

FOR THE RECORD

S. Panneerchelvam,¹ *M.Sc.*; *K. Kumara Thevan*,¹ *Lai KokFai*,¹ *M. Saravanakumar*,¹ *V. Sumathy*,¹
K. C. Yuvaneswari,¹ and *M. N. Norazmi*,¹ *Ph.D.*

Allele Frequency Distribution for 9 STR Loci in the Tamil Population of Malaysia*

POPULATION: Unrelated Tamil population, Malaysia

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

DNA database was obtained from unrelated random Tamil individuals in Malaysia. The DNA was extracted by the salting out procedure (1). Ten ng target DNA was co-amplified using the commercial typing kits, Promega Geneprint™ STR multiplex (CTT, FFv and STR III) 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 0.8458 to 0.9485.

The complete dataset can be accessed at www.ppsk.ugm.mg

¹ School of Health Sciences, Universiti Sains Malaysia, 16150 Kubang Kerian, Kelantan, Malaysia.

* This research was funded by Experimental Applied Research grant scheme, Ministry of Science, Technology and the Environment, Malaysia (09-02-05-3122 EA011).

References

1. 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.
2. Nei M, Roychoudhury AK. Sampling variances of heterozygosity and genetic distance. *Genetics* 1974;76:379–90.
3. Jones DA. Blood samples: probability of discrimination. *J Forensic Sci Soc* 1972;12:355–9.
4. Ohno Y, Sebetan IM, Akaishi S. [A simple method for calculating the probability of excluding paternity with any number of co dominant alleles.](#) *Forensic Science Int* 1982;19:93–8.

[PubMed]

[PubMed]

Additional information and reprint requests:
S. Panneerchelvam, M.Sc.
School of Health Sciences
Universiti Sains Malaysia
16150 Kubang Kerian
Kelantan, Malaysia

TABLE 1—Allele frequency for 9 STR loci in ethnic Tamil population of Malaysia (n = 102).

Allele	CSF1PO	TPOX	TH01	F13A01	Frequency FESFPS	vWA	D16S539	D7S820	D13S317
3,2	0.1730
4	0.0960
5	0.0050	0.3890	0.0240
6	0.2300	0.1640	0.0096	...
7	0.1150	0.1010	0.0100	0.0529	0.0096
8	...	0.2900	0.1850	...	0.0150	...	0.1106	0.1875	0.2067
9	0.0350	0.1550	0.3550	0.0050	0.0150	...	0.1635	0.1202	0.1250
9,3	0.0600
10	0.2500	0.1550	0.0450	...	0.1250	...	0.1395	0.2260	0.0865
11	0.3300	0.3600	0.0050	...	0.4150	...	0.2740	0.1875	0.1924
12	0.3400	0.0400	...	0.0100	0.2850	...	0.1923	0.1442	0.2548
13	0.0350	0.1150	0.0100	0.0865	0.0625	0.0769
14	0.0100	0.0140	0.0200	0.1540	0.0096	0.0096	0.0385
15	0.0430	...	0.0530	0.0096
16	0.0050	...	0.2070
17	0.2500
18	0.2070
19	0.1000
20	0.0190
H	85.26	92.08	87.78	85.59	81.93	87.49	93.86	93.99	94.85
PE	60.96	64.84	69.46	70.42	63.22	75.49	76.57	78.62	77.03
PD	0.8458	0.8910	0.8778	0.9013	0.8721	0.9266	0.9475	0.9485	0.9038
Chi	3.95	5.62	1.52	12.22	7.31	15.27	5.68	16.52	16.13
(p < 0.05)	(df 7)	(df 7)	(df 10)	(df 10)	(df 7)	(df 11)	(df 13)	(df 15)	(df 13)
CDP	0.9999999995								

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