

## FOR THE RECORD

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# Genetic Characteristics of Three New Y-STRs: DYS631, DYS634 and DYS635 in a Chinese Population

**POPULATION:** Han in eastern China

**KEYWORDS:** forensic science, DNA typing, Y-chromosome, short tandem repeats, eastern Chinese Han population, population genetics, DYS631, DYS634, DYS635

EDTA anticoagulated peripheral blood or buccal swabs for this study were drawn randomly from 79 Han-ethnic male individuals representing various geographical counties in eastern China, with their consent. Ethnic origin was determined by self-declaration.

Additionally, 20 female EDTA-blood specimens were collected from the blood banks in Suzhou, Jiangsu province, China. Genomic DNA was extracted from whole blood samples using the chelex extraction procedure (1).

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The primers of the three Y-STR loci DYS631, DYS634, and DYS635 were synthesized by Life Technologies Inc. according to the GDB primer sequence which were shown in Table 1. PCR was performed using 1–30 ng of genomic DNA in a 37.5 μL final reaction volume. In the PCR protocol, the DNA was initially denatured

TABLE 1—Locus designations and PCR primers for the three Y-STRs.

Locus	GenBank Accession ID	Motif	Primer	Sequences
DYS631	GDB:11510467	AAAT	Y4C61F Y4C61R	5' CACTCCAGCCTCGGAGATAG 5' GCGCTCTGTGGACATTATCA
DYS634	GDB: 11510473	AAGG	Y4C89F Y4C89R	5' TCAGAAGCATGCTAGAACCCTA 5' TTGCTCCTTACAGAAGAGGTGA
DYS635	GDB: 11510475	ATAG	Y4C97F Y4C97R	5' ACCAGCCCAAATATCCATCA 5' TGAATGCTCTCTTGGCTTC

TABLE 2—The allele sequences for the three Y-STRs.

DYS631	7	P1...(AAAT)3ACAT(AAAT)7...P2
	8	P1...(AAAT)3ACAT(AAAT)8...P2
	9	P1...(AAAT)3ACAT(AAAT)9...P2
	10	P1...(AAAT)3ACAT(AAAT)10...P2
DYS634	11	P1...(AAGG)6-AAGAAAGGAAAAG-(AAGG)5-...-P2
	12	P1...(AAGG)6-AAGAAAGGAAAAG-(AAGG)6-...-P2
	13	P1...(AAGG)7-AAGAAAGGAAAAG-(AAGG)6-...-P2
	14	P1...(AAGG)8-AAGAAAGGAAAAG-(AAGG)6-...-P2
	15	P1...(AAGG)9-AAGAAAGGAAAAG-(AAGG)6-...-P2
DYS635	9	P1...(ATAG)9-(ATAC)2-(ATAG)2-(ATAC)2-(ATAG)4-...-P2
	10	P1...(ATAG)10-(ATAC)2-(ATAG)2-(ATAC)2-(ATAG)4-...-P2
	11	P1...(ATAG)11-(ATAC)2-(ATAG)2-(ATAC)2-(ATAG)4-...-P2
	12	P1...(ATAG)12-(ATAC)2-(ATAG)2-(ATAC)2-(ATAG)4-...-P2
	13	P1...(ATAG)13-(ATAC)2-(ATAG)2-(ATAC)2-(ATAG)4-...-P2
	14	P1...(ATAG)14-(ATAC)2-(ATAG)2-(ATAC)2-(ATAG)4-...-P2
15	P1...(ATAG)15-(ATAC)2-(ATAG)2-(ATAC)2-(ATAG)4-...-P2	

TABLE 3—Allele frequencies of three Y-STRs loci in a Chinese population.

Locus	Allele	Frequency	Gene Diversity	Standard Error
DYS631	7	0.013	0.418	0.039
	8	0.038		
	9	0.734		
	10	0.215		
DYS634	11	0.013	0.459	0.045
	12	0.076		
	13	0.722		
	14	0.063		
	15	0.127		
DYS635	9	0.165	0.809	0.012
	10	0.253		
	11	0.278		
	12	0.152		
	13	0.076		
	14	0.063		
	15	0.013		

at 94°C for 5 min. This was followed with 94°C for 50 s, 58°C for 50 s and 72°C for 30 s. A total of 35 cycles was carried out in an Eppendorf Mastercycler gradient system. The PCR products were analyzed by non-denaturing polyacrylamide gel electrophoresis and visualized by silver staining (2). PCR products were eluted from the gels and purified before sequencing. An example of each allele was sequenced on an ABI 377 automated sequencer using Dye Terminator Cycle Sequencing Kit (PE Applied Biosystems, USA). The detailed allele sequences were shown in Table 2.

During the genotyping procedure, no PCR products were found for all the 20 female specimens at the three Y-STR loci that indicated the male specificity of the three Y-chromosome STR loci we studied. Allele determination were carried out by comparison with a sequenced human allele ladder, which was made in-house and contained all the alleles found in this study. Allele designation was established following the recommendations of the DNA commission of the ISFH (3). The allele frequencies were calculated by counting method. The gene diversity, haplotype diversity as well as the stand error (S.E.) for the three Y-STRs were calculated according the Hou's method (4).

The three loci analyzed are all tetranucleotide repeat shown in Table 1. Table 3 shows the allele frequencies and gene diversity values for all three Y-specific STR loci in a Chinese population. Four alleles at *DYS631*, five alleles at *DYS634* and seven alleles at *DYS635* were observed in our population sample. The distribution of haplotypes in the Chinese Han population is shown in Table 4. A total of 29 different haplotypes was observed in 79 males. The haplotype diversity for all three Y-specific STR loci in Chinese population was calculated to be 93.0% and the S. E. was calculated to be 0.95%.

The complete data can be obtained from the authors on request to: yuzhengao@suda.edu.cn

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TABLE 4—Haplotype assembling by three Y-specific STRs in a Chinese population.

Haplotype	Locus			Number	Haplotype Frequency (%)
	DYS631	DYS634	DYS635		
H1	9	14	12	1	1.27
H2	9	13	9	10	12.7
H3	9	13	12	6	7.59
H4	9	13	11	9	11.4
H5	9	12	11	3	3.80
H6	9	13	13	3	3.80
H7	9	14	11	1	1.27
H8	9	14	14	1	1.27
H9	9	13	10	14	17.7
H10	8	13	10	3	3.80
H11	10	15	11	6	7.59
H12	10	13	9	2	2.53
H13	10	14	12	1	1.27
H14	9	12	13	2	2.53
H15	9	14	9	1	1.27
H16	10	15	10	1	1.27
H17	10	13	12	2	2.53
H18	10	13	11	1	1.27
H19	9	15	12	1	1.27
H20	9	11	11	1	1.27
H21	9	13	14	2	2.53
H22	9	12	14	1	1.27
H23	10	13	10	1	1.27
H24	10	15	12	1	1.27
H25	10	13	13	1	1.27
H26	9	13	15	1	1.27
H27	7	13	10	1	1.27
H28	9	15	11	1	1.27
H29	10	13	14	1	1.27
Total	...	...	...	79	1.00