

FOR THE RECORD

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Polymorphism at 15 Short Tandem Repeat AmpF ℓ STR[®] Identifiler[™] Loci in Three Aboriginal Populations of India: An Assessment in Human Identification

POPULATION: Munda, Santal and Oraon are chosen in this study, as they constitute the primitive Austroloid population groups that inhabit Chotanagpur Plateau of Eastern India. Munda have lent their names to the “Mundari” branch of Austro-Asiatic language family. Santal, the third largest tribe in India also belongs to the Austro-Asiatic language family. The Oraon tribe speaks “Kurukh” classified under the Dravidian language family. These populations were hunter-gatherers but have maintained a high degree of endogamy (1)

KEYWORDS: forensic science, AmpF/STR[®] Identifiler[™], short tandem repeat (STR), Munda, Santal, Oraon, Chotanagpur Plateau, population genetics, DNA typing, D5S818, FGA, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, THO1, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51

STR polymorphisms have proven to be extremely useful in population genetics studies and human identification. The fifteen analysed STR loci were tetra-nucleotide repeats: D5S818, FGA, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, THO1, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51.

Blood samples were collected randomly by venipuncture from 185 unrelated consenting individuals of 3 tribal population of Chotanagpur Plateau of eastern India, in accordance with the ethical guidelines of the institution involved. DNA was extracted using the standard phenol-chloroform method (2). Quantitation of extracted DNA was carried out using the Quantiblot-Kit (PE Biosystem). PCR amplification was performed using the AmpF/STR[®] Identifiler[™] PCR Amplification Kit (3). The amplified products were detected using denaturing gel cast on ABI Prism[™] 377 DNA Sequencer. The reference ladder used were obtained along with AmpF/STR[®] Identifiler[™] PCR Amplification Kit. Allele designation and data analysis were carried out using the Genescan[™] and Genotyper[™] softwares.

Statistical analysis included calculations for allele frequencies, observed heterozygosity, probability of homozygosity, ex-

act test, likelihood ratio, power of exclusion and discrimination using DNATYPE Program (4). The average variance of the alleles at each locus was calculated using Microsat Software (<http://lotka.stanford.edu/microsat.html>). Results are given in Tables 1–4.

All the loci were observed to be highly polymorphic. Minimum of 120 chromosomes have been analyzed for each loci in the three tribal groups. Allele 29 at D21S11, allele 12 at CSF1PO, allele 9 at THO1, allele 8 at D13S317 and allele 11 at TPOX were found to be most frequent in the tribes. Of the 15 microsatellite loci, FGA, D8S1179, D7S820, D2S1338 and D19S433 are highly polymorphic (variance ≥ 4), while the other loci demonstrate a narrow range of variation. The tests show that most of these populations are following the Hardy-Weinberg Equilibrium and have not undergone any major population stochastic processes. The combined Power of Discrimination for the three populations Munda, Santal and Oraon are 0.972, 0.978 and 0.977 respectively. Our work demonstrates that 15 microsatellite/STR markers chosen for this study are highly suitable for individual identification and genetic characterization of highly endogamous aboriginal populations. The data generated in this study will augment the existing STR information already available for Indian populations (5–8).

The complete dataset is available on website <http://humstr.ndacdb.org> and also through electronic mail from communicating author: dtubprd@giasc101.vsnl.net.in, vkk2k@hotmail.com

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TABLE 1—Allele frequencies of fifteen STR loci in Munda (N = 128) Tribe of Chotanagpur Plateau, India.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSFIPO	D3S1358	THO1	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6								0.123							
7								0.169	0.008						
8	0.031				0.198			0.100	0.461	0.094					0.269
9	0.063				0.079	0.016		0.462	0.039	0.164		0.008			0.185
9.3					0.016			0.131							
10	0.063		0.131		0.190	0.262		0.015	0.063	0.102				0.162	0.008
10.2						0.008									
11	0.414		0.023		0.302	0.270			0.281	0.352		0.023		0.362	0.008
12	0.305		0.069		0.175	0.373			0.109	0.172		0.062		0.023	0.049
12.2															0.008
13	0.125		0.108		0.032	0.048			0.039	0.086		0.323			0.148
13.2												0.015			0.008
14			0.208		0.008	0.024	0.055			0.031		0.231	0.200		0.320
14.2												0.031			
15			0.300				0.258					0.115	0.031		0.197
15.2												0.108	0.008		0.008
16		0.025	0.138				0.367					0.069	0.192		0.131
16.2							0.008					0.008			
17			0.023				0.250				0.032		0.215		0.033
17.2												0.008			0.008
18		0.050					0.063				0.169		0.185		0.049
19		0.050									0.258		0.169		
19.2		0.008													
20		0.133									0.097				0.008
21		0.058									0.056				0.016
21.2		0.033													
22		0.208									0.056				
22.2		0.008													
23		0.200									0.177				
24		0.133									0.073				
25		0.050									0.056				
26		0.008									0.016				
26.2		0.008													
27		0.017									0.008				
28				0.055											
28.2				0.008											
29				0.297											
29.2				0.008											
30				0.188											
30.2				0.008											
31				0.039											
31.2				0.172											
32				0.039											
32.2				0.086											
33				0.031											
33.2				0.070											
H	0.641	0.850	0.862	0.828	0.730	0.619	0.766	0.739	0.594	0.719	0.790	0.769	0.769	0.862	0.754
HP	0.212	0.687	0.317	0.992	0.200	0.087	0.513	0.686	0.098	0.146	0.209	0.441	0.367	0.022	0.234
ET	0.224	0.002	0.107	0.763	0.225	0.287	0.313	0.038	0.009	0.020	0.102	0.088	0.765	0.102	0.553
LR	0.182	0.000	0.042	0.706	0.272	0.222	0.188	0.019	0.003	0.037	0.134	0.153	0.815	0.084	0.635
PD	0.711	0.868	0.813	0.827	0.795	0.716	0.729	0.715	0.690	0.792	0.848	0.807	0.813	0.736	0.813
PE	0.343	0.695	0.719	0.652	0.476	0.314	0.538	0.491	0.284	0.458	0.581	0.543	0.543	0.719	0.517

N: Number of chromosome; H: Observed heterozygosity; HP: Probability of homozygosity; ET: Exact test; LR: Likelihood ratio; PD: Power of discrimination; PE: Power of exclusion.

TABLE 2—Allele frequencies of fifteen STR loci in Santal (N = 122) tribe of Chotanagpur Plateau, India.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	THO1	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6								0.205							
7					0.008			0.189							
8	0.016				0.303			0.115	0.303	0.098				0.336	
8.2					0.033										
9	0.033				0.025	0.025		0.385	0.049	0.123		0.016		0.213	
9.3								0.082							
10	0.107		0.082		0.156	0.131		0.025	0.082	0.066				0.049	
10.2						0.008									
11	0.352		0.049		0.377	0.328			0.287	0.336		0.041		0.377	0.017
12	0.336		0.098		0.098	0.451			0.189	0.246		0.107		0.025	0.042
13	0.148		0.098			0.049			0.049	0.082		0.328			0.167
13.2												0.025			
14			0.221			0.008	0.049		0.041	0.049		0.189	0.221		0.275
14.2												0.041			
15	0.008		0.311				0.336					0.18	0.082		0.225
15.2							0.041					0.049	0.008		
16			0.115				0.262					0.025	0.148		0.158
17			0.016				0.262					0.057	0.189		0.067
18		0.025	0.008				0.049					0.238	0.246		0.033
19		0.066										0.18	0.098		
20		0.098										0.066	0.008		0.017
21		0.033										0.049			
21.2		0.016													
22		0.197										0.066			
23		0.287										0.189			
24		0.123										0.074			
24.2		0.025													
25		0.041										0.057			
25.2		0.025													
26		0.041										0.025			
26.2		0.016													
27				0.016											
28				0.082											
29				0.246											
29.2				0.008											
30		0.008		0.139											
30.2				0.025											
31				0.057											
31.2				0.148											
32				0.033											
32.2				0.148											
33.2				0.09											
34.2				0.008											
H	0.754	0.82	0.803	0.885	0.607	0.623	0.754	0.623	0.738	0.836	0.902	0.82	0.771	0.705	0.75
HP	0.651	0.616	0.861	0.52	0.03	0.446	0.842	0.018	0.462	0.362	0.273	0.785	0.351	0.886	0.21
ET	0.139	0.101	0.373	0.121	0.597	0.352	0.363	0.115	0.498	0.755	0.538	0.007	0.376	0.828	0.172
LR	0.065	0.089	0.556	0.075	0.644	0.364	0.493	0.244	0.273	0.516	0.486	0.012	0.333	0.922	0.162
PD	0.728	0.843	0.813	0.856	0.73	0.669	0.743	0.753	0.777	0.788	0.852	0.806	0.817	0.697	0.813
PE	0.517	0.637	0.605	0.765	0.299	0.319	0.517	0.319	0.489	0.667	0.8	0.637	0.546	0.436	0.51

N: Number of chromosome; H: Observed heterozygosity; HP: Probability of homozygosity; ET: Exact test; LR: Likelihood ratio; PD: Power of discrimination; PE: Power of exclusion.

TABLE 3—Allele frequencies of fifteen STR loci in Oraon (N = 120) tribe of Chotanagpur Plateau, India.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSFIPO	D3S1358	THO1	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
4								0.025							
5								0.008							
6								0.125							
7					0.017			0.2						0.008	
8	0.017		0.008		0.35	0.008		0.125	0.325	0.108				0.3	0.018
9	0.067				0.042			0.433	0.1	0.192				0.108	
9.2					0.008										
9.3								0.083							
10	0.133		0.15		0.242	0.142			0.075	0.083		0.059		0.1	
11	0.275		0.042		0.233	0.358			0.208	0.225		0.017		0.442	0.008
11.2												0.017			
12	0.292		0.092		0.008	0.358	0.025		0.233	0.233		0.068		0.042	0.008
12.2												0.008			
13	0.2		0.108		0.008	0.092	0.033		0.058	0.117		0.314	0.017		0.149
14	0.008		0.308		0.017	0.042	0.1			0.042		0.224	0.192		0.368
14.2												0.042			0.008
15	0.008		0.175				0.308					0.093	0.108		0.167
15.2												0.059	0.025		
16			0.1				0.283					0.059	0.183		0.114
16.2												0.034			
17			0.017				0.225				0.058		0.158		0.114
18		0.017					0.025				0.133		0.2		0.018
18.2		0.008													
19		0.1									0.192		0.092		0.008
19.2		0.008													
20		0.108									0.083		0.025		
21		0.042									0.05				0.008
21.2		0.008													
22		0.225									0.033				0.008
22.2		0.017													
23		0.233									0.233				
24		0.117									0.133				
25		0.075									0.042				
26		0.008									0.017				
27		0.017									0.025				
27.2				0.008											
28				0.067											
29				0.283											
29.2				0.008											
30		0.008		0.217											
30.2				0.005											
31				0.042											
31.2		0.008		0.133											
32				0.008											
32.2				0.108											
33.2				0.067											
34.2				0.008											
H	0.833	0.9	0.85	0.833	0.733	0.8	0.817	0.633	0.85	0.817	0.783	0.746	0.733	0.75	0.79
HP	0.292	0.286	0.54	0.943	0.693	0.136	0.317	0.08	0.177	0.879	0.105	0.126	0.02	0.326	0.966
ET	0.004	0.848	0.005	0.825	0.102	0.088	0.021	0.312	0.778	0.076	0.592	0.568	0.13	0.038	0.333
LR	0.002	0.805	0.003	0.844	0.083	0.198	0.018	0.154	0.853	0.11	0.633	0.482	0.231	0.038	0.351
PD	0.777	0.851	0.82	0.832	0.762	0.713	0.762	0.734	0.778	0.824	0.857	0.824	0.843	0.691	0.787
PE	0.662	0.795	0.695	0.662	0.481	0.599	0.631	0.332	0.695	0.631	0.568	0.503	0.481	0.51	0.581

N: Number of chromosome; H: Observed heterozygosity; HP: Probability of homozygosity; ET: Exact test; LR: Likelihood ratio; PD: Power of discrimination; PE: Power of exclusion.

TABLE 4—Number of alleles and their variance among three primitive Austroloid tribal populations of India.

Populations	D5S818	FGA	D8S1179	D21S11	D7S820	CSFIPO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
Munda	6 (1.328)	11 (5.004)	8 (3.725)	6 (2.167)	7 (2.341)	6 (1.110)	5 (1.000)	5 (1.277)	7 (3.008)	7 (2.355)	11 (6.442)	8 (1.768)	6 (2.951)	5 (1.591)	11 (3.512)
Santal	6 (1.193)	9 (3.872)	8 (3.237)	7 (2.371)	5 (2.137)	5 (0.801)	5 (1.037)	5 (1.630)	7 (3.389)	7 (2.529)	10 (6.898)	7 (1.714)	6 (2.864)	5 (1.882)	9 (2.654)
Oraon	6 (1.529)	9 (3.630)	8 (4.928)	6 (2.732)	6 (13.739)	5 (1.668)	6 (1.291)	6 (5.287)	5 (1.190)	6 (2.749)	11 (8.427)	8 (14.024)	7 (3.054)	5 (1.960)	6 (1.791)
Average	6 (1.35)	9.66 (4.17)	8 (3.96)	6.33 (2.42)	6 (6.07)	5.33 (1.19)	5.33 (1.11)	5.33 (2.73)	6.33 (2.53)	6.66 (2.54)	10.66 (7.26)	7.66 (5.83)	6.33 (2.96)	5 (1.81)	8.66 (2.65)

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