

Announcement of Population Data

Allele frequency distribution at 15 autosomal STR loci in Panggi, Komkar and Padam sub tribes of Adi, a Tibeto-Burman speaking population of Arunachal Pradesh, India

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Abstract

Fifteen autosomal STR loci were analyzed in 223 healthy individuals belonging to three remote, isolated Tibeto-Burman speaking sub tribes namely, Panggi, Komkar and Padam of Adi tribe of Arunachal Pradesh, India. The analyzed markers exhibited a high degree of polymorphism in the studied populations. Statistical parameters of forensic interest; observed heterozygosity, probability of homozygosity, exact test, likelihood ratio test, power of discrimination, power of exclusion, match probability and typical paternity index were determined for all loci. The average heterozygosity values were found to be low in the three populations (Panggi: 0.7747; Komkar: 0.7742 and Padam: 0.7663). The combined power of discrimination and power of exclusion were 0.9999 in the studied populations thereby revealing the high forensic significance of the chosen markers. The study indicates the utility of the tested microsatellite markers in forensic human identification, paternity testing and human population genetic studies.

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Population: Peripheral blood samples were obtained with prior informed consent from 223 healthy individuals belonging to Panggi (110), Komkar (63) and Padam (50) sub tribes of East and Upper Siang districts of Arunachal Pradesh, India. These sub tribes are categorized, along with some other sub tribes, under Adi tribe of Mongoloid ethnicity and Tibeto-Burman linguistic family and trace their origin from Tibet and migration and settlement at about 5th–7th century AD [1–3]. The studied populations differ in terms of their size, dialect, culture, ethno-historical migration and distribution on the Siang river valley. While Padam is a large and a major population of the Adi tribe, Panggi and Komkar are very small populations numbering to only about 2–3 thousand individuals. Padam of East

Siang district is located near urban area and practice agriculture whereas Panggi and Komkar of Upper Siang district are isolated in remote hilly areas and sustain on hunting-gathering subsistence economy of population structure [4–6]. These Tibeto-Burman speaking populations of India may provide significant opportunity for genetic studies due to their relative isolation in remote mountainous terrain and wide variation in population structure. However, hardly any studies are available on the ethnographic, cultural, or biological aspects among Panggi and Komkar, the two remote sub tribes of Adi tribe, although some biological anthropological studies and monographic works among Padam have been attempted [3–8]. Though Panggi and Padam have been studied for ABO blood group polymorphism earlier, Adi Komkar has not been attempted until recently [9]. This is perhaps the first molecular genetic study on these three sub tribes of Adi speaking populations of Arunachal Pradesh, India.

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Table 1
Genetic polymorphism at 15 STR loci in Adi Panggi population of Arunachal Pradesh (N = 220)

Allele	D5S818	FGA	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	THO1
5	–	–	–	–	–	–	–	0.005
6	–	–	–	–	–	–	–	0.009
7	–	–	–	–	0.006	0.012	–	0.232
8	0.06	–	–	–	0.157	0.006	–	0.068
9	0.158	–	–	–	0.105	0.098	–	0.645
9.3	–	–	–	–	–	–	–	0.036
10	0.084	–	0.014	–	0.145	0.08	–	0.005
11	0.411	–	0.023	–	0.448	0.213	–	–
12	0.158	–	0.223	–	0.087	0.5	–	–
12.2	–	–	–	–	–	–	–	–
13	0.124	–	0.186	–	0.046	0.08	–	–
13.2	–	–	–	–	–	–	–	–
14	–	–	0.227	–	0.006	–	0.151	–
14.2	–	–	–	–	–	–	–	–
15	0.005	–	0.268	–	–	0.011	0.267	–
15.2	–	–	–	–	–	–	–	–
16	–	–	0.05	–	–	–	0.445	–
16.2	–	–	–	–	–	–	–	–
17	–	–	0.009	–	–	–	0.087	–
18	–	0.113	–	–	–	–	0.05	–
19	–	0.035	–	–	–	–	–	–
20	–	0.042	–	–	–	–	–	–
21	–	0.05	–	–	–	–	–	–
22	–	0.099	–	–	–	–	–	–
23	–	0.239	–	–	–	–	–	–
24	–	0.169	–	–	–	–	–	–
25	–	0.197	–	–	–	–	–	–
26	–	0.014	–	–	–	–	–	–
26.2	–	0.007	–	–	–	–	–	–
27	–	0.014	–	0.009	–	–	–	–
28	–	0.014	–	0.009	–	–	–	–
29	–	0.007	–	0.318	–	–	–	–
30	–	–	–	0.327	–	–	–	–
30.2	–	–	–	0.077	–	–	–	–
31	–	–	–	0.046	–	–	–	–
31.2	–	–	–	0.036	–	–	–	–
32.2	–	–	–	0.155	–	–	–	–
33.2	–	–	–	0.023	–	–	–	–
pM	0.2449	0.1532	0.2110	0.2421	0.2672	0.3181	0.3022	0.4759
PD	0.7551	0.8468	0.7890	0.7579	0.7328	0.6819	0.6978	0.5241
PE	0.7137	0.6852	0.7218	0.7584	0.3731	0.3786	0.6127	0.3249
TPI	3.5587	3.2279	3.6657	4.2301	1.4828	1.5002	2.5947	1.3416
ET	0.2655	0.0065	0.0000	0.0000	0.1490	0.0795	0.0445	0.4535
LR	0.1405	0.0045	0.0000	0.0000	0.3175	0.0235	0.0250	0.3315
H	0.1405	0.1549	0.1364	0.1182	0.3372	0.3333	0.1927	0.3727
h	0.8595	0.8451	0.8636	0.8818	0.6628	0.6667	0.8073	0.6273
p	0.0242	0.9704	0.0545	0.0024	0.1409	0.7589	0.0130	0.0294
Allele	D13S317	D16S539	D2S1338	D19S433	Vwa	TPOX	D18S51	
5	–	–	–	–	–	–	–	
6	–	–	–	–	–	–	–	
7	–	–	–	–	–	–	–	
8	0.139	0.005	–	–	–	0.404	–	
9	0.059	0.167	–	0.05	–	0.165	–	
9.3	–	–	–	–	–	–	–	
10	0.079	0.464	–	0.037	–	0.142	–	
11	0.456	0.162	–	0.005	–	0.284	–	
12	0.203	0.14	–	0.06	–	0.005	0.015	
12.2	–	–	–	0.101	–	–	–	
13	0.059	0.057	0.006	0.188	–	–	0.618	
13.2	–	–	–	0.119	–	–	0.007	
14	0.005	–	–	0.156	0.273	–	0.103	
14.2	–	–	–	0.069	–	–	–	

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