

FOR THE RECORD

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STR Data for the PowerPlex[®] 16 System Loci for the Malays, Chinese and Indians Groups of the Malaysian Population

POPULATION: Unrelated individuals of 212 Malays, 234 Chinese and 287 Indians in Malaysia

KEYWORDS: forensic science, short tandem repeat (STR), population genetics, Malays, Chinese, Indians, population, PowerPlex[®] 16 system, DNA typing

A STR database for use in forensic casework was created for three major ethnic population groups in Malaysia. Blood samples were collected from unrelated individuals and DNA were extracted using Chelex method (1). PCR amplification was performed following manufactures's instructions (PowerPlex[®] 16 System, Promega Corporation). The amplified products were analyzed and detected using the ABIPRISM[®] 3100 Gene Analyzer (Applied Biosystem) with 3100 Data Collection Software (Version 1.1). The results were analyzed with GeneScan analysis software (Version 3.7.1) and genotypes were determined by comparison to allelic ladder (Promega Corporation) using Genotyper DNA fragment analysis software (Version 3.7) with the PowerTyper[™] Macros (Promega Corporation).

The allele frequencies of the 15 STR loci studied are given in Tables 1–3. Power Stats (2), DNA-View (3) was used to calculate heterozygosity (HO), power of discrimination (PD) and the probability of excluding probability (PE). The observed heterozygosity (HO) ranged from 0.560 (TPOX) to 0.921 (PENTA E). The Power of Discrimination (PD) ranged from 0.775 (TPOX) to 0.984 (FGA). The Probability of Excluding Paternity (PE) ranged from 0.246 (TPOX) to 0.839 (PENTA E). The combined probability of excluding paternity is about 0.99999932, 0.99999937, 0.99999971 and the combined probability of identity expressed as 1 in 4.362×10^{18} , 1 in 6.268×10^{18} and 1 in 2.327×10^{18} for Malays, Chinese and Indians respectively.

The exact test (4) was performed based on 2000 shuffling experiments which all loci meet the Hardy-Weinberg equilibrium except D13S317 and vWA for Malays and CSF1PO for Chinese. No departures were detected in the Indians population.

The complete dataset is available to any interested party at www.ppsk.usm.my.

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TABLE 1—Allele frequencies of 15 STR loci in Malaysian Malays population ($n = 185$).

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
5	0.030
6	...	0.146	0.003
7	...	0.322	0.014	0.024	0.005	0.011	0.005
8	...	0.073	0.003	0.003	0.235	0.235	0.005	0.003	0.043	0.562	...
9	...	0.314	0.024	0.057	0.146	0.057	0.165	0.019	0.295	...	0.003	0.122	...
9.3	...	0.078
10	...	0.062	0.035	0.292	0.141	0.222	0.170	0.216	0.176	...	0.100	0.019	...
11	...	0.005	...	0.016	0.203	0.246	0.249	0.289	0.292	0.349	0.132	...	0.081	0.268	...
12	0.003	0.073	0.084	0.208	0.170	0.159	0.224	0.343	0.189	...	0.105	0.030	...
13	0.008	0.081	0.084	0.149	0.043	0.022	0.122	0.057	0.135	0.003	0.184
14	0.057	0.184	0.100	0.011	0.005	0.005	0.022	0.005	0.022	0.186	0.214
15	0.297	0.273	0.103	0.003	0.005	0.008	0.003	0.057	0.173
16	0.346	0.173	0.068	0.008	0.181	0.119
17	0.203	0.073	0.070	0.254	0.019	...	0.003
18	0.070	0.032	0.059	0.214	0.003	...	0.005
19	0.016	0.027	0.051	0.092	0.057
20	0.035	0.032	0.014	0.076
20.2	0.003
21	0.008	0.022	0.173
21.2	0.003
22	0.011	0.003	0.197
22.2	0.022
23	0.014	0.011	0.124
23.2	0.005
24	0.003	0.176
24.2	0.003
25	0.081
26	0.003
27	0.049
28	0.065	0.014
29	0.216	0.008
29.2	0.003
30	0.222
30.2	0.046
31	0.135
31.2	0.081
32	0.019
32.2	0.159
33.2	0.046
34.2	0.008
HO	0.746	0.751	0.854	0.827	0.892	0.784	0.795	0.735	0.757	0.757	0.843	0.757	0.843	0.616	0.849
PD	0.885	0.898	0.955	0.955	0.980	0.914	0.928	0.917	0.924	0.850	0.933	0.934	0.955	0.775	0.965
PE	0.503	0.512	0.703	0.650	0.779	0.569	0.589	0.485	0.521	0.521	0.682	0.521	0.682	0.311	0.692
P	0.183	0.206	0.796	0.456	0.824	0.233	0.001	0.058	0.281	0.654	0.680	0.013	0.771	0.396	0.723

HO: Heterozygosity; PD: Power of discrimination; PE: Probability of exclusion; and P: P-values for the exact test.

TABLE 2—Allele frequencies of 15 STR loci in Malaysian Chinese population (n = 216).

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
5	0.051
6	...	0.109	0.002	0.002
7	...	0.310	0.002	0.032	...	0.005	...	0.005	0.023
8	...	0.067	0.002	0.009	0.271	0.113	0.005	0.002	0.058	0.553	...
9	...	0.456	0.007	0.086	0.134	0.074	0.222	0.056	0.363	0.123	...
9.3	...	0.016
10	...	0.039	...	0.002	0.069	0.197	0.148	0.181	0.130	0.243	0.130	...	0.106	0.016	...
11	...	0.002	...	0.002	0.148	0.313	0.236	0.352	0.285	0.287	0.104	...	0.125	0.299	...
12	0.002	0.049	0.120	0.225	0.162	0.245	0.222	0.319	0.171	...	0.150	0.009	...
12.2	0.002
13	0.169	0.081	0.118	0.037	0.021	0.125	0.081	0.100	...	0.194
14	0.042	0.155	0.058	0.014	0.012	0.007	0.009	0.005	0.037	0.264	0.181
15	0.310	0.220	0.090	0.005	0.002	0.002	0.009	0.035	0.171
16	0.343	0.118	0.081	0.002	0.134	0.063	...	0.002
17	0.248	0.120	0.065	0.002	0.252	0.009	...	0.002
18	0.051	0.065	0.056	0.213	0.030
19	0.005	0.023	0.058	0.076	0.074
20	0.009	0.051	0.023	0.028
21	0.032	0.035	0.002	0.141
21.2	0.002
22	0.016	0.012	0.185
23	0.009	0.005	0.227
23.2	0.007
24	0.005	0.005	0.139
24.2	0.009
25	0.002	0.005	0.081
25.2	0.005
26	0.042
26.2	0.007
27	0.005	0.012
28	0.060	0.007
28.2	0.002
29	0.257
29.2	0.002
30	0.308
30.2	0.012
31	0.076
31.2	0.065
32	0.023
32.2	0.137
33	0.002
33.2	0.044
34.2	0.007
HO	0.773	0.694	0.824	0.875	0.921	0.810	0.819	0.773	0.764	0.657	0.769	0.764	0.847	0.560	0.861
PD	0.863	0.838	0.932	0.964	0.984	0.925	0.925	0.906	0.923	0.898	0.934	0.930	0.955	0.768	0.964
PE	0.550	0.420	0.644	0.745	0.839	0.618	0.636	0.550	0.534	0.365	0.542	0.534	0.689	0.246	0.717
P	0.814	0.117	0.356	0.737	0.789	0.995	0.485	0.214	0.742	0.006	0.458	0.877	0.939	0.496	0.616

HO: Heterozygosity; PD: Power of discrimination; PE: Probability of exclusion; and P: P-values for the exact test.

TABLE 3—Allele frequencies of 15 STR loci in Malaysian Indian population ($n = 195$).

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
5	0.056	0.003
6	...	0.267	0.005
7	...	0.118	0.069	...	0.021	0.044	...	0.003	0.005
8	...	0.118	0.005	...	0.233	0.236	0.100	...	0.026	0.315	...
9	...	0.351	0.018	0.033	0.110	0.067	0.144	0.028	0.269	...	0.005	0.174	...
9.3	...	0.131
10	...	0.015	...	0.010	0.031	0.136	0.092	0.241	0.108	0.156	0.205	...	0.187	0.077	...
11	0.026	0.141	0.318	0.236	0.228	0.328	0.310	0.249	...	0.069	0.405	...
12	0.005	0.074	0.118	0.300	0.208	0.156	0.195	0.415	0.118	...	0.085	0.026	...
13	0.003	0.108	0.059	0.190	0.069	0.026	0.103	0.079	0.087	0.003	0.167	0.003	...
14	0.056	0.256	0.074	0.015	0.031	...	0.023	0.005	0.026	0.131	0.200
15	0.333	0.215	0.069	0.005	0.003	0.010	0.113	0.192
16	0.300	0.141	0.136	0.003	0.203	0.079
17	0.174	0.082	0.097	0.262	0.013
18	0.126	0.033	0.067	0.172	0.003	...	0.005
19	0.003	0.031	0.026	0.110	0.056
20	0.021	0.013	0.008	0.141
21	0.010	0.100
21.2	0.003
22	0.003	0.156
22.2	0.003
23	0.003	0.179
23.2	0.003
24	0.003	0.003	0.182
25	0.003	0.118
25.2	0.003
26	0.003	0.049
27	0.013	0.003
28	0.144
29	0.208
29.2	0.005
30	0.174
30.2	0.013
31	0.028
31.2	0.121
32	0.010
32.2	0.192
32.2	0.085
34.2	0.005
HO	0.738	0.774	0.841	0.805	0.903	0.692	0.754	0.851	0.815	0.718	0.841	0.851	0.831	0.656	0.877
PD	0.895	0.898	0.953	0.955	0.981	0.904	0.942	0.921	0.931	0.847	0.926	0.938	0.953	0.865	0.960
PE	0.490	0.552	0.677	0.609	0.801	0.416	0.516	0.697	0.628	0.457	0.677	0.697	0.657	0.364	0.749
P	0.685	0.120	0.517	0.498	0.338	0.074	0.198	0.148	0.758	0.206	0.662	0.312	0.618	0.578	0.508

HO: Heterozygosity; PD: Power of discrimination; PE: Probability of exclusion; and P: P-values for the exact test.