Allele frequencies and haplotype diversity of 12-loci male-specific Y-chromosome (STRs) among Thai population in Yala province of Thailand

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Abstract

Twelve Y-STR loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439 and DYS385a/b) were analyzed in 99 unrelated Thai male individuals from Yala province of Thailand using the PowerPlex® Y System (Promega, USA). Among the 99 individuals studied, 95 different haplotypes were observed and 91 were unique, while 4 haplotypes found more than once. The overall haplotype diversity for the 12 Y-STR loci in this study was 0.9992.

Keywords: Y-STR, Allele frequency, Haplotype, PowerPlex® Y System, Yala population, Thailand.

Introduction

Y chromosomes inherited from father to son only without alteration from generation to generation except event mutations. Y chromosomal short tandem repeats (Y-STRs) reside in the non – recombining portion of the Y chromosome (NYR) [1], Moreover, the Y-STRs, particularly their markers, are useful in forensic science as well as for lineage and genealogy studies.

This study was aimed to investigate allele frequencies and haplotype diversity of Thai population in Yala province in deep southern Thailand by using 12 Y-STR loci markers of the PowerPlex® Y system (Promega,USA).

Material and methods

DNA samples

Buccal cell samples stored on FTA® card (Whatman Bioscience) were used for DNA extraction. The samples were collected from 99 unrelated Thai male individuals residing in Yala province in deep southern Thailand (Fig 1). This population study was approved by the Ethical Committee of Mahidol University.

DNA extraction

Genomic DNA was extracted from the buccal cell samples according to the manufacturer's protocols for FTA® extraction.

PCR amplification

Twelve Y-chromosomal short tandem repeats (STR) loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439 and DYS385a/b) were amplified using the commercial kit PowerPlex® Y System (Promega, USA) according to the manufacturer's recommendations. The reaction was performed using GeneAmp® PCR System 9700 Thermal Cycler (Applied Biosystems). The PCR thermocycling parameters were as follows: pre-denaturation step at 95 °C for 11 min and 96 °C for 1 min; denaturation 10 cycles at 3 temperatures at 94 °C for 30 sec, 60 °C for 30 sec and 70 °C for 45 sec. The annealing 22 cycles at 3 temperatures, 90 °C for 30 sec, 58 °C for 30 sec and 70 °C for 45 sec followed by the extension process at 60 °C for 30 min and final soak at 4 °C [2].

DNA Fragment Analysis

PCR products were analyzed using the ABI Prisms® 3100 Genetic Analyzer (Applied Biosystems, USA) and GeneMapper® *ID* Software version 3.2. Alleles were designated according to the International Society of Forensic Genetics (ISFG) guidelines for forensic STR analysis [3].

Statistical analysis

Allele frequencies were estimated by direct gene counting. The gene or haplotype diversity (GD) was calculated according to Nei formula [4]; GD = n $(1-\sum p_i^2) / (n - 1)$., Where n is the number of individuals and p_i is the allele frequency in the given population sample. Analysis of molecular variance (AMOVA) and exact test of population differentiation were performed by using ARLEQUIN Software (version 3.1) [5].

Results and discussion

Analyses of Y-STR loci for allele frequencies and gene diversity values of 10 Y-STR loci (except DYS385a/b) is shown in Table 1. The value of DYS385a/b is summarized in Table 2. The analysis for haplotype is shown in Table 3.

Table 1 Allele frequencies and gene diversity (GD) value of 10 Y-STR loci analyzed from DNA of Thai male population residing in Yala province of Thailand.

	YS	YS	YS	YS	YS	YS	YS	YS	YS	YS
Allele	**9**	**89I**	**89II**	**90**	**91**	**92**	**93**	**37**	**38**	**39**
					.04040				.08081	
0					.66667	.04040			.65657	.08081
1		.02020			.28283	.22222	.02020		.24242	.29293
2	.01010	.37374			.01010	.06061	.22222		.02020	.45455
3	.01010	.40404				.39394	.45455		–	.15152
4	.10101	.19192				.25253	.26263	.71717		.02020
5	.48485	.01010				.03030	.04040	.20202		
6	.30303							.08081		
7	.08081									
8	.01010									
0				.02020						
1				.02020						
2				.08081						
3				.28283						
4				.28283						
5			.01010	.30303						
6				.01010						
7			.02020							
8			.26263							
9			.29293							
0			.25253							
1			.13131							
2			.03030							
D	**.66275**	**.66646**	**.77056**	**.74830**	**.47866**	**.73284**	**.67986**	**.44280**	**.50835**	**.68460**

Allele	DYS385a/b	Allele	DYS385a/b	Allele	DYS385a/b
9,17	0.01010	12,20	0.01010	14.18	0.03030
11,11	0.02020	12,21	0.01010	14,19	0.03030
11,12	0.01010	13,13	0.03030	15.16	0.01010
11,14	0.05051	13,14	0.04040	15,17	0.02020
11,15	0.01010	13,15	0.02020	15.18	0.04040
11,17	0.01010	13,16	0.05051	15,19	0.01010
11,18	0.01010	13,17	0.01010	15,20	0.03030
12,12	0.03030	13,18	0.09091	15.21	0.04040
12,13	0.03030	13,19	0.04040	15,22	0.01010
12.14	0.05051	13,20	0.01010	15,23	0.01010
12,15	0.02020	13.21	0.01010	16,18	0.01010
12.16	0.03030	13,22	0.01010	16,19	0.03030
12.17	0.01010	13,23	0.01010	16,21	0.01010
12,18	0.02020	14,14	0.02020		
12.19	0.03030	14,17	0.01010		
GD	**0.97464**				

Table 2 Allele frequency and gene diversity (GD) value of DYS385a/b analyzed from DNA of Thai population residing in Yala province of Thailand. *Haplotype diversity = 0.9992*

	YS 9	YS 891	YS 8911	YS 90	YS 91	YS 92	YS 93	YS 37	YS 38	YS 39	YS 85a/b
01	2	4	1	4	1	3	3	5	0	1	3,17
02	3	4	0	4	0	1	3	5	0	1	2,15
03	4	2	8	4	0	4	1	5	1	2	3.18
04	4	2	8	5	1	4	2	5	1	2	3,18
05	4	2	9	2	0	4	1	5	0	3	3,19
06	4	2	8	3	0	4	2	4	1	2	5.18
07	4	3	9	3	0	0	4	6	1	1	3.18
08	4	3	9	2	1	0	4	6	1	2	4,19
09	4	4	0	3	0	1	3	5		2	2,18
10	4	4	0	3	1	0	4	6	1	1	2,18
11	4	4	9	3	0	0	4	4	1	2	3.20
12	4	4	0	3	1	2	3	5	1	1	3,23
13	5	2	8	3	0	5	3	4	0	3	2.12
14	5	2	8	3	0	4	3	4	0	2	2,13
15	5	2	8	3	0	4	3	4	0	1	2,14
16	5	2	0	1		2	3	4	0	1	2,15
17	5	2	8	4		3	3	4	0	2	2.16
18	5	2	8	5	0	1	2	4	1	2	2,16
19	5	2	5	4	0	3	3	5	0	2	2.17
20	5	2	8	5	0	3	2	4	10	2	2,19
21	5	2	1	4	1	3	3	4	10	1	2.21
22	5	2	0	4	0	1	3	5	9	1	3,15
23	5	2	8	4	0	2	2	4	10	2	3,16
24	5	2	8	4	0	3	3	5	10	4	3,16
25	5	2	8	4	0	1	2	5	9	2	3.18
26	5	2	8	4	0	4	2	5	11	2	4,18
27	5	2	8	2	0	1	2	4	9	1	5,16
28	5	3	0	4	0	1	3	4	12	1	1,14
29	5	3	0	5	1	1	3	4	11	0	1,15
30	5	3	9	3	0	5	3	4	10	12	2,12

Table 3 List of 95 Y-STR haplotypes (H) obtained from DNA analysis of 99 unrelated Thai population (N) residing in Yala province of Thailand.

Table 3 *(Continued)*

	YS	YS	YS	YS	YS	YS	YS	YS	YS	YS	YS
	9	891	89II	90	91	92	93	37	38	39	85a/b
31	**5**	**3**	**1**	**3**	**0**	**3**	**2**	**4**	**0**	**1**	**2,19**
32	5	3	1	4	0	1	3	4		1	3,16
33	5	3	0	4	1	3	4	4	0	2	3,18
34	5	3	9	3	0	3	2	5	0	2	3.21
35	5	3	9	5	0	3	4	4	0	3	4,19
36	**5**	**3**	**9**	**2**	**0**	**1**	**2**	**4**		**1**	**5,17**
37	5	3	9	5	0	3	3	4	0	3	5,18
38	5	3	9	2	0	4	4	4	0	3	5,18
39	5	3	9	5	1	3	3	4	0	2	5,18
40	5	3	8	5	1	3	4	4	0	2	5,19
41	5	3	0	4	0	4	4	4	0	2	5,20
42	5	3	0	6	0	4	4	4	0	2	5,20
43	5	3	0	5	0	3	4	4	0	3	5,20
44	5	3	9	5	0	3	4	4	0	2	5,21
45	5	3	9	4	1	3	4	4	0	1	5,21
46	5	3	0	5	0	4	4	4	0	2	5,22
47	5	3	9	5	0	3	4	4	0	3	5,23
48	5	3	9	5	0	3	4	4	0	1	6.18
49	5	3	0	5	0	3	4	4	0	1	6,19
50	5	4	1	5	0	1	3	4	1	0	1,11
51	5	4	2	5	0	1	3	4	1	0	1,12
52	5	4	2	4	1	3	3	6	1	4	2.12
53	5	4	0	0	0	3	3	6	0	3	2,13
54	5	4	0	0	0	3	3	6	0	3	2.14
55	5	4	0	2	0	1	3	5	0	2	3,18
56	5	4	1	5	1	3	4	4	0	1	6,19
57	5	4	0	4	1	3	4	4	0	2	6,21
58	**6**	**1**	**8**	**5**	**1**	**4**	**5**	**4**	**0**	**2**	**3,18**
59	6	2	7	3	1	4	3	4	0	2	2,13
60	6	2	0	5	1	1	3	4	1	0	2.14
61	6	2	0	4	0	4	4	4	0	3	3,13
62	6	2	7	3	0	4	3	4	0	2	3.14
63	6	2	8	3	0	1	3	4	1	1	3,14
64	6	2	0	3	0	4	3	4	0	2	3,14
65	6	2	8	3	1	4	3	4	0	1	3,14
66	6	2	8	3	0	4	3	4	0	2	3,15
67	**6**	**2**	**8**	**3**	**0**	**4**	**3**	**4**	**0**	**2**	**3,16**
68	6	2	9	3	0	4	3	4	0	1	4.14
69	6	2	8	5	0	3	2	4	0	2	4.17
70	6	3	1	5	1	1	3	4	1	0	1,14
71	6	3	9	3	1	1	5	4	0	2	1.17
72	6	3	9	3	0	1	4	4	0	1	1,18
73	6	3	1	3	1	4	3	4	0	2	2.14
74	6	3	9	4	0	3	3	5	0	2	2,16
75	6	3	9	4	1	3	4	4	0	3	2,20

Table 3 *(Continued)*

	YS	YS	YS	YS	YS	YS	YS	YS	YS	YS	YS
	9	891	8911	90	91	92	93	37	38	39	85a/b
76	6	3	9	4	1	3	4	4	0	2	3,19
77	6	3	9	5	1	3	5	4	0	3	3,19
78	6	3	9	4	0	3	2	5	0	3	3,22
79	6	3	9	5	1	3	3	4	0	2	6,19
80	6	3	9	2	0	5	2	6	0	1	,17
81	6	4	0	5	0	1	3	4	1	0	1,11
82	6	4	1	5	0	1	3	4	2	0	1,14
83	6	4	1	5	1	1	3	4	1	0	1,14
84	6	4	1	5	0	3	4	4	0	2	3,18
85	6	4	1	5	0	3	2	5	0	2	5,21
86	6	5	2	3	0	2	2	4		1	3,16
87	7	2	9	3	0	2	4	4	0	3	1,14
88	7	2	8	3	0	4	3	4	0	1	3,13
89	7	2	8	4	0	3	2	5	1	2	4,18
90	7	2	8	4		3	2	5	1	2	4,19
91	7	2	9	4	0	3	2	4	1	3	5,21
92	7	3	0	4	1	3	3	6	1	2	3,13
93	7	3	9	5	2	3	4	4	0	2	3,19
94	7	3	0	3	0	4	3	4	0	1	4,14
95	8	2	0	1		2	3	4	0	1	2,14

A total of 95 different haplotypes were observed in the analyzed 99 Thai population residing in Yala province, of which 91 haplotypes (91.92%) were unique, 4 haplotypes were found in 2 individuals. Gene diversity values among 12 Y-STR loci ranged from 0.44280 (DYS437) to 0.97464 (DYS385a/b) whereas the haplotype diversity for the 12 Y-STR loci was 0.9992. Comparative analysis between our data and previously published data for the same set of Y-STR loci [6-7] has been performed by calculating Fst- values and applying AMOVA (Arlequin 3.1 software). The Fst values between pairwise population of our data and East Malaysian (n=315) was, (F_{st} = 0.04383, $p < 0.05$), and Southwest Chinese population (n=320) was, (F_{st} = 0.01416, $p < 0.05$) respectively. The present investigation showed significant differences between Thai population residing in Yala province with the neighbor populations. These Y haplotype study provided the useful data in forensic application.

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