J Forensic Sci, Mar. 2004, Vol. 49, No. 2
Paper ID JFS2003232
Published 19 Feb. 2004
Available online at: www.astm.org

FOR THE RECORD

Meili Lv[1]*; Weibo Liang*[1]*; Meiyun Wu*[1]*; Miao Liao*[1]*; Bin Zhou; Yi Jia; and Lin Zhang*[1,2]

Allele Frequency Distribution of Two X-Chromosomal STR Loci in Han Population in China*

POPULATION: 127 unrelated female and 118 unrelated male volunteer donors, Southwest China

KEYWORDS: forensic science, X-chromosome, DXS6789, HumSTRX1, short tandem repeat, the mean exclusion chance (MEC)

Blood specimens were obtained from 127 unrelated female and 118 unrelated male volunteer donors living in Chengdu, Southwest China.

DNAs were extracted from blood specimens using Chelex-100 (1). Genotyping was carried out by PCR in a PE9600 cycler. The components of a 20 μL reaction mixture were as follows: template DNA 20 ng, primer 0.2 μmol/L each, dNTPs 200 μmol/L each, KCl 50 μmol/L, Tris-HCl (pH8.3) 10 mmol/L, $MgCl_2$ 1.5 mmol/L, Taq polymerase 1U.

[1] College of Forensic Medicine, Sichuan University, Chengdu 610041, P. R. China.
[2] Key Lab of Biotherapy of Human Diseases, Ministry of Education, P. R. China.

* The research was supported by grants from the Chinese Natural Sciences Foundation (No.- 30171033) and State Ministry of Education (No. 01143) as well as Sichuan Youth Foundation (2001–2).

PCR conditions: start at 94°C for 3 min, followed by 30 cycles consist of 35 s at 94°C, 40 s at 57°C, 50 s at 72°C followed by a 10 min extention at 72°C. The amplified products were electrophoresed in 6% polyacrylamide gel by using 100 bp ladder and allelic markers as size markers, followed by silver staining. The amplified products were examined by using an ABI PRISM™ 310 Genetic Analyzer.

Both DXS6789 and HumSTRX1 loci are tetranucleotide. DXS6789 exhibited 10 clearly distinguishable alleles ranging from 146 bp to 182 bp. HumSTRX1 exhibited six clearly distinguishable alleles ranging from 214 bp to 234 bp.

The polymorphism information content (PIC), the mean exclusion chance (MEC) (2), the expected probability of exclusion (PE), average power of discrimination in females (PD^F) and in males (PD^M) was shown in Table 1. The genotype frequencies of both loci were shown in Table 2. 25 and 12 genotypes were found in

TABLE 1—*Allele frequency distributions of DXS6789 and HumSTRX1.*

DXS6789						HumSTRX1					
Allele	Female Number	Female (%)	Male Number	Male (%)	Total Freq. (%)	Allele	Female Number	Female (%)	Male Number	Male (%)	Total Freq. (%)
14	3	1.2	0	0	0.6	11	0	0	2	0.8	0.4
15	53	20.9	40	16.9	19.0	12	7	2.8	8	3.4	3.1
16	77	30.3	74	31.4	30.8	13	41	16.1	40	16.9	16.5
17	8	3.1	14	5.9	4.5	14	117	46.1	98	41.5	43.9
18	1	0.4	0	0	0.2	15	75	29.5	76	32.2	30.8
19	14	505	2	0.8	3.3	16	14	5.5	12	5.1	5.3
20	51	20.1	46	19.5	19.8	...	...	...	...	...	...
21	37	14.6	44	18.6	16.5	...	...	...	...	...	...
22	8	3.1	16	6.8	4.9	...	...	...	...	...	...
23	2	0.8	0	0	0.4	...	...	...	...	...	...
Total	127	1	118	1	1	Total	127	1	118	1	1
PD^F: 0.931; PD^M: 0.792; MEC: 0.769; PE*: 0.769; PE†: 0.644; PIC: 0.77						PD^F: 0.837; PD^M: 0.691; MEC: 0.637; PE*: 0.751; PE†: 0.621; PIC: 0.63					

* Both mother and child are tested.
† Only the child is tested.

TABLE 2—*Genotypes of DXS6789 and HumSTRX1 found in females.*

DXS6789		HumSTRX1	
Genotypes	Number	Genotypes	Number
14–16	3	12–13	1
15–15	4	12–14	2
15–16	11	12–15	4
15–17	2	13–13	6
15–18	1	13–14	12
15–19	4	13–15	15
15–20	11	13–16	1
15–21	12	14–14	24
15–22	4	14–15	47
16–16	14	14–16	8
16–19	4	15–15	2
16–20	13	15–16	5
16–21	12	...	...
16–22	4	...	...
16–23	2	...	...
17–20	4	...	...
17–21	2	...	...
19–20	5	...	...
19–21	1	...	...
20–20	6	...	...
20–21	6	...	...
21–21	2	...	...
HWE exact test: $P = 0.309 > 0.05$; Het: 0.795		HWE exact test: $P = 0.174 > 0.05$; Het: 0.748	

DXS6789 and HumSTRX1 loci respectively and they are in good agreement with the HWE. Additionally, we investigated the loci in 50 true trios with female children,which suggested a codominant X-linked inheritance. No mutations and no mother-child exclusions were found. It is suggested that these ChrX markers are useful for forensic analyses, especially in solving complicated kinship testing and paternity testing of lacking mother.

The complete data set is available to any interested researcher at http://www.legalmed.org/dna/DXS6789andHumSTRX1.htm.

Acknowledgment

Thanks to Sandra Hering and Jeanett Edelmann for supplying the formula of MEC.

References

1. Singer-Sam J, Tanguary RL, Riggs AD. Use of Chelex to improve the PCR signal from a small number of cells. Amplification 1989;(3):11.
2. Hering S, Kuhisch E, Szibor R. Development of the X-linked tetrameric microsatellite marker HumDXS6789 for forensic purposes. Forensic Sci Int 2001;42–6. [PubMed]
3. Kishida T, Wang W, Fukuda M, Tamaki Y. Duplex PCR of the Y-27H39 and HPRT loci with reference to Japanese population data on the HPRT locus (Japanese). J Legal Med 1997;51:67–9.
4. Desmarais D, Zhong Y, Chakraborty R, Perreault C, Busque L. Development of a highly polymorphic STR marker for identity testing purposes at the human androgen receptor gene (HUMARA). J Forensic Sci 1998;43:1046–9. [PubMed]
5. Edelmann J, Hering S, Kuhlisch E, et al. Validation of the STR DXS7424 and the linkage situation on the X-chromosome. Forensic Sci Int 2002;125:217–22. [PubMed]

Additional information of primer:
DXS6789:
P1:5′-TGT CCT ATT GTA TTA GTC AGG GAT C-3′;
P2:5′-ATG TAA GTT GGT ACT TAA TAA ACC CTC-3′.
HumSTRX1:
P1:5′-GTT TCC TCC TGC AAA ATA CAG C-3′;
P2:5′-TCC AGC ACC CAA GGA AGT C-3′.

Additional information and reprint requests:
Prof. Zhang Lin
College of Forensic Medicine
Sichuan University
Chengdu, 610041, Sichuan
P. R. China
E-mail: kjc@scu.edu.cn