FOR THE RECORD

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Allelic Variation at 15 Microsatellite Loci in One Important Australoid and Two Indocaucasoid Groups of Chhattisgarh—India*

POPULATION: Oraon, Chhattigarhi-Brahman and Vaish of Chhattisgarh, India.

KEYWORDS: forensic science, forensic applications, microsatellite loci, human identification, STR, Chhattisgarh

DNA profiling with STR loci is comprehensively used for human identification since the last decade. In this perception many data are available (1), but India being a multi-ethnic country and following strict endogamous rules, each community is a distinct group. Their genetic signatures as reported till date also highlight this distinction. To create a complete DNA data bank for identification of individuals precisely—all communities spread in different part of India need to be extensively studied. Chhattisgarh is a newly formed state of India. In order to contribute DNA profiles to the database, this study is based on three important and predominant populations of the province and their allele variation in 13 tetra-nucleotide STR loci and two penta-nucleotide STR loci. Till now, no microsatellite study is reported for any of the selected populations of Chhattisgarh. Among the studied population groups—Oraon is a tribal group, conventionally agriculture based and ethnically Australoid. They are confined to the small villages and do not prefer to marry outside their community thus maintaining the genetic make-up without any admixture. Chhattisgarhi-Brahmans belong to community of learned priest with Indo-caucasoid facial appearance, their traditional occupation was teaching and officiating all ceremonial functions; they practice strict endogamy. Vaish is a trading population of Chhattisgarh. They also have Indo-caucasoid features and follow endogamy (2).

Blood samples of 143 unrelated healthy individuals were collected and DNA was extracted from blood by organic method (3). Two nanograms of template DNA was used for co-amplification of fluorescently labeled 15 STR loci (Powerplex^{TM} 16 Kit) according to the manufacturer's manual. Analysis was done on Long Ranger gel using ABI Prism 377 Automated DNA Sequencer Machine (Applied Biosystems). Statistical analysis (4–5) of allele was done by calculating allele frequency, likelihood ratio test, exact test, homozygosity test, power of discrimination (PD), power of exclusion (PE), least common allele (LCA) and most common allele (MCA).

MCA is same at TH01 (MCA = 9), TPOX (MCA = 11), D18S51 (MCA = 14),CSF1PO (MCA = 11) and D16S539 (MCA = 11) in all studied populations whereas LCA is same only at one loci TPOX (LCA = 12) (Tables 1–4). In studied populations average PD computed is 0.8021 whereas average PE is 0.498 (Table 5). Among the studied fifteen STR loci highest PD was observed at Penta E locus in Brahmin (PD = 0.8953), Oraon (PD = 0.8914) population and FGA in Vaish group (PD = 0.8823). Hardy Weinberg Equilibrium expectation was not followed at few loci among all of the studied populations (Tables 1–3).

The data generated from this study will contribute to the expansion of Indian database for forensic applications and population genetic studies. It can be searched at http://hgvbase.cgb.ki.se by interested researchers.

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TABLE 1—*Allelic variation at fifteen microsatellite loci in Vaish (N = 100) of Chhattisgarh, India.*

Allele	D3S1358	THO1	D21S11	TPOX	D18S51	Penta E	vWA	D8S1179	FGA	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D
5	...	...	...	...	...	0.071	...	...	...	...	...	...	...	...	...
6	...	0.136	...	...	...	...	...	...	...	...	...	...	...	...	...
7	...	0.125	...	...	...	0.082	...	...	...	...	0.010	0.114	...	...	0.021
8	...	0.182	...	0.313	...	...	...	0.031	...	0.051	0.210	0.094	0.040	...	0.266
9	...	0.386	...	0.146	...	0.041	...	0.020	...	0.031	0.080	0.063	0.070	0.010	0.139
9.3	...	0.171	...	...	...	...	...	...	...	...	...	...	...	...	...
10	...	...	...	0.094	...	0.051	...	0.153	...	0.092	0.150	0.302	0.060	0.245	0.277
11	...	...	...	0.405	...	0.194	...	0.102	...	0.235	0.110	0.208	0.520	0.306	0.032
12	...	...	...	0.042	0.041	0.184	...	0.092	...	0.122	0.360	0.156	0.160	0.296	0.117
13	...	...	...	...	0.122	0.021	...	0.194	...	0.275	0.050	0.063	0.130	0.143	0.053
14	0.040	...	...	...	0.337	0.092	0.085	0.143	...	0.153	0.030	...	0.020	...	0.085
15	0.290	...	...	...	0.153	0.082	0.117	0.204	...	0.041	...	...	...	...	0.010
16	0.270	...	...	...	0.102	0.051	0.223	0.061	...	...	...	...	...	...	...
17	0.320	...	...	...	0.122	0.112	0.341	...	...	...	...	...	...	...	...
18	0.080	...	...	...	0.041	0.010	0.106	...	0.022	...	...	...	...	...	...
18.2	...	...	...	...	...	...	...	...	0.045	...	...	...	...	...	...
19	...	...	...	...	0.041	...	0.117	...	0.056	...	...	...	...	...	...
20	...	...	...	...	0.041	...	0.011	...	0.067	...	...	...	...	...	...
20.2	...	...	...	...	...	...	...	...	0.022	...	...	...	...	...	...
21	...	...	...	...	...	0.010	...	...	0.111	...	...	...	...	...	...
22	...	...	...	...	...	...	...	...	0.144	...	...	...	...	...	...
22.2	...	...	...	...	...	...	...	...	0.033	...	...	...	...	...	...
23	...	...	...	...	...	...	...	...	0.133	...	...	...	...	...	...
24	...	...	...	...	...	...	...	...	0.211	...	...	...	...	...	...
25	...	...	...	...	...	...	...	...	0.078	...	...	...	...	...	...
25.2	...	...	...	...	...	...	...	...	0.011	...	...	...	...	...	...
26	...	...	...	...	...	...	...	...	0.067	...	...	...	...	...	...
27	...	...	0.060	...	...	...	...	...	...	...	...	...	...	...	...
28	...	...	0.090	...	...	...	...	...	...	...	...	...	...	...	...
29	...	...	0.240	...	...	...	...	...	...	...	...	...	...	...	...
30	...	...	0.250	...	...	...	...	...	...	...	...	...	...	...	...
30.2	...	...	0.060	...	...	...	...	...	...	...	...	...	...	...	...
31	...	...	0.050	...	...	...	...	...	...	...	...	...	...	...	...
31.2	...	...	0.090	...	...	...	...	...	...	...	...	...	...	...	...
32.2	...	...	0.100	...	...	...	...	...	...	...	...	...	...	...	...
33.2	...	...	0.050	...	...	...	...	...	...	...	...	...	...	...	...
34.2	...	...	0.010	...	...	...	...	...	...	...	...	...	...	...	...
PD	0.7326	0.7545	0.8414	0.7061	0.8161	0.8817	0.7880	0.8529	0.8823	0.8172	0.7818	0.8114	0.6766	0.7382	0.8079
PE	0.562	0.368	0.637	0.584	0.669	0.669	0.538	0.63	0.519	0.451	0.599	0.475	0.398	0.591	0.576
H	0.5190	0.1048	0.5539	0.2279	0.8223	0.2249	0.6016	0.3567	0.0031	0.0405	0.8581	0.1026	0.9584	0.4208	0.5980
ET	0.9190	0.0510	0.0555	0.0195	0.5220	0.0005	0.0240	0.2085	0.0100	0.0005	0.2185	0.0050	0.2090	0.0335	0.1300
LR	0.8955	0.0940	0.0740	0.0060	0.3995	0.0010	0.0150	0.1800	0.0020	0.0005	0.1885	0.0060	0.1900	0.0250	0.2045

N = Number of chromosome; PD = Power of discrimination; H = HWE homozygosity test; ET = Exact test; LR = Likekihoodratio test; PE = Power of exclusion.

TABLE 2—*Allelic variation at 15 microsatellite loci in Brahman (N = 102) of Chhattisgarh, India.*

Allele	D3S1358	TH01	D21S11	TPOX	D18S51	Penta E	vWA	D8S1179	FGA	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D
5	...	0.021	...	...	...	0.041	...	...	...	...	...	...	...	...	...
6	...	0.271	...	...	...	0.010	...	...	...	...	...	...	...	...	...
7	...	0.177	...	0.083	...	0.102	...	...	...	0.025	0.059	0.059	...	...	...
8	...	0.115	...	0.271	...	...	...	0.030	...	0.051	0.147	0.176	0.010	0.010	...
9	...	0.281	...	0.146	...	0.020	...	0.010	...	0.167	0.069	0.118	0.170	0.010	0.167
9.3	...	0.135	...	...	...	...	...	...	...	...	...	...	...	...	...
10	...	...	...	0.167	...	0.061	0.020	0.120	...	0.013	0.098	0.127	0.150	0.167	0.186
11	...	...	...	0.302	0.010	0.214	0.010	0.090	...	0.295	0.216	0.275	0.230	0.375	0.225
12	...	...	...	0.031	0.050	0.112	...	0.160	...	0.154	0.255	0.245	0.330	0.314	0.118
13	0.040	...	...	...	0.120	0.071	...	0.110	...	0.192	0.078	...	0.100	0.062	0.137
14	0.082	...	...	...	0.230	0.082	0.153	0.150	...	0.090	0.020	...	0.010	0.062	0.118
15	0.265	...	...	...	0.240	0.061	0.112	0.140	...	0.013	0.058	...	...	...	0.049
16	0.265	...	...	...	0.120	0.041	0.061	0.110	...	...	...	...	...	...	...
17	0.224	...	...	...	0.060	0.061	0.153	0.050	...	...	...	...	...	...	...
18	0.124	...	...	...	0.070	0.092	0.224	0.030	0.021	...	...	...	...	...	...
18.2	...	...	...	...	...	...	0.235	...	...	...	...	...	...	...	...
19	...	...	...	...	0.040	0.010	...	...	0.085	...	...	...	...	...	...
20	...	...	...	...	0.030	0.020	0.031	...	0.106	...	...	...	...	...	...
20.2	...	...	...	...	...	...	...	...	0.021	...	...	...	...	...	...
21	...	...	...	...	0.010	...	...	...	0.064	...	...	...	...	...	...
22	...	...	...	...	0.020	...	...	...	0.085	...	...	...	...	...	...
22.2	...	...	...	...	...	...	...	...	0.021	...	...	...	...	...	...
23	...	...	...	...	...	...	...	...	0.074	...	...	...	...	...	...
23.2	...	...	...	...	...	...	...	...	0.032	...	...	...	...	...	...
24	...	...	...	...	...	...	...	...	0.170	...	...	...	...	...	...
24.2	...	...	...	...	...	...	...	...	0.011	...	...	...	...	...	...
25	...	...	...	...	...	...	...	...	0.170	...	...	...	...	...	...
25.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
26	...	...	0.010	...	...	...	...	...	0.074	...	...	...	...	...	...
27	...	...	0.031	...	...	...	...	...	0.064	...	...	...	...	...	...
28	...	...	0.143	...	...	...	...	...	...	...	...	...	...	...	...
29	...	...	0.255	...	...	...	...	...	...	...	...	...	...	...	...
30	...	...	0.153	...	...	...	...	...	...	...	...	...	...	...	...
30.2	...	...	0.020	...	...	...	...	...	...	...	...	...	...	...	...
31	...	...	0.051	...	...	...	...	...	...	...	...	...	...	...	...
31.2	...	...	0.051	...	...	...	...	...	...	...	...	...	...	...	...
32.2	...	...	0.204	...	...	...	...	...	...	...	...	...	...	...	...
33.2	...	...	0.082	...	...	...	...	...	...	...	...	...	...	...	...
34.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
PD	0.7857	0.7843	0.8361	0.7784	0.8466	0.8953	0.8412	0.8812	0.8946	0.8128	0.8390	0.7992	0.7766	0.7250	0.8378
PE	0.63	0.441	0.554	0.296	0.755	0.484	0.519	0.562	0.475	0.416	0.643	0.437	0.342	0.206	0.501
H	0.6943	0.1502	0.1809	0.0020	0.6176	0.0001	0.1131	0.0128	0.0002	0.0316	0.6353	0.0647	0.0130	0.0009	0.0458
ET	0.1565	0.5520	0.1930	0.0040	0.1080	0.0720	0.0450	0.0005	0.3435	0.0330	0.7695	0.0280	0.0190	0.0010	0.1980
LR	0.0895	0.7115	0.2165	0.0050	0.0320	0.0480	0.0725	0.0005	0.3625	0.0415	0.8115	0.0640	0.1105	0.0025	0.2535

N = Number of chromosome; PD = Power of discrimination; H = HWE homozygosity test; ET = Exact test; LR = Likekihoodratio test; PE = Power of exclusion.

TABLE 3—*Allelic variation at 15 microsatellite loci in Oraon (N = 84) of Chhattisgarh, India.*

Allele	D3S1358	THO1	D21S11	TPOX	D18S51	Penta E	vWA	D8S1179	FGA	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D
5	...	0.038	...	...	...	...	...	...	...	...	...	...	...	...	...
6	...	0.200	...	...	...	...	...	...	...	...	...	...	...	...	...
7	...	0.075	...	...	...	0.016	...	...	...	...	0.038	0.047	...	...	...
8	...	0.063	...	0.333	0.031	...	...	0.016	...	0.202	0.363	0.375	0.045	...	0.015
9	...	0.488	...	0.067	...	...	...	0.078	...	0.012	0.025	0.109	0.227	...	0.167
9.3	...	0.125	...	...	...	...	...	...	...	...	...	...	...	...	...
10	...	0.013	...	0.067	...	...	0.061	0.172	...	0.119	0.025	0.156	0.106	0.157	0.212
11	...	...	...	0.500	0.031	0.141	...	0.031	...	0.274	0.188	0.125	0.348	0.329	0.227
12	0.012	...	...	0.017	0.078	0.125	0.015	0.047	...	0.226	0.188	0.172	0.227	0.314	0.167
13	0.012	...	...	0.017	0.016	0.063	...	0.188	...	0.143	0.088	0.016	0.030	0.071	0.046
14	0.048	...	...	...	0.266	...	0.212	0.188	...	0.024	0.050	...	0.015	0.057	0.091
15	0.321	...	...	...	0.266	0.109	0.091	0.125	...	...	0.038	...	...	0.071	0.045
15.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
16	0.286	...	...	...	0.125	0.141	0.167	0.109	0.042	...	...	...	...	...	0.030
17	0.310	...	...	...	0.031	0.156	0.273	0.047	...	...	...	...	...	...	...
18	0.012	...	...	...	0.047	0.094	0.121	...	...	...	...	...	...	...	...
18.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
19	...	...	...	...	0.031	0.016	0.045	...	0.042	...	...	...	...	...	...
20	...	...	...	...	0.047	0.063	0.015	...	0.104	...	...	...	...	...	...
20.2	...	...	...	...	...	...	...	...	0.021	...	...	...	...	...	...
21	...	...	...	...	0.016	0.031	...		0.021	...	...	...	...	...	...
22	...	...	...	...	0.016	0.047	...	...	0.167	...	...	...	...	...	...
22.2	...	...	...	...	...	...	...	...	0.042	...	...	...	...	...	...
23	...	...	...	...	...	...	...	...	0.250	...	...	...	...	...	...
23.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
24	...	...	...	...	...	...	...	...	0.208	...	...	...	...	...	...
24.2	...	...	...	...	...	...	...	...	0.021	...	...	...	...	...	...
25	...	...	...	...	...	...	...	...	0.063	...	...	...	...	...	...
25.2	...	...	0.024	...	...	...	...	...	0.021	...	...	...	...	...	...
26	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
27	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
28	...	...	0.098	...	...	...	...	...	...	...	...	...	...	...	...
28.2	...	...	0.012	...	...	...	...	...	...	...	...	...	...	...	...
29	...	...	0.195	...	...	...	...	...	...	...	...	...	...	...	...
30	...	...	0.122	...	...	...	...	...	...	...	...	...	...	...	...
30.2	...	...	0.049	...	...	...	...	...	...	...	...	...	...	...	...
31	...	...	0.061	...	...	...	...	...	...	...	...	...	...	...	...
31.2	...	...	0.171	...	...	...	...	...	...	...	...	...	...	...	...
32	...	...	0.012	...	...	...	...	...	...	...	...	...	...	...	...
32.2	...	...	0.122	...	...	...	...	...	...	...	...	...	...	...	...
33.2	...	...	0.037	...	...	...	...	...	...	...	...	...	...	...	...
34	...	...	0.024	...	...	...	...	...	...	...	...	...	...	...	...
34.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
35	...	...	0.049	...	...	...	...	...	...	...	...	...	...	...	...
35.2	...	...	0.024	...	...	...	...	...	...	...	...	...	...	...	...
PD	0.7094	0.6956	0.8816	0.6295	0.8280	0.8914	0.8237	0.8608	0.8446	0.7976	0.7841	0.7754	0.7608	0.7551	0.8342
PE	0.63	0.441	0.554	0.296	0.755	0.484	0.519	0.562	0.475	0.416	0.643	0.437	0.342	0.206	0.501
H	0.8513	0.0323	0.0000	0.9383	0.3528	0.9397	0.0084	0.0014	0.1091	0.0209	0.7665	0.7315	0.5355	0.2616	0.0008
ET	0.1090	0.0160	0.3825	0.1150	0.3230	0.0340	0.0005	0.0025	0.1950	0.1090	0.1550	0.4935	0.0290	0.0010	0.3015
LR	0.0720	0.0145	0.4015	0.2045	0.4095	0.0125	0.0020	0.0105	0.1035	0.1815	0.1185	0.4205	0.0400	0.0015	0.1720

N = Number of chromosome; PD = Power of discrimination; H = HWE homozygosity test; ET = Exact test; LR = Likekihoodratio test; PE = Power of exclusion.

TABLE 4—*The most common allele and least common allele at 15 STR loci in Brahman, Vaish and Oraon of Chhatisgarh, India.*

		Vaish		Brahman		Oraon	
S.No.	Locus	MCA	LCA	MCA	LCA	MCA	LCA
1	D3S1358	17	14	15,16	13	17	12,13,18
2	THO1	9	7	9	5	9	10
3	D21S11	30	34.2	29	26	29	28.2
4	TPOX	11	12	11	12	11	12,13
5	D18S51	14	12,19,20	14	11,21	14,15	13,21,22
6	Penta E	11	18,21	11	6,19	17	7,19
7	vWA	17	20	19	11	17	12,20
8	D8S1179	14	7	12	9	13,14	8
9	FGA	24	25.2	24,25	20.2	23	20.2,21
10	D5S818	13	9	11	10,15	11	9
11	D13S317	12	7	12	14	8	9
12	D7S820	10	9,13	11	7	13	13
13	D16S539	11	14	12	8,14	11	14
14	CSF1PO	11	9	11	8,9	11	14
15	Penta D	10	15	11	15	11	8

MCA = Most common allele; *LCA* = Least common allele.

TABLE 5—*Average power of exclusion and discrimination at 15 STR loci in Brahman, Vaish and Oraon of Chhatisgarh, India.*

Locus	Vaish	Brahman	Oraon
Average PE	0.551	0.484	0.460
Average PD	0.793	0.822	0.792

PD = Power of discrimination; PE = Power of exclusion.

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