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Characterization of eight Y-STR loci and haplotypes in a Chinese Han population

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Abstract In this study we analyzed the eight Y-STR loci, DYS443, DYS444, DYS448, DYS453, DYS455, DYS456, DYS457 (DYS437) and DYS458, investigated haplotype distributions of these Y-STR loci in a Chinese Han population, and sequenced alleles of the eight loci for clarifying the structure. Extracted DNA was amplified by PCR and the PCR products were analyzed by non-denaturing horizontal polyacrylamide gel electrophoresis with a discontinuous buffer system. Alleles were sequenced on an ABI 3700 using a Dye Terminator Cycle sequencing kit. DYS443, DYS453, DYS455 and DYS456 were found to be simple repeat systems, while DYS444, DYS448, DYS457 (DYS437) and DYS458 were complex repeat systems. The gene diversities of DYS443, DYS444, DYS448, DYS453, DYS455, DYS456, DYS457 (DYS437) and DYS458 were 0.7742, 0.7671, 0.7453, 0.3545, 0.0549, 0.6988, 0.6148 and 0.8213, respectively. The haplotype diversity for 8 Y-STR loci was 0.9996, and the discrimination capacity was 0.9815. The results indicate that these eight loci are useful Y-linked markers for forensic applications.

Keywords Y chromosome · STRs · Sequence · Haplotypes · Chinese Han population

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Introduction

STR analysis is now a powerful tool for forensic applications (Shimada et al. 2002) and polymorphic markers on the Y chromosome are hotspots of forensic DNA analysis. Y-specific markers are haploidly inherited with a paternal lineage (Jobling and Tyler-Smith 1995) and these properties make Y-STRs a key tool for analyzing mixed stains and kinship testing of paternal lines relative to forensic science. Panels of Y-STR loci are recommended for forensic applications (Jobling et al.1997; White et al. 1999; Ayub et al. 2000; Hou et al. 2001a; Iida et al. 2001, 2002; Butler et al. 2002; Bosch et al. 2002; Redd et al. 2002). 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, which were named as DYS443, DYS444, DYS448, DYS453, DYS455, DYS456, DYS457 and DYS458 (Ayub et al. 2000; Hou et al. 2001a; Iida et al. 2001, 2002; Butler et al. 2002; Redd et al. 2002; http://www.gdb.org), to improve the discrimination power of Y-STR haplotypes for forensic applications. DYS457 is also known as DYS437. DYS443, DYS444, DYS453, DYS455, DYS456, DYS457 and DYS458 are tetranucleotide repeat STR loci, and DYS448 is a hexanucleotide repeat STR locus. We analyzed allelic sequences of eight loci, and investigated haplotype distributions for the eight Y-STR loci in a Chinese Han population.

Materials and methods

Population sample

Blood samples were collected from 108 unrelated male volunteers donating for a blood bank (Chengdu, China), ethnic origin was determined by self-declaration. Also, blood samples were collected from 20 unrelated female volunteers in Chengdu (China), and 10 samples of bloodstains from males.

Experimental details

The Chelex method was utilized to extract DNA (Singer-Sam et al. 1989) which was quantified using a primate-specific alpha-satellite

Table 1 Sequences of primers of eight Y-STR loci

Locus	GDB Accession ID	Sequence
DYS443	GDB: 10807127	L: tctttagctttttgcagccc R: tcattggccacctgcatta
DYS444	GDB: 10807128	L: tttctctcttcccactttaaccag R: ctcacgttgttcaagggtca
DYS448	GDB: 10877524	L23: tcttccttacgtgaatttcctc U22: tgtcaaagagcttcaatggaga
DYS453	GDB: 11498119	P1: gggtaacagaacaagacagt P2: ctaaaagtatggatattcttc
DYS455	GDB:11498125	P1: ggggtggaaacgagtgtt P2: atctgagccgagccgagagaatgata
DYS456	GDB: 11498127	P1: cccatcaactcagcccaaaac P2: ggaccttgtgataatgtaagata
DYS457	GDB: 11498129	P1: tgcagcctcaatttcctggt P2: tatagatagatagataaccacag
DYS458	GDB: 11498131	P1: agcaacaggaatgaaactccaat P2: ccaccacgcccaccctcc

probe assay (Waye et al.1989). Primers of DYS448, DYS453, DYS455, DYS456, DYS457 and DYS458 were retrieved from the GDB (http://www.gdb.org, Table 1), while primers of DYS443 and DYS444 were redesigned by us using Primer3 software (http: // www.genome.wi.mit.edu/cgi-bin/primer/). Each PCR reaction contained 2–10 ng DNA, 1×Taq buffer, 1.5 mM $MgCl_2$, 200 µM each dNTP (Pharmacia Biotech), 1.5 U Taq polymerase (Promega) and 0.3 µM each primer. The reaction volume was 37.5 µl. PCR amplifications were performed in a thermocycler (Perkin-Elmer 9600) with denaturing for 2 min at 94°C, followed by 30 cycles of 94°C for 50 s, 55°C for 50 s and 72°C for 25 s. PCR products were analyzed by utilizing horizontal non-denaturing polyacrylamide gel electrophoresis with a discontinuous buffer system (Allen et al.1989; Hou et al. 1994), and gels were stained with silver. The allelic ladders for STR typing were made in house, constructed by mixing PCR products with different genotypes for each locus. For the analysis of allelic sequences, PCR products of each allele were recovered from the gels, and cloned into the plasmid vector by using the pGEM-T Easy Vector system I kit in accordance with the technical manual (Promega), and for each allele two clones were chosen to be exactly sequenced on both strands. Each cloned allele was sequenced on an automated sequencer (ABI Model 3700).

Nomenclature

Alleles were designated according to the recommendations of the International Society of Forensic Genetics (formerly International Society of Forensic Haemogenetics) (Bär et al. 1994; Gill et al. 2001). The nomenclature of alleles applied for these loci, except for DYS444, DYS448 and DYS458, also followed the published descriptions (Butler et al. 2002; Iida et al. 2002; Redd et al. 2002).

Statistical calculations

The gene diversity, the haplotype diversity and the standard error of diversity were calculated in accordance with the method of Hou et al. (2001a). The discrimination capacity was calculated according to published methods (Shin et al. 2001; Tsai et al. 2002).

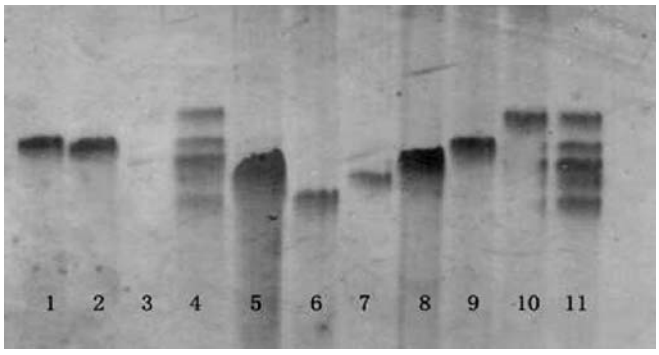

Fig. 1 Electropherogram of DYS453. The top is the anode, and the bottom is the cathode. *Lanes* 4 and 11 are the allelic ladder, which contains alleles 10–14, *lanes* 1–3 are bloodstains, *lanes* 5–10 are male samples, *lanes* 1, 2 and 9 are allele 11, *lanes* 5–8 and 10 are alleles 13, 14, 13, 12 and 10, respectively, and a PCR product of the sample in *lane* 3 was not observed

Results and discussion

An electropherogram for DYS453 is shown in Fig. 1 as a representative example for the Y-chromosome systems tested.

Specifications for the Y-chromosome

The length of amplified products of DYS443 and DYS444 was about 300 bp using the GDB primers. The fragments were too long to be easily genotyped using horizontal non-denaturing polyacrylamide gel electrophoresis with a discontinuous buffer system (Hou et al. 2001b), so primers of these loci were redesigned.

All female samples were analyzed by utilizing identical primers for all loci and no amplification products were observed. A single band was observed for each male sample showing that these are single-copy Y-STR loci.

Allelic sequences

Analyzed allelic sequences indicated that DYS443, DYS453, DYS455 and DYS456 loci have simple repeat structures, and that DYS444, DYS448, DYS457 (DYS437) and DYS458 are complex repeat systems in our sample population. Allelic sequences of the eight loci are shown in Table 2.

There were interruptive sequences in the repeat stretch of DYS444 and differences between the repeat array structure of our data and the data of Iida et al. (2002) at DYS444. A total of two interruptive sequences, TAGATACA and TAAAT, and three repeat blocks which contained two repeat motifs with TAGG and TAGA were observed for DYS444. The repetitive structure of our data differed from representative sequences of the data of Iida et al. at DYS444. Our consensus structure was $(TAGG)_5$TAGATACA$(TAGA)_2$TAAAT$(TAGA)_n$, while the representative sequence data was $(TAGG)_2$TAAG$(TAGG)_2$TAGATACA

Table 2 Allelic sequences of eight Y-STR loci

DYS443	
Consensus structure	L(20 bp)tct(ttcc)$_n$ttcttctttccttattttaaattagaagtccaattgaactatgccttgagctttttttgatgtaacataggctttaaaatgttactgattggac-cgtR(19 bp)
Allele (bp)	Sequence
11 (179)	L(20 bp)tct(ttcc)$_{11}$ 79 bp R (19 bp)
12 (183)	L(20 bp)tct(ttcc)$_{12}$ 79 bp R (19 bp)
13 (187)	L(20 bp)tct(ttcc)$_{13}$ 79 bp R (19 bp)
14 (190)	L(20 bp)tct(ttcc)$_{14}$ 79 bp R (19 bp)
15 (194)	L(20 bp)tct(ttcc)$_{15}$ 79 bp R (19 bp)
16 (198)	L(20 bp)tct(ttcc)$_{16}$ 79 bp R (19 bp)
17 (202)	L(20 bp)tct(ttcc)$_{17}$ 79 bp R (19 bp)
DYS444	
Consensus structure	L(24 bp)gtatacagaaagaactctaagtattaatttacaatacaacacatgaattatagtgcaatagata(tagg)$_5$tagataca(taga)$_2$taaat(taga)$_n$taa-agtR(20 bp)
Allele (bp)	Sequence
12 (219)	L(24 bp)64 bp(tagg)$_5$tagataca(taga)$_2$taaat(taga)$_{10}$taaagtR(20 bp)
13 (223)	L(24 bp)64 bp(tagg)$_5$tagataca(taga)$_2$taaat(taga)$_{11}$taaagtR(20 bp)
14 (227)	L(24 bp)64 bp(tagg)$_5$tagataca(taga)$_2$taaat(taga)$_{12}$taaagtR(20 bp)
15 (231)	L(24 bp)64 bp(tagg)$_5$tagataca(taga)$_2$taaat(taga)$_{13}$taaagtR(20 bp)
16 (235)	L(24 bp)64 bp(tagg)$_5$tagataca(taga)$_2$taaat(taga)$_{14}$taaagtR(20 bp)
17 (239)	L(24 bp)64 bp(tagg)$_5$tagataca(taga)$_2$taaat(taga)$_{15}$taaagtR(20 bp)
DYS448	
Consensus structure	U22(22 bp)atatttctggccggtctggaaatttatctctatctttacctctct(atctct)$_n$ttctct(atct)$_{2(}$atctct)$_3$ct(atctct)at(atctct)$_n$ctttactcat-gtctctatctccctttctgtctcgcgatctctatttctaaL23(23 bp)
Allele (bp)	Sequence
21 (280)	U22(22 bp)45 bp(atctct)$_8$ttctct(atct)$_2$(atctct)$_3$ct(atctct)at(atctct)$_9$ 50 bp L23(23 bp)
22 (286)	U22(22 bp)45 bp(atctct)$_8$ttctct(atct)$_2$(atctct)$_3$ct(atctct)at(atctct)$_{10}$ 50 bpL23(23 bp)
23 (292)	U22(22 bp)45 bp(atctct)$_9$ttctct(atct)$_2$(atctct)$_3$ct(atctct)ct(atctct)$_{10}$ 50 bpL23(23 bp)
24 (298)	U22(22 bp)45 bp(atctct)$_9$ttctct(atct)$_2$(atctct)$_3$ct(atctct)at(atctct)$_{11}$ 50 bpL23(23 bp)
25 (304)	U22(22 bp)45 bp(atctct)$_8$ttctct(atct)$_2$(atctct)$_3$ct(atctct)at(atctct)$_{13}$ 50 bpL23(23 bp)
26 (308)	U22(22 bp)45 bp(atctct)$_9$ttctct(atct)$_2$(atctct)$_3$ct(atctct)at(atctct)$_{13}$ 50 bpL23(23 bp)
27 (314)	U22(22 bp)45 bp(atctct)$_8$ttctct(atct)$_2$(atctct)$_3$ct(atctct)at(atctct)$_{14}$ 50 bpL23(23 bp)
DYS453	
Consensus structure	P1(20 bp)gtctcaaaaa(taaa)$_n$ataagctatctgcagggctggaggctctgactP2(22 bp)
Allele (bp)	Sequence
10 (127)	P1(20 bp)gtctcaaaaa(taaa)$_{10}$ataagctatctgcagggctggaggctctgactP2(22 bp)
11 (131)	P1(20 bp)gtctcaaaaa(taaa)$_{11}$ataagctatctgcagggctggaggctctgactP2(22 bp)
12 (135)	P1(20 bp)gtctcaaaaa(taaa)$_{12}$ataagctatctgcagggctggaggctctgactP2(22 bp)
13 (139)	P1(20 bp)gtctcaaaaa(taaa)$_{13}$ataagctatctgcagggctggaggctctgactP2(22 bp)
14 (143)	P1(20 bp)gtctcaaaaa(taaa)$_{14}$ataagctatctgcagggctggaggctctgactP2(22 bp)
DYS455	
Consensus structure	P1(18 bp)cttccg(ttat)$_n$tttagatatatggtctcacagtgttgcccaggctggagtgccctcgggtgatcacagctcactgcagccttgaccttgtgggct-taggcagP2(21 bp)
Allele (bp)	Sequence
10 (176)	P1(18 bp)cttccg(ttat)$_{10}$ 91 bp P2(21 bp)
11 (180)	P1(18 bp)cttccg(ttat)$_{11}$ 91 bp P2(21 bp)
12 (184)	P1(18 bp)cttccg(ttat)$_{12}$ 91 bp P2(21 bp)
DYS456	
Consensus structure	P1(21 bp)ttcttaaactgatgtattagggttctctagagggacagaactaatggaa(tatc)$_n$P2(19 bp)
Allele (bp)	Sequence
11 (133)	P1(21 bp)49 bp(tatc)$_{11}$ P2(19 bp)
12 (137)	P1(21 bp)49 bp(tatc)$_{12}$ P2(19 bp)
13 (141)	P1(21 bp)49 bp(tatc)$_{13}$ P2(19 bp)
14 (145)	P1(21 bp)49 bp(tatc)$_{14}$ P2(19 bp)
15 (149)	P1(21 bp)49 bp(tatc)$_{15}$ P2(19 bp)
16 (153)	P1(21 bp)49 bp(tatc)$_{16}$ P2(19 bp)
17 (157)	P1(21 bp)49 bp(tatc)$_{17}$ P2(19 bp)

Table 2 (continued)

18 (161)	P1(21 bp)49 bp$(tatc)_{18}$ P2(19 bp)
19 (165)	P1(21 bp)49 bp$(tatc)_{19}$ P2(19 bp)
20 (169)	P1(21 bp)49 bp$(tatc)_{20}$ P2(19 bp)
DYS457	
Consensus structure	P1(20 bp)ctcaagtgatcctcctacctcagtctcctgagtagctgggactatgggcgtgagtcccatccgg$(tcta)_n(tctg)_n(tcta)_4$tcatctgtgaatgatgtctatctacttatctatgaatgatatttatP2(23 bp)
Allele (bp)	Sequence
12 (205)	P1(20 bp)64 bp$(tcta)_7$tctc$(tctg)_1(tcta)_4$ 46 bp P2(23 bp)
14 (209)	P1(20 bp)64 bp$(tcta)_8(tctg)_2(tcta)_4$ 46 bp P2(23 bp)
14 (209)	P1(20 bp)64 bp$(tcta)_9(tctg)_1(tcta)_4$ 46 bp P2(23bp)
15 (213)	P1(20 bp)64 bp$(tcta)_9(tctg)_2(tcta)_4$ 46 bp P2(23 bp)
16 (217)	P1(20 bp)64 bp$(tcta)_{10}(tctg)_2(tcta)_4$ 46 bp P2(23 bp)
17 (221)	P1(20 bp)64 bp$(tcta)_{11}(tctg)_2(tcta)_4$ 46 bp P2(23 bp)
18 (225)	P1(20 bp)64 bp$(tcta)_{12}(tctg)_2(tcta)_4$ 46 bp P2(23 bp)
DYS458	
Consensus structure	P2(18 bp)$(tttc)_n$cttcct$(tttc)_3$ P1(23 bp)
Allele(bp)	Sequence
11 (91)	P2(18 bp)$(tttc)_8$cttcct$(tttc)_3$ P1(23 bp)
12 (95)	P2(18 bp)$(tttc)_9$cttcct$(tttc)_3$ P1(23 bp)
13 (99)	P2(18 bp)$(tttc)_{10}$cttcct$(tttc)_3$ P1(23 bp)
14 (103)	P2(18 bp)$(tttc)_{11}$cttcct$(tttc)_3$ P1(23 bp)
15 (107)	P2(18 bp)$(tttc)_{12}$cttcct$(tttc)_3$ P1(23 bp)
16 (111)	P2(18 bp)$(tttc)_{13}$cttcct$(tttc)_3$ P1(23 bp)
17 (115)	P2(18 bp)$(tttc)_{14}$cttcct$(tttc)_3$ P1(23 bp)
18 (119)	P2(18 bp)$(tttc)_{15}$cttcct$(tttc)_3$ P1(23 bp)
21 (131)	P2(18 bp)$(tttc)_{18}$cttcct$(tttc)_3$ P1(23 bp)

$(TAGA)_2TAAA(TAGA)_{14}$ (Iida et al. 2002). There was a TAAG interruptive sequence interspersed between two TAGG blocks in the representative sequence data of Iida et al. (2002), while there was a TAGG repeat in the counterpart sequence of our data. An additional thymine was observed between the second interruptive sequence and the second TAGA block in our population sample, as opposed to the counterpart of the representative sequence of the GDB. All allelic sequences demonstrated that the TAGG block and the first TAGA block were invariable at this locus in our sample, while the second TAGA block was variable. Allelic nomenclature of this locus was based on the numbers of all TAGA repeats in accordance with the recommendations of the ISFG and other publications (Bär et al. 1994; Gill et al. 2001; Iida et al. 2002).

A total of three interruptive sequences and four repeat blocks with an ATCTCT motif were observed for DYS448 in our population sample, the same as the GDB. However there was a small difference between the sequence of allele 23 in our data and the representative sequence of GDB at DYS448. A single nucleotide change (A→C) was observed in the third interruptive sequence of allele 23 in contrast to the representative sequence of GDB and other alleles at the DYS448 locus (Butler et al. 2002; Redd et al. 2002). The first block and the fourth block were variable in our population.

DYS457 (DYS437) was found to be a complex repeat system which contains two variable repeats with TCTA and TCTG motifs in our sample, some interspersed and three repeat blocks were observed. Two allelic variants composed of 14 repeats, which showed a different mobility in the gels, were observed in our sample. The repetitive structure of one allele designated as allele 14 was $(TCTA)_8(TCTG)_2(TCTA)_4$, while the repetitive structure of another allele named as allele 14′ was $(TCTA)_9(TCTG)_1(TCTA)_4$. A single nucleotide change of G→C for allele 12 was observed at this locus in our population sample. A TCTG repeat of allele 12 was changed into the TCTC interruptive sequence interspersed between the first TCTA and TCTG blocks, as opposed to other alleles of our data and the representative sequence of the GDB. The first repeat block and the second repeat block of our data were variable at DYS457 (DYS437), and the sequences of our data were different from the sequence of Ayub et al. (2000) and Hou et al. (2001a). Future studies should be performed to clarify other allelic variants of this locus.

Our results indicate that an interruptive sequence CTTCCT is located in the repeat array of DYS458, the same as the representative sequence retrieved from the GDB, and that the first TTTC block at DYS458 is variable in our population.

Population genetic data for forensic science

Gene diversities and standard errors are shown in Table 3. Haplotype diversity and standard error were 0.9996 and 0.0237, respectively. A total of 7 alleles at DYS443, 6 al-

Table 3 Diversities and standard errors of eight Y-STR loci in a Chinese Han population

Locus	Alleles	Number	Frequency	Gene diversity	SE
DYS443	11	3	0.0278	0.7742	0.0154
	12	12	0.1111		
	13	40	0.3703		
	14	21	0.1944		
	15	20	0.1852		
	16	10	0.1019		
	17	1	0.0093		
DYS444	12	3	0.0278	0.7671	0.0104
	13	29	0.2685		
	14	34	0.3148		
	15	23	0.2130		
	16	16	0.1481		
	17	3	0.0278		
DYS448	20	1	0.0093	0.7453	0.0102
	21	32	0.2963		
	22	31	0.2870		
	23	31	0.2870		
	24	2	0.0185		
	25	10	0.0926		
	26	1	0.0093		
DYS453	10	9	0.0833	0.3545	0.0397
	11	86	0.7963		
	12	3	0.0287		
	13	9	0.0833		
	14	1	0.0093		
DYS455	10	1	0.0093	0.0549	0.0214
	11	105	0.9722		
	12	2	0.0185		
DYS456	11	1	0.0093	0.6988	0.0211
	12	1	0.0093		
	14	26	0.2407		
	15	50	0.4629		
	16	19	0.1759		
	17	5	0.0463		
	18	5	0.0463		
	19	1	0.0093		
DYS457	12	2	0.0185	0.6148	0.0312
	14	10	0.0926		
	14′	63	0.5833		
	15	14	0.1296		
	16	17	0.1574		
	17	1	0.0093		
	18	1	0.0093		
DYS458	12	6	0.0556	0.8213	0.0096
	13	30	0.2777		
	14	18	0.1667		
	15	16	0.1481		
	16	22	0.2037		
	17	13	0.1204		
	18	120	0.0185		
	21	1	0.0093		

leles at DYS444, 7 alleles at DYS448, 4 alleles at DYS453, 3 alleles at DYS455, 8 alleles at DYS456, 7 alleles at DYS457 (DYS437) and 9 alleles at DYS458 were observed in our population sample. Table 4 lists the distribution of haplotyes for the eight loci in our population studied.

We observed the allele 11 at DYS443 in our population, while this allele was not seen in a Japanese population study (Iida et al. 2002).

We observed 7 alleles of DYS457(DYS437) with allele 12, 14′ and 18, while 3 alleles and 4 alleles were observed by Hou et al and Ayub et al., respectively, and alleles 12, 14′ and 18 were not observed in their populations. Allele 14′ was common in our population, but alleles 14 and 16 were fairly common in another Chinese Han population and Pakistan population, respectively (Ayub et al. 2000; Hou et al. 2001a).

The gene diversities of DYS443, DYS444, DYS448, DYS453, DYS455, DYS456, DYS457(DYS437) and DYS458 were 0.7742, 0.7671, 0.7453, 0.3545, 0.0549, 0.6988, 0.6148 and 0.8213, respectively, which showed that the discrimination powers of DYS443, DYS444, DYS448, DYS456, DYS457 (DYS437) and DYS458 were higher than DYS455.The most males shared allele 11 of DYS455 in our population studied, and the frequency of allele 11 was 0.9722. This study revealed that the eight Y-STR loci are suitable candidate Y-specific markers for forensic application in our population.

A total of 106 haplotypes was observed in our sample, among which 104 haplotypes were unique, and 2 haplotypes were observed in two males. The haplotype diversity was 0.9996, the discrimination capacity of haplotypes was 0.9815. The haplotype diversity of the widely used 9 Y-STR loci set was 0.945 and 0.9999 in the population studied by Caglia et al. (1998) and Tsai et al. 2002), respectively, and the haplotype diversity of 10 Y-STR loci was 0.995 in a Korean population (Shin et al. 2001). Our results revealed that haplotypes for eight loci showed high discrimination power for forensic application, and that these Y-STR loci were a suitable set of Y-linked markers for forensic applications in our population. For extending forensic applications, multiplex amplification for these loci will be developed, and analyzing the mutation rates and typing various specimens will be carried out in future.

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Table 4 Haplotypes of eight Y-STR loci in a Chinese Han population

No.	Haplotypes								Number
	DYS443	DYS444	DYS448	DYS453	DYS455	DYS456	DYS457	DYS458	
1	11	11	21	11	11	15	14′	13	1
2	11	11	21	11	11	16	14′	13	1
3	11	11	21	11	11	18	14′	14	1
4	12	10	21	11	11	19	14′	12	1
5	12	10	21	11	11	15	14′	14	1
6	12	11	21	11	11	18	14	12	1
7	12	11	21	11	11	15	14′	12	1
8	12	11	20	13	11	14	12	13	1
9	12	11	21	11	11	18	14	13	1
10	12	11	22	11	11	16	14′	13	1
11	12	11	21	11	11	18	14′	13	1
12	12	11	21	11	11	17	14′	14	1
13	12	12	22	11	11	14	16	14	1
14	12	13	22	11	11	15	14′	16	1
15	12	14	23	11	11	15	14	13	1
16	13	11	23	11	11	15	14′	12	1
17	13	11	21	10	11	15	14′	13	1
18	13	11	21	11	11	16	14′	13	1
19	13	11	23	11	11	14	14′	14	1
20	13	11	21	10	11	15	14′	14	1
21	13	11	21	11	11	17	14′	14	1
22	13	11	21	11	11	14	15	15	1
23	13	11	23	11	11	14	14′	15	1
24	13	11	21	10	11	15	14′	15	1
25	13	11	22	11	11	14	14	16	1
26	13	11	25	11	11	14	14′	16	1
27	13	11	22	12	11	14	14′	18	1
28	13	12	23	11	11	14	14′	12	1
29	13	12	22	11	11	15	14′	12	1
30	13	12	21	11	11	15	14′	13	1
31	13	12	21	11	11	17	14′	13	1
32	13	12	23	11	11	15	18	14	1
33	13	12	22	11	11	14	14′	15	1
34	13	12	21	10	11	15	14′	15	1
35	13	12	23	11	11	14	15	16	1
36	13	12	22	11	11	14	14′	16	1
37	13	12	21	12	11	14	14′	16	1
38	13	12	22	11	12	14	14′	16	1
39	13	12	21	11	11	15	14′	16	1
40	13	12	22	11	11	17	14′	16	1
41	13	12	22	11	11	15	14′	17	1
42	13	13	21	10	11	16	14	14	1
43	13	13	22	11	11	18	15	16	1
44	13	13	23	12	11	17	14′	16	1
45	13	13	21	10	11	14	14′	17	1
46	13	14	23	11	11	14	15	14	1
47	13	14	23	11	11	15	14′	15	1
48	13	14	21	11	11	14	16	16	1
49	13	14	23	11	10	15	16	16	1
50	13	14	22	11	11	15	16	16	1
51	13	14	21	10	11	15	14′	16	1
52	13	14	24	11	11	14	15	17	1
53	13	14	21	10	11	14	14′	18	1
54	13	15	21	11	11	15	15	13	1
55	13	15	21	10	11	16	14	17	1
56	14	11	25	11	11	15	14	13	1
57	14	11	23	11	11	15	14′	15	1

Table 4 (continued)

No.	Haplotypes								Number
	DYS443	DYS444	DYS448	DYS453	DYS455	DYS456	DYS457	DYS458	
58	14	11	22	11	11	16	14	16	1
59	14	11	23	11	11	15	14′	17	1
60	14	12	23	13	11	14	15	13	1
61	14	12	22	11	11	16	16	13	1
62	14	12	22	11	11	15	14′	14	1
63	14	12	22	11	11	15	14′	14	1
64	14	12	22	13	11	16	16	15	1
65	14	12	23	11	11	15	14′	16	1
66	14	12	23	11	11	15	16	17	1
67	14	12	23	11	11	15	16	17	1
68	14	13	23	13	11	16	14	13	1
69	14	13	23	11	11	15	14′	14	1
70	14	13	25	11	11	15	14′	14	1
71	14	13	23	11	11	14	14′	15	1
72	14	13	22	11	11	15	16	16	1
73	14	13	22	11	11	16	16	17	1
74	14	13	22	11	11	15	14′	17	1
75	14	13	22	11	11	15	15	21	1
76	14	14	22	11	11	15	16	17	1
77	15	11	22	11	11	15	14′	13	1
78	15	11	21	14	11	15	14′	17	1
79	15	12	23	13	11	12	14′	13	2
80	15	12	22	11	11	16	14′	13	1
81	15	12	26	11	11	15	14′	14	1
82	15	12	23	11	11	15	12	15	1
83	15	12	22	11	11	15	16	15	1
84	15	12	23	11	11	15	14′	15	1
85	15	12	25	11	11	16	16	16	1
86	15	12	23	11	11	14	14′	16	1
87	15	13	23	11	11	16	14	13	1
88	15	13	23	13	11	14	15	13	1
89	15	13	23	11	11	14	15	14	1
90	15	13	22	11	11	15	16	15	1
91	15	13	22	11	11	15	15	17	1
92	15	13	23	11	11	16	16	17	1
93	15	14	24	13	11	14	14′	13	1
94	15	14	21	11	11	15	15	16	1
95	15	15	23	11	11	15	14′	13	1
96	16	10	21	13	11	15	15	13	1
97	16	11	21	11	11	16	14′	13	1
98	16	12	23	11	11	16	14′	13	1
99	16	12	22	11	12	16	14′	14	1
100	16	13	25	11	11	16	16	13	1
101	16	13	25	11	11	15	15	15	1
102	16	13	22	13	11	11	14′	15	1
103	16	13	23	11	11	14	17	16	1
104	16	14	25	11	11	15	14′	13	1
105	16	14	25	11	11	15	16	15	2
106	17	14	25	11	11	15	14′	14	1

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