Cattle Genetic Resources of India

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PREFACE

Uttar Pradesh, the most populous state in India, is also rich in domestic animal diversity. The state possesses 23.5 million cattle, of which 97.4% are indigenous including non descripts (Pragati, 2001). There are five breeds of cattle in Uttar Pradesh. Three breeds fall within the category of draught type (Ponwar, Kenkatha and Kherigarh) and other two within the dual-purpose category i.e. milk and draught type (Gangatiri and Mewati). All the breeds are well adapted to the agro-climatic conditions of the state. Crossbreeding with semen from exotic breeds has also been used in pockets of these indigenous breeds. This has resulted in dilution of the indigenous breeds in the state. Ponwar, a draught breed of cattle is native of Pilibhit District of Uttar Pradesh. The bullocks of this breed are active, useful for light ploughing and carting and are remarkable for their speed and stamina, the cows however are poor milkers. Information on the Ponwar cattle breed is very limited in the available literature. No systematic program has been implemented for the improvement of this breed. Preliminary step for the sustainable development and exploitation of domestic animal genetic resources is the assembling of knowledge with reference to the genetic variability in the breeds. The studies of genetic variation provide an understanding of the existing and precedent evolutionary course of actions that have created biodiversity patterns, protection of which should be an imperative element of conservation strategies. Earlier studies on genetic structure exploited polymorphism of phenotypic traits or biochemical markers. The most recent molecular techniques for genetic scrutiny of population composition and genetic associations involve direct investigation of the DNA, the genetic material itself. Amongst these microsatellite markers have rapidly assumed the central position for population genetic studies as they offer benefits which are principally pertinent in conservation programmes. True to the breed type animals of Ponwar cattle are still available in the breeding tract in the interior region, which may be used to strengthen the population if conserved and bred in a systematic way. Here in this bulletin an effort has been made to present the phenotypic as well as molecular characterization of Ponwar cattle breed. The authors are grateful to the Director, National Bureau of Animal Genetic Resources, Karnal and Network Project on Animal Genetic Resources, ICAR for providing finances in carrying out the work. The assistance and contribution of State Animal Husbandry Department, Government of Utter Pradesh in the collection of blood sample from breeding tract is duly acknowledged.

(Authors)

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Introduction

Cattle has continued to be the most valuable species in India since centuries, contributing immensely in the form of milk, meat, bullock power, hides, organic manure and a variety of byproducts. Present day cattle breeds have evolved through mutation and genetic drift, as well as man directed artificial selection (Blott et al., 1998; Barker 1999; Nijman, 1999). Lately there has been a comprehensive inclination for animal production to be rooted through a few, exceptionally selected breeds, which is instigating a speedy decline in the number of local breeds (Gill and Hughes, 1998). These local breeds have evolved over centuries through the intervention of natural and human forces and have become adapted to a wide range of native conditions, climate, diseases and nutritional environment prevailing in the breeding tracts. The abundant reservoir of cattle genetic resources of India is represented by the 30 acknowledged breeds of zebu cattle (Acharya, 1982) and a number of populations even now uncharacterized and undefined. These breeds have been largely categorized as milch, draft or dual purpose derived from their predominant utility. Majority of them belong to draft category as cattle rearing in India mainly centered on production of bullock power for agricultural operations and transportation.

With increased prominence on milk and reduced draught energy requirements due to automation of agricultural operations, genetic diversity of Indian draft cattle breeds is diminishing. During the last decade overall cattle population of country exhibited decline, quite reverse to the uninterrupted positive population escalation since 1947 when India acquired independence. Thus there is an imperative necessity to conserve these locally adapted breeds. Ponwar breed of Indian zebu cattle (*Bos indicus*) is exclusively a draft purpose breed primarily employed for agricultural operations, for carrying load and transportation. Revelation of genetic variability in a breed has direct relevance with the issues of genetic conservation and biodiversity. In addition, such information should play a role in the formulation of rational breeding programmes with the objective of increasing output in the production system. The genetic structures for

most of the cattle breeds of India have not been assessed as per the internationally approved technical programmes. Limited studies available on this aspect are derived from a small number of animals and by means of lesser number of molecular markers.

Habitat and Distribution

The Ponwar also known as *Kabri* (mixture of colours) in the breeding tract seems to be a small hill type cattle breed. This breed may be a mixture of hill and plain cattle. The breed may have originated from the crossing of non-listed Nepalese hill cattle (*Morang*) and local white cattle as the breeding tract is very near to the Nepal boarder (Nivsarkar *et al.*, 2000). Pilibhit district of Uttar Pradesh, which lies on the foothills of the Himalayas is the breeding tract of Ponwar cattle. The breeding tract lies between latitude 28°42′ and 28°82′ North and between longitude 79°02′ and 80°42′ East. The main area is the Puranpur Block in the Pilibhit district comprising Mainakot, Mazara, Bhirkhera, Faizulaganj and Rajpur Semra villages. A few animals of this breed are also found in Lakhimpur-Kheri district of Uttar Pradesh. The entire breeding tract is plain area with majority of land covered with forest. The soil of the tract is alluvial type.

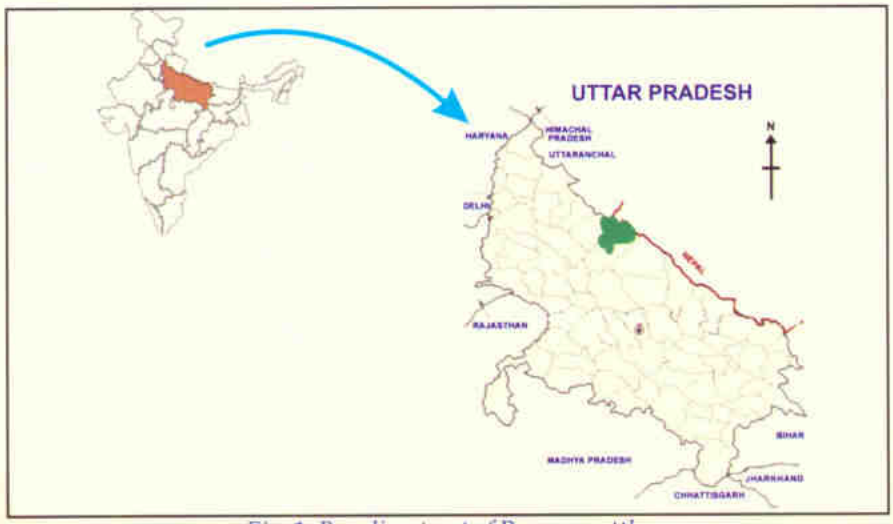

Fig. 1. Breeding tract of Ponwar cattle

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Climate of this region is tropical i.e. hot and humid. The temperature reaches upto 45°C in summer (May and June) and 5°C in winter (December and January). Annual rainfall varies from 120 to 170 cm. The peak months of rain are July, August and September. The relative humidity in the tract reaches up to 95%. Rice and sugarcane are the major crops in the area. Other crops, i.e. wheat, arhar (*Cajanus cajan*), bengal gram (*Cicer arietinum*), mustard, maize, jawar (*Sorghum vulgare*) and bajra (*Pennisetum typhoides*) are also grown in the area. The vegetable crops of the area include potato and onion, however, farmers also grow common green vegetable. The main fodder crops grown in the area are berseem (*Trifolium alexandrinum*), lucerne (*Medicago sativa*), jawar (*Sorghum vulgare*) and bajra (*Pennisetum typhoides*). Only progressive farmers were observed to grow the fodder crops.

Survey

The entire breeding tract was divided into three strata on the basis of the concentration/density of animals i.e. central (most populous area), adjacent (moderately populous area) and peripheral (least populous area). Two blocks each in the above strata i.e. a total of six blocks were selected randomly. In each of the selected blocks, two villages were selected randomly. Thus, in all, a total of 12 villages were identified for study.

Table 1. List of the villages selected for survey

Block	Category of village		
	Most populous	Medium populous	Least populous
1. Mandhotanda	Nainakot	Chokhapuri	Dharmangatpur
	Piperia Santosh	Chaugan	Takia Dinarpur
2. Puranpur	Piperia Dulai	Padaria	Jethapur Kalan
	Patabhoji	Navdia	Nandha

A total of 50 Ponwar animals from each village were randomly chosen for morphometric measurements. Production and reproduction traits of these animals were recorded by interviewing their owners. The total cattle

population of the block was obtained from the census available at District Head Quarters and the breed population was extrapolated.

Population Statistics

Breed wise population is not available in the census report of the country. However, analysis of the cattle population trend from 1982-1997 and 1997-2003 indicated a decline of 15.69% and 7.32% in Uttar Pradesh. In contrast, the cattle population of country as a whole increased by 6.98% from 1982 to 1997 and then declined by 10.06% from 1997 to 2003. The population of cattle in the breeding tract showed that majority of cattle (more than 80%) did not characteristically conform to established breeds and are commonly described as non descript. The cattle population of villages under study was 2,451 out of which 525 cattle belonged to the Ponwar breed. About 21% of the total cattle population was Ponwar. The approximate Ponwar population in the entire breeding tract was estimated as 10,667 based on the figure available for total cattle population in Puranpur block (49,800).

Table 2. Population of cattle in surveyed villages

Village	Total cattle population	Ponwar cattle population	Ponwar cattle	Distribution of Ponwar cattle measured			
				Bullocks	Cows	Calves (1yr)	Calves (2yr)
Chaugan	184	41	41	10	20	5	6
Piperia Santosh	179	69	50	9	26	5	10
Takia Dinarpur	87	25	25	9	6	5	5
Nainakot	155	57	50	10	30	5	5
Chokhapuri	71	31	31	11	12	3	5
Dharmangatpur	113	19	19	8	8	3	-
Piperia Dulai	563	94	50	12	18	10	10
Jethapur Kalan	83	14	14	6	4	2	2
Padaria	237	53	50	14	20	8	8
Nandha	62	15	15	6	4	2	3
Patabhoji	521	78	50	20	16	7	7
Navdia	196	29	29	4	17	4	4
Total	2,451	525	424	119	181	59	65

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Physical Characteristics

Coat colour of these animals is brown or black with white patches in varying proportions. Colour of muzzle, eyelids and hoofs is generally black. The tail switch is white in black animals and black in those having a greater proportion of white patches.

Fig. 2. Ponwar calves

The horns are small to medium and curve inward with pointed tips. The ears are small and erect with a sideways orientation and have pointed tips. The face is small and narrow with a slightly concave forehead, which is narrow and has a white marking. The body is small, compact and non-fleshy.

Fig. 3. A Ponwar bull

Fig. 4. A Ponwar cow

The skin is tight, the dewlap is medium and the hump is small in females and developed in males. The tail is long and reaches to below the hock. Cows have small udders and teats and milk veins are small. Animals of the breed are aggressive in nature.

Fig. 5. Alert Ponwar animals

Morphometric Measurements

Morphometric measurements (body length, height at wither and heart girth) have been recorded on 424 Ponwar animals of different categories.

Table 3. Body length, height at wither and heart girth in different category of Ponwar cattle

Category	Body length (cm)	Height at wither (cm)	Heart girth (cm)
Bullocks (119)	102.5±0.5	115.6±0.4	158.8±0.9
Cows (181)	97.1±0.5	108.9±0.4	140.6±0.5
Calves 1 year (59)	67.9±1.0	83.6±0.9	99.3±1.1
Calves 2 years (65)	79.8±0.8	97.4±0.6	122.9±1.3

Number of observations in parenthesis; Gaur *et al.*, 2004

Heart girth was highest in all categories of the animals followed by height at wither and body length giving the appearance of a small, compact body. Bullocks had higher morphometric measurements as compared to cows.

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Management Practices of the Breed

This breed is primarily maintained for draught purpose. Bullocks are quick and strong and well suited to agricultural operations. The landless labourers and marginal farmers mainly keep these animals.

Fig. 6. Ponwar bullocks in carting

The progressive farmer do not keep animals of this breed. Purebred animals are available in the interior area of the breeding tract. The *Tharu* tribe is mainly involved in rearing pure Ponwar animals. Some animals have also been maintained by *Pasi* and *Yadav* communities. Most of the animals are maintained on grazing in the forest area. Only about 5% of animals are being maintained under stall-feeding. The animals cover an average of about 10 to 15 kilometres in a day while grazing.

Fig. 7. Ponwar cattle in grazing field

Very few animals in milking stage are provided with concentrate mixture and salt. Unproductive animals, especially when fodder is scarce, are transferred to the forest for a few months. The group of animals maintained in the forest is called *Gaudi* (the livestock herd). Sometimes these animals are fed rice and wheat straw in limited amounts. Green fodder is never available to these animals. Animals are kept in the open in summer and rainy season and in rice and bamboo thatched structures called *Chappar* in winter. The average herd size varies from 1 to 50 animals.

Fig. 8. Housing system of Ponwar cattle

The occurrence of diseases in Ponwar cattle has been reported to be negligible. These animals were rarely vaccinated for Foot and Mouth Disease and Haemorrhagic Septicaemia. The animals of the Ponwar breed are never taken to veterinary hospital for the treatment and natural mating is practised in the entire population of Ponwar cattle. The farmers castrate the male calves at the age of one year or more using a local technique.

Production and Reproduction Characteristics

Information on production and reproduction characteristics has been reported on the basis of observations collected on 103 Ponwar cows. Cows produced little milk about 0.5 to 2.5 kg per day for 8 to 10 (average 8.9±0.1) months. A total of 34 cows producing 2.5 litres of milk in a day have been reported. Lactation milk yield averaged 462.5±12.1 kg. The lactation milk

yield in the Ponwar breed was lower than that reported for Hariana breed (Yadav and Rathi, 1991). Hariana is a dual-purpose breed that is also available in the Ponwar's breeding tract in limited numbers. Age at first calving ranged from 40 to 60 months (average 52.2±0.5) and the inter-calving period averaged 12.6±0.1months. The service period in Ponwar cattle varied from 60 to 100 (average 76.0±1.1) days. The cows remained dry for an average of 110.0±2.6 days.

Fig. 9. A good pair of Ponwar bullocks

Bullocks of this breed can easily transport 800 to 1000 kg load up to 10 kilometres. They can plough one acre of land in a day working for 6 to 8 hours.

Molecular Genetic Characterization

The effectiveness of microsatellite markers for the evaluation of genetic diversity and relationships among livestock breeds has been broadly acknowledged (Diez Tascon *et al.*, 2000; Canon *et al.*, 2001, Maudet *et al.*, 2002; Mukesh *et al.*, 2004). Bovine specific microsatellite markers from the FAO's recommended list have been used to evaluate the genetic variability, population structure and genetic bottleneck in Ponwar cattle.

Table 4. Microsatellite Markers, their sequences, chromosomal location & annealing temperature

Marker	Primer Sequences	Chromosome Number	Annealing Temp. (°C)
ETH152	tactcgtagggcaggctgcctg, gagacctcagggttggtgatcag	5	55
ILSTS011	gcttgctacatggaaagtgc, ctaaaatgcagagccctacc	14	58
MM8	cccaaggacagaaaagact, ctcaagataagaccacacc	2	55
BM1818	agctgggaatataaccaaagg, agtgctttcaaggtccatgc	23	58
INRA063	atttgcacaagctaaatctaacc, aaaccacagaaatgcttggaag	18	55
ETH10	gttcaggactggccctgctaaca, cctccagcccactttctcttctc	5	55
ILSTS006	tgtctgtatttctgctgtgg, acacggaagcgatctaaacg	7	56
CSRM60	aagatgtgatccaagagagaggca, aggaccagatcgtgaaaggcatag	10	55
ILSTS005	ggaagcaatgaaatctatagcc, tgttctgtgagtttgtaagc	10	55
ETH225	gatcaccttgccactatttcct, acatgacagccagctgctact	9	57
ILSTS054	gaggatcttgattttgatgtcc, agggccactatggtacttcc	21	55
HEL5	gcaggatcacttgttaggga, agacgttagtgtacattaac	21	55
ILSTS030	ctgcagttctgcatatgtgg, cttagacaacaggggtttgg	2	55
INRA035	atcctttgcagcctccacattg, ttgtgctttatgacactatccg	16	55
ILSTS034	aagggtctaagtccactggc, gacctggtttagcagagagc	5	57
MM12	caagacaggtgtttcaatct, atcgactctggggatgatgt	9	55
BM1824	gagcaaggtgtttttccaatc, cattctccaactgcttccttg	1	55
HEL1	caacagctatttaacaagga, aggctacagtccatgggatt	15	55
HEL9	cccattcagtcttcagaggt, cacatccatgttctcaccac	8	59
ILSTS033	tattagagtggctcagtgcc, atgcagacagttttagaggg	12	55
HAUT27	ttttatgttcatttttgactgg, aactgctgaaatctccatctta	26	55
INRA005	caatctgcatgaagtataaatat, cttcaggcataccctacacc	12	55
CSSM66	acacaaatcctttctgccagctga, aatttaatgcactgaggagcttgg	14	60
ETH3	gaacctgcctctcctgcattgg, actctgcctgtggccaagtagg	19	64

Sample collection

Blood samples were obtained from 40 random and unrelated Ponwar animals from the breeding region as per the guidelines of MoDAD

(Measurement of Domestic Animal Diversity) programme (FAO, 1995). To ensure unrelatedness of animals due to nonexistence of pedigree account under field situations, animals were selected from distinct villages after interviewing the owners in detail. Blood samples (5-6 ml) were collected in vacutainers containing ethylene diamine tetra acetic acid (EDTA) as anticoagulant.

Molecular techniques

Genomic DNA was isolated following the process described by Sambrook et al. (1989) with slight modifications. A set of 24 microsatellite markers recommended for cattle in FAO's DADIS-MoDAD programme were utilized for generating microsatellite genotyping data in a panel of 40 animals.

Polymerase Chain Reaction (PCR) was performed utilizing 50-100 ng genomic DNA in a 25 µl reaction volume using PTC-200 PCR machine (M J Research Inc., MA, USA). The PCR procedure comprised initial denaturation at 95º C for 1 min, 30 cycles of '95º C for 1 min, precise annealing temperature of primer for 1 min, 72º C for 1 min' and finally extension at 72º C for 5 min. The PCR products were resolved on 6% denaturing polyacrylamide gels (Sequi GT System, Bio-Rad) and sized using a 10 bp ladder (Invitrogen, Life Technologies, CA, USA) as standard for sizing. Gels were stained using silver staining (Bassam *et al.*, 1991) and genotypes scored manually.

Statistical analysis

Observed and expected heterozygosity estimates were computed after Levene (1949) and Nei (1973) as executed in POPGENE software (Yeh et al., 1999). The observed and effective numbers of alleles (Kimura and Crow, 1964) were also evaluated applying POPGENE software. Allelic frequencies were utilized for assessing Polymorphic Information Content (PIC) values as per Botstein *et al.* (1980). Departure from Hardy-Weinberg equilibrium was derived using the exact test of POPGENE. Heterogeneity of deviations from Hardy-Weinberg equilibrium among the microsatellite loci was

investigated by considering the deviations as correlation coefficient and tested accordingly (Barker *et al.*, 2001). Heterozygote deficiencies were articulated as $F_{IS} = (H_o - H_e) / H_e$ where, H_o and H_e are the observed and expected frequency of heterozygotes, respectively. Linkage (Genotypic) disequilibrium among the microsatellite loci was analyzed employing F-STAT version 2.9.3, an update version 1.2 (Goudet, 1995) for 24 microsatellite loci. Finally, the bottleneck hypothesis was explored exercising BOTTLENECK 1.2.01 software (Cornuet and Luikart, 1996).

Salient Findings

All the 24 microsatellite loci, which have been documented to be polymorphic in various *Bos taurus* and *Bos indicus* breeds amplified effectively and generated specific banding patterns from which individual genotypes could be assessed. The estimated parameters pertaining to the genetic variation in Ponwar cattle viz., observed and effective number of alleles, Shannon's Information index, observed, expected and Nei's expected heterozygosity, polymorphic information content (PIC) and heterozygote deficiency at each of the 24 microsatellite locus are provided in Table 5.

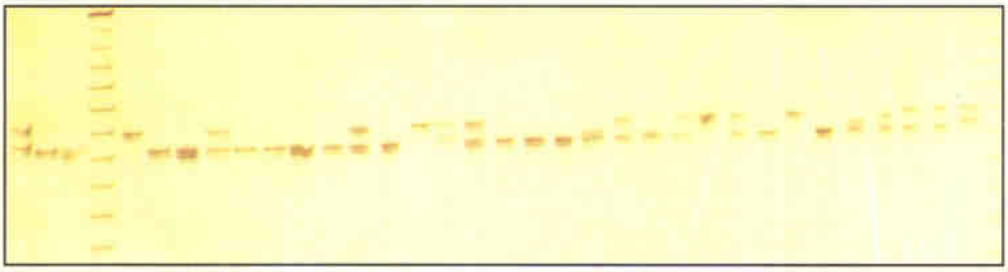

Fig. 10. A Representative gel showing alleles at microsatelite loci.

A total of 141 alleles were detected in Ponwar cattle across the 24 loci investigated with an average of 5.875±1.727 alleles per locus. Reasonable amount of polymorphism in Ponwar cattle is discernible from the allele frequency data. The number of observed alleles varied from 3 (ILSTS011, ETH3) to 10 (ILSTS034) with an overall mean of 5.875±1.727. As per FAO

four different alleles per locus are required for evaluation of genetic differences between breeds. The average numbers of alleles per locus in Ponwar cattle were well above the FAO reference and accordingly indicative of adequate polymorphism and their appropriateness for assessing genetic variation. The observed number of alleles for all the 24 loci exceeded the effective number of alleles which varied from 1.795 to 6.237 with a mean of 3.433±1.223.

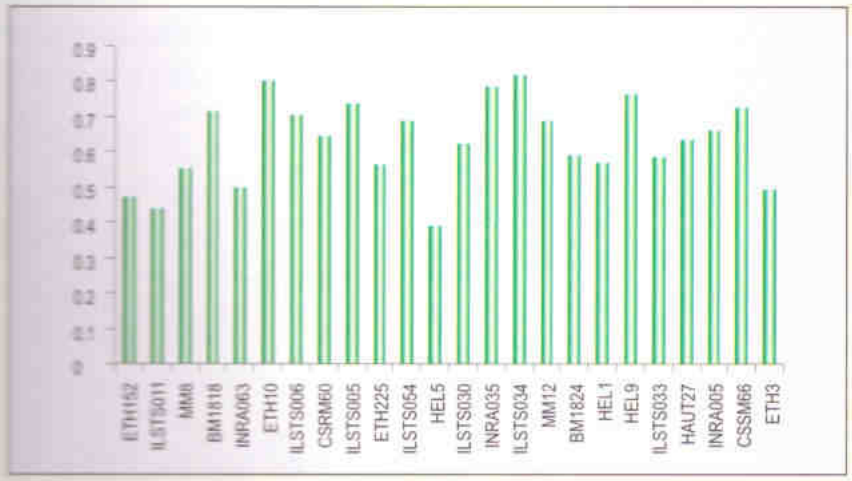

Fig. 11. PIC values at different microsatellite loci

The average PIC estimates was 0.632±0.116. Genetic markers exhibiting PIC values more than 0.5 are generally reckoned as distinctly informative in population genetic analysis (Botstein *et. al.*, 1980). Accordingly, with the exclusion of ILSTS011, INRA063, HEL5 and ETH10, all the loci were enormously informative like in taurine and indicus breeds investigated earlier (Canon *et al.*, 2001, Maudet *et al.*, 2002; Kumar *et al.*, 2003; Metta *et al.*, 2004; Mukesh *et al.*, 2004).

The average observed heterozygosity was 0.497±0.177 which was less than the expected heterozygosity. The average expected heterozygosity (Nei, 1973) within the Ponwar population varied from 0.443 (HEL5) to 0.839 (ILSTS034) with an overall mean of 0.673±0.112. Ponwar cattle, thus, had a

Table 5. Measures of Genetic variation in Ponwar cattle

Locus	N_o	N_e	Heterozygosity Observed	Heterozygosity Expected	Nei's	Heterozygote deficiency, f (F_{IS})
ETH152	5.0	1.991	0.450	0.504	0.498	0.096
ILSTS011	3.0	2.090	0.475	0.528	0.522	0.089
MM8	7.0	2.469	0.308	0.603	0.595	0.483
BM1818	8.0	4.066	0.350	0.764	0.754	0.536
INRA063	6.0	2.181	0.525	0.548	0.542	0.031
ETH10	9.0	5.597	0.447	0.832	0.821	0.455
ILSTS006	6.0	3.910	0.615	0.754	0.744	0.173
CSRM60	5.0	3.303	0.344	0.708	0.697	0.507
ILSTS005	6.0	4.443	0.750	0.787	0.775	0.032
ETH225	7.0	2.402	0.250	0.592	0.584	0.572
ILSTS054	5.0	3.752	0.550	0.743	0.733	0.250
HEL5	4.0	1.795	0.194	0.450	0.443	0.563
ILSTS030	4.0	3.161	0.303	0.694	0.684	0.557
INRA035	7.0	5.344	0.778	0.824	0.813	0.043
ILSTS034	10.0	6.237	0.595	0.851	0.839	0.292
MM12	7.0	3.583	0.500	0.730	0.721	0.307
BM1824	6.0	2.894	0.589	0.663	0.655	0.099
HEL1	5.0	2.334	0.595	0.579	0.572	-0.040
HEL9	6.0	4.878	0.800	0.809	0.795	-0.006
ILSTS033	6.0	2.839	0.700	0.656	0.648	-0.081
HAUT27	5.0	3.101	0.222	0.687	0.678	0.672
INRA005	4.0	3.505	0.543	0.725	0.715	0.240
CSSM66	7.0	4.279	0.658	0.777	0.766	0.141
ETH3	3.0	2.233	0.375	0.561	0.552	0.321
Mean	**5.875**	**3.433**	**0.497**	**0.682**	**0.673**	**0.262**
S.E.	**1.727**	**1.223**	**0.177**	**0.113**	**0.112**	

N_o Observed number of alleles
N_e Effective number of alleles [Kimura and Crow (1964)]

reduced amount of genetic variation derived from its gene diversity as judged against the genetic variation recounted in several breeds investigated globally. The average observed heterozygosity estimation in this study (0.497±0.177) is lower than reported in seven Italian cattle breeds 0.6 – 0.68 (Del Bo *et al.*, 2001), five Swiss cattle breeds 0.60-0.69 (Schmid *et al.*, 1999), twelve west/central African cattle breeds 0.506-0.697 (Ibeagha-Awemu *et al.*, 2004) and two Indian zebu cattle breeds viz Hariana (0.53) and Deoni (0.59) (Mukesh *et al.*, 2004). However, lower heterozygosity (0.42) than Ponwar has been reported for Sahiwal cattle (Mukesh *et al.*, 2004) whose population is also on a rapid decline in India.

Within-population inbreeding estimate f (F_{IS}) was positive based on table wide randomizations ($P< 0.05$). The f-estimates varied from -0.006 to 0.672 with an average of 0.262.

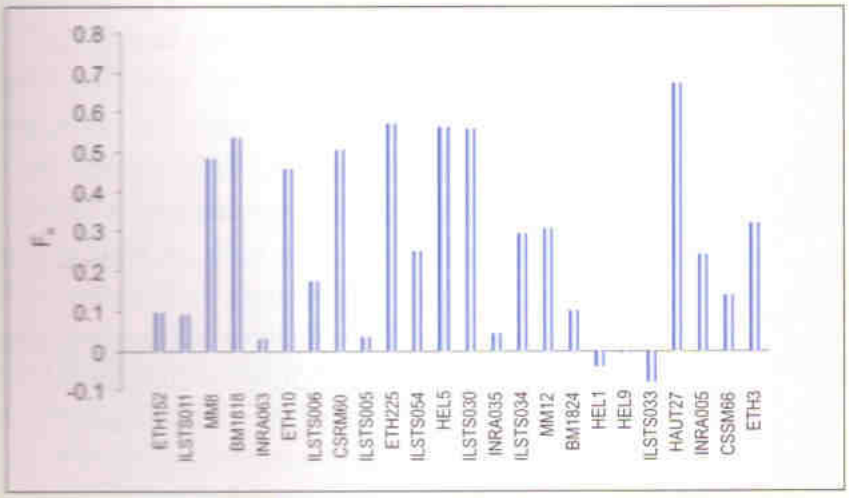

Fig. 12. F_{IS} values at different microsatellite loci

Thus on an average a significant deficit (26.2%) of heterozygote exists in the Ponwar population. All the microsatellite markers, with the exception of HEL1, HEL9 and ILSTS033, contributed to the observed heterozygote shortage. Existence of the breed in a restricted geographical region, free grazing of herds in the forests and lack of sufficient number of breeding

bulls in the population could be the likely sources for the detected loss of heterozygotes. Numerous factors viz., inbreeding, locus under selection (genetic hitchhiking), null alleles (non amplifying alleles) and presence of population sub structure (Wahlund effect) have been recognized as accountable for insufficiency of heterozygotes in a population (Nei, 1987). But the key reason for scarcity of heterozygosity in Ponwar cattle breed might be due to inbreeding brought about by above described issues and exhibited by the overall positive f-value (Weir, 1996). All the scrutinized loci were observed to be neutral (except ILSTS054 and INRA005) in Ewens-Watterson neutrality test (Manly, 1985) suggesting that homozygosity in Ponwar may not be as a consequence of selection. Null alleles are on the whole unlikely to be segregating at all the loci. Likewise prospective Wahlund effects (localities with subpopulations) may not account significantly for the observed heterozygote deficit.

Linkage disequilibrium was found between locus ILSTS033 and INRA05 in Ponwar cattle. Gametic disequilibrium could be triggered by diverse sources, including physical linkage, epistatic selection and genetic hitchhiking. Since markers ILSTS033 and INRA005 reside on the same chromosome (chromosome 12), physical linkage may be a likely source of disequilibrium. Analysis was carried out both with as well as without the locus ILSTS033 for substantiation but no disparity was detected in the overall results. Other Indian breeds showing sharp declines in breeding populations, Sahiwal and Hariana (Mukesh *et al.*, 2004) exhibited comparable deficiency of heterozygotes and decline in number of alleles. With the fall in observed number of alleles (Hariana 6.5, Ponwar 5.9 and Sahiwal 5.2) inbreeding estimates (F_{IS}) swelled to 0.211 in Hariana, 0.262 in Ponwar and 0.326 in Sahiwal cattle (Mukesh *et al.*, 2004, this study).

The investigated genetic parameters thus reveal that most likely there is inbreeding in this population presumably ensuing from reduced population restricted to limited number of villages in the jungle by river Sharda, coupled with unplanned and unsystematic breeding owing to lack

of sufficient number of breeding males required in the breeding region. Ponwar cattle population has shrunk to just about 10,000 heads in the entire breeding tract. In addition, male calves of six to twelve months of age are sold to farmers outside the breeding tract to be used in agricultural operations and transportation after castration and consequently are genetically dead. Thus, breedable males are radically reduced in the breeding tract. All together effective population size is decreased and the matings between relatives instigates genetic drift.

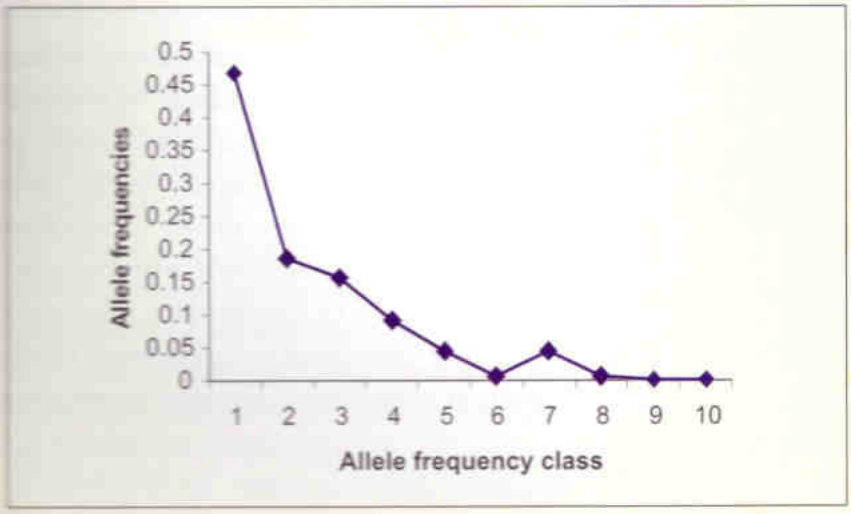

Fig. 13. L-shaped mode-shift graph

When a population suffers bottleneck, rare alleles are likely to be vanished and the average number of alleles per locus, or allelic diversity is diminished. Heterozygosity, nevertheless, is not reduced proportionately, because rare alleles add little to heterozygosity. The variation between allelic diversity and heterozygosity is exploited as the basis for statistical tests to uncover the existence of a recent genetic bottleneck in the population (Piry *et al.*, 1999). The lower extent of He (heterozygosity excess) with their corresponding Hee (heterozygosity excess expected) in frequency based method in two phase and stepwise mutation models generated by the BOTTLENECK indicated the absence of such a genetic bottleneck in Ponwar population.

In addition, qualitative graphical method of Luikart and Cornuet (1998) was also employed to visualize the allele frequency spectra (Figure 5). The microsatellite alleles were categorized in to 10 frequency classes, which permit checking whether the scattering followed the normal L-shaped form, where alleles with low frequencies (0.01-0.1) are the most abundant. The distribution further disclosed that the population had not experienced genetic bottleneck in any case in the recent past.

Recommendations

Present status of Ponwar cattle breed revealed that there is an imperative need for genetic management and conservation of this locally adapted draft breed. It is especially necessary owing to the husbandry systems practiced by local farmers, which may further influence diversity levels through the breeding of relatives. To begin with breed society needs to be created, that should be responsible for complete maintenance and improvement of the breed to make it economically sustainable in the transforming agricultural scenario of the country. Migration of purebred animals from the breeding tract should be restricted and semen of the breed must be made available in the breeding tract.

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