FOR THE RECORD

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Distribution of Allele Frequencies of Six STR Markers in North Indians

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 1–3.

Other Remarks

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

Alleles at most of the loci were in Hardy Weinberg equilibrium. There was no non-random 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	D2S297	D2S442	D2S1777	D2S2186	D5S817	D5S1492
98	0.20	…	…	…	…	…
100	0.29	…	…	…	…	…
102	0.18	…	…	…	…	…
106	0.01	…	…	…	…	…
108	0.16	…	…	…	…	…
110	0.12	…	…	…	…	…
112	0.01	0.01	…	…	…	0.19
116	…	…	…	…	…	0.32
120	…	…	…	…	…	0.42
124	…	…	…	…	…	0.06
162	0.01	…	…	…	…	…
191	…	…	0.01	…	…	…
195	…	0.13	0.04	…	…	…
199	…	0.17	0.56	…	…	…
201	…	…	…	0.16	…	…
202	…	…	0.01	…	…	…
203	…	0.51	0.20	0.10	…	…
205	…	…	…	0.23	…	…
207	…	0.16	0.15	0.02	…	…
209	…	…	…	0.01	…	…
211	…	0.02	0.01	…	…	…
215	…	…	0.01	…	…	…
219	…	…	0.01	…	…	…
227	…	…	…	0.44	…	…
229	…	…	…	0.03	0.01	…
256	…	…	…	…	0.01	…
260	…	…	…	…	0.24	…
264	…	…	…	…	0.35	0.01
268	…	…	…	…	0.31	…
272	…	…	…	…	0.06	…
276	…	…	…	…	0.01	…
H	0.761	0.660	0.620	0.735	0.667	0.620
PIC	0.765	0.627	0.579	0.673	0.663	0.623
IP	0.074	0.155	0.200	0.129	0.133	0.173
PE	0.597	0.437	0.391	0.486	0.462	0.418
p (HW)	0.810	0.530	0.780	0.600	0.890	0.260

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.

TABLE 2—*Allele frequency distribution among Chaturvedis.*

Bp	D2S297	D2S442	D2S1777	D2S2186	D5S817*	D5S1492
98	0.22	...	...	...	...	...
100	0.40	...	...	...	...	...
102	0.08	...	...	...	...	...
104	0.07	...	...	...	...	...
106	0.03	...	...	...	...	...
108	0.12	...	...	...	...	0.01
110	0.03	...	...	...	...	...
112	0.03	...	...	...	...	0.09
116	...	...	...	...	...	0.29
120	...	...	...	...	...	0.50
124	...	...	...	...	...	0.11
162	...	...	...	...	...	...
191	...	...	...	...	...	...
195	...	0.05	0.07	...	...	...
199	...	0.32	0.53	...	...	...
201	...	...	...	0.14	...	...
202	...	...	...	...	...	...
203	...	0.40	0.25	0.18	...	...
205	...	...	...	0.14	...	...
207	...	0.21	0.15	0.09	...	...
209	...	...	...	...	...	...
211	...	0.01	...	...	...	...
215	...	...	...	...	...	...
219	...	...	...	...	...	...
225	...	...	...	0.02	...	...
227	...	...	...	0.36	...	...
229	...	...	...	0.04	...	...
256	...	...	...	...	...	...
260	...	...	...	...	0.19	...
264	...	...	...	...	0.45	...
268	...	...	...	...	0.29	...
272	...	...	...	...	0.04	...
276	...	...	...	...	...	...
280	...	...	...	...	0.01	...
H	0.723	0.612	0.600	0.771	0.551	0.740
PIC	0.728	0.627	0.575	0.749	0.602	0.590
IP	0.110	0.152	0.190	0.088	0.172	0.216
PE	0.559	0.420	0.377	0.581	0.396	0.392
p (HW)	0.300	0.540	0.920	0.540	0.000	0.750

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

TABLE 3—*Allele frequency distribution among Brahmins.*

Bp	D2S297	D2S442	D2S1777	D2S2186	D5S817	D5S1492
98	0.27	…	…	…	…	…
100	0.25	…	…	…	…	…
102	0.16	…	…	…	…	…
104	0.04	0.01	…	…	…	…
106	0.03	…	…	…	…	…
108	0.10	…	…	…	…	0.01
110	0.10	…	…	…	…	…
112	0.01	…	…	…	…	0.12
116	…	…	…	…	…	0.28
120	…	…	…	…	…	0.47
124	…	…	…	…	…	0.11
166	0.01	…	…	…	…	…
191	…	0.01	0.01	…	…	…
195	…	0.06	0.12	…	…	…
199	…	0.36	0.54	0.03	…	…
201	…	…	…	0.13	…	…
202	…	…	0.01	…	…	…
203	…	0.23	0.25	0.09	…	…
205	…	…	…	0.16	…	…
207	…	0.25	0.61	0.06	…	…
209	…	…	…	…	…	…
211	…	0.03	…	…	…	…
215	…	…	…	…	…	…
219	…	0.01	…	…	…	…
223	…	0.02	…	0.01	…	…
225	…	…	…	0.01	…	…
227	…	0.02	…	0.38	0.01	…
229	…	…	…	0.09	…	…
231	…	…	…	0.01	…	…
256	…	…	…	…	…	…
260	…	…	…	…	0.22	…
264	…	…	…	…	0.38	…
268	…	…	…	…	0.28	0.01
272	…	…	…	…	0.08	…
276	…	…	…	…	0.01	…
H	0.848	0.660	0.531	0.813	0.735	0.700
PIC	0.785	0.710	0.572	0.759	0.659	0.623
IP	0.082	0.105	0.196	0.095	0.108	0.172
PE	0.628	0.528	0.378	0.601	0.459	0.427
p (HW)	0.250	0.860	0.670	0.430	0.550	0.900

H: Observed heterozygosity.
PIC: Polymorphism information content.
IP: Individualization potential.
PE: Power of exclusion.
p (HW): Significance of departive from HW equilibrium by Chi-square test.