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SHORT COMMUNICATION

Hwan Young Lee · Myung Jin Park · Chan Kwon Jeong · Seon Yeong Lee · Ji-Eun Yoo · Ukhee Chung · Jong-Hoon Choi · Chong-Youl Kim · Kyoung-Jin Shin

Genetic characteristics and population study of 4 X-chromosomal STRs in Koreans: evidence for a null allele at DXS9898

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Abstract The four X-chromosomal short tandem repeats (STRs), DXS9898, DXS6809, DXS7424 and DXS10011 were analyzed by single multiplex PCR in 150 male and 150 female Koreans. The loss of an allele at DXS9898 was observed in 13 out of 450 chromosomes (2.9%) and the PCR analysis showed that the X-chromosome with a null allele at DXS9898 has more than 1 kb deletion at the DXS9898 locus. Statistical analyses for these four X-STRs showed that they are highly informative for forensic application in Koreans. No linkage disequilibrium was observed among these four STRs and the previously reported five polymorphic STRs, HumARA, DXS101, GATA172D05, HPRTB and DXS8377 in Koreans. The test of homogeneity between allele frequencies revealed that there are some discrepancies in allele distributions between Koreans and Germans.

Keywords STR · X-chromosome · Null allele · Korea

Introduction

In comparison with autosomal and Y-chromosomal short tandem repeats (STRs) [1, 2, 3], X-chromosomal markers have so far been employed only rarely in forensic practice. However, their genetic peculiarities render X-chromosomal STRs effective in complex cases of kinship testing [4]. In our previous report, the usefulness of five highly informative X-STRs, HumARA, DXS101, GATA172D05, HPRTB and DXS8377 markers in a Korean population was discussed on the basis of their statistical parameters [5].

In the meantime, additional X-linked STRs (DXS9898, DXS6809, DXS7424 and DXS10011) have been found to be highly informative in several ethnic populations [6, 7, 8, 9, 10, 11, 12]. In the present study, we applied single multiplex PCR to analyze these four X-STRs in a Korean population. We found evidence for a null allele at the DXS9898 locus and calculated the statistical parameters for forensic efficiency. In addition, we provide relevant information regarding population differences with respect to allele distribution patterns and linkage disequilibrium among these four STRs and the five previously reported STRs.

H. Y. Lee · M. J. Park · J.-E. Yoo · U. Chung · J.-H. Choi · C.-Y. Kim · K.-J. Shin (✉)
Department of Forensic Medicine, College of Medicine, Yonsei University,
134 Shinchon-Dong, Seodaemun-Gu,
120-752 Seoul, Korea
e-mail: kjshin@yumc.yonsei.ac.kr
Tel.: +82-2-3615775
Fax: +82-2-3620860

U. Chung · K.-J. Shin
Biometrics Engineering Research Center, Yonsei University,
134 Shinchon-Dong, Seodaemun-Gu,
120-749 Seoul, Korea

C. K. Jeong · S. Y. Lee · J.-H. Choi · C.-Y. Kim · K.-J. Shin
Human Identification Research Institute, Yonsei University,
134 Shinchon-Dong, Seodaemun-Gu,
120-752 Seoul, Korea

Material and Methods

DNA samples

DNA from 300 unrelated Koreans (i.e. 150 males and 150 females) already typed for HumARA, DXS101, GATA172D05, HPRTB and DXS8377 [5] were analyzed in the present study. A male with a null allele at DXS9898 and his family members were also analyzed. Genomic DNA was extracted from buccal swabs using a QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions.

Multiplex PCR

The primer sequences and concentrations used for the PCR amplification of the four X-chromosomal STRs are shown in Table 1. Quadruplex PCR for DXS9898, DXS6809, DXS7424 and DXS10011 was carried out in a 10 µl reaction volume containing 1–2 ng DNA, 1.6 µl Gold STR 10×buffer (Promega, Madison, WI) and 2.0 U AmpliTaq Gold DNA polymerase (Applied Biosystems, Foster City, CA). Thermal cycling was conducted using a PTC-200

DNA engine (MJ Research, Waltham, MA) under the following conditions: 95°C for 11 min, 30 cycles at 94°C for 1 min, 55°C for 1 min, 72°C for 1 min and a final extension at 60°C for 45 min. The PCR products were analyzed by capillary eletrophoresis using an ABI PRISM 310 Genetic Analyzer (Applied Biosystems, Foster City, CA).

Genotyping of PCR products

Sequenced allelic ladders were constructed for all markers by combining observed alleles from each locus. Each allele was sequenced on an ABI PRISM 310 Genetic Analyzer using a BigDye Terminator Cycle Sequencing kit (Applied Biosystems, Foster City, CA). Allele typing was carried out based on the sequenced allelic ladders and by using Genotyper software (Applied Biosystems, Foster City, CA). Alleles were assigned according to the recommendations of the International Society of Forensic Genetics (ISFG) Commission [13]. The cell line sample K562, 9947A and 9948 (Promega, Madison, WI) were used for control DNA to calibrate allelic ladders.

PCR analysis for the loss of an allele at DXS9898

Since the loss of an allele was observed at the DXS9898 locus, DNA isolated from a male with a null allele at DXS9898 and from his family members were analyzed. All nine X-STRs (HumARA, DXS9898, DXS6809, DXS101, DXS7424, GATA172D05, HPRTB, DXS8377 and DXS10011) were genotyped in this family and to verify that the null allele at DXS9898 was caused by deletion of the DXS9898 locus, PCR primers were designed to include the DXS9898 locus in the center of amplification fragments (Table 1). The PCR amplifications of 392 and 1093 bp DNA regions were carried out using 50–100 ng DNA, and the resultant amplification products were analyzed by agarose gel electrophoresis.

For determination of whether female homozygotes at DXS9898 are genuine homozygotes or ostensible homozygotes due to the loss of an allele, the genotyping results of DXS9898 in females were validated by duplex-PCR in a semi-quantitative manner with a ratio of 1:1 or 1:2 of the target to the internal control [14]. A duplex-PCR for DXS9898 and amelogenin as an internal control was carried out in a 10 μl reaction volume containing 1 ng DNA, 1.6 μl Gold STR 10×buffer and 1.5 U AmpliTaq Gold DNA polymerase. The primer sequences and concentrations are shown in Table 1, and thermal cycling was conducted under the same conditions of multiplex PCR except for 28 cycles of amplification.

Statistical analysis

The following statistical analyses were carried out; expected heterozygosity (Het) [15], polymorphic information content (PIC) [16], mean exclusion chance in trio case (MEC) [17], power of exclusion in motherless case (PE) [17], power of discrimination (PD) in females and males [17]. Each of the four X-STR loci was also checked using Fisher's exact test to verify Hardy-Weinberg equilibrium. In order to compare allele distribution patterns between populations for the nine X-STRs (HumARA, DXS9898, DXS6809, DXS101, DXS7424, GATA172D05, HPRTB, DXS8377 and DXS10011), we tested the hypothesis of random distribution of different haplotypes among populations using the Arlequin statistical analysis package [18]. As the hemizygosity of gonosomes in males renders linkage analysis using male haplotype data particularly efficient for X-chromosomal loci [4], haplotype frequency estimates calculated in 150 males were used to calculate linkage disequilibrium using the Arlequin statistical analysis package under the null hypothesis of no association between the tested loci.

Results

Loss of an allele at DXS9898

The loss of an allele at DXS9898 was observed in 5 males and 8 females by multiplex PCR and semi-quantitative duplex PCR, respectively (3.3% and 2.7% in males and

Table 1 Primer sequences and concentrations for the four X-linked STR loci and the amelogenin gene

Locus	Sequence	Label	Primer conc. (μM)
DXS9898			
Primer 1	5'-CGA GCA CAC CTA CAA AAG CT-3'	-	0.38[a]/0.45[b]
Primer 2	5'-TCG ATT AGG TTC AGT TCC CA-3'	FAM	0.38[a]/0.45[b]
DXS6809			
Primer 1	5'-TGA ACC TTC CTA GCT CAG GA-3'	-	0.12
Primer 2	5'-TCT GGA GAA TCC AAT TTT GC-3'	FAM	0.12
DXS7424			
Primer 1	5'-CTG CTT GAG TCC AGG AAT TCA A-3'	FAM	0.33
Primer 2	5'-GAA CAC GCA CAT TTG AGA ACA TA-3'	-	0.33
DXS10011			
Primer 1	5'-GGA GTG AAC TCT GAA AAA AAA-3'	-	0.65
Primer 2	5'-TGA AAT CAT CTA TCT TTC TTT C-3'	HEX	0.65
DXS9898–392 bp[c]			
Primer 1	5'-GGA GAG CAG ATT GCA AAA ATG G-3'	-	0.40
Primer 2	5'-TCG TGT AAT TGT CTC CCC TTG A-3'	-	0.40
DXS9898–1093 bp[d]			
Primer 1	5'-CAC TGA ATT GGA GCC ACT TAT GG-3'	-	0.40
Primer 2	5'-CAC TGC AAA CAT TAG CAC TCC TG-3'	-	0.40
Amelogenin			
Primer 1	5'-CCC TGG GCT CTG TAA AGA ATA GTG-3'	HEX	0.40
Primer 2	5'-ATC AGA GCT TAA ACT GGG AAG CTG-3'	-	0.40

[a]Primer concentrations used for multiplex PCR consisting of DXS9898, DXS6809, DXS7424 and DXS10011.
[b]Primer concentrations used for duplex PCR consisting of DXS9898 and amelogenin.
[c]Primers used for the amplification of 392 bp DNA fragment which contains the DXS9898 locus.
[d]Primers used for the amplification of 1093 bp DNA fragment which contains the DXS9898 locus.

females, respectively, total 2.9%). STR genotyping of a family, including a male who showed a null allele at DXS9898, revealed that the presence of the null allele at the DXS9898 locus went back to his maternal grandmother and all family members in the maternal lineage were affected (Fig. 1). PCR analysis showed that the X-chromosome with a null allele at DXS9898 has a deletion of more than 1 kb at the DXS9898 locus since neither the 392 bp nor the 1093 bp PCR products of the normal X-chromosome could be amplified (Figs. 2 and 3).

Population data of DXS9898, DXS6809, DXS7424 and DXS10011 in Koreans

The four types of the representative repeat sequence structure of DXS10011 are displayed in Table 2. The DXS9898, DXS6809, DXS7424 and DXS10011 allele frequencies in a Korean population are shown in Table 3. Typing results were confirmed using standard DNA. Genotyping results of K562, 9947A and 9948 DNAs for DXS9898, DXS6809 and DXS7424 were identical with those in the literature [19]. At DXS10011, K562, 9947A and 9948 displayed genotypes, 20/20, 27/29, and 22.2, respectively.

Statistical parameters were calculated (Table 4) and no significant deviations from the Hardy-Weinberg equilibrium were found for any marker (P>0.05).

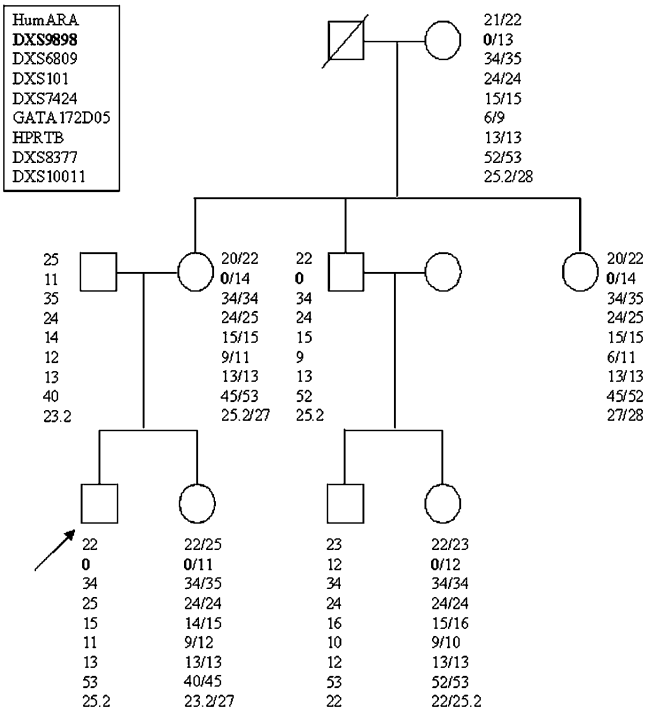

Fig. 1 Pedigree of a family, including a male who showed a null allele at DXS9898 in multiplex PCR analysis. STR genotypes are shown in the locus order depicted in the top left corner of the graph. The null allele was designated by the numeral 0. An *arrow* indicates the proband through whom the family was ascertained

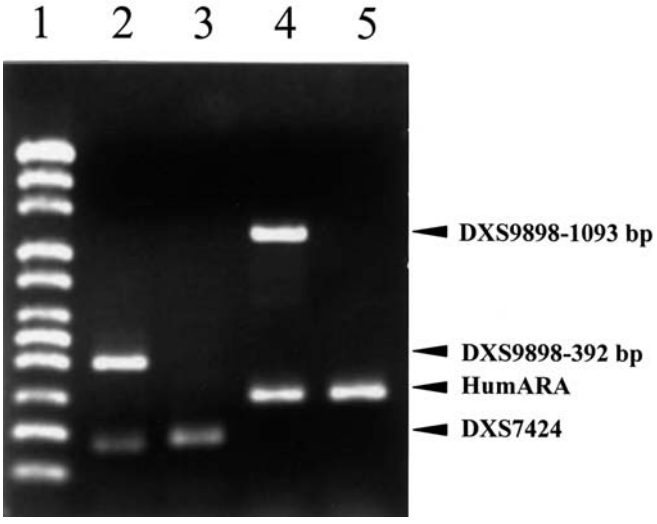

Fig. 2 PCR analysis of the loss of an allele at the DXS9898 locus. *Lane 1* 100 bp size marker, *lanes 2 and 3* the 392 bp PCR amplification of the DXS9898 locus in a common male and a male with a null allele, respectively, *lanes 4 and 5* the 1093 bp PCR amplification of the DXS9898 locus in a common male and a male with a null allele, respectively. DXS7424 and HumARA were used as internal positive standards for PCR amplification of 392 bp and 1093 bp DNA, respectively

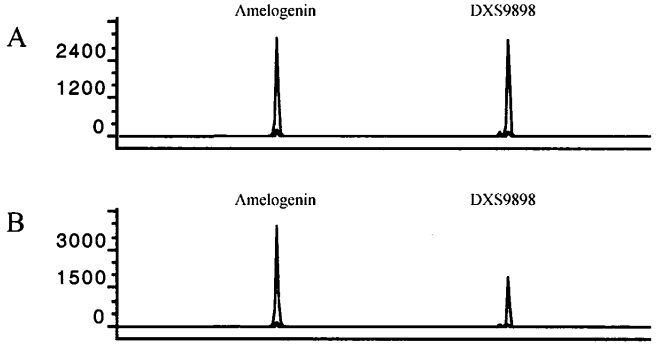

Fig. 3A-B Electropherograms of semi-quantitative duplex-PCR to validate the genotype results at DXS9898 in females. Genuine homozygotes **A** and ostensible homozygotes due to the loss of an allele **B** displayed 2 peaks with a ratio of 1:1 and 2:1 of the internal control to DXS9898, respectively. The amelogenin gene was used as an internal control

Population differences and linkage disequilibrium test for the nine X-STRs

Testing for allele frequency homogeneity in the German and Korean populations using the Alequin statistical analysis package yielded a P-value of <0.00001 at eight X-STR loci with the exception of DXS10011 (P=0.0899) [6, 9, 10, 12]. For homogeneity testing in the Japanese and Korean populations, the P-values were 0.0304, 0.4056 and 0.0065 for HumARA, HPRTB and DXS10011, respectively [11, 20, 21].

Since all markers are located on the q-arm of X-chromosome [4], intermarker linkage disequilibrium among the nine X-STRs was checked. However, exact test of linkage disequilibrium using male haplotype data

Table 2 Representative repeat sequence structures of DXS10011

DXS10011 repeat type	Sequence structure
Type 1 -AAGAA$(GAAA)_n$-	
20 (157 bp)	P_{F21}-AAGAA **$(GAAA)_{20}$**GAAGGAAAG(GAAG)-N16-P_{R22}
27 (185 bp)	P_{F21}-AAGAA **$(GAAA)_{27}$**GAAGGAAAG(GAAG)-N16-P_{R22}
38 (229 bp)	P_{F21}- AAGAA **$(GAAA)_{38}$**GAAGGAAAG(GAAG)-N16-P_{R22}
Type 2 -CAGAA(GAAA)GA$(GAAA)_6$(GAGA)($GAAA)_n$-	
22.2 (167 bp)	P_{F21}-**C**AGAA**(GAAA)GA$(GAAA)_6$(GAGA)$(GAAA)_{14}$**GAAGGAAAG(GAAG)-N16-P_{R22}
27.2 (187 bp)	P_{F21}-**C**AGAA**(GAAA)GA$(GAAA)_6$(GAGA)$(GAAA)_{18}$(GGAA)** GAAGGAAAG (GAAG)-N16-P_{R22}
Type 3 -AAGAAA$(GAAA)_n$-	
28.1 (190 bp)	P_{F21}-AAGAA**A$(GAAA)_{28}$** GAAGGAAAG(GAAG)-N16-P_{R22}
36.1 (222 bp)	P_{F21}-AAGAA**A$(GAAA)_{36}$**GAAGGAAAG(GAAG)-N16-P_{R22}
Type 4 -AAGAA$(GAAA)_2$ (GAA)$(GAAA)_n$-	
35.3 (220 bp)	P_{F21}-AAGAA**$(GAAA)_2$(GAA)$(GAAA)_{33}$** GAAGGAAAG(GAAG)-N16-P_{R22}

revealed that no linkage disequilibrium exists among these markers (P>0.05).

Discussion

As an extension of our previous study on the five polymorphic X-STRs, HumARA, DXS101, GATA172D05, HPRTB and DXS8377 in Koreans [5], we analyzed allele sequence structures and allele frequencies at the four X-STRs, DXS9898, DXS6809, DXS7424 and DXS10011. In the present study, DXS9898, DXS6809 and DXS7424 showed the identical allele sequence structures with those of the previous reports [6, 10]. DXS10011 showed four types of allele according to the sequence characteristics (Table 2). As the sequence structure of allele 31.3 in a Japanese population has not been available [12], we isolated the allele 35.3 which was expected to have the similar allele sequence structure with that of 31.3 and found the corresponding allele structure: $(GAAA)_2GAA(GAAA)_{33}$. On the other hand, we did not observe the allele structure like that of 28.2 in a Japanese population, with a GA dinucleotide insertion or an AA dinucleotide deletion between GAAA repeat units without an A to C transversion in the flanking region (**A**AGAA to **C**AGAA) (Table 2).

The null allele at the DXS9898 locus was identified and found to have a significant frequency in Koreans (as much as 2.9%). DXS9898 has been studied in Germans, Chinese and Koreans [6, 7, 8], and yet there has been no report about the null allele at this locus. Accordingly, it remains to be determined if the occurrence of the loss of an allele at the DXS9898 locus is specific for Koreans. Allele distribution patterns of DXS9898 showed a discrepancy between Koreans and Germans [6, 9]. The allele 8.3 which is the second most prevalent allele (25.9%) in Germans was encountered only in 4.7% of Koreans. Also, Germans displayed a relatively even allele distribution across the alleles 8.3, 11, 12, and 13 (25.9%, 21.9%, 29.3% and 16.4%, respectively), while Koreans show a concentrated allele distribution at allele 12 (47.8%).

To investigate the forensic utility of X-STRs in Koreans and to compare this with those of other ethnic populations, statistical methods were applied. The four X-STRs are confirmed to be highly informative along with the previously reported five X-STRs, HumARA, DXS101, GATA172D05, HPRTB and DXS8377. Also, statistical parameters values in Koreans were similar to those of Germans at all nine X-STR loci [9, 12]. That is, DXS10011 was the most informative marker in Germans followed by DXS8377, HumARA, DXS101, DXS6809, GATA172D05, DXS7424, HPRTB and DXS9898 in sequence, and this order was the same in Koreans except that the order of DXS101 and DXS6809 and the order of DXS9898 and HPRTB was reversed (Table 4). However, statistical parameters for forensic efficiency were generally lower in Koreans than in Germans [9].

Testing of the random distribution of the different haplotypes in populations revealed that there are discrepancies in the allele distributions of all eight X-STR loci (P<0.01) except for DXS10011 (P>0.01) between Koreans and Germans. Considering the much higher allele number at DXS10011, the relatively small population size of Germans and Koreans (215 and 450 chromosomes, respectively) might have been inadequate to produce reliable allele frequencies or allow allele frequency data comparisons between the populations. The allele distribution homogeneity test for DXS10011 in the Korean and Japanese populations (450 and 456 chromosomes, respectively) showed a discrepancy between the two populations (P<0.01). However, Korean and Japanese populations did not show the significant differences at HumARA or HPRTB (P>0.01). This is inferred to be the result of relatively less polymorphic characteristics of HumARA and HPRTB than DXS10011 and the geographic proximity of the Korean and Japanese populations.

According to the genetic localization of the nine X-STR loci [9, 10], several linkage groups have been reported, of

Table 3 Allelic frequencies of the four X-chromosomal loci in Koreans

Allele	DXS9898			DXS6809			DXS7424			DXS10011		
	Female	Male	Total	Female	Male	Total	Female	Male	Total	Female	Male	Total
0[a]	0.027	0.033	0.029									
8.3	0.043	0.053	0.047									
10	0.013	0.007	0.011									
11	0.110	0.073	0.098									
12	0.483	0.467	0.478				0.010	0.000	0.007			
13	0.253	0.267	0.258				0.070	0.060	0.067			
14	0.060	0.087	0.069				0.170	0.160	0.167			
15	0.007	0.013	0.009				0.293	0.300	0.296			
16	0.003	0.000	0.002				0.407	0.393	0.402			
17							0.033	0.060	0.042	0.003	0.000	0.002
18							0.017	0.027	0.020	0.010	0.007	0.009
19										0.023	0.033	0.027
20										0.020	0.047	0.029
21										0.037	0.033	0.036
21.2										0.023	0.020	0.022
22										0.033	0.047	0.038
22.2										0.037	0.053	0.042
23										0.040	0.067	0.049
23.2										0.073	0.053	0.067
24										0.037	0.020	0.031
24.2										0.040	0.013	0.031
25										0.033	0.053	0.040
25.2										0.033	0.013	0.027
26										0.040	0.087	0.056
26.2										0.023	0.007	0.018
27										0.060	0.047	0.056
27.2										0.003	0.000	0.002
28										0.070	0.053	0.064
28.1										0.000	0.007	0.002
29				0.007	0.007	0.007				0.083	0.080	0.082
30				0.023	0.013	0.020				0.067	0.033	0.056
31				0.177	0.187	0.180				0.030	0.020	0.027
32				0.153	0.160	0.156				0.037	0.013	0.029
33				0.277	0.327	0.293				0.030	0.047	0.036
34				0.180	0.167	0.176				0.017	0.020	0.018
35				0.117	0.080	0.104				0.027	0.033	0.029
35.3										0.003	0.000	0.002
36				0.053	0.053	0.053				0.020	0.033	0.024
36.1										0.003	0.000	0.002
37				0.007	0.000	0.004				0.020	0.013	0.018
38				0.007	0.000	0.004				0.010	0.013	0.011
39				0.000	0.000	0.000				0.003	0.007	0.004
40				0.000	0.007	0.002				0.003	0.007	0.004
41										0.000	0.000	0.000
42										0.003	0.013	0.007
43										0.000	0.007	0.002
44										0.003	0.000	0.002

[a]*Numeral 0* in allele column represents null allele

which the DXS101 and DXS7424 linkage group was found to show significant linkage disequilibrium in Germans [9]. However, the test for association in Koreans indicated the absence of linkage disequilibrium between DXS101 and DXS7424. Such a difference between populations in terms of linkage disequilibrium is regarded as being due to the fact of linkage disequilibrium not being a monotonic function of the distance between marker pairs [22]. Also, linkage disequilibrium is usually detected for markers as close as 10–20 kbp, and the distance between DXS101 and DXS7424 is 794 kb (http://www.ensembl.org). Other than linkage between loci, there are some other

Table 4 Comparison of the statistic parameters of the nine X-STR markers in Koreans

Markers	PIC	MEC	PE	PD^F	PD^M	Het
DXS10011	0.953	0.953	0.909	0.996	0.953	0.959
DXS8377	0.897	0.897	0.814	0.983	0.901	0.908
HumARA	0.880	0.880	0.812	0.978	0.899	0.893
DXS6809	0.795	0.795	0.642	0.943	0.796	0.822
DXS101	0.790	0.790	0.662	0.942	0.810	0.816
GATA172D05	0.706	0.706	0.596	0.898	0.762	0.743
DXS7424	0.667	0.667	0.536	0.871	0.722	0.716
DXS9898	0.642	0.642	0.510	0.859	0.694	0.686
HPRTB	0.621	0.621	0.520	0.839	0.711	0.682

PIC Polymorphic information content.
MEC Mean exclusion chance in trio cases.
PE Power of exclusion in motherless cases.
PD^F Power of discrimination in females.
PD^M Power ofdiscrimination in males.
Het Expected heterozygosity.

potential sources of linkage disequilibrium, like random drift, the founder effect, mutation, selection and population admixture or stratification [23]. Therefore, the linkage disequilibrium between DXS101 and DXS7424 in Germans is thought to be the complex result of some of the above parameters rather than a linkage between markers. In Koreans, no linkage disequilibrium was found between markers, and accordingly the allele frequencies of the nine X-STRs could be employed independently for forensic use.

To summarize, we investigated four highly informative X-STRs using interpopulation and intrapopulation statistical analyses and we report new findings regarding population differences and the loss of an allele at the DXS9898 locus.

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References

1. Urquhart A, Kimpton CP, Downes TJ, Gill P (1994) Variation in short tandem repeat sequences: a survey of twelve microsatellite loci for use as forensic identification markers. Int J Legal Med 107:13–20
2. Brinkmann B (1998) Overview of PCR-based systems in identity testing. Methods Mol Biol 98:105–119
3. Jobling MA, Pandya A, Tyler-Smith C (1997) The Y chromosome in forensic analysis and paternity testing. Int J Legal Med 110:118–124
4. Szibor R, Krawczak M, Hering S, Edelmann J, Kuhlisch E, Krause D (2003) Use of X-linked markers for forensic purposes. Int J Legal Med 117:67–74
5. Shin KJ, Kwon BK, Lee SS et al. (2004) Five highly informative X-chromosomal STRs in Koreans. Int J Legal Med 118:37–40
6. Edelman J, Hering S, Michael M et al. (2001) 16 X-chromosome STR loci frequency data from a German population. Forensic Sci Int 124:215–218
7. Son JY, Lee YS, Choung CM, Lee SD (2002) Polymorphism of nine X chromosomal STR loci in Koreans. Int J Legal Med 116:317–321
8. Huang DX, Liang WB, Wu MY (2002) Genetic polymorphism of the STR DXS9898 locus in Han population. Fa Yi Xue Za Zhi 18:150–151, 154
9. Edelmann J, Hering S, Kuhlisch E, Szibor R (2002) Validation of the STR DXS7424 and the linkage situation on the X-chromosome. Forensic Sci Int 125:217–222
10. Edelmann J, Deichsel D, Plate I, Kaser M, Szibor R (2003) Validation of the X-chromosomal STR DXS6809. Int J Legal Med 117:241–244
11. Watanabe G, Umetsu K, Yuasa I, Suzuki T (2000) DXS10011: a hypervariable tetranucleotide STR polymorphism on the X chromosome. Int J Legal Med 113:249–250
12. Tamura A, Iwata M, Takase I, Miyazaki T, Matsui K, Nishio H, Suzuki K (2004) Analysis of two types of novel alleles in the DXS10011 locus. Legal Med 6:52–54
13. Bär W, Brinkmann B, Budowle B et al. (1997) 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 110:175–176
14. Cirigliano V, Lewin P, Szpiro-Tapies S, Fuster C, Adinolfi M (2001) Assessment of new markers for the rapid detection of aneuploidies by quantitative fluorescent PCR (QF-PCR). Ann Hum Genet 65:421–427
15. Nei M, Roychoudhury AK (1974) Sampling variances of heterozygosity and genetic distance. Genetics 76:379–390
16. Botstein D, White RL, Skolnick M, Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am J Hum Genet 32:314–331
17. Desmarais D, Zhong Y, Chakraborty R, Perreault C, Busque L (1998) Development of a highly polymorphic STR marker for identity testing purposes at the human androgen receptor gene (HUMARA). J Forensic Sci 43:1046–1049
18. Schneider S, Roessli D, Excoffier L (2000) Arlequin ver. 2000: a software for population genetics data analysis. Genetics and Biochemistry Laboratory, University of Geneva, Switzerland
19. Szibor R, Edelmann J, Hering S et al. (2003) Cell line DNA typing in forensic genetics—the necessity of reliable standards. Forensic Sci Int 138:37–43
20. Kishida T, Tamaki Y (1997) Japanese population data on X-chromosomal STR locus AR. Nippon Hoigaku Zasshi 51:376–379
21. Kishida T, Wang W, Fukuda M, Tamaki Y (1997) Duplex PCR of the Y-27H39 and HPRT loci with reference to Japanese population data on the HPRT locus. Nippon Hoigaku Zasshi 51:67–69
22. Lonjou C, Zhang W, Collins A, Tapper WJ, Elahi E, Maniatis N, Morton NE (2003) Linkage disequilibrium in human populations. Proc Natl Acad Sci U S A 100:6069–6074
23. Chakravarti A (1999) Population genetics—making sense out of sequence. Nat Genet 21:56–60