

## FOR THE RECORD

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# Allele Frequencies of Microsatellite Repeat Loci in Bhargavas, Chaturvedis, and Brahmins of North India

**POPULATION:** Fifty healthy unrelated individuals were randomly chosen from each of the following three populations viz., Bhargava, Chaturvedi, and Brahmin. Three generation pedigree charts were prepared to ensure (i) surname endogamy in Bhargavas and Chaturvedies, and caste endogamy in Brahmins. Subjects were chosen from several parts of Uttar Pradesh, a northern state of the Indian republic.

**KEYWORDS:** forensic science, DNA, STR, North Indian population, Bhargava, Chaturvedi, Brahmin

**Extraction:** Modified salting out technique (1) followed by phenol—chloroform extraction and ethanol precipitation.

### PCR

1–2 ng of target DNA, using flanking primers (2–4) purchased from Research Genetics, one of which was fluorescently labeled.

**Typing:** ABI 373A genetic analyzer, Genescan T, Genotype T.

**Analysis of data:** POPGENE (5) TFPGA (6) CERVUS (7)

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### Results

See Tables 1 to 3.

### Other Remarks

The allele frequency estimates of these STR markers reveal that alleles are not equally distributed in all the three populations included in the study.

Alleles at most of the loci were in Hardy Weinberg equilibrium. There was no nonrandom association between alleles at two different loci. Markers are informative and can be used for forensic DNA analysis and paternity testing.

### References

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TABLE 1—Allele frequency distribution among Bhargavas.

Bp	D13S894*	D14S297	D16S2622	D17S1298	D19S1034	D1S551*
75	...	...	0.02	...	...	...
79	...	...	0.33	...	...	...
83	...	...	0.53	0.01	...	...
87	...	...	0.08	...	...	...
91	...	...	0.03	...	...	...
97	...	0.08	...	...	...	...
99	...	0.08	...	...	...	...
101	...	0.40	...	...	...	...
103	...	0.19	...	...	...	...
105	...	0.23	...	...	...	...
107	...	0.01	...	...	...	...
122	0.01	...	...	...	...	...
136	...	...	0.01	...	...	...
176	0.02	...	...	...	...	...
180	0.01	...	...	...	...	...
188	0.21	...	...	...	...	...
192	0.66	0.01	...	...	...	...
196	0.08	...	...	...	...	...
200	0.01	...	...	...	...	...
220	...	...	...	...	0.07	...
224	...	...	...	...	0.01	...
228	...	...	...	...	0.22	...
230	...	...	...	...	...	0.01
232	...	...	...	...	0.52	0.32
234	...	...	...	...	...	0.39
236	...	...	...	...	0.15	0.24
238	...	...	...	...	...	0.02
240	...	...	...	...	0.01	...
245	...	...	...	0.65	0.01	...
249	...	...	...	0.02	...	...
253	...	...	...	0.30	...	...
256	...	...	...	0.01	...	...
257	...	...	...	0.01	...	...
H	0.500	0.840	0.540	0.560	0.612	0.638
PIC	0.468	0.699	0.535	0.410	0.604	0.610
IP	0.315	0.138	0.229	0.377	0.172	0.172
PE	0.290	0.515	0.339	0.231	0.411	0.398
p (HW)	0.000*	0.740	0.310	0.880	0.490	0.000*

H: Observed heterozygosity.  
 PIC: Polymorphism information content.  
 IP: Individualization potential.  
 PE: Power of exclusion.  
 p (HW): Significance of departure from HW equilibrium by Chi-Square test.  
 \*Deviation from HWE.

TABLE 2—Allele frequency distribution among *Chaturvedis*.

Bp	D13S894	D14S297	D16S2622	D17S1298	D19S1034	D1S551
75	...	...	0.04	...	...	...
79	...	...	0.35	...	...	...
83	...	...	0.53	...	...	...
87	...	...	0.08	...	...	...
91	...	0.01	...	...	...	...
93	...	0.01	...	...	...	...
97	...	0.11	...	...	...	...
99	...	0.01	...	...	...	...
101	...	0.46	...	...	...	...
103	...	0.01	...	...	...	...
105	...	0.35	...	...	...	...
107	...	...	...	...	...	...
109	...	0.01	...	...	...	...
111	...	0.03	...	...	...	...
176	...	...	...	...	...	...
180	0.13	...	...	...	...	...
188	0.25	...	...	...	...	...
192	0.40	...	...	...	...	...
196	0.14	...	...	...	...	...
200	0.07	...	...	...	...	...
204	0.01	...	...	...	...	...
220	...	...	...	...	0.16	...
224	...	...	...	...	0.03	...
228	...	...	...	...	0.35	0.02
230	...	...	...	...	...	0.03
232	...	...	...	...	0.34	0.25
234	...	...	...	...	...	0.33
236	...	...	...	...	0.06	0.33
238	...	...	...	...	...	0.03
240	...	...	...	...	0.06	...
241	...	...	...	0.01	...	...
245	...	...	...	0.57	...	...
249	...	...	...	0.05	...	...
253	...	...	...	0.32	...	...
256	...	...	...	...	...	...
257	...	...	...	0.05	...	...
H	0.720	0.540	0.620	0.440	0.720	0.729
PIC	0.697	0.592	0.513	0.497	0.683	0.659
IP	0.128	0.165	0.244	0.247	0.119	0.139
PE	0.511	0.395	0.315	0.304	0.495	0.458
p (HW)	0.890	0.990	0.970	0.130	0.610	0.940

H: Observed heterozygosity.

PIC: Polymorphism information content.

IP: Individualization potential.

PE: Power of exclusion.

p (HW): Significance of departure from HW equilibrium by Chi-Square test.

\*Deviation from HWE.

TABLE 3—Allele frequency distribution among Brahmins.

Bp	D13S894	D14S297	D16S2622	D17S1298	D19S1034	D1S551*
71	...	...	0.02	...	...	...
75	...	...	0.02	...	...	...
79	...	...	0.32	...	...	...
83	...	...	0.50	0.01	...	...
87	...	...	0.12	...	...	...
91	...	...	0.01	...	...	...
93	...	0.03	...	...	...	...
97	...	0.07	...	...	...	...
99	...	0.02	...	...	...	...
101	...	0.49	...	...	...	...
103	...	0.11	...	...	...	...
105	...	0.19	...	...	...	...
107	...	0.04	...	...	...	...
109	...	0.01	...	...	...	...
111	...	0.01	...	...	...	...
115	...	0.02	...	...	...	...
130	0.01	...	...	...	...	...
136	...	...	0.01	...	...	...
180	0.06	...	...	...	...	...
184	0.03	...	...	...	...	...
188	0.22	...	...	...	...	...
192	0.57	0.01	...	...	...	...
196	0.09	...	...	...	...	...
200	0.02	...	...	...	...	...
220	...	...	...	...	0.06	...
224	...	...	...	...	0.04	...
228	...	...	...	...	0.35	...
230	...	...	...	...	...	0.02
232	...	...	...	...	0.27	0.29
234	...	...	...	...	...	0.43
236	...	...	...	...	0.22	0.20
238	...	...	...	...	...	0.03
240	...	...	...	...	0.03	0.01
241	...	...	...	0.05	...	...
245	...	...	...	0.54	...	...
249	...	...	...	0.03	...	...
253	...	...	...	0.35	0.01	...
257	...	...	...	0.02	...	...
H	0.560	0.720	0.800	0.600	0.714	0.592
PIC	0.572	0.674	0.570	0.507	0.697	0.619
IP	0.199	0.145	0.286	0.254	0.114	0.167
PE	0.387	0.502	0.372	0.313	0.508	0.415
p (HW)	0.780	0.090	0.540	0.890	0.750	0.000*

H: Observed heterozygosity.  
 PIC: Polymorphism information content.  
 IP: Individualization potential.  
 PE: Power of exclusion.  
 p (HW): Significance of departure from HW equilibrium by Chi-Square test.  
 \*Deviation from HWE.