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FOR THE RECORD

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DNA Polymorphism Study at D1S80, DYS19, DYS287, and DYF155S2 in Two Tribal Populations from Central India

POPULATION: DNA polymorphism study of four well-studied loci: D1S80, DYS19, DYS287 (YAP), and DYF155S2 have been carried out among two tribal population groups (Bison Horn Maria and Muria) from Bastar district of Madhya Pradesh in Central India. For this study, 82 random, unrelated individuals were analyzed for D1S80 minisatellite, where as 46 random, unrelated male individuals were studied for DYS19 microsatellite and two Y-linked biallelic loci viz, DYS287 (Y-chromosomal alu polymorphic locus, YAP), and DYF155S2.

KEYWORDS: forensic science, D1S80, DYS19, DYS287 (YAP), DYF155S2, Indian populations

Genomic DNA was extracted from peripheral blood samples using a rapid non-enzymatic method (1). The PCR primers and the amplification parameters of D1S80 were as described by Kasai et al. (2) for DYS19 as per Kayser et al. (3) and de Knjiff et al. (4) for DYS287 (YAP) as per Hammer and Horai (5) and for DYF155S2 as per Jobling and Tyler-Smith (6). PCR amplification of all the four loci was achieved by using locus specific primers flanking the repeat region and was carried out in an eppendorf™ Master Cycler. For D1S80 and DYF155S2, the amplimers were resolved on 4% non-denaturing polyacrylamide gel followed by silver staining, whereas for DYS287 (YAP) locus, the amplimers were electrophoresed on 2% agarose gel stained with ethidium bromide. For DYS19 locus, the forward primer was labeled with flourescent CY5™ dye amidite and the amplimers were electrophoresed on 6% denaturing urea gel (7M) using ALF Express DNA Sequencer (Amersham Pharmacia Biosciences, PVT. Ltd., Uppasala, Sweden). Internal ladders were used in addition to external standards (CY5™ labeled 50–500 bp DNA ladder) for accurate size determination. The amplimers of DYS19 locus were also compared with the standards, kindly supplied by Dr. Chris Tyler-Smith from Oxford University, Oxford, UK, for confirmation.

Allele frequencies, gene diversities, and exact tests were performed using the software ARLEQUIN Ver 1.1 (7). The polymorphic information content (PIC) was determined according to Botstein et al. (8) and the power of discrimination (PD) was calculated as by Fisher (9).

At D1S80 locus, 14 alleles were observed among Bison Horn Maria population group, whereas 12 alleles were observed among Murias. Allele 18 was observed to be predominant in both groups. A bimodal distribution of alleles 18 and 24 was observed among Murias, whereas Bison Horn Maria population group showed a clear unimodal pattern of allele 18 (Table 1). The expected and observed heterozygosity showed no significant differences. At DYS19 locus, two alleles were detected among Bison Horn Maria

TABLE 1—*Allele frequency distribution of D1S80 among Indian tribals.*

	Maria (N = 48)		Muria (N = 34)	
Allele (Repeats)	No. Obs.	Frequency	No. Obs.	Frequency
14	0	0	1	0.015
15	1	0.010	1	0.015
16	2	0.021	1	0.015
17	1	0.010	0	0
18	46	0.479	38	0.559
19	2	0.021	0	0
21	4	0.042	1	0.015
22	6	0.063	1	0.015
23	1	0.010	0	0
24	9	0.094	16	0.235
25	3	0.031	1	0.015
26	5	0.052	0	0
28	7	0.073	2	0.029
29	0	0	2	0.029
30	3	0.031	1	0.015
31	6	0.063	3	0.044
H	0.79		0.79	
h	0.75 ± 0.04		0.64 ± 0.05	
PIC	0.76		0.67	
PD	0.86		0.92	
Exact test	0.643 ± 0.0008		0.606 ± 0.0008	

N = No. of individuals; H = Observed heterozygosity; h = Expected heterozygosity; PIC = Polymorphic Information Content; PD = Power of Discrimination.

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TABLE 2—*Allele frequency distribution of three Y-chromosomal loci among Indian tribals.*

Allele frequency distribution at *DYS287(YAP)*.				
	Maria ($N = 21$)		Muria ($N = 25$)	
Allele	No. Obs.	Frequency	No. Obs.	Frequency
13	0	0	4	0.160
14	0	0	0	0
15	10	0.476	8	0.320
16	11	0.524	12	0.480
17	…	…	1	0.040
Gene diversity	0.50		0.64	
Allele frequency distribution at DYS287(YAP)				
	Maria ($N = 21$)		Muria ($N = 25$)	
Allele (bp)	No. Obs.	%	No. Obs.	%
YAP+	0	0.0	0	0
YAP−	21	100	25	100
Allele frequency distribution at DYS155S2				
	Maria ($N = 21$)		Muria ($N = 25$)	
Allele (bp)	No. Obs.	%	No. Obs.	%
196	21	100	25	100

N = No. of individuals, No. Obs. = Number observed.

population, whereas four alleles were found among Murias. Allele 16 was predominant in both the groups (Table 2). A PCR product of 150 bp was observed for all the male individuals studied at DYS287, indicating lack of alu insertion (YAP-) in these two population groups (Table 2). At DYF155S2 locus, a PCR product of 196 bp was observed among all the males from these two population groups (Table 2).

The complete data set is available to all interested parties via electronic mail from the corresponding author at msesh@apsara.bare.ernet.in or birajalaxmi@yahoo.co.in

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