

# Haplotype distribution of four new Y-STRs: DYS630, DYS631, DYS634 and DYS635 in a Chinese population

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**Abstract.** In this study, we analyzed four new Y-STR loci, DYS630, DYS631, DYS634 and DYS635, investigated haplotype distributions of these Y-STR loci in a Chinese Han population (eastern China) and sequenced alleles of the four loci for clarifying the structure. DYS630, DYS631 and DYS635 were found to be simple repeat systems, while DYS634 was complex repeat systems. The gene diversities of DYS630, DYS631, DYS634 and DYS635 were 0.797, 0.418, 0.459 and 0.809, respectively. A total of 50 different haplotypes was observed in 79 males. The haplotype diversity for all the four Y-specific STR loci in Chinese population was calculated to be 98.3% and the stand error (S.E) was calculated to be 0.3%. The results indicate that these four loci are useful Y-linked markers for forensic applications. © 2005 Elsevier B.V. All rights reserved.

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## 1. Introduction

Because Y-specific markers are haploidly inherited with a paternal lineage and these properties make Y-STRs a powerful tool for analyzing mixed stains and kinship testing of paternal lines relative to forensic science [1], polymorphic markers on the Y chromosome have become hotspots of forensic DNA analysis. However, some Y-STR loci show poor discrimination power, so it is necessary to develop more informative Y-STR loci. We chose a new set of Y-STR loci from GDB, which were named as DYS630, DYS631,

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Table 1  
Allele frequencies of four Y-STR loci in a Chinese population

Number	Haplotype				Number	Frequency (%)
	DYS630	DYS631	DYS634	DYS635		
1	16	9	14	12	1	1.27
2	19	9	13	9	1	1.27
3	15	9	13	12	1	1.27
4	18	9	13	11	2	2.53
5	18	9	12	11	1	1.27
6	17	9	13	11	3	3.80
7	19	9	12	11	1	1.27
8	18	9	13	13	1	1.27
9	19	9	14	11	1	1.27
10	16	9	14	14	1	1.27
11	19	9	13	10	2	2.53
12	18	8	13	10	1	1.27
13	15	10	15	11	1	1.27
14	17	9	13	12	3	3.80
15	15	9	13	11	2	2.53
16	18	10	13	9	2	2.53
17	18	9	13	9	4	5.06
18	18	10	14	12	1	1.27
19	18	9	13	10	2	2.53
20	18	9	12	13	2	2.53
21	17	9	13	10	7	8.86
22	19	9	14	9	1	1.27
23	16	10	15	10	1	1.27
24	16	10	15	11	3	3.80
25	18	10	15	11	1	1.27
26	17	9	13	13	1	1.27
27	17	9	13	9	3	3.80
28	19	9	13	13	1	1.27
29	16	9	13	12	2	2.53
30	15	10	13	12	1	1.27
31	17	8	13	10	2	2.53
32	16	9	13	9	2	2.53
33	17	10	13	11	1	1.27
34	20	9	13	10	1	1.27
35	17	9	12	11	1	1.27
36	14	10	15	11	1	1.27
37	16	9	13	11	2	2.53
38	15	9	15	12	1	1.27
39	17	9	11	11	1	1.27
40	19	9	13	14	2	2.53
41	19	9	12	14	1	1.27
42	16	10	13	10	1	1.27
43	15	10	15	12	1	1.27
44	16	10	13	13	1	1.27
45	17	9	13	15	1	1.27
46	16	9	13	10	2	2.53
47	16	7	13	10	1	1.27
48	17	9	15	11	1	1.27

(continued on next page)

Table 1 (continued)

Number	Haplotype				Number	Frequency (%)
	DYS630	DYS631	DYS634	DYS635		
49	15	10	13	14	1	1.27
50	20	10	13	12	1	1.27
Total					79	1.00

DYS634 and DYS635, analyzed allelic sequences of four Y-STR loci and investigated haplotype distributions for the four loci in a Chinese Han population.

## 2. Materials and methods

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, under 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 [2]. PCR, genotyping and sequencing method were performed as described previously [3].

Allele determination was carried out by comparison with a sequenced human allele ladder, which was made in-house. Allele designation was established following the recommendations of the DNA commission of the ISFH [4]. The allele frequencies were calculated by counting method. The gene diversity, haplotype diversity, as well as the stand error (S.E.) for the four Y-STRs, were calculated according to Hou's method [5].

## 3. Results and discussion

During the genotyping procedure, no PCR products were found for all the 20 female specimens at the four Y-STR loci which indicated the male specificity of the four Y-chromosome STR loci. A single band was observed for each male sample showing that these are single-copy Y-STR loci. DYS630, DYS631 and DYS635 were found to be simple repeat systems, while DYS634 was a complex repeat system. The gene diversities of DYS630, DYS631, DYS634 and DYS635 were 0.797, 0.418, 0.459 and 0.809, respectively. A total of 50 different haplotypes was observed in 79 males (Table 1). The haplotype diversity for all the four Y-specific STR loci in Chinese population was calculated to be 98.3% and the stand error (S.E) was calculated to be 0.3%. The results indicate that these four loci are useful Y-linked markers for forensic applications.

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