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Announcement of population data

STR data for the Amp F*l*STR Profiler Plus loci among 27 populations of different social hierarchy from southern part of Andhra Pradesh, India

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Abstract

Allele frequency for the 9 STR loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820) were estimated from a total of 1096 individuals belonging to 27 endogamous populations from the state of Andhra Pradesh, India, covering the entire gamut of socio-economic variation of the linguistic region. These loci are found to be highly polymorphic within the populations with high levels of average heterozygosity (>0.80). However, the allele frequency distributions are fairly uniform across the populations in case of these loci suggesting relatively greater homogeneity among the populations. Regrouping populations into five broad socio-economic categories further reiterated the homogenous pattern of genetic diversity.

Keywords: DNA profiling; Forensic science; Profiler Plus loci; Hierarchical caste groups; Tribes; Southern India

Populations: Representative samples (1096 individuals) from 27 populations distributed in the southern areas of Andhra Pradesh were analysed for nine autosomal STR loci. These populations belong to not only all the major social or hierarchical groups of Hindu caste system, but also include three different tribes. All these populations presently speak one of the Dravidian languages, Telugu. They represent upper (Brahmin, Kshatriya and Vysya), upper middle (Pokanati, Panta, Vanne, Akuthota, Kapu and Kamma), lower middle (Ekila Dora, Balija, Yadava, Thogata, Kurava, Ediga, Gandla and Jangam), lower (Mangali, Chakali and Vaddi) and Pancham (Mala and Madiga) ranking castes, besides including Sheik and Dudekula from Muslim communities and Sugali, Erukula and Yanadi tribes. While most of the caste populations and the Muslim groups are Caucasoid ethnically, the tribal populations barring Sugali are Proto-Australoids. The Sugali tribe, which is known to have migrated from Rajasthan, originally speaks Indo-European language, besides showing Caucasoid features.

Material and methodology: DNA was isolated from the above samples following standard protocol. Erythrocytes were lysed with 15.0 ml of EL buffer (10 mM Tris pH 8.0, 320 mM sucrose, 5 mM $MgCl_2$, 1% Triton X-100) for 5 min. After complete lysis of erythrocytes, leucocytes were pelleted by centrifugation at 1500 rpm for 5 min. Leucocyte pellet was dissolved in 8.0 ml of LL buffer (400 mM Tris, 60 mM EDTA, 150 mM NaCl and 1% SDS) and mixed thoroughly. To this 2.0 ml of 5 M sodium perchlorate was added and mixed thoroughly for 2–3 min. DNA was precipitated after extracting once with phenol–chloroform and once with chloroform. DNA was washed with 70% ethanol and dissolved in TE Buffer (pH 8.0). The extracted DNA was quantified by spectrophotometer

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followed by quantification in 0.8% agarose gel [1]. AmpF*l*STR Profiler Plus kit (ABI, USA), which co-amplifies 9 STR (D3S1358, D8S1179, D5S818, vWA, D21S11, D13S317, FGA, D7S820 and D18S5) loci at a time was analysed on ABI Prism 377 automated DNA sequencer with the GeneScan and Genotyper softwares (Perkin Elmer) to obtain the allelic designations.

Analysis of data: The allele frequencies representing repeat numbers were computed by simple gene counting method. Arleqiun software version 2.00 [2] (http://anthropologie. unige.ch/arlequin) was used to obtain observed and expected heterozygosity and the exact test for Hardy-Weinberg equilibrium probabilities. Polymorphism information content (PIC), power of discrimination (PD) and power of exclusion (PE) probability were calculated for each locus using powerstatsv12.xls software (http://www.promega. com/geneticidtools/powerstats/). This article follows the guidelines for publication of allele frequency data of population requested by the journal [3] and the data can be accessed via electronic mail from the communicating author.

Results: The allele frequency data along with observed and expected heterozygosity, and exact test for all the 27 populations are presented in Tables 1–3. The estimated

Table 1
Allele frequencies of the 9 STR loci among upper and upper middle ranking caste populations

Locus	Populations								
	Brahmin	Kshatriya	Vysya	Akuthota	Kamma	Kapu	Pokanati	Panta	Vanne
D3S1358									
13	–	–	–	–	–	–	0.018	0.012	–
14	0.019	0.012	–	0.017	0.031	0.025	0.018	0.037	0.016
15	0.296	0.341	0.300	0.397	0.388	0.325	0.263	0.366	0.375
16	0.352	0.317	0.350	0.190	0.306	0.375	0.307	0.317	0.250
17	0.204	0.232	0.275	0.293	0.143	0.225	0.263	0.159	0.219
18	0.130	0.098	0.075	0.103	0.122	0.050	0.105	0.085	0.094
19	–	–	–	–	–	–	0.018	0.024	0.031
20	–	–	–	–	0.010	–	0.009	–	0.016
N	54	82	40	58	98	40	114	82	64
Obs. Ht	0.5556	0.7073	0.7500	0.5517	0.6531	0.8500	0.7193	0.5610	0.8438
Exp. Ht	0.7666	0.7284	0.7244	0.7254	0.7273	0.7180	0.7618	0.7489	0.7505
Exact Test	0.0659	0.5438	0.7482	0.0189	0.0344	0.6729	0.7584	0.0265	0.6203
PIC	0.6818	0.6675	0.6488	0.6592	0.6728	0.6435	0.6875	0.7138	0.6966
PD	0.8669	0.8602	0.8300	0.8419	0.8605	0.8050	0.8792	0.9030	0.8594
PE	0.2409	0.4397	0.5098	0.2030	0.3594	0.6949	0.2466	0.4587	0.6826
vWA									
13	–	0.012	–	–	–	–	–	0.013	–
14	0.204	0.146	0.125	0.086	0.173	0.075	0.140	0.263	0.172
15	0.074	0.134	0.050	0.121	0.112	0.050	0.088	0.038	0.094
16	0.148	0.159	0.075	0.138	0.204	0.300	0.219	0.225	0.172
17	0.222	0.329	0.400	0.379	0.255	0.350	0.307	0.225	0.328
18	0.167	0.195	0.275	0.138	0.173	0.125	0.202	0.138	0.125
19	0.148	0.024	0.075	0.103	0.071	0.100	0.026	0.063	0.031
20	0.019	–	–	0.034	0.010	–	0.018	0.038	0.063
21	0.019	–	–	–	–	–	–	–	0.016
N	54	82	40	58	98	40	114	80	64
Obs. Ht	0.7037	0.7561	0.7000	0.7586	0.8367	0.7500	0.7368	0.7750	0.7188
Exp. Ht	0.8519	0.7980	0.7539	0.8107	0.8237	0.7731	0.7955	0.8196	0.8165
Exact Test	0.2146	0.7156	0.9051	0.5260	0.7692	0.1937	0.0940	0.3679	0.0332
PIC	0.8087	0.7580	0.6964	0.7594	0.7891	0.7166	0.7759	0.7571	0.7789
PD	0.9300	0.9185	0.8900	0.9108	0.9279	0.8700	0.9175	0.9098	0.9043
PE	0.4340	0.5203	0.4283	0.5246	0.6689	0.5098	0.5535	0.4875	0.4579
FGA									
17	–	–	–	–	–	0.026	–	–	–
18	–	–	–	0.017	–	–	0.018	–	–
18.2	–	–	–	–	0.010	–	–	–	0.016
19	–	–	–	0.017	0.042	–	0.009	0.025	–