

FOR THE RECORD

Meisen Shi,^{1,2} Ph.D.; Yingbi Li,² M.D.; Jianpin Tang,³ Ph.D.; Haijun Zhang,² Ph.D.; and Yiping Hou,² M.D.

Southwest China Han Population Data for Nine Y-STR Loci by Multiplex Polymerase Chain Reaction

POPULATION: One hundred and twenty unrelated Han ethnic individuals from Chengdu, southwest China.

KEYWORDS: forensic science, Y-chromosome, Y-STR, DYS434, Y-GATA-A10, DYS438, DYS439, DYS531, DYS557, DYS448, DYS456, DYS444, multiplex PCR, haplotype, DNA typing, population genetics

Extraction

Whole-blood samples of 120 unrelated males of the Chinese Han ethnic group who live in Sichuan province, southwest of China, were collected and anticoagulant with EDTA. DNA was extracted using the Chelex-100 method (1). Polymerase chain reaction (PCR): The co-amplification of DYS434, Y-GATA-A10, DYS438, DYS439, DYS531, DYS557, DYS448, DYS456, and DYS444 was performed using a nonplex reaction. About 2–10 ng of genomic DNA was used in a 37.5 μ L reaction volume containing 9.4 μ L of Y-STR 9plex primer mix (0.20–0.45 μ M primers), 200 μ M dNTP (Pharmacia Biotech, Stockholm, Sweden), 1 $\times$ buffer, 2.5 mM MgCl₂, and 2.0 μ L of home-product MBI Taq polymerase (5 U/ μ L). Amplification reactions were performed in a GeneAmpPCR systems 9600 (Applied Biosystems, Foster City, CA) under the following conditions: 94°C, 10 min; 10 cycles of 94°C, 1 min; 56°C, 50 sec and 72°C, 40 sec; 25 cycles of 90°C for 30 sec, 56°C for 40 sec, and 72°C for 30 sec; and 72°C for 35 min and 4°C until the samples were removed from the thermal cycler. The positive control (1–3 ng of male DNA, ATCC 45514) and the negative control (1–3 ng of female DNA, ATCC 45510) were amplified with every batch of amplification reaction.

Typing

The amplified products were detected and separated by capillary electrophoresis using an ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Foster City, CA). An appropriate matrix in this study was established with matrix standards for the four dyes 6FAM, HEX, TAMRA, and ROX. The samples for analysis were prepared by combining 0.5 μ L of PCR product and 10.0 μ L Hi-Di formamide

containing 0.2 μ L GeneScan[®]—500(ROX) Size Standard in a 200 μ L tube, followed by denaturation at 95°C for 3 min using a 9600 Thermal Cycler (Perkin-Elmer, Applied Biosystems). Fragment sizes were determined automatically using the GeneScan Analysis Software V.3.7 and by comparison with allelic ladders. Alleles were designated according to the recommendation of the DNA commission of the International Society of Forensic Genetics (2).

Results and Analysis

Data of population genetics and forensic science were analyzed according to Hou's method (3). The allelic frequencies and haplotype distribution of the nine loci in the groups studied are given in Tables 1 and 2. The most common allele for each locus was DYS434 allele 10; Y-GATA-A10, 13; DYS438, 10; DYS439, 12; DYS444, 12; DYS448, 21; DYS456, 14; DYS531, 10; and DYS557, 16. Almost all Y-STRs reached a gene diversity value of >0.5, except for DYS434 (0.2506) and DYS531 (0.4601). Most males share allele 11 of DYS531, and the frequency of allele 11 is 0.7089. A total of 105 haplotypes were observed in 120 individuals, of which 97 haplotypes were unique. The most common haplotype was 10, 11, 15, 11, 23, 12, 10, 23, 12 (DYS434, DYS531, DYS456, GATA-A10, DYS557, DYS444, DYS438, DYS448, DYS439). Our data showed that differences in allele frequency at loci DYS434, DYS438, DYS439, and DYS456, compared with those of YCC Asian cell lines, can be enormous. Therefore, establishing databases of haplotypes in different populations is a requirement for forensic biostatistic calculation. The combination of the allelic states of the nine Y-STR loci allowed us to construct highly informative haplotypes. The cumulative haplotype diversity was calculated to be 0.9968; the discrimination capacity of haplotypes was 0.9815. The data generated revealed that the nine Y-chromosome haplotype is highly polymorphic and discriminative in the Chengdu, southwest China population.

The complete data can be accessed at <http://fayi.med.stu.edu.cn/y-str.doc>

¹Department of Forensic Medicine, Shantou University Medical College, 22 Xin Ling Road, Shantou, Guangdong 515031, China.

²Institute of Forensic Medicine, Sichuan University (West China University of Medical Sciences), Chengdu 610041, Sichuan, China.

³Department of Forensic Medicine, Guangdong Medical College, No. 2, Wenming Donglu, Xiashan District, Zhanjiang, Guangdong 524023, China.

TABLE 1—Allele frequencies and gene diversity values at nine Y-STRs in the Chengdu Han population ($n = 120$).

Allele	DYS434	GATA-A10	DYS438	DYS439	DYS531	DYS557	DYS448	DYS456	DYS444
9	0.0594		0.0583		0.0432				
10	0.7345		0.6500	0.1250	0.3998				0.0333
11	0.1056	0.0346	0.2500	0.1667	0.2170			0.0103	0.2500
12	0.1005	0.3254	0.0417	0.4000	0.3206			0.0103	0.3083
13		0.3610		0.2418	0.0194			0.2507	0.2167
14		0.2404		0.0665				0.4029	0.1500
15		0.0386				0.0103		0.1960	0.0417
16						0.1879		0.0563	
17						0.3022		0.0563	
18						0.2432		0.0172	
19						0.1044			
20						0.1044	0.0103		
21						0.0373	0.3292		
22						0.0103	0.3189		
23							0.2798		
24							0.0206		
25							0.0309		
26							0.0103		
h^a	0.4394	0.7092	0.5141	0.7399	0.6938	0.7975	0.7560	0.7357	0.7766

 h^a , gene diversity value.TABLE 2—Distribution of nine Y-STRs haplotypes in the Chengdu Han population ($n = 120$).

Haplotype	DYS434	DYS531	DYS456	Y-GATA-A10	DYS557	DYS444	DYS438	DYS448	DYS439	n	$f\%$
1	10	11	15	11	17	12	10	23	12	5	4.17
2	10	11	16	14	17	11	10	22	12	3	2.50
3	10	11	15	11	17	14	10	23	12	3	2.50
4	10	11	16	15	17	12	10	23	12	3	2.50
5	10	9	15	11	17	12	10	23	12	3	2.50
6	11	13	17	11	19	12	10	23	10	2	1.67
7	11	12	16	14	17	13	10	20	11	2	1.67
8	10	11	14	13	18	13	10	22	12	2	1.67
9	10	11	12	15	17	12	10	23	12	1	0.83
10	10	11	13	12	18	11	10	23	14	1	0.83
11	10	10	12	11	17	14	10	21	13	1	0.83
12	9	11	15	12	17	12	10	22	12	1	0.83
13	12	12	19	11	15	12	10	23	13	1	0.83
14	12	12	17	13	16	13	11	25	13	1	0.83
15	12	11	16	11	18	13	11	25	13	1	0.83
16	12	11	15	15	21	12	10	23	10	1	0.83
17	12	11	15	11	18	15	9	23	11	1	0.83
18	12	11	15	13	18	10	10	23	13	1	0.83
19	12	10	17	11	15	12	10	24	12	1	0.83
20	12	10	15	14	19	11	10	21	10	1	0.83
21	12	10	15	12	17	12	11	23	11	1	0.83
22	12	10	15	13	19	12	9	24	13	1	0.83
23	12	10	15	12	21	12	11	25	13	1	0.83
24	12	10	18	12	20	12	12	24	12	1	0.83
25	12	9	16	13	16	13	10	23	13	1	0.83
26	12	9	16	15	18	14	10	23	12	1	0.83
27	11	13	15	15	17	13	10	22	13	1	0.83
28	11	12	15	12	15	13	10	25	12	1	0.83
29	11	12	15	14	18	11	10	22	12	1	0.83
30	11	12	15	13	18	15	10	23	14	1	0.83
31	11	12	17	13	20	12	12	24	11	1	0.83
32	11	12	17	11	20	13	9	26	12	1	0.83
33	11	12	14	11	15	12	10	23	12	1	0.83
34	11	12	14	14	17	12	11	22	11	1	0.83
35	11	12	16	11	17	12	11	23	13	1	0.83
36	11	12	14	14	16	13	11	24	13	1	0.83
37	11	11	14	15	16	13	10	25	14	1	0.83
38	11	11	17	13	19	12	12	24	12	1	0.83
39	11	11	15	14	16	13	10	22	10	1	0.83
40	11	10	15	14	19	12	10	23	12	1	0.83
41	11	10	13	12	16	12	10	24	13	1	0.83
42	11	10	13	13	16	11	10	23	12	1	0.83
43	11	9	15	15	21	12	11	23	10	1	0.83
44	11	9	13	11	16	13	11	23	11	1	0.83
45	10	13	16	13	18	11	11	23	11	1	0.83
46	10	13	17	11	17	12	12	24	13	1	0.83

TABLE 2—Continued.

Haplotype	DYS434	DYS531	DYS456	Y-GATA-A10	DYS557	DYS444	DYS438	DYS448	DYS439	<i>n</i>	<i>f</i> %
47	10	12	17	14	17	10	9	21	13	1	0.83
48	10	12	16	14	17	12	10	23	12	1	0.83
49	10	12	16	14	16	10	10	21	13	1	0.83
50	10	12	16	12	16	12	10	24	11	1	0.83
51	10	12	15	14	19	11	10	22	12	1	0.83
52	10	12	16	11	17	14	10	23	12	1	0.83
53	10	12	15	12	16	12	11	21	14	1	0.83
54	10	12	15	13	17	10	11	23	13	1	0.83
55	10	12	15	13	17	13	11	23	12	1	0.83
56	10	12	16	11	16	11	12	23	13	1	0.83
57	10	11	18	13	15	13	9	22	10	1	0.83
58	10	11	18	15	17	15	10	22	12	1	0.83
59	10	11	18	14	16	12	11	21	13	1	0.83
60	10	11	17	13	16	10	10	24	11	1	0.83
61	10	11	17	12	19	12	10	24	10	1	0.83
62	10	11	16	13	21	12	10	20	11	1	0.83
63	10	11	16	13	16	12	11	23	13	1	0.83
64	10	11	16	15	15	15	9	25	12	1	0.83
65	10	11	16	14	17	10	11	21	10	1	0.83
66	10	11	16	13	21	13	10	22	14	1	0.83
67	10	11	16	12	15	12	11	23	11	1	0.83
68	10	11	16	13	16	11	10	23	13	1	0.83
69	10	11	15	15	17	12	10	23	10	1	0.83
70	10	11	15	13	18	12	11	24	14	1	0.83
71	10	11	15	14	17	12	10	23	11	1	0.83
72	10	11	15	11	16	12	11	23	11	1	0.83
73	10	11	15	15	16	10	10	21	13	1	0.83
74	10	11	15	13	16	11	10	20	13	1	0.83
75	10	11	15	13	16	12	10	23	11	1	0.83
76	10	11	15	11	15	12	10	22	10	1	0.83
77	10	11	15	13	18	12	9	23	11	1	0.83
78	10	11	15	11	20	13	11	25	13	1	0.83
79	10	11	15	15	15	13	11	22	11	1	0.83
80	10	11	15	15	18	11	11	21	10	1	0.83
81	10	11	15	14	17	12	11	26	12	1	0.83
82	10	11	15	14	16	11	10	23	14	1	0.83
83	10	11	15	13	18	13	10	21	13	1	0.83
84	10	11	15	13	16	12	10	22	10	1	0.83
85	10	11	15	13	16	13	10	22	11	1	0.83
86	10	11	15	12	16	11	10	22	13	1	0.83
87	10	11	15	11	17	12	10	25	11	1	0.83
88	10	11	14	11	22	12	10	23	12	1	0.83
89	10	11	14	12	17	10	10	22	13	1	0.83
90	10	11	13	15	16	12	10	20	12	1	0.83
91	10	11	13	15	16	12	10	21	11	1	0.83
92	10	11	12	11	18	12	10	23	12	1	0.83
93	10	10	19	12	16	12	11	22	13	1	0.83
94	10	10	14	13	20	12	11	23	12	1	0.83
95	10	10	13	13	15	15	10	22	10	1	0.83
96	10	9	19	11	19	13	11	20	13	1	0.83
97	10	9	18	12	15	13	11	23	13	1	0.83
98	10	12	16	12	17	11	11	24	13	1	0.83
99	9	11	16	13	16	13	10	22	12	1	0.83
100	9	11	16	12	16	11	10	22	10	1	0.83
101	9	10	17	13	19	10	11	23	13	1	0.83
102	9	13	14	12	17	11	11	23	12	1	0.83
103	9	11	14	13	17	11	11	24	13	1	0.83
104	9	9	14	15	16	12	11	22	12	1	0.83
105	9	10	15	11	18	13	11	23	13	1	0.83

n, number of individuals observed for each haplotype; *f*, haplotype frequency of each haplotype in 120 individuals.

References

- Walsh BS, Petzger DA, Higuchi R. Chelex-100 as medium for simple extraction of DNA for PCR-based typing from forensic material. *Biotechniques* 1991;10(4):506–13.
- Gusmao L, Butler JM, Carracedo A, et al. DNA Commission of the International Society of Forensic Genetics (ISFG): an update of the recommendations on the use of Y-STRs in forensic analysis. *Forensic Sci Int* 2006;157(2–3):187–97.
- Hou Y, Zhang J, Li Y, Wu J, Zhang S, Prize M. Allele sequence of six new Y STR loci and haplotype in the Chinese Han population. *Forensic Sci Int* 2001;118(2–3):147–52.

Additional information and reprint requests:

Meisen Shi, Ph.D.
Department of Forensic Medicine
Shantou University Medical College
Shantou Guangdong 515031
China
E-mail: shimeisen2000@yahoo.com.cn