

FOR THE RECORD

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Population Genetic Data at Two Minisatellites (D19S20 and APOB 3' VNTR) Between Two Tribal Populations From Central India

POPULATION: Two minisatellites (D19S20 and ApoB 3' VNTR) have been analyzed among two anthropologically distinct tribal populations from Bastar district of Madhya Pradesh in Central India, namely Bison Horn Maria and Muria. DNA typing was carried out on a total of 54 individuals for D19S20 minisatellite and 79 individuals for ApoB 3' VNTR.

KEYWORDS: forensic science, DNA typing, D19S20, ApoB 3' VNTR, population genetics, Madhya Pradesh, Indo-European, Indian tribal population

TABLE 1—Distribution of allele frequencies at D19S20 minisatellite among two Indian tribal populations.

Alleles (repeats)	Bison Horn Maria (n = 60)		Muria (n = 48)	
	No. Obs.	Frequency	No. Obs.	Frequency
1	8	0.133	1	0.021
6	32	0.533	21	0.438
7	13	0.217	12	0.250
8	2	0.033	4	0.083
9	1	0.017	1	0.021
10	1	0.017	2	0.042
11	1	0.017	0	0.0
13	0	0.0	1	0.021
14	0	0.0	2	0.042
15	1	0.017	2	0.042
17	0	0.0	1	0.021
18	1	0.017	1	0.021
H		0.56		0.07
h		0.65 ± 0.09		0.75 ± 0.09
PIC		0.61		0.70
PD		0.82		0.86

n = number of chromosomes; No. Obs. = numbers observed; H = Observed heterozygosity; h = expected heterozygosity; PIC = polymorphic information content; PD = power of discrimination.

Genomic DNA was extracted using a rapid non-enzymatic method (1). PCR amplification of both loci was achieved by using locus specific primers flanking the repeat region (2,3) and carried out in an eppendorf thermocycler™ using Taq polymerase (Roche Molecular Diagnostics, GmbH, Germany). Amplimers were electrophoresed on 6% denaturing urea gel (7M) and analyzed in ALF™ Express DNA Sequencer (Amersham Biosciences Ltd., Uppsala, Sweden) using the software Fragment manager. Allelic

TABLE 2—Distribution of allele frequencies at ApoB 3' VNTR among two Indian tribal populations.

Alleles (repeats)	Bison Horn Maria (n = 68)		Muria (n = 90)	
	No. Obs.	Frequency	No. Obs.	Frequency
31	2	0.029	0	0.0
32	1	0.015	0	0.0
33	0	0.0	3	0.033
34	5	0.074	2	0.022
35	4	0.059	7	0.078
36	16	0.235	14	0.156
37	16	0.235	18	0.200
38	6	0.088	15	0.167
39	4	0.059	7	0.078
40	4	0.059	11	0.122
41	2	0.029	5	0.056
46	1	0.015	2	0.022
47	5	0.074	4	0.044
48	1	0.015	2	0.022
51	1	0.015	0	0.0
H		0.59		0.67
h		0.87 ± 0.04		0.88 ± 0.04
PIC		0.87		0.89
PD		0.93		0.95

n = number of chromosomes; No. Obs. = numbers observed; H = Observed heterozygosity; h = expected heterozygosity; PIC = polymorphic information content; PD = power of discrimination.

ladders for both loci were developed in our laboratory and used for the correct assignment of the alleles.

Analysis of Data

The expected genotype frequencies for both loci were calculated under the assumption of Hardy-Weinberg equilibrium expectation. The expected heterozygosity or gene diversity was calculated as described by Nei et al. (4). The Polymorphic Information Content

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was determined according to Botstein et al. (5), and the Power of Discrimination was calculated as by Fisher (6).

A total of 12 alleles at D19S20 and 15 alleles at ApoB 3' VNTR was observed among these two populations studied. At D19S20 locus, allele 6 was found to be the predominant allele among both population groups (Table 1). At ApoB locus, a bimodal distribution pattern of alleles 36 and 37 was observed among Bison Horn Maria, whereas among Murias, the distribution of predominant alleles was trimodal at alleles 36, 37, and 38 (Table 2). The expected and observed heterozygosity showed no significant differences at both the loci. The allele frequency data are comparable with the results published earlier in other Indian population groups (7).

The complete dataset can be accessed by any interested party via electronic mail from communicating authors: birajalaxmi@yahoo.co.in and msesh@apsara.barc.ernet.in.

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