

FOR THE RECORD

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Y-Chromosome STR Haplotypes in a Han Ethnic Group of Chinese Population

POPULATION: Chinese

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Blood samples were obtained from 120 healthy unrelated males 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 at the three Y-STR loci, named as DYS447, DYS449 and DYS450, were analyzed by PCR amplification system. Each PCR reaction was performed in a 37.5 μ L containing 2–10 ng DNA, 1 \times Taq buffer, 1.5 mM MgCl₂, 200 μ M each dNTP (Pharmacia Biotech, Sweden), 1.5 U Taq polymerase (NEB, UK), 0.3 μ M each primer in a Perkin-Elmer 9600 thermocycler (ABI, Foster City, CA). The PCR products were analyzed by horizontal non-denaturing polyacrylamide gel electrophoresis with discontinuous buffer system and visualized by silver staining (2). Alleles were designated according to recommendation of the International Society of Forensic Genetics (3). The gene diversities, the haplotypes diversity and the standard errors of diversity were calculated in accordance with Hou's method (4).

The complete dataset can be accessed at: <http://www.legalmed.org/dna/DYS449.htm>.

References

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

Allele	DYS447	DYS449	DYS450
12			0.0500
13		0.0417	0.0133
14		0.0583	0.2083
15		0.0833	0.3750
16		0.0833	0.1583
17		0.1667	0.0750
18		0.2500	
19		0.1500	
20	0.1083		
21	0.2833		
22	0.1917		
23	0.1500		
24	0.1250		
25	0.0500		
26	0.0417		
28	0.0500		
Total	1.0000	1.0000	1.0000
Gene diversity	0.8333	0.8580	0.7714
SE	0.0105	0.0089	0.0150

TABLE 2—*Y-STR haplotypes of Han ethnic group in Chengdu of China.*

Haplotype	<i>n</i>	F	DYS447	DYS449	DYS450	Haplotype	<i>n</i>	F	DYS447	DYS449	DYS450
H1	3	0.0250	20	13	18	H27	1	0.0083	22	16	17
H2	2	0.0167	20	15	15	H28	1	0.0083	22	17	14
H3	4	0.0333	20	15	18	H29	2	0.0167	23	13	16
H4	1	0.0083	20	17	13	H30	3	0.0250	23	14	18
H5	3	0.0250	20	17	15	H31	3	0.0250	23	14	21
H6	1	0.0083	21	12	20	H32	4	0.0333	23	15	16
H7	2	0.0167	21	13	14	H33	6	0.0500	23	15	18
H8	2	0.0167	21	13	17	H34	1	0.0083	24	12	13
H9	1	0.0083	21	13	18	H35	3	0.0250	24	13	19
H10	3	0.0250	21	14	16	H36	7	0.0583	24	14	20
H11	2	0.0167	21	14	17	H37	1	0.0083	24	15	18
H12	2	0.0167	21	15	13	H38	2	0.0167	24	15	19
H13	1	0.0083	21	15	15	H39	1	0.0083	24	17	19
H14	4	0.0333	21	15	19	H40	1	0.0083	25	14	13
H15	5	0.0417	21	15	20	H41	2	0.0167	25	14	20
H16	2	0.0167	21	16	15	H42	1	0.0083	25	15	18
H17	6	0.0500	21	16	17	H43	2	0.0167	25	17	18
H18	2	0.0167	21	16	18	H44	2	0.0167	26	14	15
H19	1	0.0083	21	16	19	H45	3	0.0250	26	16	21
H20	2	0.0167	22	12	18	H46	3	0.0250	28	15	17
H21	2	0.0167	22	12	19	H47	1	0.0083	28	15	18
H22	3	0.0250	22	13	18	H48	1	0.0083	28	16	16
H23	2	0.0167	22	14	19	H49	1	0.0083	28	17	18
H24	6	0.0500	22	15	17	HVD		0.9801			
H25	3	0.0250	22	15	19	SE		0.0019			
H26	3	0.0250	22	16	14						

n: individuals observed for each haplotype; F: frequency for each haplotype in 120 individuals; HVD: haplotype diversity value; SE: standard errors of diversity.