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A Review on Current Knowledge of Genetic Diversity of Domestic Goats (*Capra hircus*) Identified by Microsatellite Loci: How those Efforts are Strong to Support the Breeding Programs?

Getinet Mekuriaw[1,2,3,4]✉, Solomon Gizaw[2], Tadelle Dessie[2], Okeyo Mwai[5], Appolinaire Djikeng[4] and Kassahun Tesfaye[1]

[1]*Addis Ababa University, Department of Microbial, Cellular and Molecular Biotechnology, Addis Ababa, Ethiopia*
[2]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*
[3]*Department of Animal Production and Technology; Biotechnology Research Institute, Bahir Dar University, Ethiopia*
[4]*Biosciences for eastern and central Africa (BecA), Nairobi, Kenya*
[5]*International Livestock Research Institute (ILRI), Nairobi, Kenya*
✉ *yafetgetinet@gmail.com*

ABSTRACT: Genetic characterization requires knowledge of genetic variation that can be effectively measured within and between populations. It is considered as an important tool for sustainable management or conservation of a particular population. Presence of limited diversity may hamper the possibility of populations to adapt the local environment in the long term, but loss of genetic diversity can also more immediately lead to decrease fitness within populations. In this paper, genetic diversity of more than 120 domestic goat populations found in various parts of the world has been summarized. The paper is limited only to the diversity study conducted by microsatellite loci. In all the goat populations reviewed, the within population genetic diversity is extremely higher than between population variation which might be due to the uncontrolled and random mating practiced among the breeding flock. However, the technical as well as statistical data management deficiencies, like selection of microsatellites and other sampling biases, observed in the reports could have their own influences on the limited and weak variations obtained within and among populations. The genetic distance among populations is very narrow especially populations found within states. In general, goats are the most transported animals during the lengthy commercial and exploratory journeys took place in the old world long time ago. This contributed the goat to have narrow genetic differentiation compared to other ruminant livestock. The technical fissures observed in the past efforts on identification and structure analyses of the goat populations might also demand further works to design appropriate conservation and breeding management programs.

Keywords: Domestic goat, Genetic distance, Heterozygosity, Microsatellite marker, Polymorphic information content

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INTRODUCTION

Genetic diversity has been shaped by past population processes and will also affect the sustainability of species and populations in the future [1]. Maintenance of genetic diversity in livestock species requires adequate implementation of conservation priorities and sustainable management programs [2]. It is also a key to the long-term survival of most species [3] and widely used to categorize animals in the world [4]. However, isolation-by-distance [5], historical and geological factors [6], physical barriers [7,8] and ecological factors through morphological adaptation to local conditions [9] are some of the factors which are suspected in disrupting patterns of genetic structure and gene flow of a given population. Especially in domestic animals, the gene flow disruption is overseen more by human intervention than by physical barriers [10].

Farm animal genetic diversity is required to meet current production needs in various environments, to allow sustained genetic improvement, and to facilitate rapid adaptation to changing breeding objective and serves as a tool for animal breeding and selection [11- 13]. However, classifying the genetic diversity based on historical, anthropological and morphological evidences [14] as well as their geographical origin are not satisfactory and enough for the purpose of conservation and utilization of these resources. In addition, phenotypic characterization provides a crude estimate of the average of the functional variants of genes carried by a given individual or population, and the appropriateness of phenotypic traits to study the genetic variation between populations is very limited [15]. Hence, comprehensive knowledge of the existing genetic variability is the first step for the conservation and exploitation of domestic animal diversity [16].

Goats are considered the most prolific ruminant among all domesticated ruminants especially under harsh climatic conditions [17]. The high versatility, moderate size and hardy nature of goats made them ideal as a food resource in the lengthy commercial and exploratory journeys that took place in the old world a long time ago [18]. Today, there are >1,000 goat breeds (www.fao.org/corp/statistics/en/), and recently >861.9 million goats are kept around the world with the respective continental share in Million: Asia (514.4), Africa (291.1), South America (21.4), Europe (18.0), Central America (9.0), Caribbean (3.9), Northern America (3.0) and Oceania (0.9) [19]. The existence of such a large gene pool is important for the potential future breed preservation and for the development of a sustainable animal production system [2].

The absence of well-managed conservation genetics programs and the uncontrolled introgression between indigenous as well as foreign breeds are seriously threatening the future of many populations in various parts of the world [20]. The high gene flow and the admixture of the breeds can result low level of genetic differentiation [21]. This has also an implication of the presence of terrible risk that most breeds may perish before they have been exclusively recognized and exploited. Microsatellite marker is the main molecular markers employed to identify and characterize genetic diversity of domestic goats found in various corners of the world by various scholars. However, following financial and other reasons, most of the efforts conducted may not be as supportive as expected in revealing the required information for designing appropriate and sustainable goat breeding programs. Therefore, given the limited number of efforts conducted on domestic goats, strength and gaps (with emphasis) of past efforts have been summarized and possible 'the way forward' is suggested in this paper.

GENETIC DIVERSITY AND POLYMORPHIC INFORMATION CONTENT

Genetic diversity refers to the total number of genetic characteristics in the genetic makeup of a species that serves as a way for populations to adapt to changing environments. It represents diversity within a population [22] and it is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Those individuals are more likely to survive to produce offsprings bearing that allele. The population will continue for more generations because of the success of these individuals (http://genetics.nbii.gov/GeneticDiversity.html).

Choosing the appropriate breed or population for conservation is one of the most important problems in the conservation of genetic diversity in domestic animals. Some of the parameters which can help the study of genetic diversity within a population are expected heterozygosity estimates and allelic distribution; and they are believed as they are good indicators of genetic polymorphisms within a population [22-24]. On the other hand, the precision of estimated genetic diversity is a function of the number of loci analyzed, the heterozygosity of these loci and the number of animals sampled in each population [25].

Estimation of heterozygosities

Estimations of expected and observed heterozygosities are measures of genetic variability within a given population [23]. The expected heterozygosity is the proportion of heterozygotes expected in a population; whereas, observed heterozygosity is the percentage of loci heterozygous per individual or the number of individuals heterozygous per locus [26].

As it is indicated in the table, several reports confirmed the status of genetic variability of different goat populations (Table 1) and genetic diversity (H_E and H_O) estimates observed in goat of Sri Lanka, Australia, Korean, Botswana and in some Indian and Brazilian goat populations were below 0.5. This is because of maintaining microsatellite loci which had registered heterozygosity estimates below 0.5 in the respective breeds during the analysis. Literatures suggest that heterozygosity estimates having greater than 0.5 heterozygosity estimates are believed to be appropriate for genetic diversity study [44, 45]. Similarly, some of the estimated values were also closer to the margin. These low estimates imply that there might have been high selection pressure, small population size, minimal or null immigration of new genetic materials into the populations. Similar low genetic diversity estimates were reported for Argentinean and Chilean goat populations despite the small sample sizes used in the analysis [18].

Whereas the remaining estimates conclude that the studied populations have substantial and high amount of within population genetic diversity. This might be due to low selection pressure, large population size and immigration of new genetic materials [41]. High value of average expected heterozygosity within the populations could also be attributed to the large allele numbers detected in the tested loci [46]. In most of the above diversity estimates, the observed heterozygosity (H_O) and expected heterozygosity (H_E) estimates for each locus and goat population are closer to each other indicating no overall loss in heterozygosity (allele fixation) [40]. However, few

of the microsatellites studied by various scholars (e.g. [41]) had higher observed heterozygosity than expected heterozygosity estimates that probably indicate the existence of sampling bias [45].

Table 1. Estimation of genetic heterozygosity of indigenous goats

Breed	Country	H_E	H_O	No.MS	Author
Sri Lanka and Australian goats (12)	Sri Lanka-Australian	0.45-0.49	--	22	[27]
Korean goats	Korean	0.38	0.36	9	[28]
Indian goat populations	India	0.54-0.79	0.505	17- 25	[29-32]
Swiss goats (11)	Swiss3-24	0.66	--	47	[13]
Canary Island goats	C. Islands	0.62	--	27	[33]
Kalahari Red goats	--	0.63	--	8	[34]
Sub-Saharan breeds	*	0.54	0.56	11	[35]
Spanish Guadrrama goat	Spain	0.81	0.78	10	[36]
Croatian spotted goat	Croatia	0.77	0.76	20	[37]
Chinese ten goat populations	China	0.54-0.64	0.55-0.62	14	[38,39]
Brazilian goats and herds	Brazil	0.50-0.70	0.61-0.70	11	[40]
Guinea Bissau goat	W. Africa	0.60	0.61	14	[39]
Iranian goat populations	Iran	0.65-0.80	--	13	[2]
Ardi	S.Arabia	0.68	0.55	11	[41]
Twelve Chinese breeds	China	0.61- 0.78	0.60 - 0.78	17	[16]
Three Egyptian and two Italian goat breeds	Egypt and Italy	0.67- 0.79	--	7	[42]
Tswana goat	Botswana	0.16	0.12	12	[43]
Ethiopian goat populations	Ethiopia	0.55-0.69	0.52-0.68	15	[22,24]

MS=Microsatellite;* Uganda (4), Tanzania (5), Kenya (2), Mozambique (2), Nigeria (3), Mali (1) and Guinea Bissau (1)

On the other side, heterozygosity estimates of nine domestic Swiss goat herds were higher than Wild Ibex goats and Bezoar goats with the mean H_E ranging from 0.51 to 0.58 for domestic herds and from 0.17 to 0.19 for the wild species [47]. The lowest heterozygosity, the lowest genetic variation within the population, estimates are comparable with the mean observed (H_O=0.12±0.16) and expected heterozygosity (H_E=0.16±0.20) values of Tswana goat population [43] which is because of the effects of inbreeding and selective breeding in small and closed population. This idea is supported by Caňón et al. [48] who stated the positive correlation (r = 0.35) of population size with heterozygosity estimates. Low amounts of genetic diversity increase the vulnerability of populations to catastrophic events such as disease outbreaks that indicates high levels of inbreeding with its associated problems of expression of deleterious alleles or loss of over-dominance [2]. It can also destroy local adaptations and break up co-adapted gene complexes ultimately leading to the probability of population or species extinction [2].

Estimation of allelic distribution and locus variability

The allelic distribution is the other measure of genetic variability in a given population [23, 43]. The primary disadvantage of using allelic richness, i.e. the corrected mean number of alleles reflected in the standardized sample size [49], as a measure of genetic diversity is that it is highly dependent on sample size: large samples are expected to contain more alleles than small samples [50]. Similarly, more alleles are expected to be found in a region sampled many times than in a region sampled few times. Private allelic richness has the same problem: large samples are expected to have more private alleles than small ones. On the other hand, intensive sampling of genetically similar populations may reduce the number of private alleles to any population. Therefore, a region that has been sampled intensively may appear to have fewer private alleles than a region sampled less intensively. These problems have a straightforward statistical solution: rarefaction can be used to compensate for differences in sample size and number [50]. The mean number of alleles and expected heterozygosities are very accurate indicators of the genetic polymorphism within a population [41]. Mean observed alleles (n_a) that explain high level of polymorphism of the studied microsatellites were reported for several goat populations (Table 2).

Though the mean number of alleles (MNAs) indicated in table 2 showed the suggested minimum estimates, except some Ethiopian, Brazilian, Egyptian, Italian and Iran goat populations, comparatively the average as well as the range of alleles estimated were the highest estimation (14.9 mean number of alleles with a range of five to 43 alleles per locus for 45 breeds) for the 45 goat populations studied in the Mediterranean regions [48] (Table 2). In addition to this, all the microsatellites (30 microsatellites, which is the maximum coverage) were covered during the study. One of the reasons for the lowest estimates of MNA per locus, in many of the studies, might be because

of using very few bucks, e.g. 3-5 bucks per year for Tswana goat for 16 years of almost closed breeding program at BCA farm [43]; and it might also be because of directional selection for parasite resistance/tolerance coupled with increased productivity [51] that possibly accumulates inbreeding. Similarly, among the 26 loci of twelve Chinese goat populations, 17 were polymorphic and the number of alleles varied between 4 (ILSTS005) and 19 (BM2113); the remaining nine loci (excluded from the analysis) tested had less than four alleles or non-specific PCR products [16]. The later screening procedure was not undertaken by many of the authors. For studies like genetic distance, microsatellite loci should have no fewer than four alleles to reduce the standard errors of distance estimates [25].

For the other goat populations relatively encouraging estimates of MNA were reported. However, though those reports explain the existence of high polymorphism, the average number of alleles depends on sample size, number of observed alleles tends to increase with increasing population size and the number of sires used in a breeding program. This is because of the presence of unique alleles in populations which occur at very low frequencies [41, 43].

In general, heterozygosity deficiency may be resulted because of the presence of a null allele which is the allele that fails to multiply during PCR using a given microsatellite primer due to a mutation at the primer site [25, 53], small sample size where rare genotypes are likely to be included in the samples [2], Wahlund effect, that is presence of fewer heterozygotes in population than predicted on account of population subdivision and decrease in heterozygosity because of increased consanguinity (inbreeding) [11]. Higher heterozygosity provides better assignment performance [54] and the loss of alleles is probably the consequence of repeated founder effects during migration events [55].

Estimation of polymorphic information content (PIC)

Literatures state that the polymorphic information content (PIC) values depict the suitability of the markers and their primers used in the study for analyzing the genetic variability of a given population. Hence, microsatellite markers having greater than 0.5 PIC value are considered as highly informative and highly polymorphic [56, 57]. Therefore, highly polymorphic markers were employed for the goat populations indicated in Table 2.

In contrast to this, lower PIC values of microsatellites (for instance Korean goats PIC = 0.35, [28]; for Egyptian and Italian goats of few loci PIC=0.221, 0.482 & 0.389 [42] and for India goat having 28% of the loci <0.5 PIC [58]) which were expected to be excluded were included in the analysis. In fact, the PIC is determined by heterozygosity and number of alleles [41] and this makes microsatellite markers the choice for genetic characterization and diversity studies. In particular, the high PIC values of a particular marker suggest its usefulness for genetic polymorphism and linkage mapping studies in goats and 60% of microsatellite loci had significant hardy-Weinberg equilibrium (HWE).

Level of inbreeding (F_{IS})

F_{IS} is a measurement of the reduction in heterozygosity of an individual as a result of non-random mating within its subpopulation [59]. It is an average increase of homozygous loci by decreasing the heterozygous loci with the same proportion [43]. It is less suited to reflect historical processes because it has a different, more rapid dynamic than does gene diversity [59]. A high positive F_{IS} indicates a high degree of homozygosity and vice versa [45]. Inbreeding coefficients is estimated for populations which show significant deviation from the HWE [26]. This indirectly implies that inbreeding coefficient (F_{IS}) [59] is significant for significant HWE estimation; but it may not work for all loci of a population.

Based on this background, moderate and high level of inbreeding coefficients were reported by various scholars for different goat populations; for instance, for Marwari (F_{IS}=0.26; [32]), Jamunapari (F_{IS}=0.19; [66]), Mehsana (F_{IS}=0.16; [60]) and Kutchi (F_{IS}=0.23; [31]) breeds of India, Ardi goat breed (F_{IS} =0.18 with only 50% of the markers under HWE; [41]) of Saudi Arabia, Tswana goat breed (F_{IS} =0.12; [43]) of Botswana are some of the reports having high level of inbreeding. However, particularly for Tswana goat breed, the F_{IS} estimate ranged from -0.2340 (INRA006) indicating low levels of inbreeding at that marker locus to 0.8772 (MCM527) depicting high levels of inbreeding. This might be because of the small population size, closed breeding system and very limited number of breeding bucks used for many consecutive years in the farm [43]. The lowest heterozygosity and MNA estimates indicated in table1 and 2 above strengthen this rationale. However, tolerable mean value of F_{IS} (0.03) with the range of -0.223 to 0.220 was obtained for 17 microsatellites (with 12 MNA per locus and a range of 0.586 to 0.790 H_E estimates) of 12 Chinese indigenous goat populations [16].

The moderate level of inbreeding may be a result of moderate levels of mating between closely related individuals under field conditions and may be the uncontrolled and unplanned mating that caused high level of

inbreeding. On the contrary, very low inbreeding value (F_{IS}=0.10) were reported within 45 rare breeds of 15 European and Middle Eastern countries [48] compared with the above reports and the discrepancy between the observed and expected heterozygosities and the difference between the observed and effective number of alleles could confirm the existence of inbreeding [48]. Still the level of inbreeding estimates in all the 45 breeds studied except the two populations (St. Gallen Booted goat breed of Switzerland, F_{IS} = 0.048 and Thuringian forest goat breed of Germany F_{IS} =0.049) are not tolerable because the estimated values obtained were higher than 0.05.

Table 2. Estimated mean number of alleles and polymorphic information content

Breed	Country origin/Region	MNA per breed	MNA per MS	PIC per locus	Author	MS (No.)
Egyptian and Italian goat breeds (5)	Italy	6.48	3.8-9.8	0.22 -0.87	[42]	7
Indian goat breeds (10) f	India	6.33-9.7	4-24	0.08-0.90	[23,40,59,60]	17-25
Taleshi goat	Iran	6.7	2.4-5.2	0.54-0.81	[61]	9
Iranian goat breeds (6)	Iran	6.46 -8.15		0.71-0.86	[2,62]	13
Croatian spotted goat	Croatia	8.1	8.1	0.74	[37]	20
Ardi goat	Saudi Arabia	6.64		0.63	[41]	
Brazilian goat breed (3)	Brazil	3.5 -7.2	3-11	NA	[40]	11
Namibian goat breeds (4)	Namibia		4.67 – 6.00		[63]	18
Kalahari Red goat	South Africa	7.77	7.77	NA	[34]	18
Tete goat	Mozambique	5.58			[64]	
Pafuri goat	Mozambique	6.94			[64]	
45 breeds	Mediterranean regions	5.2-9.1	5-43	NA	[48]	30
Chinese goat populations (22)	China	5.24 -9.1	4-19	0.62-0.88	[16,65]	17-20
Tswana goat	Botswana		1.83	0.58	[43]	12
Indigenous goat populations (17)	Ethiopia	5.13 -6.73	2.06-23	NA	[22,24]	15

Key:- MS=Microsatellite

From thirty microsatellites used, twenty-four of them were in H–W equilibrium (p>0.05) and is more than 90% of the total 45 populations of European and Middle East goats studied [48]. However, small number of loci which were in Hardy-Weinberg Equilibrium: only seven loci (ILSTS011, SPS113, ILSTS029, SRCRSP3, MAF70, ILSTS005 and OarAE54) i.e., only 50% of the total fourteen microsatellite markers, showed Hardy Weinberg Equilibrium (HWE) (p>0.05) in Ardi goat population of Saudi Arabia [41]. Similarly, only 55% of the total microsatellites used showed HWE (P>0.05) in Alpine Saanen and Moxotó dairy goat populations in Brazil [40]. Such findings indicate the presence of effect of selection or uncontrolled breeding practice in the study populations [41]. Huge deviation from HWE (16 out of 20 loci), i.e. only 20% showed HWE (P>0.05), was observed on Kanniadu goats of India [67]; the possible reasons for the deviations pointed out were existence of "null" alleles, high mutation rate and size of homoplasy of microsatellite loci, besides the small study population. On the other hand, four out of the 12 loci (SRCRSP5, MCM527, ILST087 and INRA006) that differed significantly from the Hardy-Weinberg equilibrium (HWE) were observed indicating subjection of, particularly, those loci to systematic selection and dispersive forces such as genetic drift and inbreeding [43]. In this study, five out of the total 12 loci were monomorphic (fixed allele) that could be linked to genes responsible for parasitic resistance, and this goes in line with the study made by Beh et al. [68].

The large proportion of loci without of HWE might be because of those loci being under within major histocompatibility complex [69] and under strong natural selection pressure [70]; or it might be because of the presence of null or non-amplified alleles, allele grouping defects, a sampling structure effect, selection against heterozygotes or inbreeding [40]. In other study, it is also stated that deviations from Hardy-Weinberg equilibrium could also be due to a variety of causes including: excess of heterozygote individuals than homozygote individuals [71] in contrast Mahmoudi et al. [2] who stated heterozygosis deficiency is one of the parameters underlying departure from HWE), migration, high mutation rate at microsatellite loci and artificial selection .

GENETIC DISTANCE AMONG POPULATIONS

The simplest parameters for assessing diversity among breeds are the genetic differentiation or fixation indices. Several estimators have been proposed (e.g. F_{ST} and G_{ST}), the most widely used being F_{ST} [72], which measure the degree of genetic differentiation of subpopulations through calculation of the standardized variances

in allele frequencies among populations. Statistical significance can be calculated for the F_{ST} values between pairs of populations [73] to test the null hypothesis of lack of genetic differentiation between populations and, therefore, partitioning of genetic diversity [74]. Hierarchical analysis of molecular variance (AMOVA) can be performed to assess the distribution of diversity within and among groups of population [75].

In relative to other markers, microsatellite data are commonly used to assess genetic relationships between populations and individuals through the estimation of genetic distances [76-80]. The most commonly used measure of genetic distances is Nei's standard genetic distance (D_S) [81]. However, the modified Cavalli-Sforza distance (D_A) is recommended for closely related populations where genetic drift is the main factor of genetic differentiation, as is often the case in livestock populations particularly in the developing world [82].

Genetic relationship between populations is often visualized through the reconstruction of a phylogeny, most often using the neighbor joining (N-J) method [83]. However, a major drawback of phylogenetic tree reconstruction is that the evolution of lineages is assumed to be non-reticulated, i.e. lineages can diverge, but can never result from crosses between lineages. This assumption will rarely hold for livestock where new breeds often originate from cross-breeding between two or more ancestral breeds. The visualization of the evolution of breeds provided by phylogenetic reconstruction must, therefore, be interpreted cautiously.

Multivariate analysis and more recently Bayesian clustering approaches have been suggested for admixture analysis of microsatellite data from different populations [84]. Probably the most comprehensive study of this type in livestock is a continent-wide study of African cattle [85], which reveal the genetic signatures of the origins, secondary movements, and differentiation of African cattle pastoralism.

Based on comparison of genetic distances that measure genetic drift, with microsatellite data set, the Reynolds distances underestimate the divergence of eastern Mediterranean goat populations (Saudi Arabia, Turkey, Albania and Cyprus) with a high heterozygosity [48]. Model-based clustering [84] of the goat microsatellite genotypic values indicates that the most significant subdivision is at the level of breeds or groups of closely related breeds [48]. Analysis at lower *K*-values may indicate a subdivision of the goat population [86] that preceded breed formation.

In relative to other reports, lower average values of F_{ST} for the four goat populations clusters (East Mediterranean: F_{ST}=0.033, Central Mediterranean: F_{ST}=0.040, West Mediterranean: F_{ST}=0.051 and Central-north European: F_{ST}=0.069) were obtained [48] than the values of 0.14 recorded for Asian goats [27], of 0.17 for Swiss goat populations [49] and of 0.10 for a set of Chinese goat populations [16]. Similar low estimate of mean differentiation among populations (F_{ST} = 0.0717) was also reported that indicates presence of mixing among population and the most variability occurs within a population [40]. This might be because of gene flow among most breeds has probably been restricted by geographical isolation rather than adherence to pedigree; i.e. a geographical restriction of genetic contacts of population may cause geographical clines or maintain clines that predate breed formation [48].

F_{ST} values for each pair of the goat populations in Ethiopia varied from 0.001 to 0.040 [22]. The average F_{ST} values over all microsatellite loci was 0.026, indicating that a 2.6% of total genetic variation corresponded to differences among populations, whereas 97.4% was explained by difference among individuals. Similarly, it was also noted that 5% of the total variation occurred due to population subdivision, while the remaining 95% of the variation existed among individuals within the goat ecotypes [24].

It was recommended that the highest genetic distance (F_{ST}) to be higher than 0.25, moderate to be between 0.05 and 0.25 and the lowest estimate below 0.05 [46, 87]. In general, the genetic distance between populations obtained by many of the scholars [16, 21, 22, 24, 40] is almost negligible (<0.05) and/or moderate ($0.05<F_{ST}<0.25$) values. Some of the authors revealed significant genetic distance estimates among populations. This implies that, despite the limitations of sampling and other related statistical management limitations stated above there is relatively moderate genetic sub-differentiation among the goat populations. A fixation index (F_{ST}) of about 0.15 is considered to be an indication of significant differentiation among populations [88]. In line with this, as an indirect way to measure quantitative genetic diversity, a fixation index (F_{ST}) of about 0.25 total genetic variance could be explained among-breed genetic variance [49].

In the phylogeny tree analysis employing both the NJ and UPGMA trees might be good. However, it would have been more informative if the fitness of the trees were statistically tested. This limitation makes the result blurred and difficult to arrive at certain conclusion with either of the phylogenetic tree analyses. In addition, besides to the polymorphic nature of microsatellites there might be a chance to face monomorphic nature of them. Hence, this demands some techniques to isolate such loci. However, there is no clear methodology that describes whether such techniques were employed or not. Monomorphic microsatellite loci were obtained while studying the Indian domestic goat populations and dropped out from the analysis [30]. Probably, the minimum

estimates of MNA per locus obtained in the microsatellite loci genotyped might be an indication of absence of employing some screening techniques. Such limitations were seen in many of the studies.

GAPS IDENTIFIED

Apart from the least sample size used in some of the studies, e.g. Halima et al [24] who used eight animals to represent a population and which is quite far from FAO recommendation for SSR marker analysis [89], the number of samples used for a study was not equal which leads the genetic diversity parameters like HWE and MNA to be sensitive for biasness; or there is no any technique indicated in the papers which was employed to handle such a limitation [90]. Large samples are expected to have more alleles than small samples [91]; however, the degree of influence of small sample size is weak as compared with the size of number of markers to be used [90].

In addition to the procedures to be followed in handling unequal sample size, selection of microsatellite loci which are efficient in polymorphism and techniques of screening monomorphic loci [93] and design of statistical genetic analysis in general are not clearly indicated in the papers and might bias the readers. This ultimately could have their own influence on implementation of further activities of improvement and conservation breeding programs. On the other hand, only very few or no microsatellite loci used in the analysis showed higher observed heterozygosity values than expected heterozygosity values [16, 22, 24, 39, 40]. This probably implies the existence of sampling bias [45]. In addition, some of the microsatellite loci (table 1) had shown H_E and H_O estimates of less than 0.5; however, it was suggested that such loci having values less than 0.5 are not appropriate for heterozygosity evaluation [44,45]. Similarly, the number of alleles found per locus is the other indicative in evaluating the efficiency of loci; hence, though it was not seen in some of the studies found in table 2, the number of alleles to be found per locus for remarkable genetic diversity of a population should be equal or greater than four [25, 92]. These all points remark as the microsatellites could be dropped out or could require to be prudent in selecting microsatellite. Apart from that it is important to note to be keen in selecting microsatellites to deliver strong recommendation that serves for effective sustainable conservation and breeding management strategies.

CONCLUSIONS AND RECOMMENDATION

Genetic diversity studies carried out on domestic goat at various parts of the world were compiled in this paper. More than 120 goat populations were included in the review. These all goat populations were studied with microsatellite markers. The results indicated that there is high within population genetic variations and very narrow population differentiation among the goat populations studied. On the other side, limited sample sizes which are not equal for the populations included in the respective studies, weak efficiency of the markers employed for the analysis (e.g. few numbers of alleles per marker, very low heterozygosity estimate per marker, etc) which lead to bias the parameters measured or absence of handling techniques to capture those limitations are observed in most of the studies. In general these all demand further works to support the goat breeding interventions.

Competing Interests
The authors have declared that there is no competing interest

REFERENCES

1. Soule M. 1987. Viable populations for conservation. Cambridge Univ. press, Cambridge.
2. Mahmoudi B, Babayev M. Sh., HayeriKhiavi F, Pourhosein A and Daliri M. 2011. Breed characteristics in Iranian native goat populations. Journal of Cell and Animal Biology Vol. 5(7), pp. 129-134, July 2011.
3. Väli Ü, Annika E, Lisette W and Hans E. 2008. To what extent do microsatellite markers reflect genome-wide genetic diversity in natural populations? Molecular Ecology 17: 3808–3817.
4. Cardellino RA and Boyazoglu J. 2009. Research opportunities in the field of animal genetic resources. Livestock Sci. 120:166–173.
5. Wright S. 1943. Isolation by distance. Genetics 38 : 114 March 1943.
6. Gübitz T, Thorpe RS andMalhotra A. 2000. Phylogeographic and natural selection in the Tenerife gecko Tarentoladelalandii: testing historical and adaptive hypotheses. Molecular Ecology 9: 1213–21.

7. Nicholls JA and Austin JJ. 2005. Phylogeography of an east Australian wet-forest bird, the satin bowerbird (Ptilonorhynchusviolaceusi), derived from mtDNA, and its relationship to morphology. Molecular Ecology 14: 1485–96.
8. Trizio I, Crestanello B, Galbusera P, Wauters A, Tosi G, Matthysen E and Hauffe C. 2005. Geographical distance and physical barriers shape the genetic structure of Eurasian squirrels (Sciurus vulgaris) in the Italian Alps. Molecular Ecology 14: 469–81.
9. Brown RP and Thorpe RS. 1991. Description of within-island microgeographic variation in body dimensions and scalation of the skink Chalcidessexlineatus, which testing of causal hypotheses. Bio.J. of the Linnean Society 44: 47-64.
10. Gizaw S, Van Arendonk JAM, Komen H, Windig JJ and Hanotte O. 2007. Population structure, genetic variation and morphological diversity in indigenous sheep of Ethiopia. Animal Genetics, 38: 621–628.
11. Kumar S, Gupta T, Kumar N, Dikshit K, Navani N, Jain P, Nagarajan M. 2006. Genetic variation and relationships among eight Indian riverine buffalo breeds. Mol. Ecol., 15: 593-600.
12. Kevorkian SEM, Georgescu SE, Manea MA, Zaulet M, Hermenean AO, Costache M. 2010. Genetic diversity using microsatellite markers in four Romanian autochthonus sheep breeds. Rom. Biotechnol. Lett. 15(1): 5059-5065.
13. Glowatzki-Mullis ML, Muntwyler J, Bäumle E, Gaillard C. 2008. Genetic diversity measures of Swiss goat breeds as decision-making support for conservation policy. Small Rum. Res. 74(1-3): 202-211.
14. Ali BA. 2003. Genetics similarity among four breeds of sheep in Egypt detected by random amplified polymorphic DNA markers. African Journal of Biotechnology Vol. 2 (7): 194–197.
15. Meghen C, MacHugh DE and Bradley DG. 1994. Genetic characterization and West African cattle. World Anim. Rev.,78: 59-66.
16. Li MH, Zhao SH, Bian C, Wanng HS, Wei H, Liu B, Mei Yu M, Fan B, Chen SL, Zhu MJ, Li SJ, Xiong TA, Li K. 2002. Genetic relationships among twelve Chinese indigenous goat populations based on microsatellite analysis. Genet. Sel. Evol. 34: 729–744.
17. Yadav A and Yadav BR. 2008. DNA Fingerprint: Genetic relationship in six Indian goat breeds. Indian J. Biotechnol. 7: 487-490.
18. Amills M, Ramı´rez O, Toma`s A, Badaoui B, Marmi J, Acosta J, Sa`nchez A and Capote J. 2008. Mitochondrial DNA diversity and origins of South and Central American goats. Animal Genetics, 40: 315–322.
19. Abdel-Aziz M. 2010. Present status of the world goat populations and their productivity. Lohmann information. Vol. 45 (2).
20. Pariacote F. 2006. The goat in South America and development perspectives. In: International Symposium Goat Farming Central, Eastern European countries, present and future. IGA-CAPRIROM. Constanta, Romania.
21. Hoda A, Sena L and Hykaj G. 2012. Genetic diversity revealed by AFLP markers in Albanian goat breeds. Archives of Biological Sciences 64, (2): 799-807.
22. Tesfaye AT. 2004. Genetic characterization of indigenous goat populations of Ethiopia using microsatellite DNA markers. A PhD thesis submitted to the national dairy research institute, Deemed University. Karnal-Haryana, India.
23. Ramamoorthi J, Thilagam K, Sivaselvam SN and Karthickeyan SMK. 2009. Genetic characterization of Barbari goats using microsatellite markers. Journal of Veterinary Science 10(1): 73-76.
24. Halima H, Samer L, Barbara R, Michael B and Markos T. 2012. Molecular characterization of Ethiopian indigenous goat populations. Trop Anim Health Prod 44:1239–1246.
25. Barker JSF. 1994. A global protocol for determining genetic distances among domestic livestock breeds. In: V World Congress on Genetics Applied to Livestock Production, Gelph: sd, v. 21, pp 501-508.
26. Ojango JM, Mpofu N, Marshall K and Andersson-Eklund L. 2011. Quantitative methods to improve the understanding and utilisation of animal genetic resources In:Animal Genetics Training Resource, version 3, 2011. Ojango, J.M., Malmfors, B. and Okeyo, A.M. (Eds). International Livestock Research Institute, Nairobi, Kenya, and Swedish University of Agricultural Sciences, Uppsala, Sweden.
27. Barker JSF, Tan SG, Moore SS, Mukherjee TK, Matheson JL and Selvaraj OS. 2001. Genetic variation within and relationships among populations of Asian goats (Capra hircus). Journal of Animal Breeding and Genetics 118: 213–23.
28. Kim KS, Yeo JS, Lee JW, Kim JW and Choi CB. 2002. Genetic diversity of goats from Korea and China using microsatellite analysis. Asian-Australasian Journal of Animal Science 4: 461-465

29. Fatima S, Bhong CD, Rank DN and Joshi CG. 2008 Genetic variability and bottleneck studies in ZalawadiGohilwadi and Surti goat breeds of Gujarat (India) using microsatellites. Small Ruminant Research 77: 58-64.
30. Pramod KR, Manjunath BJ, Ajoy M, Laloe D, Singh L and Thangaraj K. 2008. Microsatellite-based phylogeny of Indian domestic goats. BMC Genetics 9:11.
31. Dixit SP, Verma NK, Aggarwal RAK, Kumar S, Chander R, Vyas MK and Singh KP. 2009. Genetic Structure and Differentiation of Three Indian Goat Breeds. Asian-Aust. J. Anim. Sci. Vol. 22, No. 9 : 1234 – 1240
32. Kumar D, Dixit SP, Sharma R, Pandey AK, Sirohi G, Patel AK, Aggarwal RAK, Verma NK, Gour DS and Ahlawat SPS. 2005. Population structure genetic variation and management of Marwari goats. Small Ruminant Research. 59:41-48.
33. MartínezAM, Carrera MP, Acosta JM, Rodríguez-Gallarda PP, Cabello A, Camacho E, Delgado JV. 2004. Genetic characterization of the Blanca Andaluza goat based on microsatellite markers. S. Afr. J. Anim. Sci. 34(1):17-19.
34. Kotze A, Swart H, Grobler JP and Nemaangani A. 2004. A genetic profile of the Kalahari Red goat breed from Southern Africa. South African Journal of Animal Science 34(1):10-12.
35. Muema EK, Wakhungu JW, Hanotte O and Jianlin H. 2009. Genetic diversity and relationship of indigenous goats of Sub-saharan Africa using microsatellite DNA markers. Livestock Research for Rural Development. Volume 21, Article #28. http://www.lrrd.org/lrrd21/2/muem21028.htm
36. Serrano M, Calvo JH, Martínez M, Marcos-Carcavilla A, Cuevas J, González C, Jurado JJ, de Tejada PD. 2009. Microsatellite based genetic diversity and population structure of the endangered Spanish Guadarrama goat breed. BMC Genet.10: 61.
37. Jelena R, Mio B, Curkovic M, Pavic V, Ivankovic A and Medugorac I. 2011. Genetic diversity measures of the Croatian spotted goat. ActaVeterinaria (Beograd), Vol. 61, No. 4: 373-382.
38. Verma NK Dixit SP, Aggarwal RAK, Chander R, Kumar S, Ahlawat SPS. 2007. Genetic analysis of the Sirohi breed of Indian goat (Capra hircus). Korean J. Genetics. 29:129-136.
39. Di R, FarhadVahidi SM, Ma YH, He XH, Zhao QJ, Han JL, Guan WJ, Chu MX, Sun W and Pu YP. 2010. Microsatellite analysis revealed genetic diversity and population structure among Chinese cashmere goats. J. Animal Genetics. doi: 10.1111/j.1365-2052.2010.02072.x
40. Araújo AM, Guimarães SEF, Machado TMM, Lopes PS, Pereira CS, da Silva FLR, Rodrigues MT, Columbiano VS and Fonseca CG. 2006. Genetic diversity between herds of Alpine and Saanen dairy goats and the naturalized Brazilian Moxotó breed. J. Genetics and Molecular Biology, 29, No.1: 67-74.
41. Aljumaah RS, Musthafa MM, Al-Shaikh MA, Badri OM and Hussein MF. 2012. Genetic diversity of Ardi goat based on microsatellite analysis. African Journal of Biotechnology Vol. 11(100): 16539-16545
42. Agha SH, Pilla F, Galal S, Shaat I, D'Andrea M, Reale S, Abdelsalam AZA and Li MH. 2008. Genetic diversity in Egyptian and Italian goat breeds measured with microsatellite polymorphism. J. Anim. Breed. Genet. 125: 194–200.
43. Maletsanake D, Nsoso SJ and Kgwatalala PM. 2013. Genetic variation from 12 microsatellite makers in an indigenous Tswana goat flock in South-eastern Botswana. Livestock Research for Rural Development 25 (2)
44. Davila SG, Gil Resino-Talavan MG and Campo JL. 2009. Evaluation of diversity between different Spanish chicken breeds, a tester line and White Leghorn population based on microsatellite markers. Poult.Sci., 88: 2518-2525
45. Dorji N, Duangjinda M and Phasuk Y. 2012. Genetic characterization of Bhutanese native chickens based on an analysis of Red Junglefowl (Gallus gallusgallus and Gallus gallusspadecieus), domestic Southeast Asian and commercial chicken lines (Gallus gallusdomesticus). Genetics and Molecular Biology, 35, 3: 603-609.
46. Kalinwski ST. 2002. How many alleles per locus should be used to estimated genetic distances? Heredity, 88: 62-65.
47. Saitbekova N, Gaillard C, Obexer-Ruff G and Dolf G. 1999. Genetic diversity in Swiss goat breeds based on microsatellite analysis. Animal Genetics 30, 36–41.
48. Cañón J, Garcı´a D, Garcı´a-Atance MA, Obexer-Ruff G, Lenstra JA, Ajmone-Marsan P, Dunner S and The ECONOGENE Consortium. 2006. Geographical partitioning of goat diversity in Europe and the Middle East. J.Animal Genetics, 37: 327–334.
49. Nomura K, Ishii K, Dadi H, Takahashi Y, Minezawa M, Cho CY, SutopoFaruque MO, Nyamsamba D and Amano T. 2012. Microsatellite DNA markers indicate three genetic lineages in East Asian indigenous goat populations. Animal Genetics, 43: 760–767

50. Kalinowski ST. 2004. Counting alleles with rarefaction: Private alleles and hierarchical sampling designs. Conservation Genetics 5: 539–543, 2004.
51. Nsoso SJ, Machete JB, Molatole M, Ndebele RT, Lebani NN, Chabo RG, Kalake AM, Jacyna L, Segadimo BW and Mine OM. 2001. The impact of traditional management on seasonal internal parasite burdens and productivity of indigenous Tswana goats in southern Botswana. Onderstepoort Journal of Veterinary Research 68: 101-104
52. Callen DF, Thompson AD, Shen Y, Phillips HA, Richards RI, Mully JC, Sutherland GR. 1993. Incidence and origin of "null" alleles in the (AC)n Microsatellite markers. Am. J. Hum. Genet., 52: 922-927.
53. Pemberton JM, Slate J, Bancroft DR, Barrett JA. 1995. Non amplifying alleles at microsatellite loci: A caution for parentage and population studies. Mol. Ecol., 4: 249-252.
54. Manel S, Berthier P and Luikart G. 2002. Detecting wildlife poaching: identifying the origin of individuals with Bayesian assignment test and multilocus genotypes. Conservation Biology 16: 650–9.
55. Cymbron T, Freeman AR, Isabel Malheiro M, Vigne JD and Bradley DG. 2005. Microsatellite diversity suggests different histories for Mediterranean and northern European cattle populations. Proceedings of the Royal Society of London Series B, Biological Sciences 272: 1837–43.
56. Botstein D, White RL, Skolnick M, Davis RW. 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. American Journal of Human Genetics, 32, 314–331.
57. Marshall TC, Slate J, Kruuuk LEB and Pemberton JM. 1998. Statistical confidence for likelihood-based paternity inference in natural population. Molecular Ecology (1998) 7, 639-655.
58. Kumar S, Dixit SP, Verma NK, Singh DK and Pande A, Kumar S, Chander R, Singh LB. 2009. Genetic diversity analysis of the Gohilwari breed of Indian goat (Capra hircus) using microsatellite markers. Am. J. Anim. Vet. Sci., 4: 49-57. DOI: 10.3844/ajavsp.2009.49.57.
59. Widmer A and Lexer C. 2001. Glacial refugia: sanctuaries for allelic richness, but not for gene diversity. TRENDS in Ecology & Evolution Vol.16 No.6.
60. Aggarwal RAK, Dixit SP, Verma NK, Ahlawat SPS, Kumar Y, Kumar S, Chander R and Singh KP. 2007. Population genetics analysis of Mehsana goat based on microsatellite markers. Current Science 92: 1133–1137
61. Mahmoudi B and Babayev MS. 2009. The investigation of genetic variation in Taleshi goat using microsatellite marker. Res. J. Biol. Sci. 4(6):644-646.
62. Mahmoudi B, Mansour B, Reza S, Majnun SB and Hamed A. 2010. Genetic Diversity among Three Goat Populations Assessed by Microsatellite DNA Markers in Iran. J. Global Veterinaria 4 (2): 118-124.
63. Els JF, Kotze A and Swart H. 2004. Genetic diversity of indigenous goats in Namibia using microsatellite markers: preliminary results. South African Journal of Animal Science, 34 (Supplement 2).
64. Garrine CMLP, Kotze A, Els H and Grobler JP. 2010. Genetic characterization of the indigenous Landim and Pafuri goat breeds from Mozambique. African Journal of Agricultural Research 5(22): 3130-3137
65. Qi YJ, Luo XF, Han YZ, Zhu C, Chen JX, Liu and Sheng HJ. 2009. Genetic diversity and relationships of 10 Chinese goat breeds in the Middle and Western China. Small Rumin. Res. 82:88-93.
66. Gour DS, Malik G, Ahlawat SPS, Pandey AK, Sharma R, Gupta N, Gupta SC, Bisen P and Kumar D. 2006. Analysis of genetic structure of Jamunapari goats by microsatellite markers. Small ruminant research 2006; 66:140-149.
67. Thilagam K, Ramamoorthi J, Sivaselvam SN, Karthickeyan SMK and Thangaraju P. 2006. Kanniadu goats of Tamilnadu, India: genetic characterisation through microsatellite markers. Livestock Research for Rural Development 18 (10): http://www.lrrd.org/lrrd18/10/thil18149.htm
68. Beh KJ, Hulme DJ, Callaghan MJ, Leish Z, Lenane I, Windon RG and Maddox JF. 2002. A genome scan for quantitative trait loci affecting resistance to Trichostrongyluscolubriformisin sheep. Animal Genetics 33: 97–106
69. Schwaiger FW, Buitkamp J, Weyers E, Epplen JT. 1993. Typing of MHC-DRB genes with the help of intronic simple repeated DNA sequences. Molecular Ecology 2, 55–9.
70. Hedrick PW and Kim KJ. 2000. Genetics of complex polymorphisms: parasites and maintenance of the major histocompatibility complex variation. In: Evolutionary Genetics: from Molecules to Morphology (Ed. by R.S. Singh & C.B. Krimbas), pp. 204–234.Cambridge University Press, Cambridge
71. Aminafshar M, Amirinia C and Torshizi RV. 2008. Genetic diversity in buffalo population of Guilan using microsatellite marker. Journal of Animal and Veterinary Advances 7(11): 1499-1502
72. Weir BS and Basten CJ. 1990. Sampling strategies for distances between DNA sequences. Biometrics46:551-582.

73. Weir BS and Cockerham CC. 1984. Estimating Fstatistics for the analysis of population structure. Evolution, 38: 1358–1370.
74. Mburu DN, Ochieng JW, Kuria SG, Jianlin H and Kaufmann B. 2003. Genetic diversity and relationships of indigenous Kenyan camel (Camelusdromedarius) populations: implications for their classification. Animal Genetics, 34(1): 26–32.
75. Excoffier L, Smouse PE and Quattro JM. 1992. Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data. Genetics, 131: 479–491.
76. Beja-Pereira A, Alexandrino P, Bessa I, Carretero Y, Dunner S, Ferrand N, Jordana J, Laloe D, Moazami-Goudarzi K, Sanchez A and Canon J. 2003. Genetic characterization of southwestern European bovine breeds: a historical and biogeographical reassessment with a set of 16 microsatellites. Journal of Heredity, 94: 243–50.
77. Ibeagha-Awemu EM, Jann OC, Weimann C and Erhardt G. 2004. Genetic diversity, introgression and relationships among West/Central African cattle breeds. Genetics Selection Evolution, 36: 673–690.
78. Joshi MB, Rout PK, Mandal AK, Tyler-Smith C, Singh L and Thangaraj K. 2004. Phylogeography and origin of Indian domestic goats. Molecular Biology and Evolution, 21: 454–462.
79. Sodhi M, Mukesh M, Mishra BP, Mitkari KR, Prakash B and Ahlawat SP. 2005. Evaluation of genetic differentiation in Bosindicuscattle breeds from Marathwada region of India using microsatellite polymorphism. Animal Biotechnology, 16: 127–137.
80. Tapio M, Tapio I, Grislis Z, Holm LE, Jeppsson S, Kantanen J, Miceikiene I, Olsaker I, Viinalass H and Eythorsdottir E. 2005. Native breeds demonstrate high contributions to the molecular variation in northern European sheep. Molecular Ecology, 14: 3951–3963.
81. Nei M. 1972. Genetic distance between populations. The American Naturalist, 106: 283–292.
82. Nei M, Tajima F And Tateno Y. 1983. Accuracy of estimated phylogenetic trees from molecular data. II. Gene frequency data. Journal of Molecular Evolution, 19: 153–170.
83. Saitou N and Nei M. 1987. The neighbour-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution, 4: 406–425.
84. Pritchard JK, Stephens M and Donnelly P. 2000. Inference of population structure from multilocus genotype data. Genetics 155: 945–59.
85. Hanotte O, Bradley DG, Ochieng JW, Verjee Y, Hill EW and Rege JEO. 2002. African pastoralism: genetic imprints of origins and migrations. Science 296: 336–9.
86. Rosenberg NA, Pritchard JK, Weber JL, Cann HM, Kidd KK, Zhivotovsky LA and Feldman MW. 2002. Genetic structure of human populations. Science 298: 2381–5.
87. Weir BS. 1996. Genetic Data Analysis II. Sinauer Associates, Inc, Sunderland, MA.
88. Frankham R, Briscoe DA and Ballou JD. 2002. Introduction to conservation genetics. Cambridge University Press, New York, New York, USA.
89. FAO. 2011. Food and Agricultural organization. Molecular genetic characterization of animal genetic resources. FAO Animal Production and Health Guidelines. No. 9. Rome.
90. Landguth EL, Fedy BC, Oyler-McCance SJ, Garey AL, Emel SL, Mumma M, Wagner HH, Fortin MJE and Cushman SA. 2012. Effects of sample size, number of markers, and allelic richness on the detection of spatial genetic pattern. Molecular Ecology Resources, 12: 276–284.
91. Kalinowski ST. 2005. Do polymorphic loci require large sample sizes to estimate genetic distances? Heredity 94: 33–36
92. Nassiry MR, Javanmard A and Tohidi R. 2009. Application of statistical procedures for analysis of genetic diversity in domestic animal populations. Am J Anim Vet Sci 4:136-141.
93. Takezaki N and Nei M. 1996. Genetic distances and reconstruction of phylogenetic trees from microsatellite DNA. Genetics 144:389-399.