu sites and Tehuledere and Habru sites. Measurements of ear length and horn length for the Kutaber population were found to be similar with those of sample populations from Gimba and Were-Ilu sites whereas in heart girth it was closer to Tehuledere and Habru sites.

Table 2. Least squares means of quantitative variables by study site for the female sample populations (n = 680)

Variables* (n)	Gimba (100)	Were-Ilu (105)	Kutaber (114)	Tehuledere (115)	Habru (116)	Raya (107)	Afar (23)
Body length	115.26bc	115.92c	113.59ab	112.91a	112.74a	117.76d	124.64e
Height at withers	108.98b	106.23a	107.24a	106.52a	106.55a	111.02c	115.53d
Heart girth	139.95b	140.42b	135.47a	136.49a	135.52a	136.86a	146.44c
Pelvic width	33.29b	33.23ab	32.59a	32.14a	32.99a	34.61c	38.09d
Ear length	17.78a	17.74a	17.90a	19.30b	18.88b	18.94b	20.31c
Horn length	17.41a	16.55a	16.40a	24.12b	31.13c	47.66d	60.83e

* Least Squares means with different superscripts in a row are statistically significant at P<0.05.

Quantitative variation for the male population

As with the female population, the quantitative data from the male sample populations was analysed by considering site and dentition as fixed effects. However, the number of sites in this model was six instead of seven considered for female populations, because no male animals were sampled from site 7 (Afar). The analysis of variance showed significant differences (P<0.05) between sites for all variables (Table 3).

A significant (at least P<0.05) difference was also noted between dentition categories for half of the variables. Height at withers, ear length and horn length did not vary significantly (P>0.05) between dentition categories, indicating that these variables are less affected by age of animals. This pattern is similar to the observation by Hall (1991) who pointed out that height at withers, which is related to inherent size of animals, is little affected by environmental factors when compared to other measurements such as heart girth and body length.

Horn length and height at withers had respectively the maximum and minimum R^2 value and CV, respectively. Horn length had the highest variability between sites (Table 3). Similar to the female population, horn length had the highest coefficient of variation followed by pelvic width and ear length. Generally the coefficients of variation of all variables on male animals were higher than those of females partly due to small sample sizes.

Table 3. Level of significance of main effects for the quantitative variables and their associated R^2 and CV for male sample populations (n = 129)

Variables	P-value for site	P-value for dentition	R2 (%)	C.V.(%)
Body length	= 0.0005	= 0.0033	20.25	6.52
Height at withers	= 0.0248	= 0.1355	11.29	4.61
Heart girth	< 0.0001	= 0.0019	29.83	7.17
Pelvic width	< 0.0001	= 0.0088	22.94	10.67
Ear length	< 0.0001	= 0.7129	25.87	9.66
Horn length	< 0.0001	= 0.1324	64.07	33.42

Pair-wise comparisons of the least squares means of body linear measurements of male populations between sites (Table 4) revealed that those from Were-Ilu (site 2) have the highest measurement values for three variables namely body length, heart girth and pelvic width, indicating that they have the largest body frame. But they have shorter ear and horn length, similar to those from sites 1 (Gimba) and site 3 (Kutaber). Similarly, males from site 6 (Raya/Kobo) have the longest horn and ear measurements. Males from Tehuledere and Habru sites tend to maintain intermediate values for these variables (Table 4). This may be explained by their adjacent location and likely continual interbreeding (admixture) with cattle populations from lowland (Afar, Raya) and highland (Were-Ilu, Gimba) cattle. This hypothesis is also strengthened by the observation that both highland and lowland type cattle are found in these mid-altitude areas.

Table 4. Least squares means of quantitative variables and pair-wise comparisons by study sites for male sample populations (n =129)

Variables* (n)	Gimba (23)	Were-Ilu (21)	Kutaber (22)	Tehuledere (20)	Habru (20)	Raya (23)
Body length	121.62a	129.70b	120.51 a	121.03a	119.38a	120.57a
Height at withers	116.12b	115.89b	112.28a	113.33ab	112.04a	115.44b
Heart girth	145.78b	156.45c	142.89ab	147.27b	139.46a	137.34a
Pelvic width	33.00a	37.51b	33.51a	33.54a	32.22a	32.34a
Ear length	16.69a	17.64ab	18.09bc	18.89cd	19.85d	19.02cd
Horn length	16.13a	18.95a	20.93a	30.29b	36.34c	49.31d

* Means with different superscripts in a row are statistically significant at P <0.05

In general, within site adult males have larger measurements than females for body length, height at withers and heart girth, but shorter horn and ear lengths, which is generally expected for the species. This is consistent with what has been reported before for growth related traits in cattle (Saeed *et al*., 1987; Mwandotto, 1985). However, this difference was more conspicuous at Were-Ilu site (e.g. 156.4 vs. 140.4cm for heart girth) due to the better management practice of farmers for males as they prepare them for a lucrative beef animal market in Addis Ababa.

Qualitative variation

The chi-square test results showed highly significant differences (*P*<0.0001) between sample populations in all categorical variables (Table 5). Generally, most of the variables had medium to high association values with the study sites. Navel flap size and facial profile had respectively the maximum and minimum phi and contingency coefficient values. Among the lowland cattle owners, size of navel flap is considered as good selection criterion for breeding females. Naval flap had the highest association value or discriminating power in the present study. The importance of this trait as selection criteria of breeding females was also documented by Zewdu Wuletaw (2004) from the adjacent North and South Gonder Zones of the Amhara Region.

Table 5. Chi-square tests and level of association between sites and categorical variables for both female and male sample populations (n = 809)

Variables	P-value	Phi-coefficients	Contingency coefficients	Cramer's V
Coat pattern	< 0.0001	0.33	0.31	0.23
Body score	< 0.0001	0.28	0.26	0.16
Hump size	< 0.0001	0.29	0.29	0.17
Hair type	< 0.0001	0.66	0.55	0.66
Dewlap size	< 0.0001	0.74	0.59	0.52
Horn shape	< 0.0001	0.68	0.56	0.30
Face profile	< 0.0001	0.26	0.25	0.19
Size of navel flap	< 0.0001	0.84	0.64	0.48
Size of sheath	< 0.0001	0.32	0.30	0.18

Discriminant analysis

Putting equal a priori probability levels for all sample populations, the known sample cases were subjected to reclassification using discriminant analysis separately for female and male sample populations to determine the matching hit rate. The overall classification rates (hit rate) of female and male sample populations were 55.2 and 60.1 per cent, respectively (Tables 6 and 7).

The overall hit rate was not very high as the hit rates observed for some sites or sample populations were small. This is due to phenotypic similarities observed between some sites (for example the first three sites) in their cattle populations. For female populations, the highest hit rate of 73.9 per cent was obtained for Afar site, followed by 69.2 per cent for Raya site (Table 6), indicating that the female cattle of these sites are relatively more homogenous and distinct from such populations of other sites, suggesting that cattle keepers may be exerting directional selection pressure on the female population, for instance for traits perceived to be related to dairy production. In case of male populations, where the Afar sample population was missing, the highest hit rate was 91 per cent for site 6 followed by the Were-Ilu site with 66.7 per cent (Table 7). Unlike female sample populations, the male sample population from Were Ilu site had a relatively high hit rate, apparently due to the special selective management practices of the farmers in their desire to participate in the lucrative Addis Ababa beef market.

Table 6. Per cent classified into each site for female sample populations using discriminant analysis (n=680)

From site	Gimba	Were-Ilu	Kutaber	Tehuledere	Habru	Raya	Afar
Gimba	41.0	23.0	20.0	14.0	2.0	0.0	0.0
Were-Ilu	21.9	52.4	10.5	15.2	0.0	0.0	0.0
Kutaber	18.4	23.7	45.6	12.3	0.0	0.0	0.0
Tehuledere	6.9	13.0	7.8	45.2	26.9	0.0	0.0
Habru	4.3	0.9	0.9	24.1	59.5	9.5	0.9
Raya	0.0	0.0	0.9	0.0	14.0	69.2	15.9
Afar	0.0	0.0	0.0	0.0	13.0	13.0	73.9

Table 7. Per cent classified into each site for male populations using discriminant analysis (n = 129)

From site	Gimba	Were-Ilu	Kutaber	Tehuledere	Habru	Raya
Gimba	56.5	30.4	8.7	4.4	0.0	0.0
Were-Ilu	14.3	66.7	19.1	0.0	0.0	0.0
Kutaber	27.3	13.6	40.9	9.1	9.1	0.0
Tehuledere	5.0	5.0	10.0	50.0	15.0	15.0
Habru	0.0	0.0	10.0	5.0	55.0	30.0
Raya	0.0	0.0	0.0	0.0	8.7	91.0

Stepwise discriminant analysis

The stepwise discriminant analysis procedure revealed that in both sexes all the variables had good discriminating power between sites or sample populations. This was confirmed by a high significant value ($P<0.0001$) associated for each variable against Wilk's Lambda. For both female and male sample populations, horn length was found to have the highest discriminating power. This can be explained by the sexual dimorphism in this trait and the strong variations between breed populations.

In all variables, the standard deviations for female populations were lesser than those of the male populations, partly due to the small sample size of males. The difference in standard deviation particularly for heart girth measurement was very high: 7.3 for females and 11.6 for males. The discriminating importance of horn length was also confirmed by the large pooled-within class standardized class mean value obtained from stepwise discriminant analysis of female and male sample populations.

Canonical discriminant analysis

All squared Mahalanobis' distances obtained between sites or sample populations for females were significant ($P<0.0001$), indicating the existence of measurable differences between female sample populations or sites (Table 8). The smallest (0.49) and largest (46.9) distances were observed between Gimba and Kutaber, and Were-Ilu and Afar, respectively.

All multivariate tests (i.e. Wilk's Lambda, Pillia's Trace, Hotelling-Lawley Trace and Ray's Greatest Root) obtained from canonical discriminant analysis showed significant differences ($P<0.0001$) between sites or sample populations. This result is consistent with that of the univariate analysis that tests the hypothesis that class means are equal. In this test, values of all quantitative variables considered (i.e. class means) were highly significantly different ($P<0.0001$) between sites or sample populations.

Table 8. Squared Mahalanobis' distances between sites or sample populations for female sample populations

Sites	Gimba	Were-Ilu	Kutaber	Tehuledere	Habru	Raya	Afar
Gimba	***						
Were-Ilu	0.5106	***					
Kutaber	0.4991	0.9363	***				
Tehuledere	2.2939	2.8604	1.8441	***			
Habru	5.7897	6.7963	5.4181	1.3518	***		
Raya	22.5274	25.0677	22.9129	13.8558	6.9531	***	
Afar	43.9221	46.9647	46.2479	32.6251	22.4665	5.5646	***

The procedure of canonical discriminant analysis extracted six canonical variates of which the first two canonical variates (CAN1 and CAN2) accounted for about 97 per cent of the total variation. Therefore the rest four canonical variates that accounted for about 3 per cent of the variance were dropped as these were less important in separating sample populations.

The plot of the first two canonical variates (CAN1 and CAN2) showed that CAN1 best separated sample populations of the Raya and Afar sites, which have mainly Sanga characteristics, from those of the first three sites (Gimba, Were-Ilu and Kutaber), which have more of zebu type characters. Sample population from Tehuledere and Habru were positioned in between these two groups. The second canonical variate further separated sample populations of Were-Ilu and Afar from those of Habru, with the other sample populations positioned more or less in between (plot not shown).

In case of the male sample populations, the squared Mahalanobis' distances between sites or sample populations were slightly higher than it was for female populations (Table 9). The nearest distance (2.19) was observed between populations of Tehuledere and Habru and the largest distance between populations of Were-Ilu and Raya with value of 25.98 standard units (Table 9). The distance observed between sample populations is due to distinct phenotypic differences observed between them in quantitative traits. Both univariate and multivariate tests generated from canonical discriminant analysis once again confirmed the existence of highly significant differences ($P<0.0001$) between male sample populations sampled from different sites.

Table 9. Squared Mahalanobis' distance between sites or sample populations for male sample populations

Sites	Gimba	Were-Ilu	Kutaber	Tehuledere	Habru	Raya
Gimba	***					
Were-Ilu	2.87269	***				
Kutaber	2.71533	3.19062	***			
Tehuledere	7.15578	7.23198	2.21367	***		
Habru	15.20410	15.70844	6.47770	2.19370	***	
Raya	23.33843	25.97509	14.45410	7.54204	2.94131	***

A total of five canonical variates were extracted from canonical discriminant analysis using male sample populations. The first two canonical variates (CAN1 and CAN2) altogether explained about 94.3 per cent of the total variation, with the remaining three variates accounting for only about 5 per cent of the total variation. The plot of the first two canonical variates showed to some extent similar pattern with that of female populations. As with the female populations, the first canonical variate (CAN1) separated sample population of the first three sites (Gimba, Were-Ilu and Kutaber) from that of Habru and Raya, with Tehuledere site positioned in between. The second canonical variate (CAN2) further differentiated sample populations of Gimba and Raya from those of Were-Ilu and Habru (plot not shown).

Cluster analysis

Results of cluster analysis using Unweighted Pair-Group Method (UPGM) (Sneath and Sokal, 1973) revealed the existence of four different clusters for female as well as male populations, but the length of the branch in the dendogram formed was different for the two sexes. In case of female populations (Figure 1), the first cluster consisted of sample population of three sites (Gimba, Were-Ilu and Kutaber) whereas in males (Figure 2), it consisted of two sites (Gimba and Kutaber), perhaps due to the preferential management of males in Were-Ilu area. The second and third clusters consisted of sample populations of two sites (Tehuledere and Habru), and one site (Raya/Kobo), respectively, for both female and male sample populations. The fourth cluster consisted of the Afar sample in case of females and Were-Ilu sample in case of males.

In the male sample population, where the Afar sample was missing, the Were-Ilu site came out separately forming one cluster but it was clustered with Gimba and Kutaber sites in the female classification tree. This is due to the fact that males of this site appear to be selected for larger body size (body length, heart girth and pelvic width) than males of other sites. It was also noted that the standard deviation of heart girth (7.3) for females of this site was by far less than that of males (11.6). The reason for this divergence of the male population at Were-Ilu is that farmers in this area have got special treatment for males and therefore they tend to have bigger body size and better body condition when compared to other areas.

According to Nei *et al*. (1983), error in topology and branch length is expected from the sample populations due to differences in branching pattern and deviations of branch length. For this case, the difference between classification trees constructed for female and male populations could be attributed to differences in sample size, and other sex-linked characters such as heart girth and pelvic width.

Generally it is believed that phenogram tends to reflect the evolutionary process of population development though it may not represent the true genetic relationships among the populations. It may therefore be difficult to verify the relative merit of classification trees. However; classification tree constructed from females seems to represent the true difference between sample populations because on one hand the formation of clusters go with the geographical proximity of the populations and on the other hand the sample size of female population is larger than males making it more likely to reflect real differences.

Though no classification method is yet available for testing significant differences between clusters, the clusters formed in this study can be taken as true and natural differences between sample populations because in most cases the results are in line with the outcome of group discussions conducted in the area. The other is that the quantitative variables used in this study have been proven to be cattle breed descriptors (FAO, 1986) that could make the results even more realistic and acceptable.

Finally, combining the results of both female and male sample populations with the outcome of group discussions, the following three clusters can be considered as the most meaningful clusters to biologically explain and tentatively classify cattle genetic resources of the area into three breed types but the fourth cluster is considered as intermediate type and hence not taken as breed type.

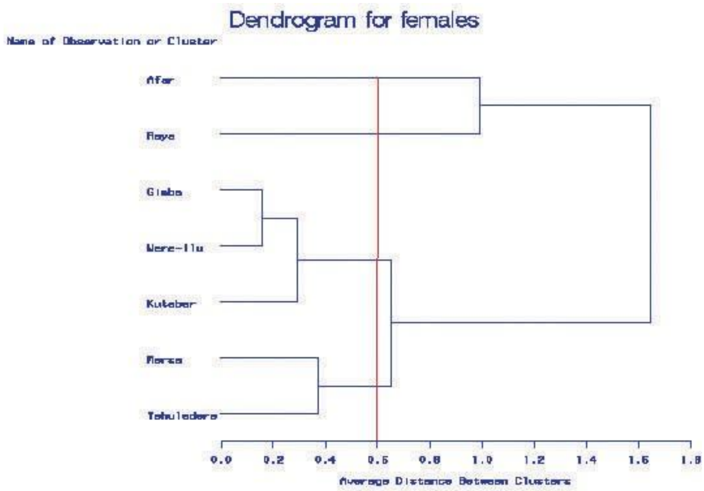

Figure 1. Dendrogram for female sample population by sites

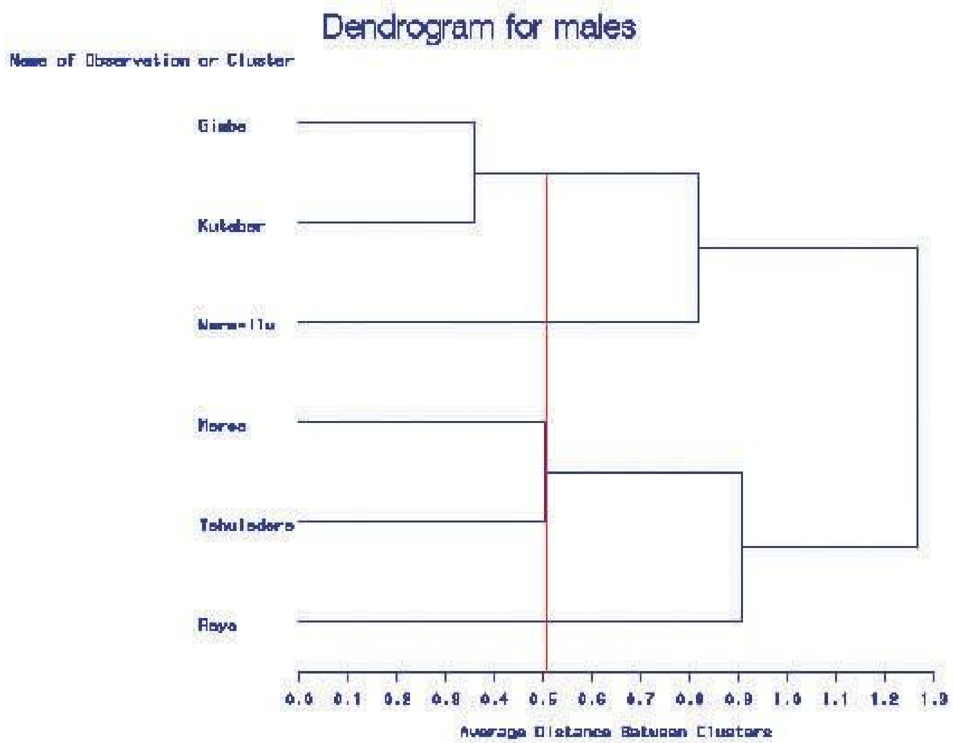

Figure 2. Dendrogram for male sample population by sites

Cluster 1: Wollo Highland Zebu

This cluster consists of the cattle populations from Gimba, Were-Ilu and Kutaber sites. This cluster appears to reflect more zebu-like characteristics. This cattle type is not known before in the literature. This cattle type is found in the highlands of Wollo, well adapted to cold climatic conditions. The main production functions of these cattle are traction, reproduction, milk and meat. Based on the information of cattle population size of each Wereda and the percentage distribution of the main agro-ecologies of the two zones, the population size of this breed type is estimated to be about 450,000.

They are short and compact animals with short legs and predominantly black coat color. They are characterized by having short ears (17.7± 0.14cm) and horns (18.0± 0.49cm). Mature females measure 116.8 (± 0.47cm) for body length, 107.5 (± 0.35cm) for height at withers and 33.8 (± 0.17) cm for pelvic width, which are smaller than those of the Raya and Afar Sanga breed types. Their heart girth measurement (141.5± 0.48 cm) is smaller than that of Afar Sanga type. Owner-recalled estimates of daily milk yield, calving intervals and lactation length of this breed type is about 2.3 liters, 16 months and 8.6 months, respectively (Figure 3).

Cluster 2: Raya Sanga

This cluster consists of the Raya cattle of site 6. They stood alone separately from others in both female and male classification trees. They are known by the name Raya cattle and already known in literature but not well described in terms of population size and reproductive performances in the study area. They are found in North Wello Zone particularly in Kobo Wereda with the Raya people. The main functions of this cattle breed type are traction, milk, meat and reproduction. The population size of this cattle type in this area is estimated to be around 120,000.

They have big body frame and long horns (48.7± 0.67 cm), which are thick at the base with an upward and slightly forward orientation to 50% of the length and then turning inward, and continue to grow upward. In some animals, the tip of the horn turns backwards. Predominantly, they have light red coat color. Their ear is longer (18.9± 0.19 cm) than that of the Wollo Highland Zebu but smaller than the Afar Sanga. Mature females measure 119.0 (±1.65) cm for body length, 110.9 (± 0.49) cm for height at withers, 138.2 (± 0.66) cm for heart girth and 35.2 (± 0.24) cm for pelvic width. Estimated daily milk yield, calving intervals and lactation length of these cattle is about 1.8 liters, 19 months and 11 months, respectively (Figure 4).

Cluster 3: Afar Sanga

This cluster consists of the Afar cattle of site 7 that came out separately from other populations in the classification tree. The name Afar is already known in the literature. Apart from their existence in the study area, their distribution and population size are not well described in earlier reports. The Afar people keep these cattle for reproduction and milk production, which is the main staple food for the pastoralists. Their number is very limited within the South and North Wollo Zones and is estimated to be not more than 4,500 based on the information obtained from Wereda Agricultural Offices where the Afar breed type is believed to exist and based on the frequency of their existence within the herds of the two zones during the survey.

They are long framed but look thinner when compared to Raya cattle. Many animals have a combination of black and white spots being distributed over the body giving them ashy or grey or light chestnut colors. They have straight facial profile and the longest horns (61.9± 1.45 cm) of all cattle types in the area, with an upward and outward orientation at the base and slightly inward orientation around the tips. In most animals the tip of the horn turns backward after forming a spiral-twisting curve. The horns appear thinner at the base than they are for the Raya breed type. They have also the longest ear (20.3 ± 0.42 cm). Mature females are 126.0 (± 1.39) cm long and 115.4 (± 1.05) cm high. They also measure 147.9 (± 1.42) cm for heart girth and 38.7 (± 0.51) cm for pelvic width (Figure 5).

Figure 3. Picture of Wollo highland zebu

Figure 4. Picture of Raya Sanga

Figure 5. Picture of Afar Sanga

Conclusion

The present study confirmed the existence of three cattle breed types in the North and South Wollo Zones of Amhara Region: the Wollo Highland Zebu, the Raya Sanga and the Afar Sanga. Results of both quantitative and qualitative analyses clearly showed population level differentiation into distinct breed types.

All the study sites covered differed in climatic conditions, vegetation cover, topography, and to some extent cattle husbandry practices. The existence of interbreeding at least between sites that are proximal to each other is highly likely as a result of exchange of breeding males and females through livestock markets, social transactions, and occasional matings at times of transhumant cattle movements. Cyclical famines that have been occurring for the past several decades in these areas and the subsequent restocking activities are believed to cause large scale movement of breeding cattle from place to place which could lead to population admixtures; however, this cannot be substantiated based on the data generated in this study. Traditional selection practices of breeding animals within and between populations are also one potential external force that could lead to gradual genetic differentiation and breed divergence. Adaptation of animals to specific environmental stresses is another force responsible for genetic variations between cattle populations.

Nevertheless the results of these morphological classifications need to be verified through genetic characterization to substantiate genetic breed differences.

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