

FOR THE RECORD

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Genotype Profile for Fifteen Tetranucleotide Repeat Loci in Two Tibeto-Burman Speaking Tribal Populations of Arunachal Pradesh, India

POPULATION: Two Tibeto-Burman-speaking Adi tribal populations of Arunachal Pradesh, India, Adi Pasi ($n = 121$) from Upper Siang district, and Adi Minyong ($n = 33$) from East Siang district were analyzed for polymorphisms at 15 microsatellite loci. The populations belong to Mongoloid ethnicity and are of special significance in genetic studies due to their small population size, relative isolation in remote hilly areas, and traditional subsistence patterns.

KEYWORDS: forensic science, DNA typing, short tandem repeats, population genetics, microsatellite loci, D3S1358, THO1, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, CSF1PO, vWA, D8S1179, TPOX, D2S1338, D19S433, FGA, Tibeto-Burman populations, Arunachal Pradesh

Genomic DNA was extracted from collected blood samples using the standard phenol/chloroform extraction method (1), and the quantitation of DNA was carried out by using the Quantiblot[®] Human DNA Quantification Kit according to the manufacturer's instructions (Applied Biosystems, Foster City, CA). PCR amplification of the 15 loci was performed using the AmpFI STR[®] Identifiler kit (Applied Biosystems) according to the manufacturer's recommendations (2). The amplified fragments were then detected on a 4% denaturing polyacrylamide gel using the ABI Prism[™] 377 automated DNA sequencer (Applied Biosystems). The resultant data analysis and the allele designation were carried out by GeneScan[™] Analysis Software (Version 3.7; Applied Biosystems) and Genotyper[™] DNA Fragment Analysis Software (Version 3.7; Applied Biosystems), respectively.

The allele frequencies and other forensically important statistical parameters like observed heterozygosity (H_{obs}), probability of homozygosity ($H [P]$), exact test (ET), and the likelihood ratio (LR) test were calculated using DNATYPE software (3). The power of discrimination (PD) (4) and the probability of match (P_m) (5) were also computed. The allele frequencies and the estimated statistical parameters in the two studied populations are shown in Tables 1 and 2.

The observed heterozygosity values indicate a high degree of polymorphism for the studied loci in the two populations. Locus CSF1PO was the least heterozygous in both Adi Pasi (53.2%) and

Adi Minyong (45.45%) and loci D8S1179 and D18S51 were most heterozygous in Adi Pasi (91.7%) and Adi Minyong (100%), respectively. ET and LR values indicate divergence from HWE at six loci (D8S1179, CSF1PO, D3S1358, THO1, vWA, and TPOX) in Adi Pasi and at one locus (THO1) in Adi Minyong populations.

The PD of the analyzed markers was high for the populations, thereby facilitating the validation and efficacy of these STR markers in human identification. The most discriminating loci in both the populations were D2S1338 (PD = 0.8888 in Adi Pasi and 0.8786 in Adi Minyong), followed by FGA, and the least discriminating locus was THO1 (PD = 0.6142 in Adi Pasi and 0.6235 in Adi Minyong) in the two populations. The data generated will contribute to the Indian DNA database (6–8) suitable for human identification in forensic studies and also genetic diversity studies.

The complete dataset is available from the corresponding author upon request at vasulu@isical.ac.in

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References

1. Sambrook J, Fritsch EF, Maniatis T. Molecular cloning. A laboratory manual. 2nd ed. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, 1989.
2. Applied Biosystems. Applied biosystems AmpF/STR[®] identifiler[™] PCR amplification kit user's manual, instruction for use of products. Foster City, CA: Applied Biosystems, 2001.
3. Chakraborty R, King A, Strivers D, Zhong Y. CHG. DNATYPE [Computer program; Windows 95/NT ver]. Houston, TX: University of Texas, 1998.
4. Fisher RA. Standard calculations for evaluating a blood-group system. *Heredity* 1951;5:95–102.
5. Jones DA. Blood samples: probability of discrimination. *J Forensic Sci Soc* 1972;12:355–59.

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TABLE 1—Allele frequencies and other statistical parameters of 15 STR loci of Upper Siang Adi Pasi population ($N = 121$) of Arunachal Pradesh, India.

Alleles	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	THO1	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6	—	—	—	—	—	—	—	0.043	—	—	—	—	—	—	—
7	—	—	—	—	—	—	—	0.312	—	—	—	—	—	0.004	—
8	0.07	—	0.004	—	0.297	—	—	0.009	0.294	0.053	—	—	—	0.342	—
9	0.148	—	0.004	—	0.214	0.038	—	0.53	0.073	0.158	—	—	—	0.231	—
9.3	—	—	—	—	—	—	—	0.051	—	—	—	—	—	—	—
10	0.13	—	0.029	—	0.151	0.19	—	0.055	0.096	0.29	—	0.013	—	0.051	—
11	0.252	—	0.029	—	0.224	0.171	—	—	0.197	0.154	—	0.053	—	0.355	—
12	0.113	—	0.182	—	0.104	0.506	—	—	0.211	0.25	—	0.031	0.004	0.013	0.02
13	0.222	—	0.186	—	0.01	0.07	0.005	—	0.055	0.048	—	0.162	—	0.004	0.39
13.2	—	—	—	—	—	—	—	—	—	—	—	0.013	—	—	0.049
14	—	—	0.256	—	—	0.025	—	—	0.041	0.019	—	0.316	0.345	—	0.056
14.2	—	—	—	—	—	—	—	—	—	—	—	0.132	—	—	0.021
15	0.035	—	0.227	—	—	—	0.284	—	0.033	0.009	—	0.017	0.004	—	0.208
15.2	—	—	—	—	—	—	—	—	—	—	—	0.246	—	—	—
16	0.03	—	0.083	—	—	—	0.385	—	—	0.009	0.005	0.013	0.267	—	0.097
16.2	—	—	—	—	—	—	—	—	—	—	—	0.004	—	—	—
17	—	0.011	—	—	—	—	0.202	—	—	—	0.095	—	0.172	—	0.076
18	—	0.043	—	—	—	—	0.11	—	—	0.005	0.11	—	0.04	—	0.028
19	—	0.07	—	—	—	—	0.014	—	—	0.005	0.131	—	0.155	—	0.041
20	—	0.011	—	—	—	—	—	—	—	—	0.063	—	0.013	—	—
21	—	0.14	—	—	—	—	—	—	—	—	0.084	—	—	—	0.014
22	—	0.161	—	—	—	—	—	—	—	—	0.068	—	—	—	—
23	—	0.161	—	—	—	—	—	—	—	—	0.137	—	—	—	—
24	—	0.14	—	—	—	—	—	—	—	—	0.179	—	—	—	—
25	—	0.108	—	—	—	—	—	—	—	—	0.07	—	—	—	—
26	—	0.032	—	—	—	—	—	—	—	—	0.021	—	—	—	—
26.2	—	0.027	—	—	—	—	—	—	—	—	—	—	—	—	—
27	—	0.032	—	0.027	—	—	—	—	—	—	0.032	—	—	—	—
28	—	0.005	—	0.025	—	—	—	—	—	—	0.005	—	—	—	—
29	—	0.017	—	0.22	—	—	—	—	—	—	—	—	—	—	—
29.2	—	—	—	0.013	—	—	—	—	—	—	—	—	—	—	—
30	—	0.011	—	0.374	—	—	—	—	—	—	—	—	—	—	—
30.2	—	0.005	—	0.04	—	—	—	—	—	—	—	—	—	—	—
31	—	0.005	—	0.099	—	—	—	—	—	—	—	—	—	—	—
31.2	—	0.005	—	0.004	—	—	—	—	—	—	—	—	—	—	—
32	—	—	—	0.036	—	—	—	—	—	—	—	—	—	—	—
32.2	—	0.005	—	0.086	—	—	—	—	—	—	—	—	—	—	—
33	—	—	—	0.018	—	—	—	—	—	—	—	—	—	—	—
33.2	—	0.011	—	0.054	—	—	—	—	—	—	—	—	—	—	—
35	—	—	—	0.004	—	—	—	—	—	—	—	—	—	—	—
H_{obs}	0.791	0.806	0.917	0.667	0.75	0.532	0.816	0.752	0.688	0.76	0.705	0.895	0.845	0.812	0.681
$H(P)$	0.288	0.014	0.002	0.002	0.436	0.005	0.025	0.002	0.002	0.265	0	0.007	0.027	0.011	0.039
ET	0.234	0.164	0	0.271	0.253	0.001	0.002	0.0005	0.481	0.291	0.263	0.122	0	0	0.098
LR	0.001	0.074	0	0.039	0.266	0.002	0.002	0	0.080	0.067	0.204	0.004	0	0	0.208
P_m	0.172	0.113	0.194	0.214	0.218	0.328	0.282	0.386	0.190	0.201	0.112	0.209	0.246	0.299	0.220
PD	0.828	0.887	0.806	0.786	0.782	0.672	0.718	0.614	0.810	0.799	0.888	0.791	0.754	0.701	0.780

N , number of individuals; H_{obs} , observed heterozygosity; $H(P)$, probability of homozygosity; ET, exact test; LR, likelihood ratio; P_m , match of probability; PD, power of discrimination.

TABLE 2—Allele frequencies and other statistical parameters of 15 STR loci of Adi Minyong population ($N = 33$) of Arunachal Pradesh, India.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	THO1	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
6	—	—	—	—	—	—	—	0.138	—	—	—	—	—	—	—
7	—	—	—	—	—	0.045	—	0.414	0.079	—	—	—	—	—	—
8	0.04	—	—	—	0.182	—	—	—	—	0.019	—	0.019	0.039	0.519	—
9	0.14	—	—	—	0.091	—	0.035	0.431	—	0.222	—	—	—	0.222	—
9.3	—	—	—	—	—	—	—	0.017	—	—	—	—	—	—	—
10	0.26	—	—	—	0.136	0.182	—	—	0.026	0.315	—	—	—	—	—
11	0.3	—	0.017	—	0.318	0.227	—	—	0.316	0.166	—	—	—	0.222	—
12	0.16	0.063	0.15	—	0.136	0.501	—	—	0.316	0.148	—	0.037	—	0.037	—
13	0.1	—	0.15	—	0.046	—	—	—	0.158	0.093	—	0.222	—	—	0.215
13.2	—	—	—	—	—	—	—	—	—	—	—	0.074	—	—	0.071
14	—	—	0.333	—	—	—	—	—	0.105	—	0.023	0.371	0.462	—	0.286
14.2	—	—	—	—	—	—	—	—	—	0.037	—	0.074	—	—	0.071
15	—	—	0.267	—	0.091	—	0.345	—	—	—	—	—	0.019	—	0.215
15.2	—	—	—	—	—	—	—	—	—	—	0.023	0.129	—	—	—
16	—	—	0.05	—	—	—	0.293	—	—	—	—	0.055	0.23	—	0.071
16.2	—	—	—	—	—	—	—	—	—	—	—	0.019	—	—	—
17	—	—	—	—	—	0.045	0.155	—	—	—	0.023	—	0.154	—	0.071

TABLE 2—Continued.

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51
18	—	0.063	—	—	—	—	0.172	—	—	—	0.181	—	0.077	—	—
19	—	0.063	—	—	—	—	—	—	—	—	0.091	—	0.019	—	—
20	—	0.03	—	—	—	—	—	—	—	—	0.068	—	—	—	—
21	—	0.219	—	—	—	—	—	—	—	—	0.091	—	—	—	—
22	—	0.188	—	—	—	—	—	—	—	—	0.068	—	—	—	—
23	—	0.125	—	—	—	—	—	—	—	—	0.159	—	—	—	—
24	—	0.03	—	—	—	—	—	—	—	—	0.181	—	—	—	—
25	—	0.063	—	—	—	—	—	—	—	—	0.046	—	—	—	—
26	—	—	—	—	—	—	—	—	—	—	0.023	—	—	—	—
26.2	—	0.063	—	—	—	—	—	—	—	—	—	—	—	—	—
27	—	0.063	—	0.083	—	—	—	—	—	—	0.023	—	—	—	—
28	—	—	—	0.083	—	—	—	—	—	—	—	—	—	—	—
29	—	—	—	0.125	—	—	—	—	—	—	—	—	—	—	—
29.2	—	—	—	0.02	—	—	—	—	—	—	—	—	—	—	—
30	—	0.03	0.033	0.542	—	—	—	—	—	—	—	—	—	—	—
30.2	—	—	—	0.042	—	—	—	—	—	—	—	—	—	—	—
31	—	—	—	0.063	—	—	—	—	—	—	—	—	—	—	—
32.2	—	—	—	0.042	—	—	—	—	—	—	—	—	—	—	—
H_{obs}	0.520	0.813	0.867	0.708	0.636	0.455	0.621	0.724	0.684	0.778	0.955	0.704	0.615	0.667	1.000
$H(p)$	0.001	0.449	0.204	0.684	0.142	0.148	0.142	0.264	0.455	0.861	0.273	0.335	0.335	0.701	0.195
ET	0.448	0.019	0.023	0.601	0.083	0.072	0.725	0.003	0.865	0.315	0.436	0.016	0.015	0.054	0.122
LR	0.427	0.013	0.019	0.515	0.159	0.228	0.578	0.003	0.937	0.278	0.293	0.015	0.023	0.03	0.058
P_m	0.214	0.125	0.186	0.331	0.19	0.340	0.260	0.376	0.243	0.208	0.121	0.220	0.298	0.369	0.194
PD	0.786	0.875	0.814	0.669	0.810	0.660	0.740	0.624	0.757	0.792	0.879	0.780	0.702	0.631	0.806

N , number of individuals; H_{obs} , observed heterozygosity; $H(p)$, probability of homozygosity; ET, exact test; LR, likelihood ratio; P_m , match of probability; PD, power of discrimination.

6. Sahoo S, Kashyap VK. Genetic variation at fifteen autosomal microsatellite loci in three highly endogamous tribal population of Orissa, India. *Forensic Sci Int* 2002;130:189–93.
7. Gaikwad S, Kashyap VK. Genetic diversity in four tribal groups of Western India: a survey of polymorphism in 15 STR loci and their application in human identification. *Forensic Sci Int* 2003;134:225–31.
8. Sitalaximi T, Trivedi R, Kashyap VK. Genotype profile for thirteen tetra-nucleotide repeat loci in four endogamous Tamil population groups of India. *J Forensic Sci* 2002;47:1168–73.

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