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FOR THE RECORD

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Allele Frequencies for the PowerPlex® 16 STR Loci in Javanese Population in Malaysia

POPULATION: Unrelated Javanese residing in Malaysia

KEYWORDS: forensic science, genetics, Javanese population, Malaysia, short tandem repeats (STR)

Geographical proximity of Indonesia to Malaysia and better employment opportunities in Malaysia are factors for strong migration flow of Javanese in Malaysia. A STR database to be used in forensic casework was created for the Javanese population residing in Malaysia. Saliva samples obtained from 109 unrelated Javanese in Malaysia were DNA extracted using FTA paper extraction method (1). PCR amplification was performed following manufacturer's instructions (PowerPlex® 16 System, Promega Corporation). The amplified products were analyzed and detected using ABI PRISM® 3100 Gene Analyzer (Applied Biosystem) with 3100 Data Collection Software (Version 1.1). The results were analyzed with GeneScan (Version 3.7.1) and PowerTyper™ Macros.

Power Stats (2), DNA-View Version (3)—The allele frequencies of the 15 STR loci studied are given in Table 1. The observed heterozygosity (OH) ranged from 0.606 (TPOX) to 0.890 (PENTA E). The Power of Discrimination (PD) ranged from 0.606 (TPOX) to 0.964 (FGA). The Probability of Excluding Paternity (PE) ranged from 0.298 (TPOX) to 0.775 (PENTA E). The combined probability of excluding paternity is about 0.999998221 and the combined probability of identity expressed as 1 in 2.567×10^{17}. The exact test (4) was performed based on 2000 shuffling experiments and there is no deviation from Hardy-Weinberg equilibrium except for D21S11 ($P < 0.05$).

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The complete detaset is available to any interested party at http://www.ppsk.usm.my.

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References

1. Budowle B, Smith J, Moretti T, DiZinno J. DNA typing protocols: molecular biology and forensic analysis. Natick USA: Eaton Publishing, 2000; 41–2.
2. Tereba A. Tools for analysis of population statistics. Profiles DNA 1999; 2:14–6.
3. Brenner C. DNA-View version 25.43.
4. Guo SW, Thompson EA. Performing the exact test of Hardy-Weinberg proportion for multiplex alleles. Biometrics 1992;48:361–72. [PubMed]

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TABLE 1—*Allele frequencies of 15 STR loci for Javanese population in Malaysia.*

Allele	D3S1358 $n=218$	TH01 $n=218$	D21S11 $n=218$	D18S51 $n=218$	Penta E $n=218$	D5S818 $n=218$	D13S317 $n=218$	D7S820 $n=218$	D16S539 $n=218$	CSF1PO $n=218$	Penta D $n=218$	vWA $n=218$	D8S1179 $n=218$	TPOX $n=218$	FGA $n=218$
5	...	...	...	...	0.028	...	...	...	...	...	...	...	...	...	...
6	...	0.064	...	...	...	...	...	...	...	...	...	...	...	...	...
7	...	0.349	...	...	0.005	0.018	...	...	...	...	0.023	...	...	0.005	...
8	...	0.101	...	...	...	...	0.257	0.248	0.005	0.014	0.046	...	...	0.601	...
9	...	0.303	...	...	0.018	0.005	0.142	0.133	0.179	0.018	0.349	...	0.005	0.133	...
9.3	...	0.078	...	...	...	...	...	...	...	...	...	...	...	...	...
10	...	0.092	...	0.005	0.023	0.344	0.138	0.188	0.161	0.271	0.188	0.005	0.069	0.018	...
10.3	...	0.009	...	...	...	...	...	...	...	...	...	...	...	...	...
11	...	0.005	...	...	0.284	0.275	0.284	0.326	0.298	0.317	0.110	0.005	0.055	0.220	...
12	...	...	...	0.078	0.142	0.188	0.110	0.092	0.252	0.321	0.147	0.005	0.156	0.009	...
12.2	...	...	...	...	...	...	...	...	...	0.005	...	...	...	...	...
13	0.018	...	...	0.161	0.087	0.147	0.064	0.009	0.101	0.046	0.083	...	0.248	0.014	...
14	0.041	...	...	0.133	0.119	...	0.005	0.005	0.005	0.005	0.032	0.183	0.179	...	...
14.2	...	...	...	...	...	...	...	...	...	0.005	...	...	...	...	...
15	0.280	...	...	0.289	0.069	0.009	...	...	...	...	0.023	0.032	0.174	...	...
16	0.358	...	...	0.161	0.055	0.014	...	...	...	...	...	0.165	0.106	...	...
17	0.239	...	...	0.055	0.041	...	...	...	...	...	...	0.284	0.009	...	...
18	0.055	...	...	0.037	0.028	...	...	...	...	...	...	0.197	...	...	0.028
19	0.009	...	...	0.050	0.073	...	...	...	...	...	...	0.092	...	...	0.069
20	...	...	...	0.014	0.023	...	...	...	...	...	...	0.028	...	...	0.046
21	...	...	...	...	...	...	...	...	...	...	...	0.005	...	...	0.156
21.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.028
22	...	...	...	0.009	0.005	...	...	...	...	...	...	...	...	...	0.193
22.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.037
23	...	...	...	0.009	...	...	...	...	...	...	...	...	...	...	0.170
23.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.009
24	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.106
24.2	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.014
25	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.096
26	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.041
27	...	...	...	...	...	...	...	...	...	...	...	...	...	...	0.005
28	...	...	0.032	...	...	...	...	...	...	...	...	...	...	...	...
29	...	...	0.220	...	...	...	...	...	...	...	...	...	...	...	0.005
29.2	...	...	0.005	...	...	...	...	...	...	...	...	...	...	...	...
30	...	...	0.284	...	...	...	...	...	...	...	...	...	...	...	...
30.2	...	...	0.046	...	...	...	...	...	...	...	...	...	...	...	...
31	...	...	0.078	...	...	...	...	...	...	...	...	...	...	...	...
31.2	...	...	0.092	...	...	...	...	...	...	...	...	...	...	...	...
32	...	...	0.055	...	...	...	...	...	...	...	...	...	...	...	...
32.2	...	...	0.142	...	...	...	...	...	...	...	...	...	...	...	...
33	...	...	0.090	...	...	...	...	...	...	...	...	...	...	...	...
33.2	...	...	0.032	...	...	...	...	...	...	...	...	...	...	...	...
34.2	...	...	0.005	...	...	...	...	...	...	...	...	...	...	...	...
OH	0.670	0.734	0.844	0.844	0.890	0.826	0.780	0.725	0.743	0.706	0.743	0.826	0.826	0.606	0.881
PD	0.888	0.900	0.942	0.948	0.955	0.882	0.930	0.908	0.914	0.867	0.935	0.930	0.948	0.774	0.964
PE	0.383	0.483	0.683	0.683	0.775	0.648	0.562	0.468	0.498	0.438	0.498	0.648	0.648	0.298	0.756
p	0.636	0.227	0.010	0.617	0.109	0.766	0.737	0.108	0.725	0.153	0.600	0.362	0.938	0.873	0.260

OH: Heterozygosity; PD: Power of discrimination; PE: Probability of excluding paternity; *p*: values (p) of the exact tests.