

Announcement of Population Data
Allele frequencies of six miniSTR loci of three
ethnic populations in Singapore

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Abstract

MiniSTR loci has demonstrated to be an effective approach to recover genetic information from degraded sample, due to the improved PCR efficiency of their reduced PCR product sizes. This study investigated the allele frequency of six miniSTR loci, D1S1677, D2S441, D4S2364, D10S1248, D14S1434 and D22S1045, in three Singapore populations. All loci showed a moderate degree of polymorphism with observed heterozygosity >0.6 for all three populations. The allele frequencies, forensic parameters and heterozygosity comparison with other CODIS STR in similar populations are presented.

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Population: Venous blood was obtained from randomly selected Singapore Armed Forces personnel comprising 185 Chinese, 182 Malay and 178 Indian individuals. Samples were anonymised and the collection procedure approved by DMERI Research Ethics Committee. Singapore is a small multiracial state with a total resident population of 3.5 million, primarily comprising of three recognized ethnic groups; 76% Chinese, 14% Malay and 9% Indian [1]. While the Chinese and Indian communities mostly comprise migrants from Southern China and India, respectively in the last 200 years, the Malay has been resident in the region (the Malayan Peninsular) for a much longer time.

Extraction: Genomic DNA was extracted from 200 µl of whole blood using QIAamp DNA Mini Kit (Qiagen, Hilden, Germany). DNA quantified by spectrophotometry.

Marker panel and PCR: Two multiplexes (mini01 and mini02) were performed with the same primer sets as in Coble and Butler [2]. Changes were made to the fluorescent dye label to accommodate subsequent PCR fragment analysis detection

in the automated sequencer MegaBACE1000. The forward primers of D10S1248 and D4S2364 were labelled with 6FAM, D14S1434 and D2S441 with HEX, and D22S1045 and D1S1677 with TET. Each PCR multiplex was performed in a total volume of 10 µl containing 1 ng genomic DNA, 1× Amplitaq Gold buffer, 0.5 U Amplitaq Gold polymerase (Applied Biosystems, Foster City, USA), 1.5 mM MgCl₂, 200 µM of each deoxyribonucleotide triphosphate, and similar primer concentration as published [2]. Amplification were done in GeneAmp 9700 (Applied Biosystems, Foster City, USA) with slight modification in PCR condition. Pre-PCR denaturation was carried out at 95 °C for 10 min, followed by 30 cycles of 94 °C for 20 s, 55 °C for 20 s, 72 °C for 20 s, and a final extension of 60 °C for 45 min.

Genotyping: PCR products were separated on an automated capillary electrophoresis sequencer (MegaBACE1000, Molecular Dynamics, Sunnyvale, USA). Multiplex PCR product was diluted 15 times. One microlitre of the diluted product was mixed with 4 µl of loading solution (0.1% Tween 20) containing 0.125 µl of ET400-R internal size standard. Samples were denatured at 95 °C for 2 min, snap-cold on ice, and injected for 80 s at 3 kV, electrophoresis run at 10 kV for 75 min at 44 °C. Genotypes were called with Fragment Profiler (Version 1.2).

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Table 1
Allele frequency distributions of six miniSTR loci in three Singapore populations

Miniplex 01											
D10S1248			D14S1434				D22S1045				
Allele	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Allele	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Allele	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)
10	0.0027	–	–	14	0.0730	0.0824	0.171	7	–	–	0.006
11	0.0027	–	–	15	0.1676	0.1154	0.118	8	0.1784	0.1703	0.264
12	–	–	0.008	16	0.0243	0.0165	0.037	9	–	–	0.003
13	0.0784	0.0522	0.020	17	0.2838	0.2857	0.270	10	–	0.0055	0.003
14	0.3595	0.3104	0.191	17.3	0.0027	–	–	11	0.0324	0.0522	0.093
15	0.2243	0.2363	0.253	18	0.4189	0.4588	0.371	12	0.3054	0.3819	0.396
16	0.2324	0.2473	0.272	19	0.0189	0.0330	0.022	13	0.2297	0.1621	0.160
17	0.0838	0.1099	0.197	20	0.0108	0.0082	0.008	14	0.2324	0.2088	0.070
18	0.0162	0.0412	0.056	21	–	–	0.003	15	0.0189	0.0137	0.003
19	–	0.0027	0.003					16	0.0027	0.0055	0.003

Miniplex 02											
D1S1677			D2S441				D4S2364				
Allele	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Allele	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Allele	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)
9	0.0027	0.0027	–	8	–	–	0.003	8	0.0054	–	–
10	–	0.0027	0.006	9	–	–	–	9	0.1784	0.2060	0.171
11	0.0162	0.0247	0.051	10	0.2270	0.2308	0.343	10	0.4243	0.3571	0.494
12	0.1054	0.1319	0.124	11	0.3757	0.2720	0.382	11	0.3811	0.4341	0.326
13	0.4892	0.4890	0.427	11.3	0.0622	0.1896	0.062	12	0.0108	0.0027	0.008
13.1	–	0.0027	–	12	0.2027	0.1099	0.065				
14	0.3000	0.3049	0.295	12.3	–	0.0055	–				
15	0.0757	0.0357	0.093	13	0.0135	0.0110	0.017				
16	0.0108	0.0055	0.003	14	0.1135	0.1676	0.110				
17	–	–	0.003	15	0.0054	0.0137	0.014				
				16	–	–	0.006				

Table 2
Forensic parameters of six miniSTR loci in three Singapore populations

	D10S1248			D14S1434			D22S1045		
	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)
Miniplex01									
Observed heterozygosity	0.795	0.720	0.736	0.676	0.714	0.747	0.816	0.742	0.719
Power of discrimination	0.895	0.906	0.919	0.870	0.855	0.888	0.899	0.900	0.882
Polymorphism information content	0.714	0.734	0.748	0.663	0.639	0.705	0.728	0.716	0.694
Power of exclusion	0.589	0.460	0.486	0.392	0.451	0.505	0.629	0.496	0.458
Typical paternity index	2.434	1.784	1.894	1.542	1.750	1.978	2.721	1.936	1.780
HWE <i>p</i> -values	0.622	0.050	0.148	0.370	0.944	0.126	0.824	0.477	0.148
	D1S1677			D2S441			D4S2364		
	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)	Chinese (N = 185)	Malay (N = 182)	Indian (N = 178)
Miniplex02									
Observed heterozygosity	0.643	0.632	0.764	0.719	0.758	0.697	0.600	0.610	0.640
Power of discrimination	0.826	0.825	0.862	0.900	0.926	0.872	0.807	0.802	0.775
Polymorphism information content	0.599	0.591	0.658	0.711	0.765	0.671	0.570	0.567	0.547
Power of exclusion	0.346	0.331	0.534	0.458	0.524	0.423	0.291	0.303	0.342
Typical paternity index	1.402	1.358	2.119	1.779	2.068	1.648	1.250	1.282	1.391
HWE <i>p</i> -values	0.758	0.919	0.461	0.453	0.143	0.406	0.166	0.535	0.345

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