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GENETIC VARIATION OF SOME GOAT POPULATIONS IN ETHIOPIA BY MEANS OF BLOOD PROTEIN POLYMORPHISM

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ABSTRACT: Genetic variability of 298 individuals from four indigenous goat types (Afar, Hararghe Highland, Western Highland and Western Lowland of Ethiopia), two exotic breeds (Toggenburg and Anglo-Nubian) and three crossbreed populations (crosses between the exotic breeds and Hararghe Highland and Somali goat types) were investigated. The red blood cell lysates and plasma proteins were analyzed by starch gel electrophoresis. From a total of five loci studied, two were found to be polymorphic. Two alleles were detected at each of Haemoglobin (Hb) and Transferrin (Tf) loci. Only one allele was detected at each of the loci Carbonic anhydrase (CA), Albumin (Al) and Post Transferrin (PTF) in all the populations of goats studied. In most cases, the observed genotypic frequencies were not significantly different from that expected under the Hardy-Weinburg equilibrium. The proportion of polymorphic loci (P%) varied between 20.0% and 40.0%, with mean number of alleles per locus between 1.2 and 1.4, and expected heterozygosities (H_E) between 0.030 and 0.177 while mean observed heterozygosities (H_O) were between 0.032 to 0.217. Among the three groups of goat populations, higher variability was found in crossbred populations. Afar goat type was more variable (H_O=6.7%) among the indigenous goat types. Cluster analysis based on Nei's standard genetic distance and the unweighted pair-group method using arithmetic averages (UPGMA) revealed low level of genetic distance among populations. The results indicated a higher proportion of genetic variation between populations.

Key words/phrases: Afar goat, Ethiopia, Hararghe goat, Western Highland goat, Western Lowland goat.

INTRODUCTION

Goat farming is an important component of livestock system in all agroecological zones of Ethiopia. According to CSA (2010), the goat population in Ethiopia is estimated to be 21.9 million which is the second largest in Africa and the fifth largest in the world. Goats constitute about 22% of the ruminant livestock population in Ethiopia. They are a valuable source of milk and milk products, meat, manure, and skin. They also play a

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role in certain traditional and ceremonial cultural domains. Goats are kept in a wide range of production systems and are present in diverse environments of Ethiopia.

Despite these valuable merits, adequate attention has not been given to identify, characterize and improve the genetic resources of goats. The existing goat types and their numbers have not been studied in detail, except for some works on classification based on few phenotypic characters and their geographical distribution (Workneh Ayalew, 1992; FARM-Africa, 1996). The present goat breeds/types of Ethiopia are classified by FARM-Africa (1996) into four main families: Nubian, Rift Valley, Somali and Small East African families. These breeds/types are believed to have originated from the dwarf goats of West Africa and the Savanna goats of East Africa (Epstein, 1971). Based on available sources, Workneh Ayalew (1992) has traced the first entrance of goats to Ethiopia to be sometime between 2000 and 3000 B.C.

In order to use these national goat resources for sustainable development, a systematic, reliable and comprehensive breed characterization is essential. Characterization at the genetic level is the objective way to identify and quantify the available genetic diversity. Such studies could assist to design rational improvement strategies between-breeds and within-breeds. On the basis of information obtained from such studies, selection programmes could be designed to exploit available traits sustainably. Therefore, in Ethiopia, for the development of effective breeding policy and for maintaining breed diversity as well as pure form of breeds, breed identification and characterization work using genetic markers along with morphological characteristics are required. Otherwise, breeds, which can thrive and produce in adverse environmental conditions, will be lost. It would be tragic if unique genetic resources that resulted from centuries of natural and artificial selection were lost (Rege, 1994). At present, the genetic diversity in indigenous goats is confronted with interbreeding among the indigenous breeds or types and to a certain extent from the indiscriminate crossbreeding with exotic breeds (Devendra, 1999). Sustainable livestock improvement, however, cannot be guaranteed without the adaptive traits of these genetic resources. The recent developments in genomics also suggest that it will soon be possible to identify and manipulate genes, including those which confer disease resistance and physiological adaptation to the harsh environmental conditions.

The objective of the present study was to generate base-line information for identification and characterization of goat breeds by assessing blood protein polymorphisms, which could assist in the development of livestock breeding policies and for goat breed evaluation and conservation activities in Ethiopia.

MATERIALS AND METHODS

Breeds/Types/Populations

In this paper, both the terms type and breed are used for indigenous goats as there is no general agreement on whether they are breeds or types. Breed and population are used for exotic and crossbred goats, respectively.

Nine goat types/breeds/populations which included four indigenous goat types/breeds, two exotic breeds and three crossbred populations were studied using five blood protein loci, namely, Albumin (Al), Carbonic anhydrase (CA), Haemoglobin (Hb), Post Transferrin (PTF) and Transferrin (Tf). The indigenous goat types/breeds studied were Afar, Hararghe Highland, Western Highland, and Western Lowland while the exotic breeds were the synthetic European breeds, Anglo-Nubian and Toggenburg. The crosses of these exotic breeds with Hararghe Highland and Somali goat types were included.

Methods of sample collection

Animals

Animals were sampled from individual farmers in different peasant associations of four regional states namely, Benishangul Gumuz, Amhara, Afar and Oromiya (Fig. 1). Flocks and animals within the flocks were chosen in a way that ensured that animals sampled were not related. About 55-85 animals, representative of the breed/type/population from each indigenous goat type/breed, and 2-13 from exotic breeds and crossbred populations were sampled (Table 4).

Blood sample collection and separation of blood components

Blood samples were taken carefully from jugular vein with the vacutainer tubes (heparinized). Samples were kept in ice blocks until centrifugation. Whole blood was centrifuged at 3000 rpm for 10-15 minutes in the field. Then the plasma was taken carefully with a Pasteur pipette and kept in a sample vial. The buffy coat was removed without disturbing the red blood cells. Then the red blood cells and plasma were stored in liquid nitrogen and transported to the laboratory where it was stored in a deep freezer (−71°C).

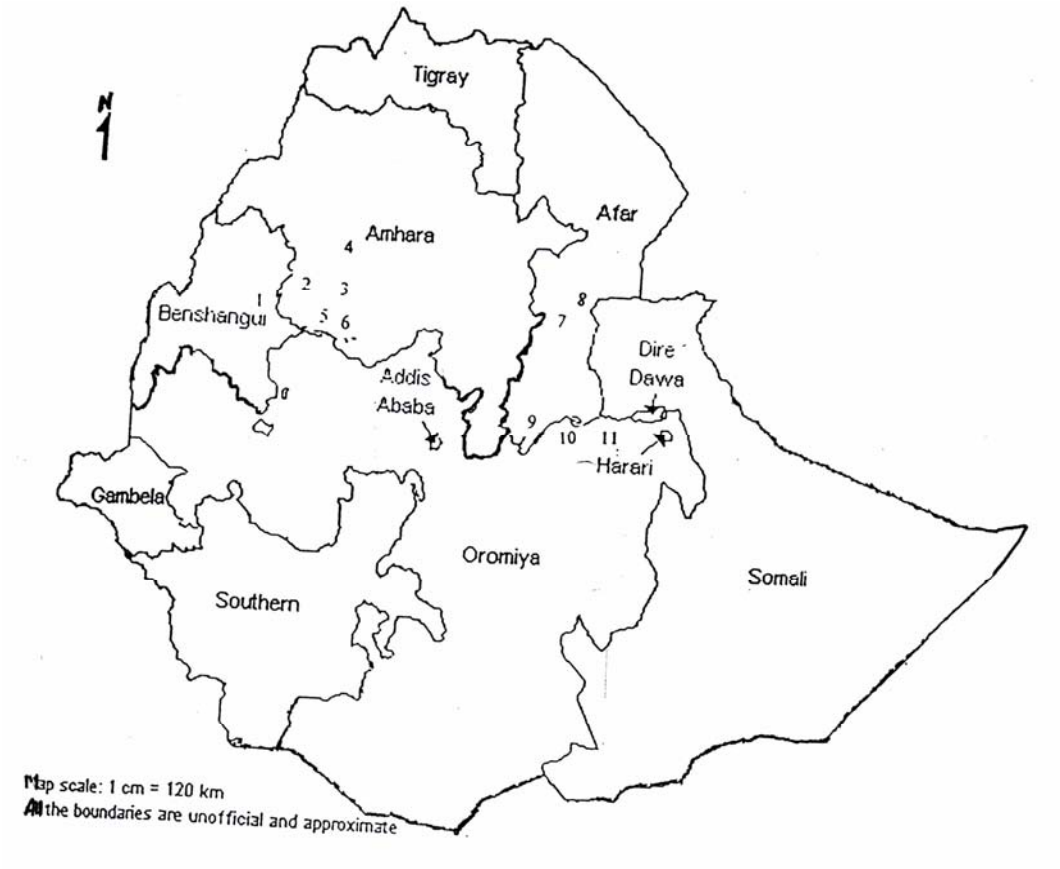

Fig. 1. Map showing the sampling sites. Key: 1 & 2: Western Lowland goat; 3, 4, 5 & 6: Western Highland goat; 7& 8: Afar goat; 9, 10 &11: Hararghe Highland and Crossbreed goats.

Sample processing

The red blood cells were washed with physiological saline solution (0.9% NaCl) three times by centrifuging at 2000 rpm for 10 minutes at 4°C. Finally, equal volume of distilled water was added and then the samples were stored at −20°C for analysis of CA and Hb. The plasma and red blood cell lysates were analyzed for polymorphism of the five protein loci by horizontal starch gel electrophoresis. Cecchini and De Nijs (1986) method of electrophoresis was used with slight modifications according to the resolution ability of the system.

Data analysis

Observed genotype frequencies based on the data of blood protein variants studied were calculated by direct count and entered into the computer

package, Biosys-1 (Swofford and Selander, 1989). All genetic parameters were calculated using the Biosys-1 computer program (Swofford and Selander, 1989). Nei (1972) genetic distances were used to construct the phylogenetic tree.

RESULTS

Genotype frequencies

The observed genotype frequencies in all populations studied are given in Table 1. Three genotypes of Hb (Hb^{AA}, Hb^{AB} and Hb^{BB}), determined by two electrophoretic codominant alleles, were observed in two populations, namely, Afar and Hararghe Highland. The frequencies of Hb^{AA} were 0.590 and 0.738 in these two populations, respectively. Two genotypes of Hb (Hb^{AA} and Hb^{BB}) were found in Anglo-Nubian and Toggenburg x Hararghe Highland goats with frequencies of 0.875 and 0.125, respectively. Only genotype Hb^{AA} was found in the rest of the studied populations. Genotype Hb^{AA} was the most common genotype in all populations studied.

Table 1. Genotype frequencies at Hb and Tf loci at the studied goat populations.

Genotype	Populations and genotype frequencies								
	Af	**HL**	**WL**	**WH**	**AN**	**TN**	**AN x HL**	**AN x Somali**	**TN x HL**
Hb^{AA}	0.590	0.738	1.000	1.000	0.875	1.000	1.000	1.000	0.875
Hb^{AB}	0.333	0.261	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Hb^{BB}	0.077	0.001	0.000	0.000	0.125	0.000	0.000	0.000	0.125
Tf^{AA}	0.959	0.919	0.840	0.684	0.286	0.500	0.250	0.600	0.500
Tf^{AB}	0.000	0.081	0.160	0.316	0.571	0.500	0.500	0.200	0.500
Tf^{BB}	0.041	0.000	0.000	0.000	0.143	0.000	0.250	0.200	0.000

Abbreviations: In this and other tables and Fig. 2: Af: Afar; HL: Hararghe Highland; WL: Western Lowland; WH: Western Highland; AN: Anglo-Nubian; TN: Toggenburg

Three genotypes of Tf (Tf^{AA}, Tf^{AB} and Tf^{BB}), determined by two electrophoretically-based codominant alleles, were found in three populations, namely Anglo-Nubian, Anglo-Nubian x Hararghe Highland and Anglo-Nubian x Somali (Table 1). The highest and lowest frequency of Tf^{AA} was observed in Afar and Anglo-Nubian x Somali goats with frequencies of 0.959 and 0.250, respectively (Table 1). The frequency of Tf^{AB} was found to be relatively higher in Anglo-Nubian goats. Two genotypes of Tf (Tf^{AA} and Tf^{AB}) were found in Hararghe Highland, Western Lowland, Western Highland, Toggenburg and Toggenburg x Hararghe Highland goats. Tf^{AA} was common in all populations studied except in the case of Anglo-Nubian and Anglo-Nubian x Hararghe Highland goats.

Al, PTF and CA loci were found to be monomorphic in all goat populations studied with banding patterns of Al^{AA}, CA^{AA} and PTF^{AA}, respectively.

Test of Hardy-Weinberg Equilibrium

The deviations of the observed genotypes from the expected were tested by chi-square test for each population and polymorphic locus. The genotypic frequencies in most of the populations were in agreement with the Hardy-Weinberg equilibrium conditions (Table 2). From a total of 18 chi-square tests, only two significant deviations were found ($p<0.001$) with degree of freedom of one. These deviations were due to the Tf locus in Afar and Hb locus in Anglo-Nubian.

Table 2. Chi-square test for deviation from Hardy-Weinberg equilibrium of the heteromorphic loci (Hb and Tf).

Locus/ allele	Population								
	Af	**HL**	**WL**	**WH**	**AN**	**TN**	**AN x HL**	**AN x Somali**	**TN x HL**
Hb	0.581	2.181	0.000	0.000	15.077*	0.000	0.000	0.000	0.492
Tf	87.022*	0.109	0.328	0.544	0.057	0.000	0.083	2.286	0.857

Note: All chi-square values were calculated at degree of freedom of 1; *P<0.001

Allelic frequency

Alleles were designated as A and B according to their rate of mobility. The allelic frequencies observed for each population is given in Table 3.

Table 3. Allelic variation parameters, heterozygosity and coefficient of heterozygosity deficiency at all loci in all populations.

Population	Mean no. of alleles per locus	Percentage of polymorphic loci *	Mean heterozygosity		Heterozygote deficiency
			Observed	**Hardy-Weinberg expected****	
Af	1.4 (0.24)	20.0	0.067 (0.067)	0.089 (0.071)	−0.247
HL	1.4 (0.24)	20.0	0.059 (0.042)	0.068 (0.051)	−0.132
WL	1.2 (0.2)	20.0	0.032 (0.032)	0.030 (0.030)	0.067
WH	1.2 (0.2)	20.0	0.063 (0.063)	0.055 (0.055)	0.145
AN	1.4 (0.24)	40.0	0.114 (0.114)	0.152 (0.104)	−0.250
TN	1.2 (0.2)	20.0	0.100 (0.100)	0.100 (0.100)	0.000
AN x HL	1.2 (0.2)	20.0	0.100 (0.100)	0.114 (0.114)	−0.123
AN x Somali	1.2 (0.2)	20.0	0.040 (0.040)	0.093 (0.093)	−0.570
TN x HL	1.4 (0.2)	40.0	0.217 (0.133)	0.177 (0.109)	0.226
Mean	1.24 (0.24)	24.4	0.088 (0.077)	0.097 (0.080)	−0.093

*A locus is considered polymorphic if the frequency of the most common allele does not exceed 0.95

** Nei (1978) unbiased estimate (standard errors in parenthesis)

Haemoglobin: Two alleles, Hb^A and Hb^B, were observed, with the Hb^A being the allele with the highest mobility. The haemoglobin allele (Hb^A) was the most frequent allele in all populations. The frequencies of Hb^A in indigenous populations varied between 0.761 and 1.000, whereas it varied between 0.625 and 1.000 in exotic breeds and crossbreds.

Transferrin: In this locus, two alleles Tf^A and Tf^B, were observed in decreasing order of mobility in all populations studied. The most frequent allele was Tf^A and its frequency ranged from 0.500 to 0.959. The frequency of Tf^A was high in all populations, particularly in indigenous populations where the frequency ranged between 0.842 (Western Highland) and 0.959 (Afar and Hararghe Highland), while it ranged between 0.500 and 0.750 in exotic and crossbred populations. The PTF, CA and Al loci were represented only by one allele each in all goat populations studied.

Average heterozygosity and polymorphism

Of the five protein loci investigated, Tf and Hb were polymorphic, while the other three were monomorphic in all populations studied. The locus Tf was polymorphic in all goat populations studied except in Afar and Hararghe Highland goats. Hb was polymorphic in four goat populations namely, Afar, Hararghe Highland, Anglo-Nubian and Toggenburg x Hararghe Highland.

Estimates of mean observed heterozygosity (H_O), expected heterozygosity (H_E), number of alleles per locus, percentage of polymorphic loci (P%) and coefficients for the heterozygote deficiency ($D = H_O - H_E/H_O$) are shown in Table 4. The mean percentage of polymorphic loci was in the range of 20.0% and 40.0% with an overall mean of 24.4%. In all populations investigated, the mean number of alleles per locus ranged from 1.2 to 1.4 with an overall mean of 1.24. The mean observed heterozygosity (H_O) in the populations studied ranged from 0.032 (Western Lowland) to 0.217 (Toggenburg x Hararghe Highland), whereas the mean expected heterozygosity (H_E) varied from 0.030 (Western Lowland) to 0.177 (Toggenburg x Hararghe Highland). Average H_O across all the populations was 0.088 while the average of H_E was 0.097. Both negative and positive deviations of heterozygotes were observed in the studied populations. Relatively higher deficiency of heterozygotes (−0.570) was found in Anglo-Nubian x Somali populations. There was a slightly excess heterozygotes in the Toggenburg x Hararghe Highland population (0.226). The grand mean coefficient of heterozygosity deficiency was negative, indicating an apparent overall deficiency of heterozygotes.

Table 4. Allelic frequencies in the goat populations studied.

Locus	Population								
	Af	**HL**	**WL**	**WH**	**AN**	**TN**	**AN x HL**	**AN x Somali**	**TN x HL**
Hb									
(N)	69	65	80	55	8	2	2	5	12
A	0.761	0.846	1.000	1.000	0.875	1.000	1.000	1.000	0.625
B	0.239	0.154	0.000	0.000	0.125	0.000	0.000	0.000	0.375
PTF									
(N)	73	74	50	19	7	2	4	5	10
A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
B	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Tf									
(N)	73	74	50	19	7	2	4	5	10
A	0.959	0.959	0.920	0.842	0.571	0.750	0.500	0.700	0.750
B	0.041	0.041	0.080	0.158	0.429	0.250	0.500	0.300	0.250
Al									
(N)	70	74	48	19	8	2	4	5	10
A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
B	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CA									
(N)	69	65	80	55	8	2	4	5	10
A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
B	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Abbreviations: (N): number of animals sampled

The crossbred populations were found to be the most variable, the H_O being 21.7% for Toggenburg x Hararghe Highland and 10.0% for Anglo-Nubian x Hararghe Highland. Exotic breeds exhibited a higher variability than the indigenous breeds, the H_O being 11.4% for Anglo-Nubian and 10.0% for Toggenburg. Of the indigenous goat types, the most variable population was Afar (H_O=6.7%), and was followed by Western Highland (H_O=6.3%), and the Western Lowland was the least variable (H_O=3.2%).

Genetic structure and differentiation

A summary of Wright's F-statistics (Wright, 1965) for all populations is given in Table 5. Tf did not show variation within populations F_{IS} (−0.036), while Hb exhibited slight variability within populations F_{IS} (0.137). The mean value of F_{ST} (0.185) indicates a moderate level of differentiation among populations, being more strongly differentiated (i.e., higher F_{ST} value) for the locus Hb. The overall average F_{IS} was 0.020, which is slightly greater than zero and indicates a deficit of heterozygosity (less variability) within the populations studied. At the same time the overall average F_{IT} across all the populations studied was 0.170. The largest proportion of this variation was attributable to the between-population component (F_{ST}=0.153)

compared to the within-population variation.

Table 5. Wright's F-statistics within (F_{IS}), among (F_{ST}) populations and total genetic differentiation (F_{IT}) in the populations.

Locus	F_{IS}	F_{IT}	F_{ST}
Hb	0.137	0.296	0.185
Tf	−0.036	0.106	0.137
Mean	0.020	0.170	0.153

Genetic distances

The matrix of genetic distances derived from the data collected, between pairwise combinations of the nine populations based on the coefficient of standard genetic distance (Nei, 1972) is presented in Table 6. Genetic distance measures ranged from 0.001 to 0.059. Among the indigenous populations the distance values varied from 0.001 (Western Highland-Western Lowland) to 0.015 (Afar-Western Highland). The distance value between exotic breeds was 0.010. The distance values between indigenous and exotic populations were greater than or equal to the largest value obtained between purebred populations except between Toggenburg and Western Highland (0.002) and Toggenburg and Western Lowland (0.006). The distance measures found between crossbreds and both of purebred populations (exotic and indigenous) were high. The distance values obtained between crossbreds themselves were also higher than the values obtained between purebreds (i.e., indigenous and exotics) and ranged from 0.009 to 0.046.

Table 6. Nei's genetic distances (below diagonal) and similarities (above diagonal) among the studied populations.

Population	Af	HL	WL	WH	AN	TN	AN x HL	AN x Somali	TN x HL
Af	-	0.998	0.988	0.985	0.964	0.978	0.941	0.973	0.987
HL	0.002	-	0.995	0.992	0.967	0.985	0.941	0.980	0.981
WL	0.012	0.005	-	0.999	0.972	0.994	0.963	0.990	0.965
WH	0.015	0.008	0.001	-	0.981	0.998	0.975	0.996	0.969
AN	0.036	0.033	0.028	0.019	-	0.990	0.999	0.997	0.978
TN	0.022	0.015	0.006	0.002	0.010	-	0.990	0.999	0.969
AN x HL	0.059	0.051	0.037	0.025	0.001	0.010	-	0.991	0.954
AN x Somali	0.027	0.020	0.010	0.004	0.007	0.001	0.009	-	0.968
TN x HL	0.013	0.019	0.035	0.031	0.022	0.031	0.046	0.032	-

Cluster analysis

An UPGMA dendrogram of relationships among the nine studied populations of goats based on the coefficient of Nei's standard genetic distance (Nei, 1972) is shown in Fig. 2. The dendrogram shows differentiation into four clusters. The first and the second clusters contain indigenous populations, Afar and Hararghe Highland, and Western Lowland and Western Highland, respectively, the third cluster contains populations of exotic breeds and the fourth cluster contains the crossbred populations.

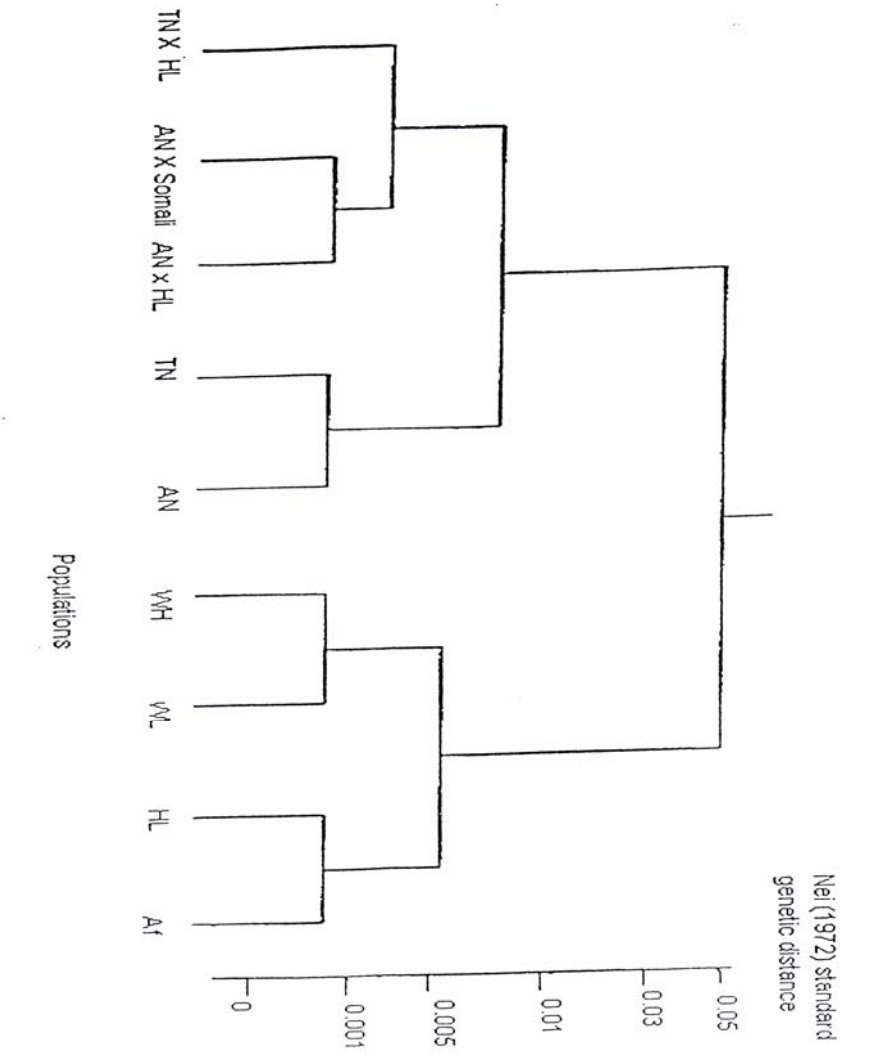

Fig. 2. Dendrogram showing the genetic relationships among the studied populations/breeds/types.

DISCUSSION

The degree of polymorphism obtained in the present study was low. The majority of the loci were monomorphic being similar to many systems studied by protein polymorphism, as also reported by Nei (1978), Pepin and Nguyen (1994) and Deza *et al*., (2000). In general, the blood proteins appear to be highly monomorphic in goats than in sheep (Bhat *et al*., 1983; Redero *et al*., 1997) and cattle (Cecchini and De Nijs, 1986; Sisay Gezahagne, 1996). The low polymorphism obtained in this study indicates the existence of low genetic variation within the Ethiopian indigenous goat populations. However, the fact that we have dealt only with blood proteins that are only a small fraction of structural genes with no information of base sequences of these genes does not necessarily reflect the overall low degree of polymorphism reported here.

Only one genotype of the albumin locus designated as Al^{AA}, was found in all goat populations studied as has been reported in several breeds of goats (e.g., Bhat and Baruah, 1980; Fesus *et al*., 1983; Tucker *et al*., 1983). However, there are exceptions to this and albumin was reported to be polymorphic in several Spanish breeds (Tunon *et al*., 1989; Redero *et al*., 1997), in Japanese Saanen goats (Nozawa *et al*., 1978), in Angora goats of South Africa (Osterhoff *et al*., 1987), in native breeds of Central Argentina (Deza *et al*., 2000) and in five goat breeds by Pepin and Nguyen (1994) with two alleles of Al^F and Al^S. The most common allele in the literature appears to be Al^S. So, the allele that was obtained in this study may be allele Al^S by inference. The observed monomorphism at this locus in exotic breeds and crossbreds studied may be due to the small number of samples used.

As was the case with albumin, the analysis for CA revealed one allele (CA^A) in all the populations investigated in this study. This is also in agreement with previous studies (Fesus *et al*., 1983; Tucker *et al*., 1983; Osterhoff *et al*., 1987; Tunon *et al*., 1989; Pepin and Nguyen, 1994; Deza *et al*., 2000). But, Barker *et al*. (2001) reported polymorphism in CA locus in 11 populations of Southeast Asian goat populations.

Of the four alleles known to exist at Hb locus of goats, only two alleles Hb^A and Hb^B were observed in the present study. This result was consistent with several previous studies (Bhat and Baruah, 1980; Bhat, 1986; Osterhoff *et al*., 1987; Garcia-Cascas *et al*., 1992). Allele Hb^A had a higher frequency than Hb^B in all the populations. The allele frequency ranged between 0.625 and 1.000, a result which was consistent with previous reports. Osterhoff *et al*. (1987) reported frequencies of Hb^A to vary from 0.740 to 1.000 in goats

of South Africa. Frequencies of Hb^A similar to the present study were also found in Indian goats (Bhat and Baruah, 1980; Bhat, 1986). However, a lower frequency of this allele (ranging between 0.00 and 0.02) was reported in goats of Central Argentina. Clearly, this allele is common both in the Asian and African goat populations, indicating a possible common ancestry, and it is quite rare in the America's, or at least Argentina's (Deza *et al*., 2000). In the Asian and South African goats, allele Hb^B was rare in goat populations studied particularly in indigenous ones. The Hb allele (Hb^A) in sheep (Agar *et al*., 1972) and in goats (Garcia-Cascas *et al*., 1992) is likely to indicate better adaptation to harsh environments, particularly to hilly areas where majority of Ethiopian indigenous goats live. They have practically high frequency and fixed Hb^A allele (Western Highland and Western Lowland). Moreover, similar to other African and Asian goats no rare variants were observed in the present study, possibility due to small sample size.

The present study was in agreement with the majority of reports (Osterhoff *et al*., 1987; Tunon *et al*., 1989), which have shown that Tf^A is the most frequent allele in European and African goat breeds. Many authors have noted substantial differences in Transferrin gene frequencies between breeds of goats with Tf^A being associated with Alpine breeds and Tf^B with Indian breeds irrespective of the geographic distances between the different groups of the goat breeds studied (Tunon *et al*., 1989).

Only one allele, PTF^A, was found in all the goat populations studied and no further information was available in the literature on this locus in goats.

Observed genotype frequencies were not significantly different from those expected from the Hardy-Weinberg (H-W) equilibrium in most of the populations. The only significant deviations observed were at Tf locus in Afar goat populations and Hb locus in Anglo-Nubian goat breed ($p<0.001$). It is common to find that a large number of loci are in H-W equilibrium, with only a few cases of significant deviations from the equilibrium, e.g., in goats of Central Argentina deviations were reported to be due the Hb locus by Deza *et al*. (2000) and it was due to three other loci (Gc, Mdh, and, Me) in Southeast Asian goats (Barker *et al*., 2001). The possible explanations for the two deviations observed in the present study include scoring bias, inbreeding, or selection against heterozygotes, as the number of observed homozygotes was greater than the expected.

The mean percentages of polymorphic loci obtained in the present study were in the range of 20.0% (77.8% of the populations) to 40.0% with an overall mean of 24.4%. In the populations investigated, the mean number of alleles per locus ranged from 1.2 (77.8% of the populations) to 1.4 with an overall mean of 1.24, which is slightly lower than the values obtained for goats in central Argentina (Deza *et al*., 2000) and Asia (Barker *et al*., 2001). The small mean number of alleles per locus might be the result of a small number of animals sampled, particularly for exotic and crossbreds and non-random sampling of goat genotypes. Fixation index within (F_{IS}), and among (F_{ST}) population, as well as the total genetic differentiation (F_{IT}) were calculated in order to demonstrate the relative distribution of genetic variation within and among populations. The average F_{IS}, as indicated in Table 5 was 0.020, which is slightly greater than zero indicating a low genetic variation within population. There was pronounced population structure, as indicated by F_{ST} value of 0.153, which means that much of the total genetic variation was among populations rather than within populations. Similar observations have been reported in goat populations elsewhere (Deza *et al*., 2000; Barker *et al*., 2001). The high genetic variations observed between populations in the present study was not surprising given that the populations studied consisted of both indigenous and exotic breeds. The excess of homozygotes observed in this study may have been caused by inbreeding, a fact, which is known in many other studies of livestock (e.g., Barker *et al*., 2001).

Among the indigenous populations, the Afar and Western Highland were more variable. Afar, which showed high heterozygosity value, lives in harsh environments, which is hot and dry, typical of the extensive pastoral system. The Western Highland goats, on the other hand, live in an intensively degraded, cold and humid area of the country. The rest of the indigenous goat populations, which showed relatively low variability, live in more benign environments, in the highlands and mid-altitude areas where mixed farming is practiced. That the average heterozygosity values were relatively higher for populations which live in somewhat extreme environments (i.e., Afar and Western Highland) may indicate that heterozygosity has an adaptive value in harsh environmental conditions. However, other possible explanations cannot be ruled out. For example, the pastoral livestock populations are known to be more exposed to interbreeding with other populations. Similar observations were made by Sisay Gezahagne (1996) in cattle breeds of Ethiopia. He reported higher heterozygosity values for Abigar, Boran and Ogaden cattle breeds, which live in hot and dry

environments characterized by semi-pastoralism and pastoralism. The average values of heterozygosity were higher for crossbreds, confirming that crossbreeding increases genetic variation. In addition, the commercial synthetic breeds were more heterozygous than indigenous populations indicating the presence of genes from other sources of goat breeds.

The general observation of low genetic variability, deficit of heterozygotes and small number of alleles per locus in the indigenous goat populations may be due to selection against heterozygotes and inbreeding. It could also be due to the limitations of markers used in the present study. That there may be higher inbreeding levels in the indigenous populations is indicated by the fact that crossbreds had the highest heterozygosity. Therefore, the common factor in the present study may be "uncontrolled" mating. In indigenous populations, breeding groups usually comprise a dominant male and large number of females. For example, the male to female ratio in Afar populations has been reported to be 1:42 (the Afar maintain a higher proportion of breeding females in their flocks because of their need for milk) (FARM-Africa, 1996). However, when one looks at the distribution of male and female under one year of age the sex ratio is 1:1 while after one year of age the number of male goat declines (Kassahun Awgichew and Hailu Getaneh, 1986). Many males may aggregate in the vicinity of oestrus females, but the dominant male generally exclude subordinate males, and presumably sires most of the offspring (O'Brien, 1988). The presence of strong inbreeding has been reported in Spanish goat breeds based on three loci (Barbancho *et al*., 1980), and in Southeast Asian goat breeds based on 59 loci (Barker *et al*., 2001). The low overall genetic variability in the present study might be due to the presence of inbreeding in, at least, some of the populations studied.

As indicated in Table 6, the distance estimates made were slightly greater than zero and ranged between 0.001 and 0.059. Thus, there was low level of differentiation among the studied populations. Nozawa *et al*. (1978) reported distance values varying from 0.004 to 0.025 in eight populations in Okinawa, Japan. Katsumata *et al*. (1981) reported values ranging from 0.001 to 0.0174 in seven native Indonesian populations. Similar values, between 0.0004 and 0.0065, were also reported in seven Japanese Saanen populations (Katsumata *et al*., 1981). Values in close agreement with those of the present study were also reported in 14 native Spanish breeds (0.003 - 0.092) by Tunon *et al*. (1989). Pepin and Nguyen (1994) reported values of 0.016 to 0.153 between five goat breeds and pointed out that, on average, the estimated distances between European and African breeds was 2 to 4

times larger than distances found between local breeds. The results obtained in the present study between the local breeds and the European breeds generally confirm the conclusion. However, the distances of Toggenburg from Western Highland and also from Western Lowland were smaller. Most distance measures found between crossbreds and purebreds tend to be relatively higher (the highest value being 0.059) than values found amongst purebreds (the highest value was 0.036). The smallest distance found between Anglo-Nubian and Western Highland was in agreement with the fact that Anglo-Nubian goats are commercial breeds produced from England breed and Nubian of Sudan including Egyptian, Ethiopian, and Indian goats (Devendra and Mcleroy, 1982). Moreover, the Nubian goats have a continuous distribution in northern parts of Ethiopia. It is, therefore, possible that some of the indigenous populations, particularly Western Highland, have had genetic influence on the Nubian goats.

Using Nei's (1972) standard genetic distance data, it was possible to construct a genetic tree showing the genetic relationships of the nine goat populations studied. A pattern related to geographical distance and historical relationship was found. The dendrogram showed indigenous populations from close geographical location and history (Afar and Hararghe Highland) and Western Highland and Western Lowland, to cluster closely together. Similarly, exotic breeds and crossbreds were clustered on a separate branch. The branching of Western Highland and Western Lowland on the same branch on the dendrogram is in agreement with the geographical proximity of their habitats, as well as, their speculated past history (as having being derived from past admixture amongst highland goat types) (FARM-Africa, 1996). Due to close proximity there may be considerable interbreeding through trade and physical movement of people. There is also evidence that farmers in Western Lowland areas use bucks from Western Highland populations in order to increase body weight of their goats (personal observation). The close relationships between the exotic breeds and the crossbred populations may be a reflection of the proportion of exotic genes in the crossbreds studied. This is further supported by the clustering of the crossbred populations together far away from the indigenous parent stock (Hararghe Highland). The relationships observed in indigenous populations were in agreement with the previous classifications based on morphology and geography (Workneh Ayalew, 1992; FARM-Africa, 1996).

CONCLUSION

This is probably the first attempt to study blood protein polymorphism of goats in Ethiopia. It has clearly shown that the genetic variation of indigenous goats is low. It is clear that the more heterogeneous goat types are found in adverse environmental conditions in the highlands and lowlands. The major cause of low genetic variability in indigenous goats of Ethiopia is probably indiscriminate interbreeding within indigenous goat types and inbreeding depression due to mating between close relatives and using small number of males in the flocks. It could also be due to the low polymorphism in the presently studied blood protein markers and thus calls for utility of more molecular markers like AFLP and SSR.

This study has shown that Afar goat has the largest variability based on blood proteins among the indigenous goat types/populations studied and could be considered as a unique breed and eligible for conservation and improvement programmes. Goat populations found in adverse environmental conditions and pastoralist production systems tended to have high blood protein based variability. Crossbred goat populations had high variability than either of the parental populations (indigenous and exotics) but they were genetically closer to their exotic parentage, possibly due to backcrossing. In general, blood protein polymorphism variability was seen to be related to production system, breeding system used and environment in which the goat populations were found.

This study has shown that some protein loci (Haemoglobin and Transferrin) are important for the characterization of goat breeds/populations/types in Ethiopia. However, Carbonic anhydrase, Albumin and Post Transferrin are not informative.

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