

FOR THE RECORD

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Distribution of Haplotypes for Four Y-STR Loci in a Han Ethnic Group of Chinese Population

POPULATION: We have analyzed the distribution of haplotypes for four Y chromosome short tandem repeat (STR) loci (Y-GATA-A10, DYS531, DYS557, DYS448) among healthy male individuals ($n = 120$) in Chengdu, China.

KEYWORDS: forensic science, Y chromosome, Y-STR, Y-GATA-A10, DYS531, DYS557, DYS448, Multiplex PCR, haplotype, DNA typing, population genetics, Chengdu, China

Blood samples for database studies were obtained from 120 healthy unrelated male individuals from the Han ethnic group in Chengdu of China. The DNA was extracted by using Chelex 100 protocol as described by Walsh et al. (1). The allelic variation

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TABLE 1—Y-STR allele frequencies and gene diversities of Han ethnic group in Chengdu.

Allele	DYS531	Y-GATA-A10	DYS557	DYS448
9	0.0432			
10	0.3998			
11	0.2170	0.0346		
12	0.3206	0.3254		
13	0.0194	0.3610		
14		0.2404		
15		0.0386		
16				
17				
18				
19				
20				0.0103
21			0.0103	0.3292
22			0.1879	0.3189
23			0.3022	0.2798
24			0.2432	0.0206
25			0.1044	0.0309
26			0.1044	0.0103
27			0.0373	
28			0.0103	
Total	1.0000	1.0000	1.0000	1.0000
Gene diversity	0.6938	0.7092	0.7975	0.7160
SE	0.0116	0.0177	0.0108	0.0122

at the four Y-STR loci named as Y-GATA-A10, DYS531, DYS557 and DYS448, were screened by ABI PRISM310 Genetic Analyzer for double fluorescent system and analyzed by Geno Typer softer. Each PCR reaction were performed in a 37.5 μ L containing 2–10 ng DNA, 6.0 μ L dNTP (0.25 mmol/L, Pharmacia Biotech, Sweden), 3.75 μ L 10 \times buffer (Mg²⁺ + -free), 3.75 μ L BSA (1.6 μ g/mL), 3.0 μ L Mg²⁺ (2.25 mmol/L), Taq polymerase 0.7 μ L (5 U/ μ L, MBI), 0.22–0.3 μ M primer in a Perkin-Elmer 9600 thermocycler. Amplified fragments were detected using the ABI Prism 310 capillary electrophoresis system. A 1.0 μ L aliquot of each amplified sample was added to 10 μ L Hi-Di formamide (Applied biosystems) and 0.3 μ L of Genescan500 ROX internal lane standard. Alleles were designated according to recommendation of the International Society of Forensic Genetics (2). The gene diversities, the haplotypes diversity and the standard errors of diversity were calculated in accordance with Hou's method (3).

The complete dataset is available to any interested researcher upon request to the corresponding author, Professor Hou Yi Ping, email: rechtsme@wcums.edu.cn

References

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TABLE 2—Y-STR haplotypes of Han ethnic group in Chengdu of China ($n = 120$).

Haplotype	N	F (%)	DYS531/Y-GATA-A10/ DYS557/DYS448	Haplotype	N	F (%)	DYS531/Y-GATA-A10/ DYS557/DYS448
H1	8	6.67	11/15/23/23	H41	1	0.83	11/14/23/23
H2	5	4.17	11/11/23/23	H42	1	0.83	11/14/23/21
H3	5	4.17	11/11/23/23	H43	1	0.83	11/14/22/23
H4	4	3.33	11/11/24/23	H44	1	0.83	11/14/22/21
H5	3	2.50	11/13/22/22	H45	1	0.83	11/14/22/22
H6	3	2.50	11/14/23/22	H46	1	0.83	11/13/27/20
H7	3	2.50	11/13/22/23	H47	1	0.83	11/13/25/24
H8	3	2.50	12/13/23/23	H48	1	0.83	11/13/24/24
H9	3	2.50	12/11/23/23	H49	1	0.83	11/13/24/21
H10	3	2.50	11/12/23/22	H50	1	0.83	11/13/22/24
H11	3	2.50	9/11/23/23	H51	1	0.83	11/13/22/20
H12	2	1.66	13/11/25/23	H52	1	0.83	11/13/21/22
H13	2	1.66	12/14/25/22	H53	1	0.83	11/12/27/22
H14	2	1.66	12/14/23/21	H54	1	0.83	11/12/21/23
H15	2	1.66	12/14/23/20	H55	1	0.83	11/12/25/24
H16	2	1.66	12/13/26/24	H56	1	0.83	11/11/26/25
H17	2	1.66	12/12/22/21	H57	1	0.83	11/11/28/23
H18	2	1.66	11/12/22/22	H58	1	0.83	11/11/23/25
H19	2	1.66	11/12/24/23	H59	1	0.83	11/11/24/25
H21	2	1.66	11/13/24/22	H61	1	0.83	10/14/25/21
H22	2	1.66	11/11/21/22	H62	1	0.83	10/13/26/23
H23	2	1.66	10/11/23/21	H63	1	0.83	10/13/25/23
H24	1	0.83	13/15/23/22	H64	1	0.83	10/13/22/23
H25	1	0.83	13/13/24/23	H65	1	0.83	10/13/25/24
H26	1	0.83	13/11/23/24	H66	1	0.83	10/13/21/22
H27	1	0.83	12/12/23/24	H67	1	0.83	10/12/27/25
H28	1	0.83	12/12/22/24	H68	1	0.83	10/12/26/24
H29	1	0.83	12/12/21/25	H69	1	0.83	10/12/22/22
H30	1	0.83	12/14/22/21	H70	1	0.83	10/12/23/23
H31	1	0.83	12/11/21/23	H71	1	0.83	10/12/22/24
H32	1	0.83	12/14/24/22	H72	1	0.83	10/11/21/24
H33	1	0.83	12/11/21/23	H73	1	0.83	9/15/27/23
H34	1	0.83	11/15/27/23	H74	1	0.83	9/15/24/23
H35	1	0.83	11/15/24/21	H75	1	0.83	9/13/22/23
H36	1	0.83	11/15/22/25	H76	1	0.83	9/12/21/23
H37	1	0.83	11/15/22/21	H77	1	0.83	9/11/25/20
H38	1	0.83	11/15/21/25	H78	1	0.83	9/11/22/23
H39	1	0.83	11/15/22/20				
H40	1	0.83	11/14/23/26				
Haplotype diversity value						0.9881	
Standard errors						0.002	

n : individuals observed for each haplotype; F: frequency of each haplotype in 120 individuals.