

## FOR THE RECORD

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# Allele Frequency Data for Nine STRs Polymorphism in a Gurkha Population of Malaysia

**POPULATION:** Random Gurkha Population, Rawang, Malaysia.

**KEYWORDS:** forensic science, DNA typing, database, Gurkha population, Malaysia, population, genetics, short tandem repeats (STRs), CSF1PO, TH01, TPOX, F13A01, FESFPS, vWA, D16S539, D7S820, D13S317

TABLE 1—Allele frequency distribution in Gurkha population of Malaysia (n = 100).

Allele	Frequency								
	CSF1PO	TPOX	TH01	FESFPS	F13A01	vWA	D16S539	D7S820	D13S317
3.2					0.105				
4					0.250				
5					0.240				
6			0.235		0.260				
7			0.055	0.065	0.065				
8		0.380	0.070	0.020			0.040	0.150	0.140
9	0.070	0.130	0.395				0.200	0.100	0.235
9.3			0.130						
10	0.210	0.075	0.115	0.085			0.135	0.215	0.190
11	0.185	0.395		0.455			0.230	0.210	0.255
12	0.435	0.020		0.295			0.245	0.295	0.140
13	0.100			0.075	0.015	0.035	0.105	0.030	0.040
14				0.005	0.045	0.150	0.045		
15						0.060			
16					0.020	0.205			
17						0.375			
18						0.175			
19									
20									
21									
H	89.70	84.56	90.84	75.71	88.74	90.90	95.00	95.52	96.35
PE	48.83	41.72	53.95	45.31	59.77	54.61	63.08	58.51	60.70
PD	0.8792	0.8204	0.9072	0.8254	0.9216	0.9042	0.9321	0.9226	0.9256
Chi	13.92	2.29	7.03	10.64	10.2	3.66	10.95	5.36	9.75
(P<0.05)	(df 9)	(df 7)	(df 10)	(df 7)	(df 10)	(df 10)	(df 12)	(df 12)	(df 12)
CDP	0.99999999991								

H, heterozygosity; PE, power of exclusion; PD, power of discrimination; Chi, Chi-square; CDP, cumulative power of discrimination.

The Gurkha population of Malaysia, comprising a total of 652 individuals, live in Rawang in Selangor state in Malaysia. They had migrated from Nepal during World War II, and they constitute a distinct minority population in Malaysia. Buccal swabs were collected from 100 unrelated Gurkha individuals. DNA was

extracted by a simple salting-out procedure (1). Using STR multiplex primer kits, Promega Geneprint TM (CTT, FFv, and STR III), and following the manufacturer's guidelines, 10 ng of DNA was PCR amplified. Allele frequencies were calculated from the numbers of each genotype by the gene count method. The randomness of the population was ascertained by subjecting the data to a  $\chi^2$  test. No deviations from Hardy-Weinberg equilibrium were observed. Heterozygosity and discrimination power were

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calculated according to the methods already reported (2–4). The allelic distribution in the Gurkha population of Malaysia (Table 1) exhibits a distinct pattern from that of other population groups in Malaysia (5–7).

The complete dataset is available to any interested party at [www.ppsk.usm.my](http://www.ppsk.usm.my)

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