Evaluation of genetic diversity of Deccani and Madgyal sheep from Southern peninsular region of India

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ABSTRACT

Information is presented on the genetic diversity analysis of Deccani and Madgyal, two peculiar sheep breeds of Maharashtra state of Southern peninsular zone of India, based on twenty five microsatellite markers recommended for ovines. All the markers were polymorphic in both the populations. Estimates of observed (na) and effective number of alleles (ne), allele diversity, gene diversity and fixation indices (f, θ and F) were obtained. Genetic variation observed in terms of allele diversity (>7) and gene diversity (>0.6) revealed high level of genetic diversity within the investigated populations. There was no indication of a recent bottleneck in either population. A higher deficit of heterozygotes (FIS) was detected in Deccani (0.132) as compared to Madgyal (0.038). The estimation of θ showed that the relative magnitude of population differentiation between the two populations was quite low at 1.4%. The Nei's standard genetic distance between Deccani and Madgyal sheep was estimated to be 0.080. Considerably higher level of gene flow (14.3) observed between them was suggested to be enough to attenuate the genetic differentiation between the two sheep populations. A fairly lower degree of reliability was obtained for the individual breed assignment from the 25 loci using the Bayesian method with an accuracy of 85% only. The results showed that though there is high genetic diversity within each of Deccani and Madgyal sheep populations but there is a relatively low level of genetic differentiation between them. Negative value of relatedness reflected the influx of new germplasm in both the investigated populations. The results reported here would provide important information for the accomplishment of genetic improvement not only in the threatened Madgyal but also in Deccani-one of the numerically abundant breed from Maharashtra.

Key Words: Deccani, Madgyal, Indian sheep, microsatellite, genetic diversity, genetic improvement

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INTRODUCTION

Ovine genetic resources in India are a major source of livelihood for pastoralists and marginal farmers. Sheep contribute substantially to the income of their keepers in terms of wool, meat, hide and dung, inspite of being reared on scarce or no input, especially in harsh agroclimatic conditions. Over the years shepherds have evolved new and improved breeds by selection. In drought prone areas of western and central regions of Maharashtra where sheep rearing is the major occupation, Deccani and recently derived Madgyal sheep raising is basically carried out for meat production.

The sheep of Deccan Plateau of Maharashtra named as Deccani sheep is the most prevalent breed (population 1.5 lakhs, NBAGR Annual Report, 2003-04) from Maharashtra and perhaps the largest contributor of mutton production in the country. Deccani- one of the unique sheep breeds of India is comprised of small to medium sized, coarse wooled, hardy animals well adapted to scanty pastures/draught conditions and capable of walking long distances during migration. Although Deccani is designated as a distinct breed, the animals exhibit heterogeneity in their colour patterns, varying from black to brown and white types. The other colour patterns in Deccani comprise animals of black colour with white patches, black-brown, white-brown and black-brown-white coloured animals. Deccani is mostly found in southeastern part of Maharashtra, neighboring areas of Andhra Pradesh and Karnataka. In Maharashtra the breed is widely distributed in Nasik, Pune, Ahmadnagar, Kolhapur, Solapur, Sangli, Satara and Beed districts (Fig.1). The animals of Deccani sheep are migratory and represent a transition between the coarse wool Rajasthani sheep of Northwestern arid and semi arid (NWASA) region and the hairy sheep of Andhra Pradesh, Tamil Nadu of the Southern peninsular region of India (Nimbkar 1994). Wool production in Deccani, is however, very low and it is mainly bred for mutton.

Sheep breeders from Madgyal and its adjacent villages of Jath Taluka of Sangli District in Maharashtra have recently evolved a new strain of sheep through selection and given the name Madgyal (Waghmode et al., 2008). Morphological characterization of Madgyal sheep has been carried out by the Punyashloka Ahilyadevi Maharashtra Mendhi Va Sheli Vikas Mahamandal (PAMMSVM) Ltd. Pune- a Government of Maharashtra undertaking. The animals are phenotypically quite different from Deccani and are generally white with brown patches, hairy type and tall. The Madgyal sheep are also much superior in respect of body gain, prolificacy, early maturity and adult weight in comparison to Deccani. In view of their superiority over Deccani, the Madgyal rams are becoming increasingly popular for upgradation of local flocks. Some Madgyal sheep flocks are also being maintained at sheep farms at Dahivadi (district Satara), Mahud (district Solapur), Ranjani (district Sangli) and Rahuri (district Ahmadnagar) maintained by PAMMSVM, Pune. The animals of Madgyal are also present in Satara district in addition to Sangli of Maharashtra, which is also the breeding tract of Deccani sheep. In view of the threatened status (5319- as per statistical Survey of Department of Animal Husbandry, Govt. of Maharashtra for the year 2003), its utility and heavy demand the Government of India, Ministry of Agriculture, Department of Animal Husbandary and Dairying, New Delhi has sanctioned a centrally sponsored scheme (2003) for Madgyal sheep conservation.

Despite peculiar characteristics of Deccani and Madgyal sheep and their immense economic importance, scanty efforts have been made for their genetic improvement. Genetic characterization of these two locally important sheep breeds of the same agro-ecological region by using DNA based microsatellite markers will, therefore, provide a molecular marker based approach to assess the current within breed genetic diversity and the extent of genetic exchange between the two breeds. Such important elements would have direct bearing on the genetic improvement and management strategies of Deccani and Madgyal sheep of Maharashtra.

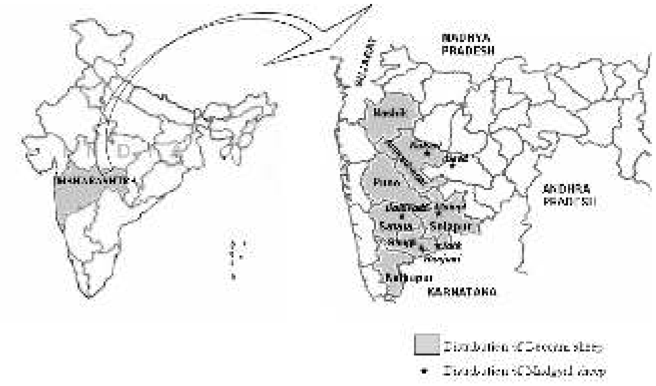

Fig. 1. Distribution of Deccani and Madgyal sheep in Maharashtra

MATERIALS AND METHODS

Sample collection and DNA extraction: Blood samples from 40 genetically unrelated sheep from each of Deccani and Madgyal were randomly collected from several flocks in villages of Satara, Solapur districts and from PAMMSVM farm, Ranjani, several villages of Sangli districts of Maharashtra respectively. Genomic DNA was isolated from the blood samples and purified using the standard phenol chloroform extraction protocol.

Genotyping with microsatellite markers: A panel of twenty-five microsatellites was genotyped on 80 DNA samples of the investigated sheep populations. The forward primer for each marker was fluorescently labeled with either FAM, NED, VIC or PET dye. Amplification of the loci was performed in a 25µl final reaction volume containing at least 100ng of genomic DNA, 5 pM of each primer, 1.5 mM $MgCl_2$, 200 µM dNTPs, 0.5 U Taq polymerase and 1x buffer. A common "Touchdown" PCR programme (FAO 1996) was used for amplification of all the twenty-five markers. Amplification was confirmed on 2% agarose gel and the genotyping were carried out on ABI 3100 automated DNA sequencer using LIZ 500 as internal size standard. Allele sizing was done using GENEMAPPER software (ABI, USA).

Statistical analysis: The GenAlEx6 (Peakall and Smouse 2006) software was used to determine allele frequencies, observed number of alleles, effective number of alleles, observed heterozygosity, expected heterozygosity, allele diversity, gene diversity, within population inbreeding estimate and Nei's genetic distance (Nei 1972). Hardy-Weinberg equilibrium (HWE) for each locus was tested with the program GENEPOP version 3.3 (Raymond and Rousset 1995). Polymorphism Information Content (PIC) was calculated using the formula given by Botstein et al., (1980). BOTTLENECK (version 1.2. 02) software (Piry et al., 1999) was used in this study for detection of bottleneck effect if any, in the investigated sheep populations. The variance-based method of Weir and Cockerham (Weir and Cockerham 1984) was used for computing population differentiation by F-statistics by the FSTAT version 2.9.3.2 programme (Goudet 1995). Mean values of the F-statistics parameters namely θ (measurement of population differentiation), F (total inbreeding estimate) and f (within population inbreeding estimate), which are analogous to Wright's (Wright 1978) FST, FIT and FIS respectively, were obtained across breeds by the Jackknifing procedure over loci (Weir 1990). The level of significance ($p < 0.05$) was determined from permutation test with the sequential Bonferroni procedures applied over all loci. The individual assignment tests were conducted by the program GENECLASS ver 1.0.02 (Cornuet et al., 1999) using the Bayesian method. A neighbour-joining (NJ) radiation tree using individual animals as taxonomic units was constructed with a distance matrix with simple allele sharing statistics.

RESULTS AND DISCUSSION

Within breed genetic diversity: The 25 investigated microsatellite loci spread over 19 ovine chromosomes revealed polymorphism and the total allele count across the analyzed loci was observed to be slightly higher in Deccani (186) than the Madgyal (181) sheep. Allele frequencies for the investigated breeds ranged from 0.013 to 0.946 (data not shown). The observed allele number, effective allele number, observed heterozygosity, expected heterozygosity and degree of inbreeding are given in Table 1 for both the investigated breeds. The number of observed alleles (Na) at each locus varied from 3 (OarAE129) to 13 (CSSM31, OarCP49) in Deccani and 3 (BM6506) to 12 (INRA63) in Madgyal with an average of 7.44 and 7.24 in Deccani and Madgyal respectively. The effective number of alleles (Ne) was observed to be lower than the observed number of alleles as expected and ranged from 1.29 (CSSM47) to 7.66 (OarCP49) in Deccani and 1.12 (CSSM47) to 8.10 (CSSM31) in Madgyal with an average of 3.81 in Deccani and 4.00 in Madgyal.

The average number of alleles (allele diversity) - a reasonable parameter of genetic variation revealed that Deccani and Madgyal harboured a good amount of genetic variation (4 or more than 4 alleles, Li et al., 2002). The allele diversity estimates in this study were observed to be higher than those reported for Garole, Nali, Chokla, Muzzafarnagri, Magra and Chhotanagpuri breeds of Indian sheep (Sodhi et al., 2003; 2006; Arora and Bhatia 2004; 2006; Mukesh et al., 2006; Bhatia and Arora 2008); Brazilian sheep (Paiva et al., 2005) and African sheep (Wafula et al., 2005) probably because of genotyping accomplishment under this study by automated DNA sequencer rather than by silver staining technique and also different set of used markers. Deccani and Madgyal exhibited 46 and 41 alleles that were not shared and specific to two sheep populations respectively. Most of these alleles had frequencies lower that 0.1. The common alleles also showed higher frequency in one population and relatively lower frequency in the other (data not shown).

Table 1. Genetic diversity measures in Deccani and Madgyal sheep across 25 microsatellite markers

Locus	Chr. Loc	Na		Ne		Ho		He		F_{IS}	
		D	M	D	M	D	M	D	M	D	M
BM 757	9	6	9	3.39	4.48	0.417	0.571	0.705	0.777	0.409	0.264
BM 827	3	5	6	3.79	4.36	0.500	0.577	0.736	0.771	0.321	0.251
BM1314	22	4	9	3.56	4.93	0.750	0.657	0.719	0.797	-0.043	0.176
BM6506	1	4	3	1.89	1.86	0.444	0.348	0.470	0.461	0.053	0.246
BM6526	26	5	7	3.36	2.92	0.676	0.816	0.702	0.657	0.038	-0.241
BM8125	17	4	5	2.24	2.69	0.410	0.600	0.553	0.628	0.258	0.045
CSRD247	14	12	9	5.15	5.24	0.725	0.912	0.806	0.809	0.100	-0.127
CSSM31	23	13	9	7.33	8.10	0.500	0.333	0.864	0.877	0.421	0.620
CSSM47	2	4	4	1.29	1.12	0.081	0.054	0.222	0.104	0.635	0.481
HSC	20	11	11	6.83	7.86	0.788	0.867	0.854	0.873	0.077	0.007
INRA63	14	9	12	5.47	5.77	0.667	0.813	0.817	0.827	0.184	0.017
MAF214	16	8	9	2.45	3.17	0.487	0.758	0.592	0.685	0.177	-0.106
OarAE129	5	3	4	1.98	2.28	0.647	0.816	0.496	0.561	-0.304	-0.455
OarCP20	21	7	4	1.76	1.41	0.359	0.185	0.430	0.291	0.166	0.365
OarCP34	3	6	7	3.41	3.84	0.763	0.895	0.706	0.740	-0.080	-0.210
OarCP49	17	13	9	7.66	6.59	0.925	0.971	0.869	0.848	-0.064	-0.144
OarFCB128	2	6	4	2.97	2.16	0.895	0.842	0.663	0.537	-0.349	-0.568
OarFCB48	17	8	5	4.44	2.58	0.541	0.391	0.775	0.612	0.302	0.361
OarHH35	4	9	9	3.82	4.13	0.711	0.923	0.738	0.758	0.038	-0.218
OarHH41	10	6	11	3.55	4.69	0.459	0.541	0.718	0.787	0.360	0.313
OarHH47	18	12	11	5.04	6.20	0.517	0.611	0.801	0.839	0.355	0.271
Oarhh64	4	9	7	3.45	3.58	0.667	0.692	0.710	0.721	0.061	0.039
OarJMP29	24	8	6	3.44	3.58	0.825	0.923	0.709	0.721	-0.164	-0.281
OarJMP8	6	8	5	4.94	3.43	0.641	0.947	0.798	0.708	0.196	-0.338
OarVH72	25	6	6	2.00	3.00	0.419	0.552	0.499	0.666	0.160	0.172
Mean		7.44	7.24	3.81	4.00	0.593	0.664	0.678	0.682	0.132	0.038

Chr.Loc-Chromosomal location; D-Deccani; M-Madgyal Na-Observed allele number; Ne- Effective allele number; Ho-Observed heterozygosity; He-Expected heterozygosity, FIS - within population inbreeding estimates

The observed heterozygosity values ranged from 0.081 (CSSM47) to 0.925 (OarCP49) in Deccani and from 0.054 (CSSM47) to 0.971 (OarCP49) in Madgyal. Expected heterozygosity that is considered to be a better estimator of the genetic variability present in a population (Kim et al., 2002) per locus varied from 0.222 (CSSM47) to 0.869 (OarCP49) in Deccani and 0.104 (CSSM47) to 0.877 (CSSM31) in Madgyal sheep. Most of the loci exhibited substantial heterozygosity (>0.5) in both the studied breeds. The mean observed heterozygosity and expected heterozygosity (gene diversity) values of Deccani and Madgyal were 0.593, 0.678 and 0.664, 0.682 respectively. The mean observed heterozygosity values, though lower than the expected values, exhibited failure of significant differences in both the populations/breeds using ANOVA test (p>0.05). The observed heterozygosity (Ho) averages and gene diversity (He-expected heterozygosity) values of Deccani and Madgyal were comparable to values reported for Indian sheep breeds investigated earlier (Sodhi et al., 2003; Arora and Bhatia 2004, Mukesh et al., 2006; Bhatia et al., 2008). This diversity analysis demonstrated considerable level of genetic variation in both the breeds, with Madgyal displaying somewhat higher levels in comparison to Deccani sheep.

Heterozygote deficiency analysis revealed significant deviation from HWE (P<0.001) at several loci in both the Deccani (BM757, CSSM47, CSSM31, OarVH72, BM6506, OarFCB48, OarJMP8, OarHH35, OarCP49, CSRD 247, MAF214) and Madgyal (BM757, CSSM47, BM6506, BM6526, Oar129, OarCP49). The exact basis of this departure is difficult to explain, however the presence of low frequency null alleles segregating at these loci may be a possible reason. Another reason for this deviation could be the positive FIS (within population inbreeding estimates) values obtained in both the populations (Deccani=0.132 and Madgyal=0.038). Analysis for linkage disequilibrium revealed no significant evidence of linkage (P > 0.01) between loci. Since there was no consistent pattern of deviation from HWE across all the loci or populations, subsequent analyses were carried out on the basis that Hardy-Weinberg equilibrium prevailed in the investigated populations (Marshall et al., 1999).

High degree of polymorphic information content (PIC) was found at each locus and all loci averaged 0.637 and 0.641 in Deccani and Madgyal respectively. Similar results were obtained from microsatellite markers in earlier reported breeds of Indian sheep (Sodhi et al., 2003; Arora and Bhatia 2004; 2006; Mukesh et al., 2006). Following the criteria of Botstein et al., (1980), in the present study 80% markers were highly informative (PIC >0.5), 16% moderately informative (0.25<PIC<0.5) and 4% least informative (PIC<0.25) across Deccani and Madgyal sheep suggesting high utility of these markers for population assignment (MacHugh et al., 1998) and genome mapping (Kayang et al., 2002) studies in addition to genetic diversity analysis in Indian sheep.

Analysis of genetic bottleneck: Efforts were made for estimation of genetic bottleneck by using the qualitative graphical method based on mode-shift distortion under the SMM (Stepwise Mutation Model), which is the most suited model for evolution of microsatellites. No Mode shift was detected in the frequency distribution of alleles and a normal L-shaped form was observed (Fig. 2) for both Deccani and Madgyal sheep. This finding suggested that both the breeds of same agroecological region did not encounter any genetic bottleneck up to 40-80 generation back and thereby reflected absence of any recent reduction in their effective population size. These findings are in agreement with the earlier reports in two sheep breeds viz; Muzzafarnagri and Marwari (Arora and Bhatia 2009) inhabiting the same North western arid and semi arid region of the country. The observed frequency distribution further reflected non- bottlenecked populations of Deccani and Madgyal under mutation drift equilibrium as also revealed by similar tendencies of three variables namely allele diversity, mean observed heterozygosity and gene diversity parameters (Hanslik et al., 2000).

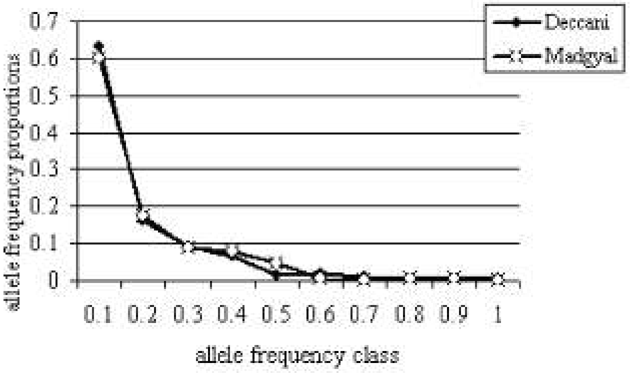

Fig. 2. Normal L-shaped curve indicating no mode shift in Deccani and Madgyal sheep

Analysis of heterozygosity deficiency: Results of within population inbreeding estimate observed at each locus (Table 1) revealed substantial amount of heterozygosity deficit in Deccani (13.2%) in comparison to Madgyal (3.8%). The average FIS value for several of the loci in Deccani and Madgyal were significantly different from Zero. Global analysis showed 9.4% deficit of heterozygotes across the populations and the total population had heterogygote deficiency of 10.7% (Table 2). The main cause for high level of genetic homogeneity or lack of heterozygotes in these Indian sheep breeds might be ascribed to inbreeding as is evident from global analysis (Table 2) by overall positive f value (0.094) and F (0.107) > θ (.014) (Weir 1996). However, the possibility of this heterozygote deficiency to Wahlund effect may also not be ruled out due to pooling samples (within breed) from different breeding flocks i.e. different villages in the same area. Nevertheless, the effect of relatedness of few samples otherwise deemed unrelated during collection cannot be denied in view of absence of pedigreed data under field conditions. The level of inbreeding observed in the present study as per global analysis (f=9.4%) nevertheless suggested unplanned and indiscriminate breeding in both the investigated breeds.

Genetic differentiation between populations: Population differences examined by global analysis of ? (F_{ST})-coefficient of multilocus genetic differentiation fixation index for each of 25 microsatellite loci, across Deccani and Madgyal revealed that levels of differentiation per locus were relatively low and ranged from -0.015 (BM827) to 0.073 (CSRD24) with an average value of 0.014, which was not significant. This finding showed that most of the total genetic variation was attributed to differences among individuals (98.6%) and only 1.4% is the result of differences among the populations. These values of genetic differentiation are lower than those reported for Indian sheep breeds namely Marwari-Sonadi (FST = 5.8%, Bhatia and Arora 2007), Nali-Chokla (FST =8.3%, Sodhi et al., 2006), Korean and Chinese domestic goats (FST =20.2%, Kim et al., 2002) and Asian goat populations (FST =14.3%, Barker et al., 2001). The present findings thus suggested comparatively low level of genetic differentiation between Deccani and Madgyal sheep.

Table 2. F-statistics analyses for 25 microsatellite loci in Deccani and Madgyal sheep populations

Locus	***F***	***θ***	***f***
BM757	0.358	0.034	0.335
BM827	0.290	-0.015	0.300
BM1314	0.184	0.005	0.181
BM6506	0.140	-0.005	0.145
BM6526	-0.077	0.007	-0.085
BM8125	0.166	0.012	0.156
CSRD24	0.082	0.073	0.010
CSSM31	0.492	0.002	0.491
CSSM47	0.600	0.011	0.595
HSC	0.074	0.014	0.061
INRA63	0.120	0.000	0.120
MAF214	0.063	-0.006	0.068
OarAE129	-0.369	0.006	-0.376
OarCP20	0.258	0.019	0.244
OarCP34	-0.135	-0.002	-0.133
OarCP49	-0.079	0.007	-0.087
OarFCB128	-0.417	0.014	-0.436
OarFCB48	0.366	0.045	0.337
OarHH35	-0.080	0.001	-0.081
OarHH41	0.366	0.028	0.348
OarHH47	0.321	-0.002	0.322
OarHH64	0.083	0.021	0.063
OarJMP8	-0.007	0.030	-0.038
OarJMP29	-0.209	0.001	-0.210
OarVH72	0.206	0.029	0.183
Over all loci	0.107	0.014	0.094

The high value of migration (Nm = 14.29) detected between Deccani and Madgyal points towards high level of gene flow thereby substantiating low level of genetic differentiation between the two populations living close to each other. In agreement with present findings high genetic similarity has also been observed between Nali, Chokla Indian sheep (Nm=4.80, Mukesh et al., 2006) and Chinese, Saanen goat (Nm =3.18, Kim et al., 2002) breeds. On the other hand low values of Nm between Korean and Chinese (0.71), Korean and Saanen (0.70) reflected very high genetic differentiation between Korean and two other breeds of goats (Kim et al., 2002). Trexler (1988) showed that gene flow (Nm) >1.0, is enough to attenuate the genetic differentiation between populations. The high level of genetic exchanges between Deccani and Madgyal may be attributed to the fact that sheep breeders are adopting Madgyal rams for breeding their Deccani ewes since they have a better growth rate and body weight. The high level of gene flow between these two sheep breeds may also be attributed to their occurrence as an admixture in Sangli and Satara districts of Maharashtra.

Negative values of relatedness (Relatc = -0.147) observed in the present study, despite high inbreeding, suggested influx of other germplasm in the investigated population. Both these populations are losing their purity because of paucity of pure rams for breeding.

Nei's genetic distance, another parameter for estimating the genetic differentiation between breeds was estimated to be 0.080. This value was comparable to those reported earlier for closely related sheep breeds from India (Sodhi et al., 2006) and Indian buffalo breeds (Tantia et al., 2006). This finding further supported substantial genetic similarity between these two Indian sheep as might be anticipated from the recent derivation of Madgyal sheep in Deccani tract. Moreover, high genetic similarity between these two sheep breeds may also be ascribed to highly migratory nature of Deccani. The route of migration of Deccani sheep from Ahmadnagar, Pune, Satara, Kolhapur, Solapur districts to coastal areas of Konkan of Maharashtra passes through Sangli which is a major breeding tract of Madgyal. High level of genetic similarity between these two breeds of Indian sheep was further confirmed by the NJ radiation tree (Fig. 3).

Evaluation of population differentiation was also done using individual assignment tests. The results based on Bayesian assignment method (Fig.4) demonstrated that the overall accuracy of correct assignment of individuals in the investigated breeds was 85% (80/94). In the present study simulated genotypes from Deccani and Madgyal sheep breeds were observed to be assigned with relatively less accuracies, similar to earlier reports in Nali and Chokla (85.3% Mukesh et al., 2006), Marwari and Sonadi sheep (81%, Bhatia and Arora 2007) and Charolais (93%), Friesian (94%) cattle (MacHaugh et al., 1998) in comparison to perfect assignments (100%) for the individuals of Garole and Pugal sheep (Mukesh et al., 2006; Mishra et al., 2009) and four British Isle and Swiss Simmental breeds (99%) of cattle (MacHaugh et al., 1998). Less percentage assignments further supported relatively high gene flow and intermixing of gene pool between these two breeds which may be attributed to the fact that the provenance of Madgyal sheep is from within the breeding tract of Deccani.

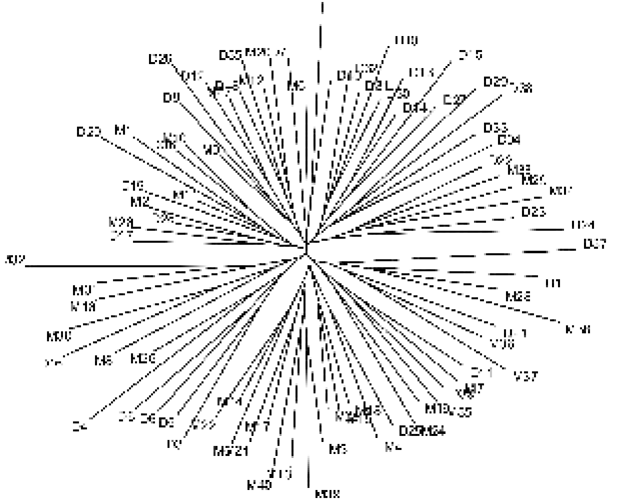

Fig. 3. Radiation tree based on allele sharing distance and neighbour joining algorithm. D-Deccani; M-Madgyal.,

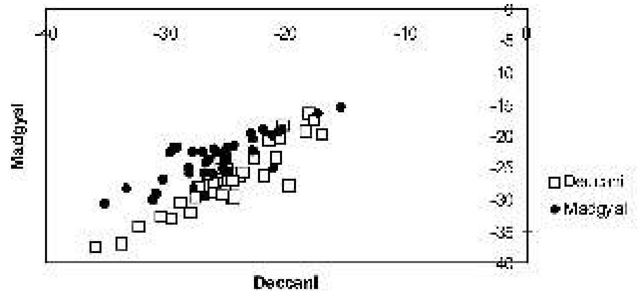

Fig. 4. Population assignment of the individuals in Deccani and Madgyal sheep.

The present study provides valuable insight into the genetic structure of Deccani and Madgyal sheep from Maharashtra. High level of genetic variability within Deccani having normal population status and Madgyal with threatened status is indicative of a valuable reservoir of genetic diversity in both these breeds which can be utilized in their future breeding strategies. Within/ between genetic variability results further emphasized the need for initiating steps for reduction in the levels of inbreeding (f=0.094) and dilution in the genetic material (Relatc=-0.147) of both the investigated sheep populations. Concerted efforts required could include generation of awareness among farmers for the frequent exchange of rams between their flocks and use of selected rams of the specific population to combat high levels of inbreeding and maintenance of breed purity respectively. Moreover, strategies for the genetic improvement should involve selective breeding by using superior rams of the respective breeds for enhancing mutton production in Deccani and Madgyal sheep instead of recent practice of introducing Madgyal rams into Deccani flocks by the small holders. This crossbreeding has led to concerns about the genetic dilution as also evident from this study or possible extinction especially of Deccani sheep (Nimbkar 2006). Practical and effective pastoral management practices would further help to curb continued genetic exchanges (high gene flow, Nm=14.29, low level of genetic differentiation, FST=0.014 and Nei's genetic distance measures =0.080) and also to preserve their adaptive genetic diversity by geographical demarcation of both the sheep groups (Giovambattista et al., 2001). Finally, elucidation of genetic structure and variability between Deccani and Madgyal revealed its direct relevance with the issues of genetic management for their improvement to make such indigenous sheep sustainable in the future.

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