

FOR THE RECORD

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Genetic Analysis for Y Chromosome Short Tandem Repeat Haplotypes of Chinese Han Population Residing in the Ningxia Province of China

POPULATION: One hundred and one unrelated, autochthonous healthy males of the Chinese Han population living in Yongning county of the Ningxia Hui Autonomous Region of China.

KEYWORDS: forensic science, DNA typing, genetic analysis, Y chromosome STR haplotypes, Chinese Han population, living in Yongning county of the Ningxia Hui Autonomous Region of China, population genetics, Y-PLEXTM 12 kit, China, DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS438, DYS439, DYS385a,b

Whole-blood samples were obtained by venipuncture and collected into ethylenediaminetetraacetic acid (EDTA) tubes. Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. (1). Eleven Y-chromosomal short tandem repeats (STRs) loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS438, DYS439, and DYS385a,b) were performed in a fluorescence-based multiplex reaction using the Y-PLEXTM 12 kit (Reliagene Technologies Inc., New Orleans, LA). The amplification reactions of 10 μ L in total contained 4.0 μ L of 2.5 $\times$ Y-PLEXTM 12 Primer Mix, 0.20 μ L of AmpliTaq Gold DNA Polymerase (Applied Biosystems, Foster City, CA) (5 U/ μ L), 3.8 μ L of deionized water, and 2.0 μ L of Genomic DNA (c. 1 ng). Thermal cycling conditions were conducted according to the manufacturer's kit protocols using GeneAmp PCR system 9700 (Applied Biosystems) (2). Detection and genotyping of all

polymerase chain reaction (PCR) products were accomplished using an ABI 3100 DNA Genetic Analyzer (Applied Biosystems). Allele designations were determined by comparison of the sample PCR fragments, together with the allelic ladders provided with the kit using GeneScan and Y12-Typer3100v 2.0 Macros (Reliagene Technologies Inc.).

Quality control was adhered to laboratory internal control standards and kit controls. Haplotype and allele frequencies were estimated by the direct counting method. Haplotype and gene diversities were estimated according to Nei (3). A comparative analysis between these haplotype data and previously published data was carried out by the method of a pairwise differentiation test as described by Chen and Huang (4) using SPSS11.5 (SPSS Inc., Chicago, IL). See Tables 1 and 2 for results. As shown in Table 1, a total of 97 haplotypes were identified in the 11 Y-STR loci, among which 93 were unique, while four occurred more than once. The overall haplotype diversity for the 11 Y-STRs loci was 0.9893, and the discrimination capacity was 0.9992. As shown in Table 2, 47 alleles (nine STR loci) and 38 phenotypes (DYS385a,b) were detected in Chinese Han population, with the allele frequencies ranging from 0.0099 to 0.7723. The gene diversity value of all 11 Y-STR loci ranged from a minimum of 0.3739 for the DYS438 locus to a maximum of 0.9698 for the DYS385a,b loci. A comparative analysis between our data and previously published data for the same set of Y-STR loci has been made using the statistical method of the pairwise differentiation test. The comparative results showed that the Chinese Han population in the Ningxia province of China has significant differences from the Tunisian population ($p < 0.001$), (5) and the Basque population ($p < 0.001$) (6). There were no significant differences between the studied population and some neighboring populations including Chinese Mongol (7), Uigur (8), Ewenki (9), Yi population (10),

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TABLE 1—Y-STR haplotypes in 101 unrelated healthy males of Chinese Han population.

Haplotypes	<i>n</i>	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	DYS385a,b
H1	1	13	12	29	24	10	11	13	10	12	13,13
H2	1	13	12	29	25	12	12	12	10	12	12,18
H3	1	13	14	29	24	9	15	14	11	11	15,20
H4	1	13	14	30	24	9	14	14	12	11	15,21
H5	1	14	12	27	24	10	13	12	11	13	12,17
H6	1	14	12	27	24	10	14	12	11	11	13,18
H7	1	14	12	28	23	10	14	12	11	11	13,18
H8	1	14	12	28	24	10	11	13	10	10	14,18
H9	2	14	12	28	24	11	14	12	11	12	13,19
H10	1	14	12	29	22	10	11	14	10	11	14,15
H11	1	14	12	29	23	11	12	12	10	12	13,17
H12	1	14	12	31	23	10	11	12	10	12	11,18
H13	1	14	13	28	22	11	14	12	11	12	13,13
H14	2	14	13	29	23	11	13	14	10	10	11,12
H15	1	14	13	29	24	10	11	12	10	10	14,14
H16	1	14	13	29	24	10	14	12	11	11	13,19
H17	1	14	13	29	24	11	14	13	10	10	11,12
H18	1	14	13	30	23	11	14	13	11	11	12,12
H19	1	14	13	30	24	10	13	12	11	13	13,13
H20	1	14	13	31	23	10	14	14	10	10	11,13
H21	1	14	14	29	23	11	13	14	10	10	11,12
H22	1	14	14	30	23	10	14	13	10	11	11,13
H23	1	14	14	30	23	10	14	13	10	12	11,12
H24	1	14	14	30	23	10	14	13	10	13	11,12
H25	1	14	14	30	23	10	14	14	10	10	11,13
H26	1	14	14	30	23	11	14	13	10	10	11,13
H27	1	14	14	31	22	10	11	12	10	11	11,18
H28	1	14	14	31	22	10	13	12	10	10	13,13
H29	1	14	14	31	23	10	11	12	10	12	11,18
H30	1	14	14	31	23	10	14	13	11	11	11,12
H31	1	14	14	32	23	10	11	12	10	12	11,18
H32	1	15	12	27	23	10	12	13	10	12	12,16
H33	1	15	12	27	23	10	12	13	11	12	13,13
H34	1	15	12	28	23	10	12	12	10	11	11,16
H35	1	15	12	28	23	10	12	12	10	12	12,17
H36	1	15	12	28	23	10	13	12	10	12	12,17
H37	1	15	12	28	23	10	13	12	10	12	14,19
H38	2	15	12	28	23	11	14	13	10	11	13,14
H39	1	15	12	28	23	11	14	14	10	11	13,13
H40	1	15	12	28	24	10	12	12	10	11	13,15
H41	1	15	12	28	24	10	13	12	9	10	12,18
H42	1	15	12	28	24	10	14	12	10	11	14,18
H43	1	15	12	28	24	10	16	12	11	13	12,18
H44	1	15	12	28	24	11	10	13	10	11	13,14
H45	1	15	12	28	24	11	13	12	10	13	12,19
H46	1	15	12	28	24	11	14	13	10	11	12,13
H47	1	15	12	28	24	11	14	13	10	11	13,14
H48	1	15	12	29	23	10	12	12	10	12	12,17
H49	1	15	12	29	23	10	13	12	10	12	12,19
H50	1	15	12	29	23	11	14	13	10	11	13,14
H51	1	15	12	29	24	10	10	12	10	11	16,17
H52	1	15	12	29	24	10	13	12	9	10	12,13
H53	1	15	12	29	24	10	13	12	10	11	13,19
H54	1	15	12	29	24	11	13	12	10	13	11,20
H55	1	15	12	29	24	11	14	13	10	11	13,13
H56	1	15	12	29	25	10	13	12	10	11	13,22
H57	1	15	12	30	23	10	13	12	10	12	12,19
H58	1	15	13	28	24	11	14	12	10	13	13,21
H59	1	15	13	28	25	9	14	14	10	11	15,18
H60	1	15	13	29	23	10	11	15	10	11	11,19
H61	1	15	13	29	23	10	15	13	10	12	11,13
H62	1	15	13	29	24	10	11	13	11	12	12,14
H63	1	15	13	29	24	10	11	14	10	11	12,12
H64	1	15	13	29	26	11	13	14	10	12	13,20
H65	1	15	13	30	23	10	11	15	10	12	11,20
H66	1	15	13	30	23	10	16	14	10	11	11,12
H67	1	15	13	30	24	10	11	13	11	12	12,15
H68	1	15	13	30	26	10	13	12	10	12	13,19
H69	1	15	13	30	26	10	13	14	10	12	13,20
H70	1	15	13	31	23	10	13	12	10	12	12,20
H71	1	15	14	30	24	10	11	13	11	11	12,14
H72	1	15	14	30	25	10	13	12	10	12	13,17

TABLE 1—Continued.

Haplotypes	<i>n</i>	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	DYS385a,b
H73	1	15	14	30	25	10	13	14	10	11	12,18
H74	1	15	15	31	25	10	7	13	11	14	11,11
H75	1	15	15	33	24	10	13	14	9	12	12,17
H76	1	16	12	27	25	9	15	12	10	12	12,12
H77	1	16	12	27	25	10	13	12	10	12	12,21
H78	1	16	12	28	23	10	13	12	10	13	12,14
H79	1	16	12	28	25	10	13	12	10	13	13,13
H80	1	16	12	28	25	10	13	12	10	13	13,17
H81	2	16	12	28	25	11	13	12	10	13	12,15
H82	1	16	12	30	22	10	12	14	10	12	12,14
H83	1	16	13	29	23	10	11	14	10	11	11,17
H84	1	16	13	29	23	10	13	14	10	13	12,20
H85	1	16	13	29	24	10	13	12	9	10	13,18
H86	1	16	14	30	23	10	11	14	10	12	11,19
H87	1	16	14	30	24	10	13	14	10	12	13,19
H88	1	16	14	30	25	10	13	15	10	11	12,17
H89	1	17	12	27	25	11	13	12	10	14	13,21
H90	1	17	12	28	24	10	13	12	10	11	12,18
H91	1	17	12	28	24	10	13	12	10	11	17,18
H92	1	17	12	28	24	10	13	12	10	11	17,19
H93	1	17	12	29	24	10	13	12	11	11	13,18
H94	1	17	13	29	24	9	13	12	10	13	11,12
H95	1	17	13	29	24	10	13	14	10	12	13,17
H96	1	17	13	30	24	10	13	12	10	12	12,19
H97	1	18	13	29	25	10	13	12	10	11	14,17

n, number of individuals observed for each haplotype; STR, short tandem repeat.

TABLE 2—Allele frequencies and gene diversity (GD) at 11 Y-chromosomal short tandem repeats (STRs) loci of Chinese Han population.

Allele	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	Phenotype	DYS385a,b	Phenotype	DYS385a,b
7						0.0099				11,11	0.0099	13,19	0.0594
9					0.0495			0.0396		11,12	0.0891	13,20	0.0198
10					0.6931	0.0198		0.7723	0.1287	11,13	0.0396	13,21	0.0198
11					0.2475	0.1584		0.1782	0.3663	11,16	0.0099	13,22	0.0099
12		0.5050			0.0099	0.0891	0.5248	0.0099	0.3465	11,17	0.0099	14,14	0.0099
13	0.0396	0.2871				0.4158	0.2277		0.1386	11,18	0.0396	14,15	0.0099
14	0.2871	0.1881				0.2574	0.2178		0.0198	11,19	0.0198	14,17	0.0099
15	0.4455	0.0198				0.0297	0.0297			11,20	0.0198	14,18	0.0198
16	0.1386					0.0198				12,12	0.0297	14,19	0.0099
17	0.0792									12,13	0.0198	15,18	0.0099
18	0.0099									12,14	0.0396	15,20	0.0099
22				0.0495						12,15	0.0297	15,21	0.0099
23				0.3762						12,16	0.0099	16,17	0.0099
24				0.3960						12,17	0.0594	17,18	0.0099
25				0.1485						12,18	0.0495	17,19	0.0099
26				0.0297						12,19	0.0396		
27			0.0693							12,20	0.0198		
28			0.2970							12,21	0.0099		
29			0.3168							13,13	0.0792		
30			0.2178							13,14	0.0495		
31			0.0792							13,15	0.0099		
32			0.0099							13,17	0.0396		
33			0.0099							13,18	0.0396		
GD	0.6988	0.6331	0.7602	0.6829	0.4604	0.7333	0.6307	0.3739	0.7166				0.9698

Han population in Beijing (11), Han population in Tianjin (12), Japanese (13), and southern populations from Korea (14).

The complete dataset is available via electronic mail from the corresponding author: Liuyao2002cn@yahoo.com.cn or the first author: zhubofeng7372@126.com or dengyj@genomics.org.cn

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