2nd International conference on Animal Dairy Science

Assessment of genetic variability in Marwari breed of Indian meat goat using Microsatellite DNA

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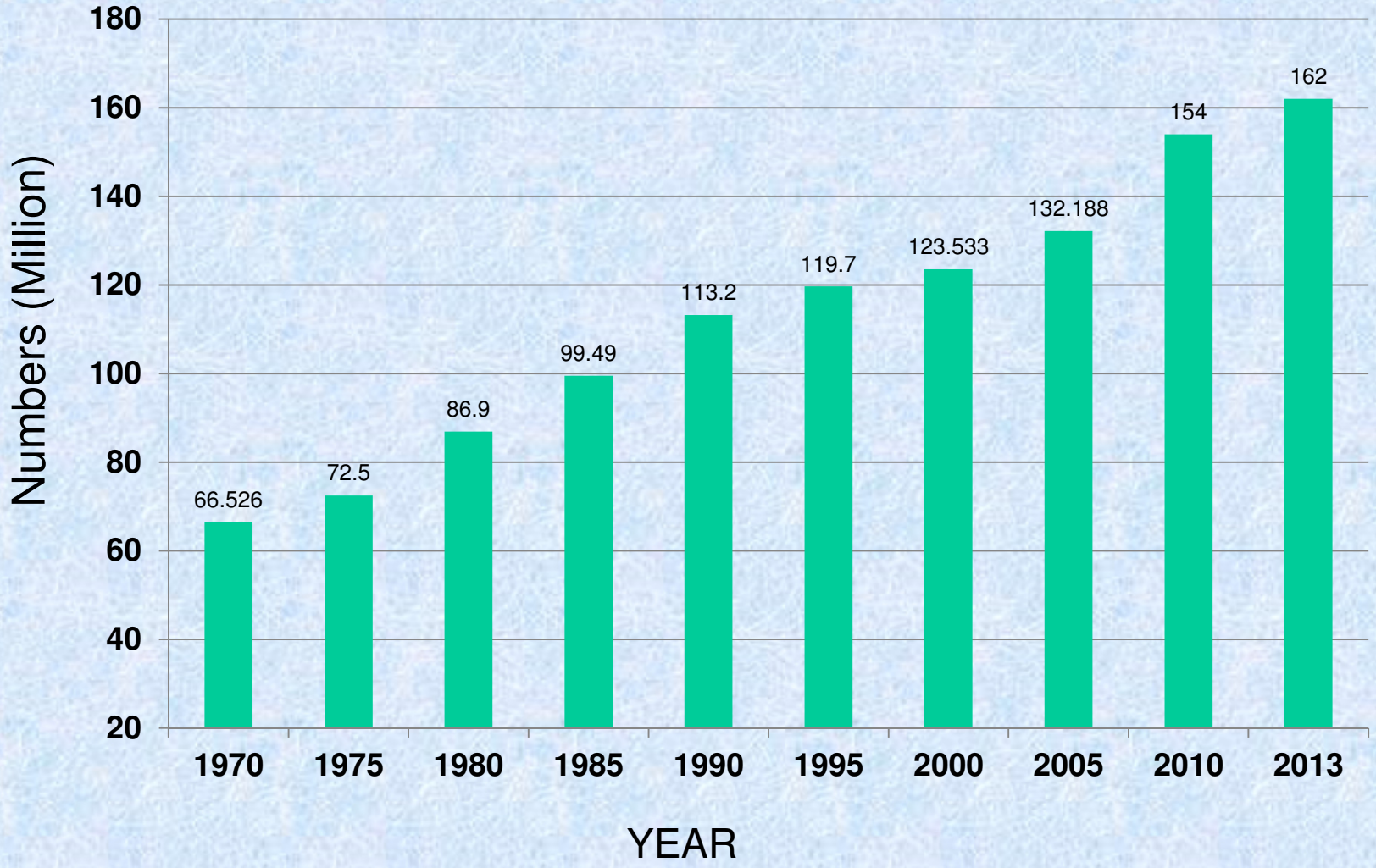
Goat Population overview

- one goat to approximately 1.17 sheep in the world (FAOSTAT, 2013).
- The largest number of goats is observed in Asia, followed by Africa, representing about 59.4% and 35.0%, summing up to 94.4% out of the total number of the world, respectively.
- The ratios of goat to sheep in Africa, Central America and Asia are approximately equal, indicating the considerable importance of goat populations in these parts of the world, especially to the poor and landless peasants.
- The total number of goats in the world increased by 146% of the total number (1005.6 million) encountered in 1990. Number of goats in the world has been increasing since 1990 by about 1% to 4% each year. During the same period, cattle number increased by 5%, while that of sheep decreased by 10%, reflecting the emergence of goats as a major livestock species.

Table1:Numbers of goats in the top ten countries, the ratio of goats to sheep & their percentages from the total number in the world (FAOSTAT, 2013)

Country	Number (Million)		Ratio		Percentage of world total (%)	
	Goats	Sheep	Goat	Sheep	Goats	Sheep
China	182.89	185.00	1	1.01	18.19	15.77
India	162.00	75.50	1	0.47	16.11	6.437
Pakistan	64.90	28.80	1	0.44	6.454	2.456
Nigeria	58.25	39.00	1	0.67	5.793	3.325
Bangladesh	55.60	19.00	1	0.34	5.529	1.62
Sudan	44.00	52.50	1	1.19	4.375	4.476
Kenya	30.00	18.50	1	0.62	2.983	1.577
Ethiopia	25.00	26.50	1	1.06	2.486	2.259
Iran	22.10	50.22	1	2.27	2.198	4.282
Mali	19.12	13.73	1	0.72	1.901	1.171
World	1005.6	1172.83	1	1.17		

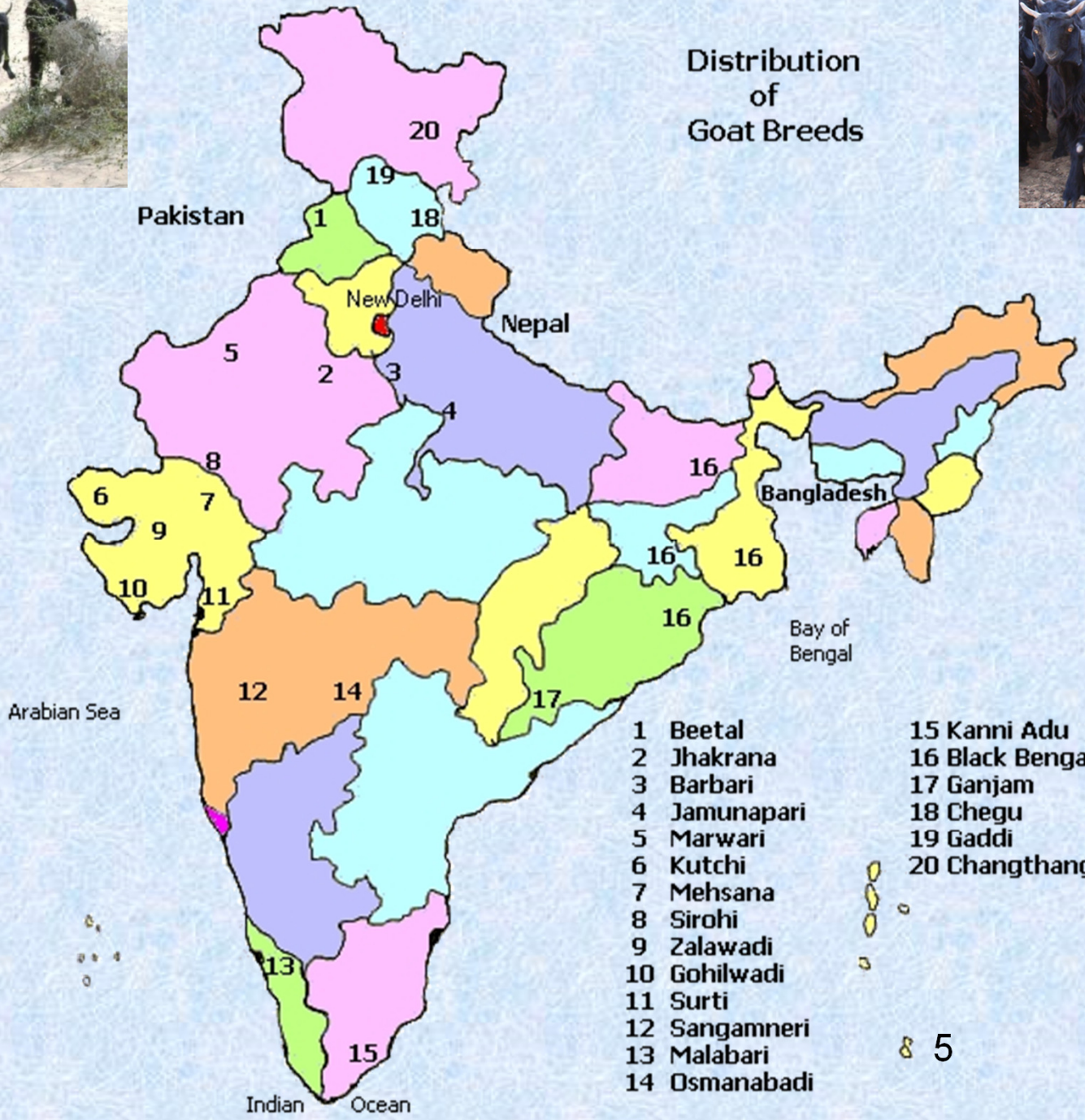
Table 2: Number of goats in the India during the period from 1970 to 2013 (FAOSTAT, 2013)







Distribution of Goat Breeds



INDIAN GOAT POPULATION DISTRIBUTION

Temperate Region

- Gaddi, Changthangi, Chegu & Shingari

Southern Region

Osmanabadi, Malabari, Sangamneri

Eastern Region

Bengal, Ganjam, Assam Hill & Jakharana

GOAT BREED

North-Western Region

Jamunapari, Beetal

Western Region

Sirohi, Barbari, Kutchi,, Mehasana, Zalawadi Surti & **Marwari**

Assessment of genetic variability in Marwari breed of Indian meat goat using microsatellite DNA

Journey for survival and co-existence--- Looking beyond Boundaries









Children normally herd goats, while their day-to-day management and the care of young stock usually fall to women.

Women, children and old men together contributed 77-92% of labor requirements in goat rearing. Women alone contributed 32-55% to it (census of India, 2010

Marwari Breed Characters

- Home Tract : Bikaner, Jodhpur, Jaisalmer, Barmer, Pali and Nagour districts.
- Utility : Meat and Milk
- Morphology : Medium sized body, predominantly black with long hairs occasionally white or brown patches.

  Hair : Lustrous hair grows with 11 to 12 cm per annum.

  Horns: 8.60 to 12.20 cm long, twisted, pointed and directed upwards and backwards

  Ears : 12.58 to19.13 cm long hanging downwards.
- Body dimensions

  Height : 60-80 cm Length : 40-67 cm
  Hearth girth: 68-80 cm Pouch girth: 70-88 cm
  Adult Wt. : Male:40-45 kg Female:35-40 Kg
- Milk yield : 84±5.7 kg to 113±7.0 kg
- Twinning : 15-20 %





OBJECTIVE: To account of the existing within-breed genetic variability in Marwari goat

Materials and methods

- ✓ Blood samples were randomly collected from 146 genetically unrelated animals of Marwari goat from different villages of Bikaner districts of Rajasthan in line with MoDAD recommendations (FAO, 1998).
- ✓ Genomic DNA was extracted from whole blood using proteinase K digestion followed by standard phenol–chloroform extraction procedure at room temperature (Sambrook *et al.*, 2001) with few modifications.
- ✓ **PCR-based microsatellite DNA typing using standard protocol.**
- ✓ All extracted samples were confirmed through horizontal electrophoresis on 0.8% agarose gel containing ethidium bromide
- ✓ **Microsatellite markers:** A panel of 15 microsatellite markers were selected from the list recommended by International Society for Animal Genetics (ISAG) and FAO's (DAD-IS) for Caprine.

Table 3 : A panel of 15 microsatellite markers used in the study

Locus	Primer sequence	Type of repeat	Size range	Chromosome No.	Annealing Temp. (in° C)
ETH-152	TACTCGTAGGGCAGGCTGCCTG GAGACCTCAGGGTTGGTGATCAG	$(CA)_{17}$	92-122	05	56.0
ETH-225	GATCACCTTGCCACTATTTCCT ACATGACAGCCAAGCTGCTACT	$(CA)_{18}$	146-160	14	54.0
ILSTS-005	GGAAGCAATGAAATCTATAGCC TGTTCTGTGAGTTTGTAAGC	$(nn)_{39}$	174-190	10	52.8
ILSTS-011	GCT TGC TAC ATG GAA AGT GC CTA AAA TGC AGA GCC CTA CC	$(CA)_{11}$	167-173	14	54.0
ILSTS-019	AAGGGACCTCATGTAGAAGC ACTTTTGGACCCTGTAGTGC	$(TG)_{10}$	142-162	Ann	53.7
ILSTS-022	AGTCTGAAGGCCTGAGAACC CTTACAGTCCTTGGGGTTGC	$(GT)_{21}$	186-202	Ann	55.0
ILSTS-028	TCC AGA TTT TGT ACC AGA CC GTC ATG TCA TAC CTT TGA GC	$(CA)_{7}$	132-150	11	50.4
ILSTS-030	CTGCAGTTCTGCATATGTGG CTTAGACAACAGGGGTTTGG	$(CA)_{13}$	159-179	2	54.0
ILSTS-033	TATTAGAGTGGCTCAGTGCC ATGCAGACAGTTTTAGAGGG	$(CA)_{12}$	151-187	12	54.6
ILSTS-034	AAGGGTCTAAGTCCACTGGC GACCTGGTTTAGCAGAGAGC	$(GT)_{29}$	153-185	5	51.0
ILSTS-044	AGTCACCCAAAAGTAACTGG ACA TGT TGT ATT CCA AGT GC	$(GT)_{20}$	142-170	Ann	50.0
ILSTS-058	GCCTTACTACCATTTCCAGC CATCCTGACTTTGGCTGTGG	$(GT)_{15}$	136-188	17	54.0
ILSTS-059	GCTGAACAATGTGATATGTTCAGG GGGACAATACTGTCTTAGATGCTGC	$(CA)_{4}(GT)_{2}$	105-135	13	55.0
ILSTS-065	GCTGCAAAGAGTTGAACACC AACTATTACAGGAGGCTCCC	$(CA)_{22}$	105-135	24	53.7
ILSTS-087	AGC AGA CAT GAT GAC TCA GC	$(CA)_{14}$	110-120	28	50.0

- ✓ PCR-amplified products were resolved on 6% urea–PAGE denaturing sequencing gel at 75 W (Sequi Gen GT apparatus. Bio-Rad, Hercules, USA) and visu*al*ized by silver staining (Bassam *et al*. 1991). *A*llele sizes were estimated using a 100-bp ladder (Invitrogen Life Technologies, Carlsbad, USA). Genotype of each individu*al* anim*al* at 25 different loci was recorded by direct counting.

Analysis of molecular data

- Genotype of each individual animal was determined and recorded from the silver-stained gels for each microsatellite locus.

- **Different measures of within-breed genetic variations, namely number of alleles, allele frequencies, effective number of alleles (ne), observed heterozygosity (Ho), expected heterozygosity (He), were estimated to evaluate variability at DNA level.**

- **Polymorphism information content (PIC) for each locus was calculated according to Botstein *et al.* (1980).**

RESULTS

- A total of 74 alleles were contributed by Marwari goat across all 15 microsatellite loci.
- The number of alleles per locus varied from two (ILSTS-087) to 9 (ILSTS-058) alleles, with a mean of 4.93 whereas the effective number of allele varied from 1.35 (ILSTS-005) to 3.129 (ILSTS011) with a mean of 2.36.
- The effective number of allele is lesser than observed number at all the loci.
- Allelic sizes ranged from 125 bp (ILSTS-028 and ILSTS-033) to 650 bp (ILSTS-011 and ILSTS-019).
- The expected heterozygosity ranged from 0.240 (locus ILSTS-005) to 0.681 (locus ILSTS-011), with an average value of 0.544.

RESULTS

- The observed heterozygosity (Ho) ranged from 0.1428 (locus ILSTS-087) to 0.9285 (locus ILSTS-034), with an average value of 0.5485 indicates substantial and very good number of heterozygotes, in the population.

- The highest polymorphic information content (PIC) value (1.1886) was observed at ILSTS-044 locus and least (0.0768) at ILSTS-065 locus for Marwari goat. Reasonably high PIC values observed for most of the marker with an average of (0.78096) are indicative of the usefulness of microsatellites biodiversity evaluation in this breed.

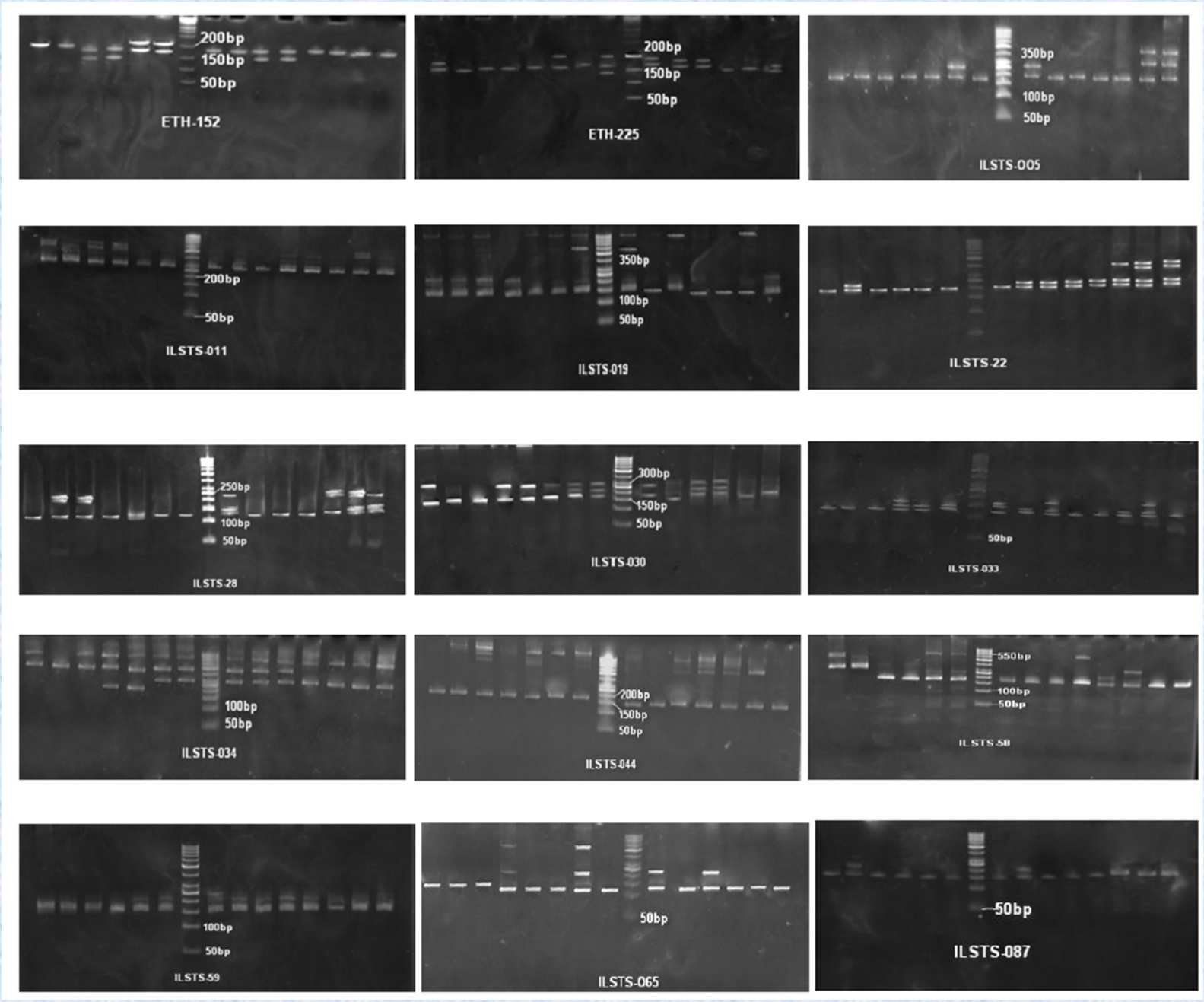
Table 4: Number and size of the *al*leles, h*e*terozygosity and PIC in Marwari goat.

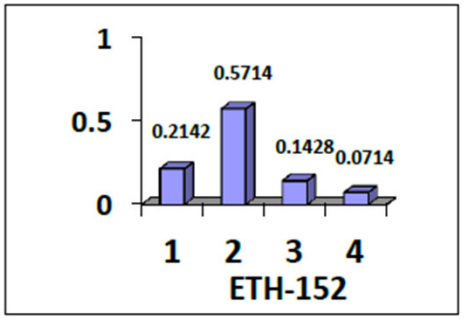
Microsatellite Marker	No. of Allele		Allele size(bp)	Heterozygosity		PIC
	A_o	A_e		H_o	$H_{(Exp)}$	
ETH-152	4	2.515	150-200	0.4285	0.603	1.1306
ETH-225	5	2.755	140-200	0.500	0.637	1.1448
ILSTS-005	3	1.315	175-350	0.2857	0.240	0.6425
ILSTS-011	7	3.129	350-650	0.5714	0.681	0.9385
ILSTS-019	5	2.932	145-650	0.7857	0.660	1.2057
ILSTS-022	4	2.143	200-350	0.5714	0.534	0.1065
ILSTS-028	4	1.44	125-245	0.4285	0.305	0.8264
ILSTS-030	6	2.853	150-310	0.6428	0.650	1.1608
ILSTS-033	4	2.939	125-175	0.514	0.655	0.1862
ILSTS-034	6	2.68	200-250	0.9285	0.627	1.1759
ILSTS-044	5	2.995	150-550	0.6428	0.666	1.1886
ILSTS-058	9	2.652	175-550	0.714	0.623	0.1279
ILSTS-059	5	1.988	150-250	0.7857	0.497	1.1534
ILSTS-065	5	2.099	145-550	0.2857	0.524	0.0768

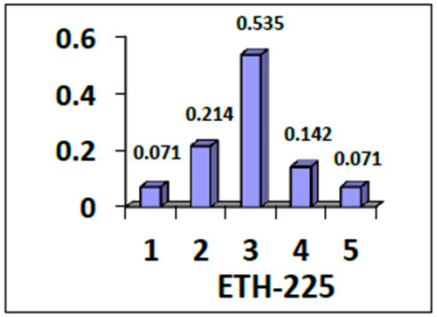
Conclusions

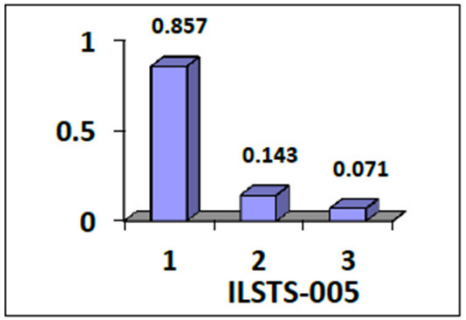
- Based on the PIC values, the microsatellite primers used in the present study are proved to be highly polymorphic in nature and hence can be well utilized for molecular characterization of goat germplasm.
- **The PIC values are suggestive of high polymorphic nature of the microsatellite loci analysed.**
- **The PIC values observed in the present study is indicative of the fact that the markers used are highly informative for characterization of Marwari goat diversity.**
- **The significant level of variability in this population reflects that the Marwari population contains a valuable genetic diversity. Hence, this population could provide a valuable source of genetic material that may be used for meeting the demands of future breeding programmes.**

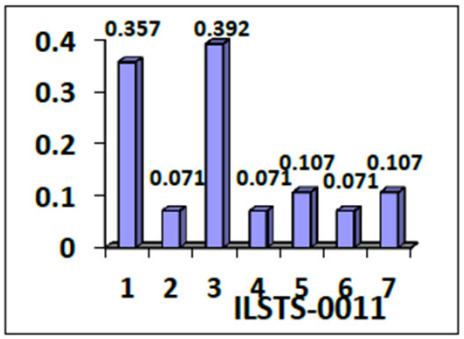
Allelic profile across the 15 microsatellite markers in Marwari goat on PAGE

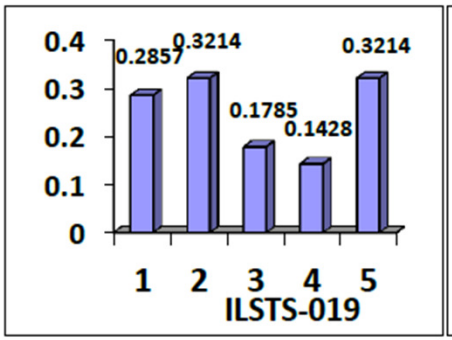


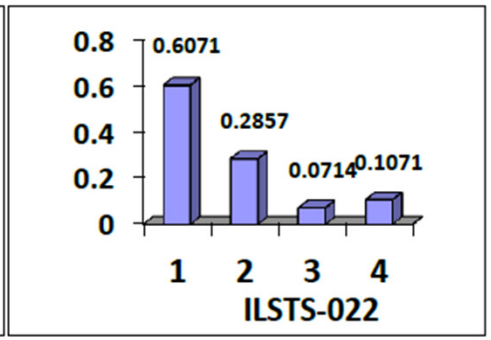


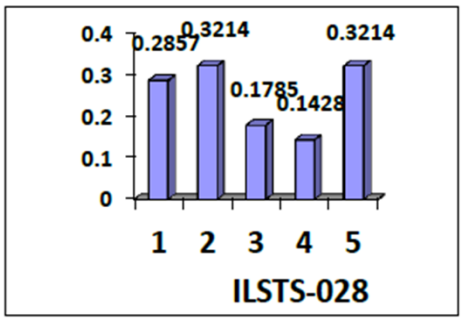


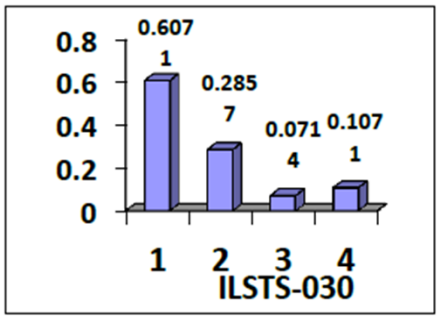


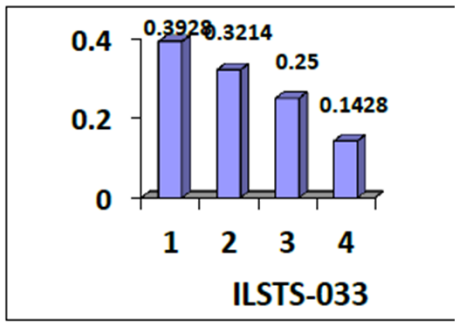


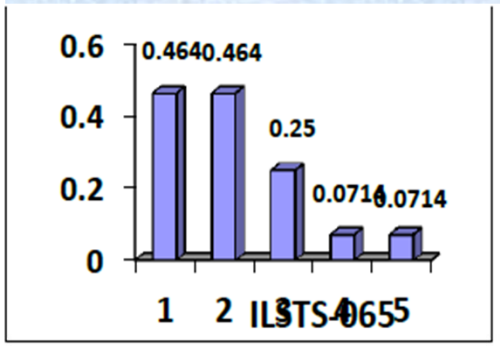


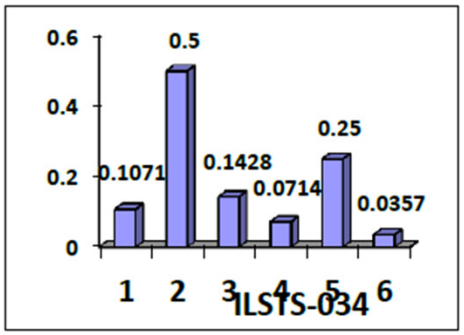


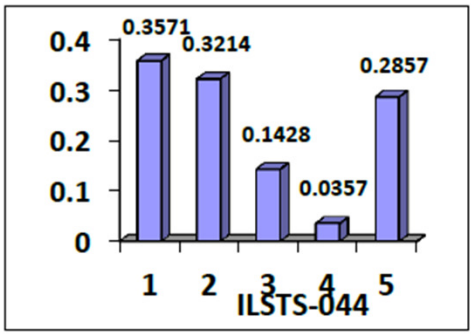


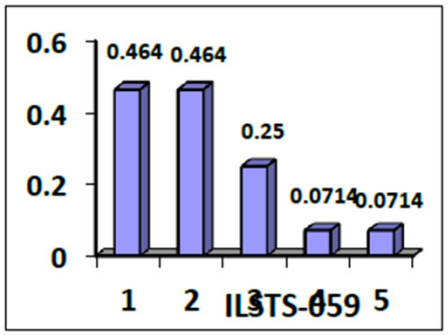












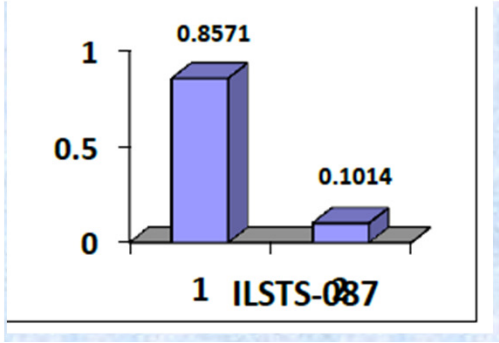


Figure :
Allelic frequency distribution across the 15 microsatellite markers in Marwari Goats.

A good cow is better than a good goat, but a good goat is better than a poor cow. Let us fulfil Gandhiji's dream with our experience.

Mahatma had the foresight of the usefulness of the humble goat for the poor. Here we see him with his pet goat.

Thank You!

