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## Phenotypic characteristics, management, performance and genetic variability in Surti breed of goat

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Genetic and phenotypic characterization of native breeds of goat is a first step in prioritization of breeds for conservation. The Surti, an important goat breed of Gujarat state, known for meat and milk production, is believed to have evolved from small Arabian milking goats. The Surti goat population is rapidly dwindling (Deshpande *et al.* 2009). The characteristics of Surti goats have not been well defined and there is a lot of confusion about its colour variation as indicated by current field survey by the authors. Therefore, phenotypic characterization under field conditions may help to redefine breed characteristics, and an investigation for genetic variation within the breed may help to evaluate how likely various factors responsible for its change are operating so that suitable measures may be undertaken for maintaining

genetic variability and purity of the breed. The specific aim of this study was to characterize Surti goats and to estimate genetic variability within the breed using microsatellite markers.

*Phenotypic characterization:* Preliminary survey done in 2007 indicated that in Gujarat breeding tract runs across 6 districts, viz. Bharuch, Surat, Narmada, Navsari, Valsad and Vadodara. Information on the body biometric characteristics viz. body length from shoulder to pin bone, chest girth, height at wither, paunch girth, face length, ear length, tail length and horn length, and qualitative confirmation attributes and body weights of 153 animals (both male and female) selected randomly were recorded (Table 1). The information on feed, management, breeding practices and reproductive

Table 1. The average ( $\pm$ SE) body weights and biometrical characteristics of Surti breed of goat

Age / Trait	1 Month		3 Month		6 Month		Adult	
	Male	Female	Male	Female	Male	Female	Male	Female
No.	21	13	19	11	6	8	11	64
Weight (kg)	6.22 $\pm$ 0.28	5.81 $\pm$ 0.48	9.79 $\pm$ 0.61	9.93 $\pm$ 0.80	22.50 $\pm$ 1.77	17.81 $\pm$ 0.92	36.27 $\pm$ 2.34	33.26 $\pm$ 1.21
Bodyl (cm)	38.14 $\pm$ 1.23	39.38 $\pm$ 1.64	45.94 $\pm$ 1.49	48.63 $\pm$ 1.51	59.50 $\pm$ 2.63	52.75 $\pm$ 1.44	63.73 $\pm$ 2.55	64.61 $\pm$ 0.78
Height at wither (cm)	41.90 $\pm$ 0.85	40.15 $\pm$ 0.77	48.26 $\pm$ 1.37	50.18 $\pm$ 2.30	64.83 $\pm$ 2.68	58.75 $\pm$ 1.72	73.36 $\pm$ 2.79	69.80 $\pm$ 0.76
Chest girth (cm)	40.62 $\pm$ 1.01	40.77 $\pm$ 1.80	50.84 $\pm$ 0.47	52.64 $\pm$ 1.70	62.83 $\pm$ 1.85	59.88 $\pm$ 1.32	74.09 $\pm$ 2.44	72.27 $\pm$ 1.02
Paunch girth (cm)	-	-	-	-	67.33 $\pm$ 3.68	61.25 $\pm$ 2.03	76.64 $\pm$ 2.32	78.13 $\pm$ 1.23
Face length (cm)	-	-	-	-	15.83 $\pm$ 1.14	13.88 $\pm$ 0.72	17.73 $\pm$ 0.74	16.92 $\pm$ 0.31
Ear length (cm)	-	-	-	-	17.83 $\pm$ 2.52	16.63 $\pm$ 0.92	17.09 $\pm$ 1.25	16.64 $\pm$ 0.45
Tail length (cm)	-	-	-	-	15.0 $\pm$ 1.24	11.88 $\pm$ 0.67	13.91 $\pm$ 0.58	14.42 $\pm$ 0.29
Horn length (cm)	-	-	-	-	8.0 $\pm$ 0.73	9.38 $\pm$ 1.86	13.73 $\pm$ 1.29	11.89 $\pm$ 0.40

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performance in the breeding tract was collected through a structured questionnaire given to goat owners, chosen at random within a structured, stratified framework. In each district, a 2 stage stratified sampling technique was used. At least 2 villages within each district and 2 goat breeders within each village were chosen at random for the interview. In total, 50 goat breeders across 23 villages over 6 districts were interviewed and the information was recorded. The additional

information, if any, was also collected from veterinary hospital of villages. The data on body biometric attributes and body weights were analyzed using SPSS 11.5 for windows.

**Molecular techniques:** Genomic DNA was isolated from blood samples of 48 unrelated animals of the breed (Sambrook *et al.* 1989). 1–2 animals were selected per flock per farmer, and farmers were interviewed about relatedness of animals before sampling to avoid relationship among the animals. A battery of 25 heterologous microsatellite markers (Dixit *et al.* 2008) was selected to generate data in a panel of 48 animals. Polymerase chain reaction (PCR) was carried out on about 50–100 ng genomic DNA in a 25 ml reaction volume (Dixit *et al.* 2008).

The PCR products were run on automated DNA sequencer of applied biosystems. The electropherograms drawn through Gene Scan were used to extract DNA fragment sizing details using Gene Mapper software (version 3.0).

**Statistical analysis:** The observed and expected heterozygosity estimates were calculated by POPGENE software (Yeh *et al.* 1999). The observed and effective numbers of alleles were also calculated using POPGENE software. F-statistics were determined after Weir and Cockerham (1984) as used in F-Stat software with Jackknifing procedure applied over loci in deriving significance levels and bootstrapping applied over loci in deriving 95% confidence intervals for these statistics. The statistics  $F_{is}$  is an estimate of variation within populations that measures the reduction in heterozygosity in an individual due to non-random mating within its subpopulations. The tests for deviation from Hardy-Weinberg equilibrium were based on 'p' values of  $F_{is}$  statistics obtained after permuting the alleles among individuals within sample.

Finally the bottleneck hypothesis was investigated using BOTTLENECK 1.2.01 (Cornuet and Luikart 1996). The BOTTLENECK tests for the departure from mutation drift equilibrium based on heterozygosity (not heterozygote), excess or deficiency. This does not require information on historical population sizes or level of genetic variations. It requires only measurement of allele's frequency from 5–20 polymorphic loci in a sample of approximately 20–30 individuals. The bottleneck compares heterozygosity expected ( $H_E$ ) at Hardy-Weinberg equilibrium to the heterozygosity expected ( $H_{eq}$ ) at mutation drift equilibrium in same sample, that has the same size and the same number of alleles. All the 3 models of mutation were used to calculate  $H_{eq}$ : strict one step-wise mutation (SSM), infinite allele (IAM) and 2-phase (TPM) models.

**Distribution and description:** Surti breed of goat is found in Bharuch, Surat, Narmada, Navsari, Valsad and Vadodara districts of Gujarat. The animals of this breed are of medium size and of varied colour patterns, viz. white, black, tan, coffee colour, and grayish. Mottled animals are also found. Muzzle and hoofs are grayish black to black, pink and light

brown. Presence or absence of horns was observed in both sexes, whereas wattles were observed only in female animals. The physical characteristics of Surti animals are presented in Table 1. The average body weight of adult animals was observed to be  $32.69 \pm 1.36$  kg. The Surti does (Fig. 1) were slightly longer than bucks (Fig. 2) and their pelvic girth was higher as compared to buck (Table 1). The higher pelvic girth of does might be due to pregnancy status or the udder development. However, the chest girth of males was higher than that of females. Ear, face, horn and tail length of does and bucks were nearly similar. In spite of breeding a white doe with a white buck, the kids were white, black, tan or white having some patches of brown, black or tan colour. This observation supported the colour variation in the breed. Out of 70 animals, 38.57% were polled.

**Management and breeding practices:** Generally goats were grazed — for at least 5 to 6 h/ day — in nearby areas in community land or fed at home by using top feed resources mainly tree leaves. The grazing schedule differed according to season and area. There was no provision of manger for feeding and group feeding was followed. The goats were not being provided with concentrate ration. Most of the goat keepers did not milk their goats and kids were allowed to suckle the does. Few farmers were having *pakka* house. Majority of goats were housed in open houses having biological boundaries.

The major fodder resources in the breeding tract were *pala* (*Zizyphus jujuba*), *khejri* (*Prosopis cineraria*), *shisham* (*Dalbergia sissoo*), *ber* (*Zizyphus rotundifolia*), *neem* (*Azadirachta indica*), *babool* (*Acacia arabica*), *keeker* (*Acacia nilotica*), *su- babul* (*Leucaena leucocephala*), tamarind (*Tamarindus indica*), banian (*Ficus benghalensis*), *peepal* (*Ficus religigosa*), *kavathi* (*kotha*) (*Limonoa acidissima*), *gundi* (*Cordia gharaf*), *hingariyu* (*Belanites aegyptiaca*), *dharo* (*dub*) (*Cynodon dactylon*), etc. In addition to these fodder resources, seasonal biomass was also available.

As there was no specific breeding policy of Surti goats in the state, Surti breeding males were available in very less number for the breeding of Surti goats. Local non-descript bucks were used for breeding of these females, resulting in loss of breed purity. Craze for sacrifice of white coat colour males on Id festival in local Muslims is another reason for low availability of males. Most of the goat keepers changed the bucks either after first or second kidding.

**Production performance:** Surti goats are good milch animals with well developed funnel/bowl shaped udder, and large, conical and pink teats. The milk production ranged from 1.5–4.0 litre/day. The average body weight of adult male and female was 36.27 and 33.26 kg, respectively (Table 1). Growth performance of kids at different ages with regards to their body weight, height, length and girth are presented in Table 1. The mean birth weight of male kids was higher as compared to female kids. The body height, length and heart

girth showed increasing trend as the age advances from birth to 6 months of age.

*Reproduction performance:* The interaction with goat breeders revealed that Surti goats were good breeders showing first oestrous at an age of 6–8 months and kid at 13–14 months of age. Twins were born to majority of does (50–60%), and triplets were rare (5%). Males also showed sexual maturity at an age of 6–7 months. The major breeding season was March-April and minor was October-November. Service period was of 1 to 2 months and 2 kiddings/13–15 months were observed.

*Genetic variation:* The various measures of genetic variation in Surti breed of goat are presented in Table 2. All loci were polymorphic, showing percentage of polymorphic loci (PPL) as 100%. This high PPL value of these loci indicated the usefulness of these markers for population analysis. Polymorphic information content (PIC) values ranged from 0.51 to 0.85 at all loci except seven loci (ETH225, OarJMP29, ILST005, ILST065, ILSTS029, ILST082 and RM4), which were having PIC values lower than 0.50. These values are comparable with the PIC values for Barbari breed ranging from 0.55 to 0.83 (Ramamoorthi

*et al.* 2009) and Chinese breed of goat (0.765) obtained by Li *et al.* (2008). Ganai and Yadav (2001) reported lower values of PIC for 3 Indian goat breeds (Sirohi, Jamunapari and Barbari). Behl *et al.* (2003) observed greater PIC values for Black Bengal and Chegu breeds in comparison to Surti. The high values indicated that the breed is more heterozygous with no selection for certain traits.

A reasonable amount of variability is discernible from allele number data. The observed number of alleles per locus ranged from 5 (ILSTS059, ETH229, RM4) to 19 (ILSTS058, RM088) with overall mean of 10.52±0.88. The effective number of alleles ranged from 1.56 (ILSTS005) to 8.96 (OarFC304) with overall mean of 4.36±0.47. The observed number of alleles across all the loci was greater than effective number of loci. The mean number of alleles observed in the present study was higher than that reported by Ganai and Yadav (2001) in Sirohi (4.12), Jamunapari (4.00) and Barbari (3.37). This value is also higher than the values obtained in various other studies (Barker *et al.* 2001, Li *et al.* 2002, Martinez *et al.* 2004).

The heterozygosity is an appropriate measure of genetic variability within a population. The observed heterozygosity

Table 2. Measures of genetic variation and F-stat. analysis for microsatellite loci in Surti breed goats.

Locus	Sample (diploid) size	Information index	PIC	Gene diversity	Allelic richness	F <sub>is</sub>	P-value	Observed number of alleles	Effective number of alleles	Heterozygosity		
										Observed	Expected	Nei's
ILST008	96	1.20	0.51	0.57	2.58	0.27	0.01	8	2.48	0.43	0.60	0.59
ILSTS059	10	1.47	0.77	0.81	3.83	0.10	0.02	5	3.84	0.20	0.82	0.74
ETH225	96	0.97	0.14	0.15	1.43	0.73	0.00	5	2.29	0.04	0.57	0.56
ILST044	96	1.81	0.50	0.52	2.68	0.20	0.01	13	4.02	0.83	0.75	0.75
ILSTS002	92	2.10	0.73	0.77	3.59	0.07	0.04	11	6.78	0.71	0.86	0.85
OarFCB304	90	2.54	0.85	0.87	4.53	0.11	0.02	20	8.96	0.73	0.89	0.88
OarFCB48	92	2.40	0.85	0.88	4.51	0.13	0.00	15	8.85	0.82	0.89	0.88
OarHH64	94	1.69	0.69	0.74	3.42	0.16	0.09	9	4.01	0.61	0.75	0.75
OarJMP29	42	1.16	0.45	0.51	2.51	0.90	0.00	6	2.23	0.04	0.56	0.55
ILSTS005	96	0.79	0.26	0.28	1.82	-0.03	0.73	6	1.56	0.31	0.36	0.36
ILSTS019	96	2.03	0.77	0.81	3.89	0.15	0.36	11	6.15	0.72	0.84	0.83
OMHC1	86	2.10	0.76	0.80	3.84	-0.07	0.36	14	5.95	0.90	0.84	0.83
ILSTS087	90	2.22	0.81	0.84	4.13	0.42	0.00	12	7.95	0.53	0.88	0.87
ILSTS30	94	1.61	0.70	0.74	3.44	0.20	0.00	8	3.90	0.59	0.75	0.74
ILSTS34	96	1.85	0.67	0.71	3.37	0.42	0.00	13	4.47	0.43	0.78	0.77
ILSTS033	62	1.43	0.52	0.56	2.79	-0.14	0.48	11	2.48	0.61	0.60	0.59
ILSTS049	96	1.66	0.68	0.73	3.35	0.04	0.37	10	3.95	0.75	0.75	0.74
ILSTS065	92	1.34	0.45	0.50	2.43	0.10	0.11	8	2.55	0.47	0.61	0.60
ILSTS058	96	2.48	0.83	0.85	4.30	-0.06	0.09	19	8.86	0.91	0.89	0.88
ILSTS029	94	1.06	0.40	0.42	2.36	0.04	0.18	11	1.72	0.40	0.42	0.42
RM088	96	1.75	0.56	0.59	3.02	0.36	0.00	19	2.72	0.37	0.64	0.63
ILSTS022	96	1.69	0.57	0.64	2.75	-0.12	0.68	8	4.40	0.83	0.78	0.77
OARE129	96	1.87	0.76	0.79	3.90	0.03	0.07	10	4.74	0.77	0.79	0.78
ILSTS082	96	1.10	0.46	0.53	2.42	-0.24	0.05	6	2.24	0.66	0.55	0.55
RM4	96	0.97	0.43	0.49	2.31	-0.01	0.31	5	2.05	0.50	0.51	0.51
Mean	87	1.65	0.60	0.64	3.16	0.15		10.52	4.36	0.57	0.71	0.70
S.E.								0.88	0.47	0.24	0.15	0.15



Figs 1–2. 1. A Surti doe. 2. A Surti Buck

ranged from 0.04 (ETH225, OarJMP 29) to 0.91 (ILSTS058) with overall mean of  $0.57 \pm 0.24$  and expected heterozygosity ranged from 0.36 (ILSTS005) to 0.89 (OarFCB304, OarFCB48 and ILSTS058) with overall mean of  $0.71 \pm 0.15$ . Most of the loci had greater value of expected heterozygosity than the observed heterozygosity. The higher values of expected heterozygosity were comparable with Chinese goat breeds reported by Li *et al.* (2008), and also with Martinez *et al.* (2004). The heterozygosity values were higher as compared to Korean and Chinese breeds (Kim *et al.* 2002) and in Asian breeds (Barker *et al.* 2001). These values are little less than values obtained for Black Bengal and Chegu breeds (Behl *et al.* 2003). There were significant differences in observed and expected heterozygosity ( $P < 0.05$ ) at majority of studied loci indicating departure from random mating, and suggested that some of the loci were homozygous in the population. Some of these loci were undergoing natural selection or linked to other loci affecting morphological, productive or adaptive traits undergoing natural selection.

The Shannon information index showed that all the loci were highly informative indicating high polymorphism across the loci and index value ranged from 0.79 (ILSTS 005) to 2.54 (OarFCB304) with the overall mean value of  $1.65 \pm 0.49$ . The gene diversity analysis across all studied loci varied from 0.15 (ETH225) to 0.88 (OarFCB48) giving an average value of 0.64 which indicated high level of genetic variability. But this variability is less in comparison with Mehsana, Marwari and Kutchi breeds of goat (Kumar *et al.* 2005, Aggarwal *et al.* 2007, Dixit *et al.* 2008). The allelic richness ranged from 1.43 (ETH225) to 4.53 (OarFCB304) with an average value of 3.16.

The heterozygote deficiency ( $F_{is}$ ) analysis showed that 72% loci (18 out of 25 loci) had positive deviation from Hardy Weinberg equilibrium (HWE). Out of these 18 loci, 12 loci revealed significant heterozygote deficiency. The deviation from HWE at these loci might be due to many causes such as existence of “null” alleles, high mutation rate and size homoplasy of microsatellite loci, besides the small

size of studied population. Significant heterozygote deficiencies were also reported in Indian goats (Kumar *et al.* 2005, Aggarwal *et al.* 2007, Verma *et al.* 2007, Dixit *et al.* 2008). The fairly high value of  $F_{is}$  (0.15) indicated that some of the loci in this breed were homozygous presumably resulting from the mating between relatives and consequent genetic drift.

The Sign and Wilcoxon tests detected significant departure from mutation-drift-equilibrium in the population under all the mutation models except sign test under single step mutation (SMM) model (data not shown). The sign test detected significant heterozygosity excess at 22 and 21 loci under indefinite allele (IAM) and 2 phase (TPM) mutation models ( $P < 0.001$ ), respectively, but nonsignificant (16 loci with heterozygosity excess  $P: 0.13733$ ) under SMM. The standardized differences test also revealed significant departure from mutation-drift-equilibrium. The deviation was positive under IAM ( $T_2 = 5.220$   $P < 0.001$ ), TPM ( $T_2 = 3.781$   $P < 0.001$ ), and SMM ( $T_2: 1.762$   $P < 0.001$ ). Microsatellites may tend to evolve under a model more similar to the SMM than IAM (Valdes *et al.* 1993). All the tests under SMM except sign test revealed that there was heterozygosity excess in the population. The heterozygosity excess could be attributed to the recent population reduction. It may be concluded that the population has under gone recent genetic bottleneck. Furthermore, an analysis of allele frequency distribution also supported the evidence of a recent genetic bottleneck in Surti goats (Fig. 3), as a mode shift from an L shaped distribution might have resulted due to recent reduced genetic variability in the population. The reduction in genetic variability may be the result of population subdivision and isolation. This seems to be true at ground level as flocks were quite isolated and males were confined to few females only and thus leading to skewed and small size effective population.

In conclusion, Surti goats had different colour variants but with well defined phenotypic characteristics and were good breeders and much animals suitable for stall fed conditions. All studied 25 microsatellite markers were highly

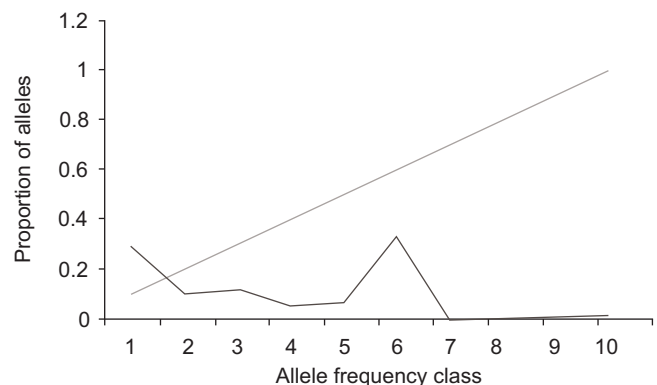


Fig. 3. Allele frequency distribution for all polymorphic studied microsatellite loci in Surti breed of goat.



polymorphic and were useful for the molecular characterization of Surti goats. There was substantial genetic variability across studied loci in Surti goats in spite of heterozygote deficiency at Hardy Weinberg equilibrium and genetic bottleneck at mutation drift equilibrium. Therefore, selective breeding strategies should be designed under field conditions for its conservation and improvement.

#### SUMMARY

Surti, an important goat breed of Gujarat, is known for meat and milk production. The average body weight of adult animals was  $32.69 \pm 1.36$  kg. The milk production ranged from 1.5–4.0 litre/day. The genetic variability in Surti goat breed was studied using 25 microsatellite markers. The gene diversity across the studied loci for Surti breed of goat varied from 0.15 (ETH225) to 0.88 (OarFCB48). The observed number of alleles per locus ranged from 5 (ILSTS059, ETH229, RM4) to 19 (ILSTS058, RM088) with overall mean of  $10.52 \pm 0.88$ . The effective number of alleles ranged from 1.56 (ILSTS005) to 8.96 (OarFC304) with an overall mean of  $4.36 \pm 0.47$ . The observed heterozygosity ranged from 0.04 (ETH225, OarJMP29) to 0.91 (ILSTS058) with overall mean of  $0.57 \pm 0.24$  and expected heterozygosity ranged from 0.36 (ILSTS005) to 0.89 (OarFCB304, OarFCB48 and ILSTS058) with overall mean of  $0.71 \pm 0.15$ . The heterozygote deficiency ( $F_{is}$ ) analysis showed that 72% loci (18 out of 25 loci) had positive deviation from Hardy Weinberg equilibrium ( $H_{WE}$ ). Out of these 18 loci, 12 loci revealed significant heterozygote deficiency. The standardized differences test also revealed significant departure from mutation-drift-equilibrium. The deviation was positive under IAM ( $T_2 = 5.220$   $P < 0.001$ ), TPM ( $T_2 = 3.781$   $P < 0.001$ ), and SMM ( $T_2 = 1.762$   $P < 0.001$ ). The information generated in this work may be utilized for studying differentiation and relationship among Indian goat breeds.

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