

## FOR THE RECORD

Suraksha Agrawal<sup>1</sup>; Bartram Müller<sup>2</sup>; Uddalak Bharadwaj<sup>1</sup>; Suhasini Bhatnagar<sup>1</sup>; Arundhati Sharma<sup>1</sup>; Faisal Khan<sup>1</sup>; S. S. Agarwal<sup>1</sup>

# DNA Short Tandem Repeat Profiling of Three North Indian Populations

**Population:** Fifty healthy unrelated individuals were randomly chosen from each of the three populations viz., Bhargavas, Chaturvedies, and Brahmins. Three generation pedigree charts were prepared to ensure surname endogamy in Bhargavas Chaturvedies and group 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 populations, Bhargavas, Chaturvedies, Brahmins.

In a North Indian population, a study was performed on the STR markers D20S115, D1S1728, D2S1329, D6S1270, D12S398, and D15S816. Each of the six STR markers were analyzed by using ABI 373 A genetic analyzer (Applied Biosystem, Inc.). This study was done on a population of 150 unrelated North Indians (Uttar Pradesh) from three different caste groups to determine allele frequencies at these STR loci and to create the database for North Indians from Uttar Pradesh, India.

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

**PCR**—1 to 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).

<sup>1</sup> Department of Medical Genetics, SGIPGIMS, Lucknow.

<sup>2</sup> Abteilung für Tropenmedizinische Grundlagenforschung, BNI, Bernhard-Nocht-Str. 74, 20359 Hamburg, Germany.

**Results**—See Table 1 to 3.

**Access to Data**—Via electronic mail from communicating author at: suraksha@sgpgi.ac.in

### Other Remarks

The allele frequency estimates of these STR markers reveal that alleles are not equally distributed in all the populations. All loci follow Hardy Weinberg equilibrium. These were 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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Additional information and reprint requests:

Dr. Suraksha Agrawal

Additional Professor

Department of Medical Genetics

Sanjay Gandhi Post Graduate Institute of Medical Sciences

Raebareli Road, Lucknow (UP) 226014 India

Phone: 091-522-440004-8 Ext 2338,2346,2347

Fax No: 091-522-440973/440017

Email: suraksha@sgpgi.ac.in

TABLE 1—Allele frequency at six STR markers in Bhargavas (North Indian populations).

bp	D20S115	D1S1728	D2S1329	D6S1270	D12S398	D15S816
104				0.01		
108						
112						
116				0.03		
120				0.44		
124				0.33		0.01
128				0.18		0.29
129					0.49	
132				0.01		0.19
133					0.22	
136						0.43
137						
140						0.08
141					0.20	
144						
145					0.06	
150					0.03	
158		0.40				
162		0.44				
166	0.02	0.16				
170	0.25					
174	0.24					
178	0.35					
182	0.14					
186						
190			0.14			
194						
198			0.51			
200			0.01			
202			0.28			
206			0.06			
H	0.840	0.700	0.740	0.680	0.640	0.800
PIC	0.695	0.552	0.590	0.616	0.625	0.644
IP	0.132	0.248	0.227	0.189	0.159	0.186
PE	0.502	0.342	0.393	0.412	0.433	0.445
p (HW)	0.820	0.200	0.690	0.970	0.820	0.760

H: Observed heterozygosity, PIC: polymorphism information content, IP: Power of exclusion, p (HW): Hardy-Weinberg test (Chi-Square) p value.

TABLE 2—Allele frequency at six STR markers in Chaturvedies (North Indian populations).

bp	D20S115	D1S1728	D2S1329	D6S1270	D12S398	D15S816
104				0.01		
108						
112				0.02		
116				0.03		0.01
120				0.39		
124				0.38		
128				0.16		0.26
129					0.43	
132				0.01		0.30
133					0.25	
136						0.29
137					0.10	
140						0.14
141					0.15	
144						
145					0.07	
150						
158		0.45				
162		0.30				
166		0.19				
170	0.16	0.03				
174	0.31	0.02				
178	0.29	0.01				
182	0.18					
186	0.06					

TABLE 2—(Continued).

bp	D20S115	D1S1728	D2S1329	D6S1270	D12S398	D15S816
190			0.08			
194			0.14			
198			0.53			
200			0.01			
202			0.14			
206			0.09			
H	0.800	0.600	0.650	0.920	0.700	0.680
PIC	0.723	0.621	0.663	0.673	0.619	0.653
IP	0.114	0.164	0.167	0.155	0.127	0.123
PE	0.538	0.417	0.449	0.418	0.483	0.492
p (HW)	0.750	0.900	0.300	0.920	0.890	0.380

H: Observed heterozygosity, PIC: polymorphism information content, IP: Power of exclusion, p (HW): Hardy-Weinberg (Chi-Square) p value.

TABLE 3—Allele frequency at six STR markers in Brahmins (North Indian populations).

bp	D20S115	D1S1728	D2S1329	D6S1270	D12S398	D15S816
104				0.03		
108						0.01
112						
116				0.04		
120				0.49		
124				0.31		
128				0.13		0.23
129					0.48	
132						0.28
133					0.19	
136						0.41
137					0.04	
140						0.05
141					0.27	
144						0.01
145					0.02	
150						
158		0.41				
162		0.31				
166	0.02	0.24				
170	0.18	0.04				
174	0.28					
178	0.37					
182	0.14					
186	0.01					
190			0.10			
194			0.08			
198			0.52			
200						
202			0.21			
206			0.09			
H	0.730	0.760	0.800	0.640	0.710	0.700
PIC	0.699	0.620	0.628	0.594	0.610	0.651
IP	0.1274	0.2024	0.1768	0.1872	0.1880	0.1407
PE	0.509	0.411	0.443	0.397	0.410	0.449
p (HW)	0.730	0.470	0.290	0.640	0.660	0.920

H: Observed heterozygosity, PIC: polymorphism information content, IP: Power of exclusion, p (HW): Hardy-Weinberg (Chi-Square) p value.