

## 22 Y-STR

1 . 1 . 1  
1 . 1.2 . 1.2  
1.2

1  
2

: 2007 10 2  
: 2007 11 2

:  
(120 - 752) 250,

: (02) 2228 - 2481  
FAX : (02) 362 - 0860  
E - mail: kjshin@yuhs.ac

### Genetic characteristics of 22 Y-STR loci in Koreans

Myung Jin Park<sup>1</sup>, Hwan Young Lee<sup>1</sup>, Na Young Kim<sup>1</sup>, Jeong Eun Sim<sup>1</sup>,  
Woo Ick Yang<sup>1,2</sup>, Sang-Ho Cho<sup>1,2</sup>, Kyoung-Jin Shin<sup>1,2</sup>

<sup>1</sup>Department of Forensic Medicine, Yonsei University College of Medicine, Seoul, Korea

<sup>2</sup>Human Identification Research Center, Yonsei University, Seoul, Korea

To construct a Korean Y-chromosomal STR database for 22 Y-STRs (DYS19, DYS385, DYS388, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS446, DYS447, DYS448, DYS449, DYS456, DYS458, DYS464, DYS635, and GATA H4.1), 708 DNA samples from unrelated Korean males were analyzed using three multiplex PCR systems. During analysis, thirty two microvariant alleles were observed at DYS449, DYS458, and DYS464, and duplicated alleles were occurred once each for DYS19, DYS390, and DYS447. In haplotype analysis for the 22 Y-STRs, a total of 693 different haplotypes were observed with overall haplotype diversity of 0.9999, and of these, 680 haplotypes were unique. By combining each marker for the extended SWGDAM haplotype, DYS458 was the most informative marker. In addition, the diversity of combined haplotypes of DYS447, DYS458, DYS635, GATA H4.1, and the SWGDAM Y-STR loci was comparable to haplotypes of 17 loci in the AmpFISTR Yfiler™ kit.

**Key words** : Y chromosome, STR, extended SWGDAM haplotype, AmpFISTR Yfiler™, microvariant allele, duplicated allele, Koreans

Y-STR  
가  
on - line 가 Y - STR Haplotype  
Reference Database (YHRD)<sup>6)</sup> 464  
9 Y - STR minimal  
haplotype<sup>3)</sup> 50,867 , 11 Y - STR extended  
SWGDAM haplotype 23,981  
가  
minimal haplotype extended SWGDAM  
haplotype 7 - 14)  
Y - STR  
Y - STR  
(76.41% - 89.96%)  
3.3%가 15 Y - STR  
가<sup>15)</sup>  
Y - STR

discriminatory capacity 가 Y-STR , YHRD 22  
 minimal haplotype diversity가 Y-STR 가 .  
 Vienna, Alcamo, Ankara  
 1.0000 Zriba 0.5699,  
 Andon Poci 0.7076  
 가 , minimal haplotype 1.  
 extended SWGDAM haplotype Y-STR mutation <sup>14)</sup> 355  
 discriminatory capacity 가 가 Y- 19 Y-STR <sup>13)</sup> 301  
 STR 708 가  
 , Y-STR autosomal STR 3 DNA 2-  
 가 microvariant, duplication null . -20  
 2.  
 가. DNA  
 kit AmpFISTR Yfiler™ QIAamp DNA Mini Kit (QIAGEN,  
 17 Y-STR (DYS19, DYS385, Hilden, Germany) DNA  
 DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DNA Picogreen dsDNA Quantitation Reagent (Molecular  
 DYS438, DYS439, DYS448, DYS456, DYS458, DYS635 Probes, Eugene, OR) TBS - 380 Mini -  
 GATA H4.1) <sup>13,14)</sup> gene Fluorometer (Turner Biosystems, Sunnyvale, CA)  
 diversity가 5 Y-STR (DYS388, DYS446, DNA  
 DYS447, DYS449 DYS464) 22 Y- -20  
 STR 708 가

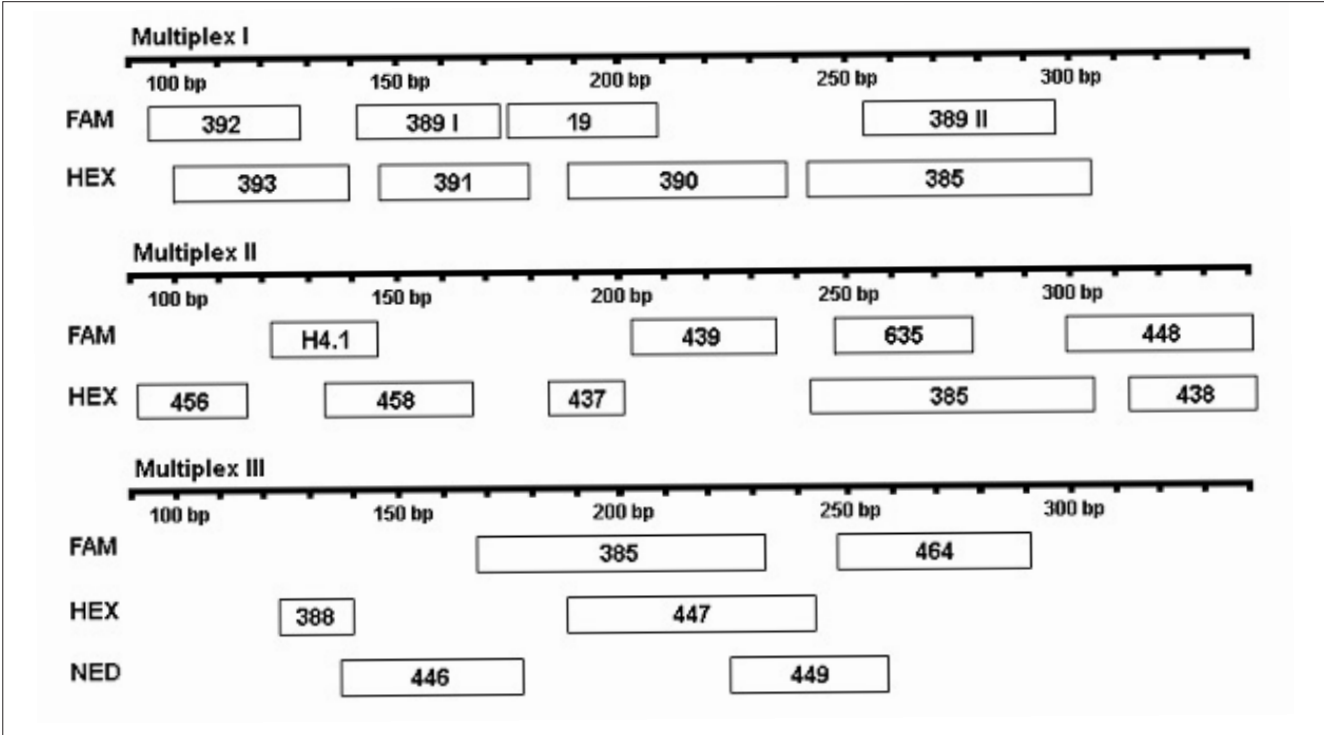


Fig. 1. Schematic of PCR product size for the loci in each multiplex. Marker names have been abbreviated (e.g. DYS392 is listed as 392)

22 Y-STR (multiplex PCR) primer (Fig. 1), PCR<sup>14)</sup> kit (Applied Biosystems, Foster City, CA) ABI 310 PRISM Genetic Analyzer Duplicated PCR pGEM-T Easy Vector Systems I (Promega, Madison, WI)

PTC-200 DNA engine (MJ Research, Waltham, MA), PCR ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Foster City, CA) capillary, GeneScan software 3.7 (Applied Biosystems, Foster City, CA) 가 Arlequin<sup>20)</sup>, discriminatoty capacity

. *Allele ladder* PCR *genotyping* ladder allele minimal haplotype extended SWGDAM haplotype Terminator Cycle Sequencing kit (Applied Biosystems, Foster City, CA) BigDye discriminatory capacity Foster City, CA) ABI PRISM 310 Genetic Analyzer, International Society for Forensic Haemogenetics (ISFG)<sup>16)</sup> haplotype Y-STR 가 PCR genotyping allele ladder GenoTyper Software 3.7 (Applied Biosystems, Foster City, CA) 1. microvariant 가 DYS447, GATA H4 GATA H4.1 Gusmão<sup>18)</sup> DYS449, DYS458 DYS464 32 (Table 1). DYS447 (core repeat unit) TAAAA - (TAATA)<sub>n</sub> (TAATA)<sub>n</sub> - TAAAA가 가 6 . 가 microvariant DYS449 (TTTC) (27.2, 28.2, 29.2, 30.2) (25, 30.1, 42)

Table 1. Microvariant alleles observed in 708 Korean males

Locus	Allele <sup>a</sup>	Structure <sup>b</sup>	N
DYS447	18	(TAATA) <sub>7</sub> TAAAA(TAATA) <sub>10</sub> <u>TAAAA(TAATA)<sub>n</sub></u>	2
	19	(TAATA) <sub>7</sub> TAAAA(TAATA) <sub>11</sub> <u>TAAAA(TAATA)<sub>n</sub></u>	4
DYS449	25 (26)	(TTTC) <sub>12</sub> -tctctctcctctc-(tttc) <sub>2</sub> -N4-(tttc) <sub>2</sub> -N12-cttc-(TTTC) <sup>14</sup>	1
	27.2	(TTTC) <sub>3</sub> TC(TTTC) <sub>10</sub> -tctctctcctctc-(tttc) <sub>2</sub> -N4-(tttc) <sub>2</sub> -N12-cttc-(TTTC) <sup>14</sup>	1
	28.2	(TTTC) <sub>3</sub> TT(TTTC) <sub>11</sub> -tctctctcctctc-(tttc) <sub>2</sub> -N4-(tttc) <sub>2</sub> -N12-cttc-(TTTC) <sup>14</sup>	1
	29.2	(TTTC) <sub>3</sub> TC(TTTC) <sub>11</sub> -tctctctcctctc-(tttc) <sub>2</sub> -N4-(tttc) <sub>2</sub> -N12-cttc-(TTTC) <sup>15</sup>	1
	30.1 (30)	(TTTC) <sub>16</sub> -tctctctcctctc-(tttc) <sub>2</sub> -N4-(tttc) <sub>2</sub> -N12-cttc-(TTTC) <sup>14</sup>	1
	30.2	(TTTC) <sub>16</sub> -tctctctcctctc-(tttc) <sub>2</sub> -N4-(tttc) <sub>2</sub> -N12-cttc-(TTTC) <sub>10</sub> TT(TTTC) <sub>4</sub>	12
DYS458	42 (33)	(TTTC) <sub>15</sub> -tctctctcctctc-[(tttc) <sub>2</sub> -N4-(tttc) <sub>2</sub> -N12-cttc] <sub>2</sub> -(TTTC) <sub>18</sub>	1
	14.1	(GAAA) <sub>14</sub> G	1
DYS464	17.2	(GAAA) <sub>15</sub> AA(GAAA) <sub>2</sub>	1
	12.3	(CCTT) <sub>7</sub> CCTT(CCTT) <sub>5</sub>	1
	14.3	(CCTT) <sub>3</sub> CCTT(CCTT) <sub>11</sub>	5

<sup>a</sup> The numbers in parentheses are genuine alleles identified by sequence analysis

<sup>b</sup> Deletion and insertion are lined and underlined, respectively.

Table 2. Allele frequencies and gene diversities of single copy 19 Y-STR loci in a Korean population

Allele	DYS 19	DYS 388	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 446	DYS 447	DYS 448	DYS 449	DYS 456	DYS 458	DYS 635	GATA H4.1
7						0.0014													
8						0.0268													
9						0.8475	0.0028	0.0014		0.0085	0.0028								
10		0.1271				0.1243	0.1554			0.5056	0.0438								
11		0.0028	0.0113				0.1017	0.3814		0.1525	0.2853	0.0763							
12		0.6850	0.3715				0.4901	0.4619	0.0014	0.0268	0.5141	0.1342				0.0169			
13	0.0240	0.1723	0.2359				0.2161	0.1073	0.6935	0.2980	0.1370	0.3573				0.0141	0.0085		
14	0.1540	0.0085	0.3729				0.0240	0.0424	0.2952	0.0085	0.0169	0.2175				0.1314	0.0085		
15	0.3799	0.0042	0.0071				0.0099	0.0056	0.0099	0.0791		0.0791				0.6766	0.0720		
16	0.3291									0.0678		0.0678				0.1201	0.1511		
17	0.1102									0.0410		0.0410		0.0339		0.0311	0.3107		
18	0.0014									0.0169		0.0169		0.0028		0.0099	0.2825		
19										0.0099		0.0099		0.0056		0.0099	0.2825		
20					0.0014									0.2345			0.1328	0.0523	0.0424
21					0.0056									0.0960			0.0254	0.2726	0.4266
22					0.1229									0.0071			0.0056	0.4661	0.4463
23					0.4873									0.1455				0.1342	0.0819
24					0.2444									0.2556				0.0466	0.0028
25*					0.1243									0.3799				0.0268	
26					0.0014	0.0113								0.0028				0.0014	
27					0.0734	0.0014								0.3573				0.0014	
28					0.2401									0.2345				0.0254	
29					0.3983									0.0960				0.0056	
30					0.2288									0.0297				0.0056	
31					0.0523									0.1455				0.1342	0.0819
32					0.0056									0.0028				0.0466	0.0028
33														0.2345				0.0268	
34														0.0960				0.0014	
35														0.0960				0.0014	
36														0.0960				0.0014	
42*														0.0960				0.0014	
Microvariants, duplicated and null alleles																			
14.1																			
17.2																			
27.2																			
28.2																			
29.2																			
30.1*																			
30.2																			
16-17	0.0014																		
22-23																			
23-24																			
Null																			
h	0.7119	0.4855	0.6681	0.7242	0.6731	0.2660	0.6789	0.6288	0.4324	0.6323	0.6342	0.7894	0.7523	0.7508	0.8521	0.5098	0.7783	0.6858	0.6112

\* At DYS449, these alleles were determined by amplicon size (i.e. ostensible allele) and contain only one of ostensible allele 25.

. DYS458    DYS464  
GAAA    CCTT

Duplicated    DYS19, DYS390    DYS447  
(Fig. 2)

diversity    가    , DYS448  
gene diversity    가

diversity    가    , extended  
SWGDAM haplotype    DYS458    가

DYS635    가    diversity  
가 가    가    가    DYS447

GATA H4.1  
diversity가    가    DYS447,  
DYS458, DYS635    GATA H4.1    extended  
SWGDAM haplotype    가    AmpFISTR

Yfiler™ haplotype    diversity

gene diversity    Table 2    multi - copy Y - STR  
DYS385    DYS464    gene

diversity    Table 3    . Single - copy  
DYS449    가 가    gene diversity (0.8521)  
, DYS446    (0.7894), DYS458    (0.7783)

가    DYS447    DYS448    가  
gene diversity    , DYS391    가 가    microvariant,  
gene diversity (0.2660)

22    Y - STR    duplicated    null  
(http://forensic.yonsei.ac.kr)    가    가    가    . Y -  
708    693    가    ISFG    Y -  
680    가    (98.12%)    STR    21)  
11    ,    2    STR    , microvariant

. Minimal haplotype, extended  
SWGDAM haplotype    AmpFISTR    Yfiler™ haplotype    가  
diversity    4

microvariant    (Table 1), DYS449  
27.2, 28.2, 29.2, 30.2    DYS458    14.1,  
17.2    DYS464    12.3, 14.3

Extended SWGDAM haplotype  
multi - copy    DYS464    Y - STR    가 가    가  
가    DYS458    가 가    가    가    diversity    (Table 5).    gene diversity    microvariant    GenoTyper

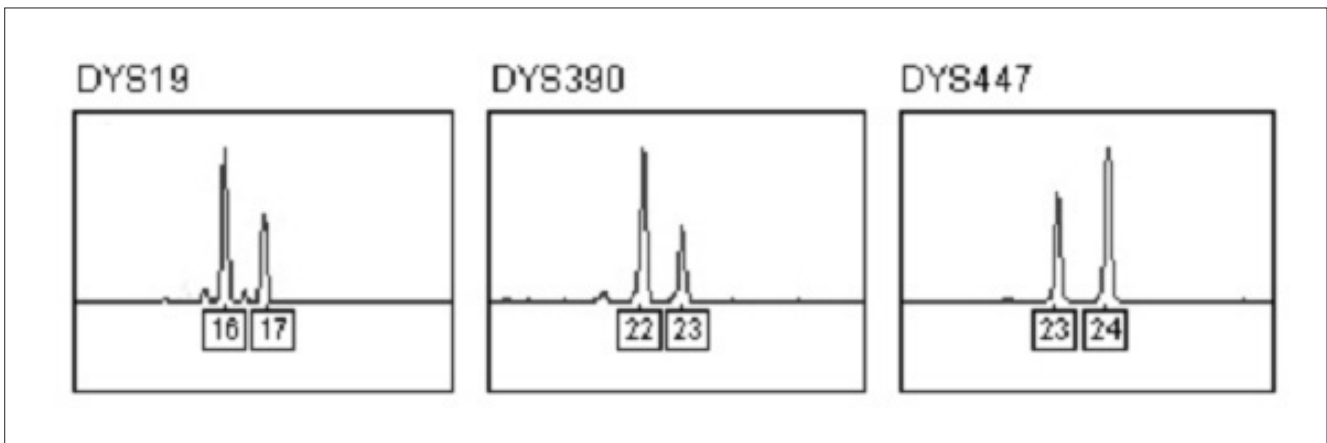


Fig. 2. Electropherogram for duplicated alleles at the single copy loci DYS19, DYS390 and DYS447

**Table 3.** Haplotype distribution and diversity of multi-copy Y-STRs in a Korean population

DYS385		DYS464					
Haplotype	Frequency	Haplotype	Frequency	Haplotype	Frequency	Haplotype	Frequency
8-20	0.0014	12-21	0.0014	12	0.0014	13-15-18	0.0127
9-16	0.0014	13-13	0.0226	13	0.0127	13-15-19	0.0014
9-18	0.0028	13-14	0.0071	14	0.0028	13-16-17	0.0282
9-19	0.0155	13-15	0.0028	15	0.0028	13-16-18	0.0113
9-20	0.0028	13-16	0.0169	16	0.0085	13-17-18	0.0028
10-10	0.0014	13-17	0.0212	17	0.0141	14-15-16	0.0042
10-16	0.0042	13-18	0.0537	11-17	0.0014	14-15-17	0.0028
10-17	0.0480	13-19	0.0381	12-13	0.0042	14-15-18	0.0014
10-18	0.1045	13-20	0.0254	12-14	0.0014	14-16-17	0.0071
10-19	0.0975	13-21	0.0028	12-16	0.0056	14-16-18	0.0028
10-20	0.0339	14-14	0.0028	13-14	0.0466	15-16-17	0.0014
10-21	0.0113	14-16	0.0028	13-15	0.0452	11-12-13-15	0.0014
11-11	0.0113	14-17	0.0141	13-16	0.0127	11-12-13-16	0.0014
11-12	0.0184	14-18	0.0212	13-17	0.0056	11-13-14-16	0.0014
11-13	0.0141	14-19	0.0113	13-18	0.0014	11-13-16-18	0.0014
11-14	0.0071	14-20	0.0155	14-15	0.0056	11-15-16-17	0.0014
11-15	0.0014	14-21	0.0085	14-16	0.0141	12-13-14-15	0.0353
11-16	0.0127	14-22	0.0042	14-17	0.0014	12-13-14-16	0.0311
11-17	0.0282	15-15	0.0028	15-16	0.0198	12-13-14-17	0.0113
11-18	0.0099	15-17	0.0014	15-17	0.0071	12-13-15-16	0.0113
11-19	0.0353	15-18	0.0014	16-17	0.0113	12-13-15-17	0.0056
11-20	0.0155	15-19	0.0071	16-18	0.0028	12-13-15-18	0.0014
11-21	0.0028	15-20	0.0184	17-18	0.0028	12-13-16-17	0.0028
12-12	0.0028	15-21	0.0127	14-14.3	0.0071	12-13-16-18	0.0042
12-13	0.0042	15-22	0.0085	10-13-15	0.0014	12-13-16-19	0.0014
12-14	0.0113	15-23	0.0014	10-14-16	0.0014	12-14-15-16	0.0311
12-15	0.0042	16-17	0.0014	11-12-17	0.0042	12-14-15-17	0.0056
12-16	0.0240	16-20	0.0028	11-13-14	0.0014	12-14-15-18	0.0014
12-17	0.0381	16-21	0.0028	11-13-15	0.0014	12-14-16-17	0.0028
12-18	0.0452	17-20	0.0028	11-14-16	0.0014	12-14-16-18	0.0014
12-19	0.0410	19-19	0.0014	12-13-14	0.0254	12-15-16-17	0.0071
12-20	0.0085	19-20	0.0014	12-13-15	0.0466	12-15-16-18	0.0014
				12-13-16	0.0042	12-15-17-18	0.0014
				12-13-17	0.0014	12.3-14-15-17	0.0017
				12-14-15	0.0254	13-14-15-16	0.0127
				12-14-16	0.0339	13-14-15-17	0.0099
				12-14-17	0.0056	13-14-15-18	0.0014
				12-15-16	0.0071	13-14-16-17	0.1045
				12-16-17	0.0028	13-14-16-18	0.0099
				12-16-18	0.0014	13-14-16-19	0.0014
				13-14-15	0.0494	13-14-17-18	0.0042
				13-14-16	0.0579	13-15-16-17	0.0282
				13-14-17	0.0198	13-15-16-18	0.0071
				13-14-18	0.0042	13-15-16-19	0.0014
				13-15-16	0.0254	14-15-16-17	0.0042
				13-15-17	0.0127		

h 0.9597 h 0.9669

가 TCTC가 T가 36 bp가  
 가 , DYS449 duplication  
 가 ISFG  
 GenoTyper 25, 30.1 42 26, 30, 33  
 , DYS449.1 DYS449.2

ISFG	30.1	haplotype	extended SWGDAM haplotype
DYS449.1*16 + DYS449.2*14 (U4Tins)		가	, extended
		SWGDAM haplotype	Y - STR 가
		discriminatory capacity	가 가
duplication triplication		DYS449	single - copy gene diversity가
22) DYS19, DYS385, DYS389I, DYS389II,		가	diversity 가 ,
DYS390, DYS391, DYS393, DYS437, DYS438, DYS439			germ line
DYS448	DYS19	<sup>14)</sup>	가
DYS385 duplication 가		extended SWGDAM haplotype	가
	DYS385	가	gene
duplication triplication		diversity	DYS446 diversity
DYS447 duplicated	23 - 24	-	가 homologous <sup>14,23)</sup>
germ line (23 - 24 24)가	<sup>14)</sup>		가 . DYS456
Y - STR		DYS446 가 X	homologous <sup>24)</sup>
가	duplication	, DYS388 DYS437	diversity
	duplication	가	
	peak가	discriminatory capacity 가	Y - STR
DNA profiles		. DYS448	AmpFISTR Yfiler™
, Y - STR	minimal	kit diversity	gene diversity 가

Table 4. Number of haplotypes and diversities for 22 Y-STRs in 708 Korean males

	Minimal 9 Y-STR haplotype	Extended SWGDAM 11 Y-STR haplotype	Y-filer™ 17 Y-STR haplotype	22 Y-STR haplotype
No. of haplotypes	485	558	657	693
No. of unique haplotypes	394	483	625	680
Discriminatory capacity (%)	68.5	78.8	92.8	97.9
Haplotype diversity (± SD)	0.9966 ± 0.0005	0.9982 ± 0.0004	0.9995 ± 0.0002	0.9999 ± 0.0001

Table 5. Numbers of haplotypes and haplotype diversities obtained by adding each marker to the extended SWGDAM haplotype

Haplotype	Gene diversity*	No. of haplotypes <sup>c</sup>	Discriminatory capacity (%)	Haplotype diversity
Extended SWGDAM haplotype		558	78.8	0.9982
Extended SWGDAM haplotype + DYS449	0.8521	612	86.4	0.9992
Extended SWGDAM haplotype + DYS446	0.7894	598	84.5	0.9989
Extended SWGDAM haplotype + DYS458	0.7783	616	87.0	0.9992
Extended SWGDAM haplotype + DYS447	0.7523	583	82.3	0.9986
Extended SWGDAM haplotype + DYS448	0.7508	565	79.8	0.9983
Extended SWGDAM haplotype + DYS635	0.6858	591	83.5	0.9988
Extended SWGDAM haplotype + GATA H4.1	0.6112	579	81.8	0.9985
Extended SWGDAM haplotype + DYS456	0.5098	574	81.1	0.9984
Extended SWGDAM haplotype + DYS388	0.4855	566	79.9	0.9983
Extended SWGDAM haplotype + DYS437	0.4324	568	80.2	0.9983
Extended SWGDAM haplotype + DYS458 + DYS635		639	90.3	0.9994
Extended SWGDAM haplotype + DYS458 + DYS447		630	89.0	0.9994
Extended SWGDAM haplotype + DYS458 + GATA H4.1		631	89.1	0.9993
Extended SWGDAM haplotype + DYS458 + DYS635 + DYS447		650	91.8	0.9996
Extended SWGDAM haplotype + DYS458 + DYS635 + GATA H4.1		649	91.5	0.9995
Extended SWGDAM haplotype + DYS458 + DYS635 + DYS447 + GATA H4.1		658	92.9	0.9996
Y-filer™ 17 Y-STR haplotype		657	92.8	0.9995

\* Gene diversity of added marker to extended SWGDAM haplotype loci

(AZFc) , DYS448 가 azoospermia factor c microdeletion null  
 가 Y 708 22 Y-STR 693  
 가 680 가  
 , DYS464 multi-copy  
 gene diversity 가  
 DNA  
 , DYS448 가 AZFc  
<sup>30,31)</sup> DYS448 null  
<sup>25)</sup> 가  
 DYS458 single-copy 가 gene diversity 가 extended SWGDAM haplotype diversity  
 가 가  
 discriminatory capacity 가  
 Y-STR , diversity 가  
 가 DYS458, DYS635, DYS447, GATA H4.1  
 4 extended SWGDAM haplotype  
 가 15 17  
 AmpFISTR Yfiler™ haplotype diversity 가 ,  
 , 15 Y-STR haplotype  
 AmpFISTR Yfiler™ haplotype discriminatory capacity 93% , Y-STR  
 haplotype  
 Y-STR 가  
 708  
 22 Y-STR  
 . Microvariant 32 가  
 DYS449 가 ,  
 microvariant  
 . DYS19, DYS390 DYS447  
 duplicated 가 ,  
<sup>25)</sup> DYS385  
 deletion AZFc  
 DYS448 DYS464 deletion

가  
 . Desciminary capacity 가  
 extended SWGDAM haplotype diversity가  
 DYS458 diversity가  
 가 가 , DYS447, DYS458, DYS635,  
 GATA H4.1 가 (15 ) 17  
 AmpFISTR Yfiler™ haplotype  
 discriminatory power 가 .

1. Roewer L, Arnemann J, Spurr NK, Grzeschik KH, Epplen JT. Simple repeat sequences on the human Y chromosome are equally polymorphic as their autosomal counterparts. *Hum Genet* 1992;89:389-94
2. Jobling MA, Pandya A, Tyler-Smith C. The Y chromosome in forensic analysis and paternity testing. *Int J Legal Med* 1997;110:118-24
3. Kayser M, Caglia A, Corach D et al. Evaluation of Y-chromosomal STRs: a multicenter study. *Int J Legal Med* 1997;110:125-133, appendix 141-9
4. de Knijff P, Kayser M, Caglia A et al. Chromosome Y microsatellites: population genetic and evolutionary aspects. *Int J Legal Med* 1997;110:134-49
5. Jobling MA, Tyler-Smith C. Fathers and sons: the Y chromosome and human evolution. *Trends Genet* 1995;11:449-56
6. Roewer L, Krawczak M, Willuweit S. Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes. *Forensic Sci Int* 2001;118:106-13
7. Shin DJ, Jin HJ, Kwak KD et al. Y-chromosome multiplexes and their potential for the DNA profiling of Koreans. *Int J Legal Med* 2001;115:109-17
8. Kim YJ, Shin DJ, Kim JM et al. Y-chromosome STR haplotype profiling in the Korean population. *Forensic Sci Int* 2001;115:231-7
9. Lee SD, Lee DH, Kim KB, Lee YS, Lee JB. Y chromosome haplotypes in Koreans. *Kor J Legal Med* 2001;25:29-33
10. Zheng ZJ, Zhang YJ, Park JC, Lin HY, Kim SY, Choi YT, Lee JB. Polymorphism and haplotypes of 10 Y-STR loci in Koreans. *Kor J Legal Med* 2003;27:62-72
11. Kwak KD, Jin HJ, Shin DJ et al. Y-chromosomal STR haplotypes and their applications to forensic and population studies in east Asia. *Int J Legal Med* 2005;119:195-201
12. Chun BW, Shin SC, Kim YJ et al. Allele frequencies and haplotypes of the STR loci of the PowerPlex Y-system in southern populations from Korea. *Forensic Sci Int* 2005;148:225-31
13. Park MJ, Lee HY, Yoo JE, Chung U, Lee SY, Shin KJ. Forensic evaluation and haplotypes of 19 Y-chromosomal STR loci in Koreans. *Forensic Sci Int* 2005;152:133-47



14. Lee HY, Park MJ, Chung U, Lee HY, Yang WI, Cho SH, Shin KJ. Haplotypes and mutation analysis of 22 Y-chromosomal STRs in Korean father-son pairs. *Int J Legal Med* 2007;121:128-35
15. Xue Y, Zerjal T, Bao W et al. Recent spread of a Y-chromosomal lineage in northern China and Mongolia. *Am J Hum Genet* 2005;77:1112-6
16. Bär W, Brinkmann B, Budowle B, Carracedo A, Gill P, Lincoln P, Mayr W, Olaisen B. DNA recommendations. Further report of the DNA Commission of the ISFH regarding the use of short tandem repeat systems. International Society for Forensic Haemogenetics. *Int J Legal Med* 1997;110:175-76
17. Mulero JJ, Budowle B, Butler JM, Gusmão L. Letter to the editor-nomenclature and allele repeat structure update for the Y-STR locus GATA H4. *J Forensic Sci* 2006;51:694
18. Gusmão L, Gonzalez-Neira A, Alves C, Lareu M, Costa S, Amorim A, Carracedo A. Chimpanzee homologous of human Y specific STRs. A comparative study and a proposal for nomenclature. *Forensic Sci Int* 2002;126:129-36
19. Nei M. *Molecular Evolutionary Genetics*. Columbia University Press, New York, 1987
20. Schneider S, Roessli D, Excoffier L. *Arlequin: a software for Population Genetics Data Analysis, Ver 2.000*. Genetics and Biometry Lab, Department of Anthropology, University of Geneva, 2000
21. Gusmão L, Butler JM, Carracedo A et al. DNA Commission of the International Society of Forensic Genetics (ISFG): an update of the recommendations on the use of Y-STRs in forensic analysis. *Int J Legal Med* 2006;120:191-200
22. Butler JM, Decker AE, Kline MC, Vallone PM. Chromosomal duplications along the Y-chromosome and their potential impact on Y-STR interpretation. *J Forensic Sci* 2005;50:853-9
23. Rodig H, Grum M, Grimmecke HD. Population study and evaluation of 20 Y-chromosome STR loci in Germans. *Int J Legal Med* 2007;121:24-7
24. Chang CW, Mulero JJ, Budowle B, Calandro LM, Hennessy LK. Identification of a novel polymorphism in the X-chromosome region homologous to the DYS456 locus. *J Forensic Sci* 2006;51:344-8
25. Park MJ, Shin KJ, Kim NY, Yang WI, Cho SH, Lee HY. Characterization of deletions in the DYS385 flanking region and null alleles associated with AZFc microdeletions in Koreans. *J Forensic Sci* In press
26. Parkin EJ, Kraayenbrink T, Opgenort JR, van Driem GL, Tuladhar NM, de Knijff P, Jobling MA. Diversity of 26-locus Y-STR haplotypes in a Nepalese population sample: Isolation and drift in the Himalayas. *Forensic Sci Int* 2006;166:176-81
27. Chang YM, Perumal R, Keat PY, Kuehn DL. Haplotype diversity of 16 Y-chromosomal STRs in three main ethnic populations (Malays, Chinese and Indians) in Malaysia. *Forensic Sci Int* 2007;167:70-6
28. Roewer L, Krüger C, Willuweit S et al. Y-chromosomal STR haplotypes in Kalmyk population samples. *Forensic Sci Int* 2007;173:204-9
29. Mizuno N, Nakahara H, Sekiguchi K, Yoshida K, Nakano M, Kasai K. 16 Y chromosomal STR haplotypes in Japanese. *Forensic Sci Int* In press
30. King TE, Bosch E, Adams SM, Parkin EJ, Rosser ZH, Jobling MA. Inadvertent diagnosis of male infertility through genealogical DNA testing. *J Med Genet* 2005;42:366-8
31. Kayser M, Kittler R, Erler A et al. A comprehensive survey of human Y-chromosomal microsatellites. *Am J Hum Genet* 2004;74:1183-97