Population Genetics in Malaysia and Japanese Populations Using Power Plex Y23 System

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Abstract

Population flow between Southeast Asian countries and Japan continues to gather pace. Accordingly, the number of foreigners involved in incidents in Japan has markedly increased, which means that forensic dentistry is now increasingly being faced with the need to analyze DNA from persons of non-Japanese extraction. The DNA test currently used for personal identification mainly utilizes short tandem repeats (STRs) on autosomal chromosomes and the Y-chromosome. This test was developed for use in personal identification, not for distinguishing among races; nonetheless, the standard method for personal identification is often used because the procedure has been established. To determine the degree to which racial differences can be distinguished by standard DNA analysis, 23 STRs located on the Y chromosome were investigated in 218 Malay and 426 Japanese males. The frequencies of each STR were calculated in the two populations. The difference in the power of discrimination between the Malay and Japanese populations ranged from a minimum of 0.01 to a maximum of 0.27; the difference in polymorphic information content ranged from 0.01 (minimum) to 0.23 (maximum). No major differences were noted in the polymorphisms in these two Mongoloid populations, but the distributions of the 17 STRs differed significantly. Short tandem repeat types demonstrating a likelihood of racial differences were identified in 14 of the STRs. Race-specific STR types were identified in 10 STRs. These results suggest that the likelihood of Malay or Japanese genetic background can be judged based on Y-chromosome STR test results.

Key words: DNA identification — Y-chromosome — STR — Malaysia —
Race determination

Introduction

The 'Out of Africa' theory of the origin of the human race is widely held. According to this theory, one part of this population then left Africa, traversing the Arabian Peninsula to reach the Malay Peninsula via the Indian Peninsula, after which it further diffused into Indonesia. From there, as one population crossed the ocean to reach Japan, another migrated northward along the south margin of Eurasia, diffusing throughout Northeast Asia and eventually migrating southward to reach Japan. Given that this migration path originated in Africa, the Southeast Asian region has been demonstrated to have played an important role in interchange with Mongoloid peoples based on MtDNA and Y-chromosome haplogroups^{1,2,6,7,10}.

At present, Malaysia is made up of approximately 65% Malay, 24% ethnic Chinese, and 8% Indian populations. Malay people are widely distributed throughout Southeast Asia, including Indonesia, Brunei, Thailand, and Singapore. An earlier study by this group used autosomal chromosomal short tandem repeats (STRs) to investigate the racial breakdown of the Malaysian population⁴. In the present study, polymorphism information on 23 STRs on the Y chromosome was acquired from 218 male Malaysians living near Kuala Lumpur in Malaysia and compared with similarly acquired population data for 426 Japanese males. The Y-STR test tool used was PowerPlex[®] Y23 (Promega, USA). This DNA test is not exclusively designed for purposes of racial differentiation; rather, it is typically used as the first choice for blood relation analysis and personal identification by the police and in the field of forensics⁹. The purpose of the present study was to determine the possibility of estimating race based on a standard DNA test that was not developed for the purpose of distinguishing racial background. Specifically, the efficacy of PowerPlex[®] was investigated in distinguishing Japanese and Malay populations.

Materials and Methods

1. Samples

Malay genomic DNA was extracted from tooth samples obtained from 218 unrelated Malay men living in or around Kuala Lumpur. Appropriate consent was obtained from the patients. Within the Malay Archipelago, the population distribution is 65% Malaysian, 24% Chinese, and 8% Indian. This study used data exclusively of Malay archipelago origin. A family history also was taken to ensure that the parents of these participants were of Malay origin. No tribal population samples were included in the study. Japanese genomic DNA was extracted from blood samples obtained from 426 unrelated Japanese men. Informed consent was obtained from all donors, including those individuals in the case samples.

The protocol of this study was approved by the Ethics Committee of Tokyo Dental College (approval no.202 and 204) and met the conditions for cooperative study at the University of Malaya.

2. DNA extraction

Isolation of genomic DNA from tooth and blood samples was performed as described previously³. Permanent teeth extracted during dental treatment were used to obtain each sample. Each tooth was crushed to facilitate extraction of DNA.

3. PCR

PCR amplification and typing of Y-chromosome STRs targeted the following loci: DYS576, DYS389I, DYS389II, DYS448, DYS19, DYS391, DYS481, DYS549, DYS533, DYS438, DYS437, DYS570, DYS635, DYS390, DYS439, DYS392, DYS643, DYS393, DYS458, DYS385a, DYS385b, DYS456, and GATA-H4. Typing was performed using the Investigator PowerPlex[®] Y23 System PCR Amplification kit (Promega).

Table 1 shows the positional information for each STR. The sequences of the primers used in this kit were not disclosed by the manufacturer.

Table 1 Physical location of 23 Y-STRs

Locus	Physical location (bp)
DYS 393	3,131,128
DYS 456	4,270,942
DYS 570	6,861,115
DYS 576	7,053,302
DYS 458	7,867,839
DYS 481	8,426,350
DYS 19	9,521,935
DYS 391	14,102,769
DYS 635	14,379,486
DYS 437	14,466,964
DYS 439	14,515,188
DYS 389 I	14,612,164
DYS 389 II	14,612,164
DYS 438	14,937,785
DYS 390	17,274,885
DYS 643	17,425,969
DYS 533	18,393,105
GATA-H4	18,743,528
DYS 385a	20,801,569
DYS 385b	20,842,336
DYS 549	21,520,190
DYS 392	22,633,848
DYS 448	24,364,964

An ABI PRISM 3130 Genetic Analyzer (Applied Biosystems, USA) was used to perform electrophoresis under the conditions described in the manufacturer's recommendations. Fragment sizes were determined automatically using GeneScan Analysis software 3.1 (Applied Biosystems) and the results analyzed using Genotyper version 2.5 (Applied Biosystems).

4. Statistical analysis

The Matching Probability (MP), the power of discrimination (PD), and the polymorphic information content (PIC) were calculated using PowerStatsV12 software (<http://www.promega.com>)⁸⁾. The p-values were determined using the Fisher's exact test from

GENEPOP software version 4.2 (<http://genepop.curtin.edu.au>)⁵⁾.

Results

Tables 2a–w show the allele frequencies of the 23 STR loci evaluated in the Malay and Japanese populations. The PD and PIC are indices of polymorphism, and the MP is the probability of coincidence. The difference in PD between the two populations ranged from a maximum of 0.27 to a minimum of 0.01, while that in PIC ranged from 0.23 to 0.01. In general, the number of polymorphisms was higher in the Malay population than in the Japanese population. As both populations are Mongoloid and of the same origin, there was no major difference between the two populations. To clarify detailed differences, any STR type with an allele frequency of less than 1% was considered to be a mutation and excluded. The allele frequency distributions in the two populations were subjected to Fisher's exact analysis. The p-values of the 6 STRs (DYS549, DYS570, DYS437, DYS19, DYS389II, and DYS392) were highly similar among the two populations, with a p-value of 0.05 or higher. A significant difference was noted for 17 STRs (p-value <0.01). A total of 8 STRs (DYS385a, DYS389I, DYS438, DYS481, DYS390, DYS533, DYS439, and DYS643) were considered the most useful for racial differentiation (Table 3). The smallest difference was noted in the allele frequency of DYS549. The distribution of this type is shown in Fig. 1. In DYS549, the allele frequency of type 12 was the highest in both populations. The distribution was unimodal, and types with many repeats (right side of the graph) were dominant, with type 12 representing the most frequent allele. The absence of any difference between the 2 populations suggests that this STR has been present for a long time without change, and may be characteristic of Mongoloids. Its usefulness for racial differentiation is low. In DYS385a, type 13 exhibited the maximum allele frequency in both populations, but the overall distribution was bimodal, with type

Table 2a Observed allele frequencies for DYS19 loci in Malay and Japanese

Locus	DYS19	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
12	1.8%	0.0%
13	3.7%	4.2%
14	17.0%	8.0%
15	50.0%	45.1%
16	17.9%	22.1%
17	8.7%	20.4%
18	0.9%	0.2%
p-Value	0.0866405	
MP	0.320	0.302
PD	0.680	0.698
PIC	0.64	0.65

p-Value: Probability value from Fisher's exact test.
MP: Matching Probability.
PD: Power of Discrimination.
PIC: Polymorphism Information content.

Table 2b Observed allele frequencies for DYS385a loci in Malay and Japanese

Locus	DYS385a	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
6	0.5%	0.0%
7	0.0%	0.0%
8	0.0%	0.0%
9	0.5%	1.2%
10	2.8%	30.0%
11	17.0%	5.9%
12	19.7%	13.4%
13	22.5%	30.3%
13.2	0.0%	0.2%
14	10.1%	12.7%
15	18.3%	4.5%
16	6.0%	1.4%
17	1.4%	0.2%
18	0.9%	0.2%
19	0.5%	0.0%
p-Value	6.18057E-07	
MP	0.167	0.222
PD	0.833	0.778
PIC	0.81	0.75

Abbreviation: shown in Table 2a

Table 2c Observed allele frequencies for DYS385b loci in Malay and Japanese

Locus	DYS385b	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
11	0.9%	0.0%
12	2.8%	2.6%
13	4.1%	3.3%
14	21.6%	3.5%
15	10.6%	4.0%
16	10.1%	6.3%
17	9.6%	25.6%
18	13.3%	20.0%
19	13.3%	16.4%
19.2	0.5%	0.0%
20	8.7%	12.7%
21	3.2%	3.8%
22	1.4%	0.7%
23	0.0%	0.5%
24	0.0%	0.2%
25	0.0%	0.2%
27	0.0%	0.2%
p-Value	0.0052308	
MP	0.124	0.158
PD	0.876	0.842
PIC	0.86	0.82

Abbreviation: shown in Table 2a

Fig. 1 Frequency distribution of DYS549
Frequency distribution of DYS549 in Malay and Japanese populations.

Fig. 2 Frequency distribution of DYS385a
Frequency distribution of DYS385a in Malay and Japanese populations.

Table 2d Observed allele frequencies for DYS391 loci in Malay and Japanese

Locus	DYS391	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
8	0.0%	0.2%
9	11.9%	1.4%
10	68.3%	88.0%
11	18.8%	9.6%
12	0.9%	0.7%
p-Value	0.00212661	
MP	0.517	0.784
PD	0.483	0.216
PIC	0.44	0.20

Abbreviation: shown in Table 2a

Table 2e Observed allele frequencies for DYS549 loci in Malay and Japanese

Locus	DYS549	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
8	0.5%	0.0%
9	0.0%	0.0%
10	0.5%	4.7%
11	11.0%	10.6%
12	54.6%	59.4%
13	28.0%	21.6%
14	5.0%	3.8%
15	0.5%	0.0%
p-Value	0.202757	
MP	0.391	0.414
PD	0.609	0.586
PIC	0.55	0.54

Abbreviation: shown in Table 2a

Table 2f Observed allele frequencies for DYS392 loci in Malay and Japanese

Locus	DYS392	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
10	2.8%	0.5%
11	33.9%	42.0%
12	12.8%	7.3%
13	28.0%	38.7%
14	18.8%	10.1%
15	2.8%	0.7%
16	0.9%	0.5%
17	0.0%	0.2%
p-Value	0.0571873	
MP	0.247	0.342
PD	0.753	0.658
PIC	0.71	0.59

Abbreviation: shown in Table 2a

Fig. 3 Frequency distribution of DYS389 I

Frequency distribution of DYS389 I in Malay and Japanese populations.

Fig. 4 Frequency distribution of DYS438

Frequency distribution of DYS438 in Malay and Japanese populations.

13.2 as a boundary, and there were clear differences in the allele frequency between the two populations. Types 10 or lower were dominant in Japanese, whereas types 15 or higher were dominant in Malay (Fig. 2). In DYS389I, the maximum allele frequency was noted in type 13 in Malay and type 14 in Japanese. The distribution was concentrated in types 12 and 13 in Malay, whereas types 11 or

lower and 14 or higher were dominant in Japanese (Fig. 3). In DYS438, the maximum allele frequency was noted in type 10 in both populations, and the overall distribution was bimodal, with type 12 as a boundary. Types 11 or lower were dominant in Malay, whereas types 13 or higher were dominant in Japanese (Fig. 4). In DYS481, the maximum allele frequency was noted in type 23 in Malay, and

Table 2g Observed allele frequencies for DYS643 loci in Malay and Japanese

Locus	DYS643	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
7	1.8%	0.0%
8	0.0%	1.2%
9	11.5%	3.1%
10	14.2%	8.5%
11	34.4%	22.3%
11.1	2.3%	0.0%
12	32.1%	50.0%
13	3.2%	11.5%
14	0.0%	3.3%
15	0.5%	0.2%
p-Value	0.000999386	
MP	0.257	0.322
PD	0.743	0.678
PIC	0.70	0.64

Abbreviation: shown in Table 2a

Table 2h Observed allele frequencies for DYS393 loci in Malay and Japanese

Locus	DYS393	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
11	0.9%	1.4%
12	20.6%	20.0%
13	43.6%	64.1%
14	29.8%	11.7%
15	5.0%	2.6%
16	0.0%	0.2%
p-Value	0.0178206	
MP	0.324	0.465
PD	0.676	0.535
PIC	0.62	0.49

Abbreviation: shown in Table 2a

Table 2i Observed allele frequencies for DYS456 loci in Malay and Japanese

Locus	DYS456	
	Malay	Japan
Total Alleles	218	425
Allele	Frequency	
12	0.0%	0.5%
13	1.4%	0.7%
14	9.6%	4.9%
15	50.0%	69.6%
16	24.3%	20.5%
17	11.9%	3.3%
18	2.8%	0.5%
p-Value	0.0172153	
MP	0.334	0.531
PD	0.666	0.469
PIC	0.62	0.42

Abbreviation: shown in Table 2a

Fig. 5 Frequency distribution of DYS481
Frequency distribution of DYS481 in Malay and Japanese populations.

Fig. 6 Frequency distribution of DYS390
Frequency distribution of DYS390 in Malay and Japanese populations.

types 21 and 26 in Japanese. The distribution was concentrated in types 22–25 in Malay, whereas types 21 or lower and 26 or higher were dominant in Japanese (Fig. 5). In DYS390, types 22–25 accounted for more than 80% in both populations, but types 21 or lower were noted only in Malay (Fig. 6). In

DYS533, the maximum allele frequency was noted in type 11 in both populations, and types 10 or lower were dominant in Malay, whereas types 12 or higher were dominant in Japanese (Fig. 7). In DYS439, the maximum allele frequency was noted in type 12 in both populations, and types 11 or lower were domi-

Table 2j Observed allele frequencies for DYS438 loci in Malay and Japanese

Locus	DYS438	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
8	0.9%	0.2%
9	6.9%	2.1%
10	67.9%	55.2%
11	22.5%	11.5%
12	1.8%	1.4%
13	0.0%	27.7%
14	0.0%	1.9%
p-Value	9.27129E-07	
MP	0.517	0.395
PD	0.483	0.605
PIC	0.43	0.55

Abbreviation: shown in Table 2a

Fig. 7 Frequency distribution of DYS533

Frequency distribution of DYS533 in Malay and Japanese populations.

Fig. 8 Frequency distribution of DYS439

Frequency distribution of DYS439 in Malay and Japanese populations.

Table 2k Observed allele frequencies for DYS437 loci in Malay and Japanese

Locus	DYS437	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
13	0.0%	0.7%
14	77.1%	85.7%
15	17.4%	12.9%
16	5.5%	0.7%
p-Value	0.132959	
MP	0.627	0.751
PD	0.373	0.249
PIC	0.33	0.22

Abbreviation: shown in Table 2a

Table 2l Observed allele frequencies for DYS481 loci in Malay and Japanese

Locus	DYS481	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
19	1.4%	0.0%
20	0.9%	2.3%
21	3.2%	21.8%
22	8.3%	5.6%
23	39.9%	14.1%
24	18.8%	10.8%
25	13.3%	8.5%
25.1	0.9%	0.0%
26	6.0%	21.4%
27	5.0%	9.9%
27.1	0.5%	0.0%
28	0.5%	2.6%
29	0.9%	1.6%
30	0.5%	0.5%
31	0.0%	0.2%
32	0.0%	0.7%
p-Value	4.27111E-06	
MP	0.227	0.146
PD	0.773	0.854
PIC	0.75	0.84

Abbreviation: shown in Table 2a

Fig. 9 Frequency distribution of DYS643

Frequency distribution of DYS643 in Malay and Japanese populations.

Table 2m Observed allele frequencies for DYS533 loci in Malay and Japanese

Locus	DYS533	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
9	1.8%	0.0%
10	24.8%	2.6%
11	43.1%	46.2%
12	25.7%	45.3%
13	4.1%	4.9%
14	0.5%	0.9%
p-Value	0.000107509	
MP	0.315	0.422
PD	0.685	0.578
PIC	0.63	0.49

Abbreviation: shown in Table 2a

Table 2n Observed allele frequencies for DYS570 loci in Malay and Japanese

Locus	DYS570	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
13	0.5%	0.0%
14	3.2%	1.2%
15	6.0%	2.3%
16	20.2%	10.8%
17	15.1%	26.3%
18	25.2%	20.0%
19	17.0%	20.0%
19.3	0.0%	0.2%
20	8.7%	12.9%
21	4.1%	4.7%
22	0.0%	1.4%
23	0.0%	0.2%
p-Value	0.190552	
MP	0.170	0.180
PD	0.830	0.820
PIC	0.81	0.80

Abbreviation: shown in Table 2a

Table 2o Observed allele frequencies for DYS390 loci in Malay and Japanese

Locus	DYS390	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
20	0.5%	0.0%
21	14.2%	0.0%
22	7.3%	22.8%
23	26.1%	25.1%
24	25.7%	17.4%
25	25.2%	31.0%
26	0.9%	3.3%
27	0.0%	0.5%
p-Value	8.61223E-05	
MP	0.224	0.242
PD	0.776	0.758
PIC	0.74	0.72

Abbreviation: shown in Table 2a

nant in Malay, whereas types 13 or higher were dominant in Japanese (Fig. 8). In DYS643, the maximum allele frequency was noted in type 11 in Malay and type 12 in Japanese. Types 11 or lower were dominant, with type 11.1 as a boundary in Malay, whereas types 12 or higher were dominant in Japanese (Fig. 9).

Discussion

Since the technique of differentiating race based on Y-chromosome single nucleotide polymorphisms (SNPs) was first demonstrated by Peter Au and others, the study of Y-chromosome haplogroups has gained much attention. The Malay and Japanese popula-

tions share the same group (haplogroup O), and have been shown to be closely related. The results of the present study based on STRs support those of these earlier investigations using SNPs. Malay people are considered to be the ancestors of the *Jomon* people, and comparison with the Japanese population is therefore anthropologically meaningful. Comparison of DNA between Malay and Japanese populations is also significant for forensic dentistry, as the number of foreign travelers and workers visiting Japan from Southeast Asian countries is increasing each year. The present results revealed dominant distribution zones in each population, suggesting that the two races can be distinguished by evaluating these STRs. Furthermore, type 15

Table 2p Observed allele frequencies for DYS576 loci in Malay and Japanese

Locus	DYS576	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
11	0.5%	0.0%
13	0.5%	0.0%
14	0.5%	0.0%
15	8.7%	0.9%
16	11.0%	5.4%
17	21.6%	13.8%
18	30.7%	26.8%
19	16.5%	32.6%
20	9.2%	15.5%
21	0.5%	3.8%
22	0.5%	1.2%
p-Value	0.00223763	
MP	0.196	0.226
PD	0.804	0.774
PIC	0.78	0.74

Abbreviation: shown in Table 2a

Table 2q Observed allele frequencies for DYS448 loci in Malay and Japanese

Locus	DYS448	
	Malay	Japan
Total Alleles	218	424
Allele	Frequency	
15	0.5%	0.0%
16	4.6%	2.8%
17	11.0%	8.5%
18	26.1%	41.0%
19	21.6%	32.1%
20	26.1%	11.3%
21	9.2%	4.0%
22	0.9%	0.2%
p-Value	0.0188783	
MP	0.206	0.294
PD	0.794	0.706
PIC	0.76	0.66

Abbreviation: shown in Table 2a

Table 2r Observed allele frequencies for DYS635 loci in Malay and Japanese

Locus	DYS635	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
18	0.9%	0.0%
19	3.2%	2.6%
20	14.7%	31.7%
21	39.9%	49.8%
22	17.4%	9.9%
23	15.1%	3.8%
24	7.3%	2.1%
25	1.4%	0.2%
p-Value	0.00177995	
MP	0.241	0.360
PD	0.759	0.640
PIC	0.73	0.58

Abbreviation: shown in Table 2a

or higher of DYS385a is the dominant distribution zone in Malay. Focusing on type 15 alone, the allele frequency was 18.3% in Malay and 4.5% in Japanese. This represents a 4-fold difference in the allele frequency. Thus, a person with type 15 is more likely to be Malay than Japanese. As type 15 of DYS385a is common in Malay but rare in Japanese, a person with this type can be presumed to be Malay. On the other hand, type 10 or lower is the dominant distribution zone in Japanese. The allele frequency of type 10 was 30% in Japanese and 2.8% in Malay. This represents a 10-fold difference in the allele frequency. Based on this difference in allele frequency, type 10 of DYS385a may be seen as common in Japanese but rare in Malay. Therefore, a person with this type can be presumed to be Japanese. It is difficult to judge a person as

Japanese based on this type alone. There are several types of STR demonstrating the likelihood of a specific race, however, such as type 10 of DYS385a. When several such types are present, the two races can be distinguished with a high degree of accuracy. Therefore, we defined a type with an allele frequency in Malay that was 4-fold or higher compared to the frequency in Japanese. The presence of an allele that is known to have a frequency of 5% or lower in Japanese can be taken as an indication of Malay heritage. Thus, the presence of types 15 and 16 of DYS385a, type 14 of DYS385b, type 9 of DYS391, type 10 of DYS392, type 18 of DYS456, type 16 of DYS437, type 10 of DYS533, type 15 of DYS576, types 23 and 25 of DYS635, type 10 of DYS439, and types 10 and 14 of GATA-H4 are types indicative of Malay identity. Similarly, we defined a type

Table 2s Observed allele frequencies for DYS439 loci in Malay and Japanese

Locus	DYS439	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
9	0.0%	0.2%
10	11.0%	1.9%
11	39.0%	17.4%
12	40.4%	61.0%
13	7.8%	15.5%
14	1.8%	3.8%
15	0.0%	0.2%
p-Value	0.000197448	
MP	0.334	0.428
PD	0.666	0.572
PIC	0.61	0.53

Abbreviation: shown in Table 2a

Table 2t Observed allele frequencies for DYS389I loci in Malay and Japanese

Locus	DYS389 I	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
11	0.0%	4.7%
12	35.3%	14.8%
13	46.8%	30.0%
14	17.4%	48.8%
15	0.5%	1.6%
p-Value	6.61623E-07	
MP	0.374	0.353
PD	0.626	0.647
PIC	0.55	0.59

Abbreviation: shown in Table 2a

Table 2u Observed allele frequencies for DYS389II loci in Malay and Japanese

Locus	DYS389 II	
	Malay	Japan
Total Alleles	218	426
Allele	Frequency	
25	0.5%	0.0%
27	2.3%	6.8%
28	23.4%	13.1%
29	34.9%	26.3%
30	21.6%	27.5%
31	11.9%	22.5%
32	4.1%	3.5%
33	1.4%	0.0%
34	0.0%	0.2%
p-Value	0.0654928	
MP	0.239	0.218
PD	0.761	0.782
PIC	0.72	0.75

Abbreviation: shown in Table 2a

with an allele frequency in Japanese 4-fold or higher than that in Malay. The presence of an allele that is known to have a frequency of 5% or lower in Malay can be taken as an indication of Japanese heritage. The presence of type 10 of DYS385a, type 10 of DYS549, type 13 of DYS643, types 21 and 28 of DYS481, type 21 of DYS576, and type 20 of DYS458 are types indicative of Japanese identity. Thus, the detailed allele distributions were compared between the two populations. There were several race-specific types that were present only in Malay or Japanese: type 12 of DYS19, types 7 and 11.1 of DYS643, type 19 of DYS481, type 9 of DYS533, type 21 of DYS390, type 33 of DYS389II, and type 13 of DYS458 were characteristic of Malay individuals; whereas types 8 and 14 of DYS643, types 13 and 14 of DYS438, type 22 of DYS570, and type 11 of DYS389I were characteristic of Japanese individuals. In

a forensic context, the use of these race-specific types may permit distinction of persons of these two backgrounds.

No major difference was noted in polymorphisms between the two Mongoloid populations, but the allele frequency of 17 STRs did differ significantly. To distinguish Malay and Japanese, a dominant distribution zone was observed in each population based on the following 8 STRs: DYS385a, DYS389I, DYS438, DYS481, DYS390, DYS533, DYS439, and DYS643. In addition, by paying attention to types demonstrating the likelihood of a specific race (Malay-like type or Japanese-like type) and race-specific types, elements indicative of Malay or Japanese heritage were identified in 21 of the 23 STRs, excluding DYS393 and DYS448, suggesting the possibility of estimated identification in the two populations. These results are shown in Table 4.

Table 2v Observed allele frequencies for GATA-H4 loci in Malay and Japanese

Locus	GATA-H4	
	Malay	Japan
Total Alleles	217	426
Allele	Frequency	
10	7.8%	1.4%
11	36.9%	50.5%
12	38.2%	43.7%
13	14.3%	4.0%
14	2.3%	0.5%
15	0.5%	0.0%
p-Value	0.00397189	
MP	0.309	0.447
PD	0.691	0.553
PIC	0.64	0.45

Abbreviation: shown in Table 2a

Table 2w Observed allele frequencies for DYS458 loci in Malay and Japanese

Locus	DYS458	
	Malay	Japan
Total Alleles	218	425
Allele	Frequency	
13	1.4%	0.0%
14	6.4%	2.4%
14.1	0.0%	0.5%
15	15.6%	26.8%
15.2	0.5%	0.0%
16	28.4%	15.3%
17	24.8%	19.1%
18	16.5%	18.4%
18.2	0.9%	0.0%
19	4.6%	11.5%
20	0.5%	4.9%
20.2	0.5%	0.0%
21	0.0%	0.5%
23	0.0%	0.7%
p-Value	0.0152059	
MP	0.200	0.182
PD	0.800	0.818
PIC	0.77	0.79

Abbreviation: shown in Table 2a

Table 3 p-Values of 23 Y-STRs

Locus	p-Value
DYS549	0.2027570
DYS570	0.1905520
DYS437	0.1329590
DYS19	0.0866405
DYS389 II	0.0654928
DYS392	0.0571873
DYS448	0.0188783
DYS393	0.0178206
DYS456	0.0172153
DYS458	0.0152059
DYS385b	0.0052308
GATA-H4	0.0039719
DYS576	0.0022376
DYS391	0.0021266
DYS635	0.0017800
DYS643	0.0009994
DYS439	0.0001974
DYS533	0.0001075
DYS390	0.0000861
DYS481	0.0000043
DYS438	0.0000009
DYS389 I	0.0000007
DYS385a	0.0000006

The results of this study suggest that the likelihood of Malay or Japanese genetic background can be judged based on Y-chromosome STR test results. As interchanges between the populations of Japan and South-east Asian countries increase in the future, the ability to distinguish between Japanese and Malay individuals may become forensically important.

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Table 4 Markers that may be useful in differentiating persons of Malay and Japanese heritage

Y-STR	Malay dominant zone	Malay-like type	Malay-specific type	Japanese dominant zone	Japanese-like type	Japanese-specific type
DYS19			12			
DYS 385a	15 or higher	15, 16		10 or lower	10	
DYS 385b		14				
DYS389 I	12, 13			11 or lower, 14 or higher		11
DYS389 II			33			
DYS390			21			
DYS391		9				
DYS392		10				
DYS437		16				
DYS438	11 or lower			13 or higher		13, 14
DYS439	11 or lower	10		13 or higher		
DYS456		18				
DYS458			13		20	
DYS481	22–25		19	21 or lower, 26 or higher	21, 28	
DYS533	10 or lower	10	9	12 or higher		
DYS549					10	
DYS570						22
DYS576		15			21	
DYS635		23, 25				
DYS643	11 or lower		7, 11.1	12 or higher	13	8, 14
GATA-H4		10.14				

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