

FOR THE RECORD

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STR Polymorphism Among Two Tribal Populations of India

POPULATIONS: Two tribal populations of India, Bison Horn Maria and Muria from Bastar district of Madhya Pradesh in Central India were studied for DNA polymorphisms at tetranucleotide short tandem repeat (STR) loci (F13A01 and HUMvWA). A total of 63 random adult individuals for F13A01 locus and 53 samples for HUMvWA were analyzed in the present study.

KEYWORDS: forensic science, STR, F13A01, HUMvWA, Indian tribal populations

Genomic DNA was isolated from peripheral blood samples using the method by Lahiri and Nurnberger (1). The samples were then PCR amplified using locus specific primers (2,3). The forward primer for both the loci were fluorescently labeled with Cy5TM dye amidite. The amplified products were analyzed on ALFTM Express DNA Sequencer (Amersham Biosciences Ltd., Uppasala, Sweden). Internal ladders were used in each lane to compensate for mobility shifts. Nomenclature for both loci was based on number of repeat units.

Allele frequencies and gene diversities were computed using Arlequin ver. 1.1 (4). Significant departure from Hardy-Weinberg equilibrium (HWE) expectations was tested using Exact test. The polymorphic information content (PIC) was determined according to Botstein et al. (5) and the Power of Discrimination (PD) was calculated as described by Fisher (6).

At F13A01 locus, a total of 15 and 12 alleles was observed among Maria and Muria, respectively, with repeats varying from 3.2 to 17 (Table 1). The predominant allele was allele 5.2 for both the populations. The observed heterozygosity was low, but high values were observed for PIC and PD. At HUMvWA locus, Maria and Muria showed 7 and 6 alleles, respectively, with repeats varying from 14 to 20 (Table 1). Among Maria, allele 17 and allele 18 both were predominant with a frequency of 0.22, while allele 14 showed an almost similar frequency of 0.20. Among Muria, the most common allele was allele 17 with a frequency of 0.40. For HUMvWA locus, both the populations showed high values for heterozygosity, PIC and PD. Using exact test the two populations were in Hardy-Weinberg equilibrium for both the loci.

The complete dataset can be accessed via electronic mail from the authors at anugh@magnum.barc.ernet.in or msesh@apsara.barc.ernet.in.

TABLE 1—STR polymorphism among two tribal populations of India.

Allele	F13A01		HUMvWA	
	Maria (n = 74)	Muria (n = 52)	Maria (n = 54)	Muria (n = 52)
3.2	0.054 (4)	0.038 (2)		
4	0.149 (11)	0.058 (3)		
5	0.094 (7)	0.192 (10)		
5.2	0.216 (16)	0.231 (12)		
6	0.149 (11)	0.173 (9)		
6.2	0.054 (4)	0.115 (6)		
7	0.054 (4)	0.019 (1)		
7.2	0.054 (4)	-		
8	0.014 (1)	-		
13	0.014 (1)	-		
14	0.068 (5)	0.019 (1)	0.200 (11)	0.096 (5)
14.2	0.014 (1)	-	-	-
15	0.027 (2)	0.077 (4)	0.070 (4)	0.019 (1)
15.2	-	0.019 (1)	-	-
16	0.027 (2)	0.038 (2)	0.180 (10)	0.096 (5)
17	0.014 (1)	0.019 (1)	0.220 (12)	0.403 (21)
18	-	-	0.220 (12)	0.260 (14)
19	-	-	0.070 (4)	0.110 (6)
20	-	-	0.018 (1)	-
Observed heterozygosity	0.57	0.60	0.88	0.82
Gene diversity	0.90 ± 0.059	0.87 ± 0.051	0.83 ± 0.084	0.75 ± 0.072
PIC	0.89	0.85	0.79	0.71
PD	0.88	0.84	0.90	0.85
Exact test (p > 0.005)	0.71	0.80	0.052	0.384

n = No. of chromosomes. The number in the parentheses denotes the observed number for each allele.

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