

FOR THE RECORD

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Allele Frequency Distribution for 10 STR Loci in the Malay Population of Malaysia*

POPULATION: Malay population, Malaysia ($n = 100$).

KEYWORDS: forensic science, DNA typing, population genetics, Malay, Malaysia

DNA data base was obtained from 100 unrelated random Malay individuals in Malaysia. The DNA was extracted by the salting out procedure (1), 20 ng target DNA was co-amplified using the commercial typing kits, Promega Geneprint™ STR multiplex (CTT, FFv, and STR III) and monoplex (LPL) systems, according to the manufacturer's instructions. Assignment of alleles was made by visual comparison between the commercially supplied reference allelic ladders and the amplified samples at the corresponding locus. Data were analyzed as per the methods already reported (2–4). No deviations from equilibrium were observed. The power of discrimination ranges from 0.7298 to 0.9311 and the combined power for the 10 loci is 0.99989.

The complete dataset can be accessed at <http://www.ppsk.usm.my>.

References

- Miller SA, Dykes DD, Polesky HF. A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Res* 1988;16:12–5.
- Nei M, Roychoudhury AK. Sampling variances of heterozygosity and genetic distance. *Genetics* 1974;76:379–90.
- Jones DA. Blood samples: probability of discrimination. *J Forensic Sci Soc* 1972;12:355–9.
- Ohno Y, Sebetan IM, Akaishi S. A simple method for calculating the probability of excluding paternity with any number of codominant alleles. *Forensic Sci Int* 1982;19:93–8.

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TABLE 1—Allele frequency for 10 STR loci in ethic Malay population of Malaysia (n = 100).

Allele	Frequency									
	CSF1PO	TPOX	TH01	F13A01	FESFPS	vWA	D16S539	D13S317	D7S820	LPL
3.2		0.2450
4		0.0900
5	0.0100	0.2450
6	...	0.0250	0.1100	0.3750
7	...	0.0100	0.2700	0.0350	0.0050	0.0100	0.0050
8	...	0.5350	0.1450	...	0.0100	...	0.0300	0.2500	0.2100	...
9	0.0250	0.1350	0.3550	0.1800	0.1500	0.0150	0.0200
9.3	0.0150
10	0.1650	0.0200	0.0950	...	0.0750	...	0.1250	0.1100	0.2450	0.6900
11	0.4050	0.2550	0.0050	...	0.3350	...	0.3150	0.2850	0.3150	0.1200
12	0.3000	0.0150	0.3850	...	0.2150	0.1700	0.1950	0.1400
13	0.0650	0.0050	0.1800	...	0.1200	0.0250	0.0100	0.0250
14	0.0400	0.0150	0.2200	0.0100	0.0050
15	0.0050	...	0.0250	0.0050
16	0.0050	...	0.1550
17	0.3100
18	0.1800
19	0.0750
20	0.0350
H	85.49	69.37	86.87	85.18	84.4	90.50	90.42	90.54	88.47	69.34
PE	47.33	42.51	54.62	49.07	44.80	59.39	59.3	59.11	52.72	38.83
PD	0.8552	0.8080	0.9016	0.8696	0.8304	0.7298	0.9311	0.9162	0.9077	0.7984
Chi	3.5294	12.061	2.2084	7.2335	8.5769	5.8241	1.7146	10.765	4.6820	4.9311
(p < 0.05)	(df 9)	(df 8)	(df 8)	(df 10)	(df 6)	(df 11)	(df 11)	(df 12)	(df 9)	(df 7)
CPE	0.99989									
CDP	0.999999999									

H: Heterozygosity; PE: Power of exclusion; PD: Power of discrimination; Chi: Chi square; CPE: Cumulative power of exclusion; CDP: Cumulative discrimination power.