Available online at www.sciencedirect.com
SCIENCE DIRECT
Forensic Science International 158 (2006) 76–79
Forensic Science International
www.elsevier.com/locate/forsciint

Announcement of population data

Patterns of genetic polymorphism at the 10 X-chromosome STR loci in Mongol population

Qingbo Liu [a,b], Shengbin Li [a,b,c,*]

[a] *Key Laboratory of Environment and Genes Related to Diseases, Xi'an Jiaotong University, Ministry of Education, Xi'an Shaanxi 710061, China*
[b] *The Key Laboratory of National Ministry of Health for Forensic Sciences, Xi'an Jiaotong University, Xi'an Shaanxi 710061, China*
[c] *Beijing Genome Institute, Chinese Academy of Sciences, Beijing 101300, China*

Received 27 September 2004; received in revised form 1 April 2005; accepted 13 April 2005
Available online 8 November 2005

Abstract

Genetic diversity at 10 X-chromosome STR loci has been approved and widely used for forensic science field. In this paper, we have studied this genetic diversity in various Mongol ethnic group with geographic backgrounds. Allele frequencies of 10 X-chromosome STR loci, including DXS7133, DXS6799, DXS8378, DXS7423, DXS6804, HPRTB, DXS7424, DXS7132, DXS6789 and DXS101, were obtained from healthy unrelated individuals (53 females and 47 males) of Mongol ethnic group lived in north China. Gene diversity analysis showed that the average heterozygosity was uniformly high (0.687) in the studied population. The coefficient of PIC was 0.99998.

Keywords: X-chromosome; Polymorphism; STR; Mongol ethnic population

Population: Blood samples (53 females, 47 males) were obtained from healthy unrelated individuals of Mongol ethnic group, whose ancestors of three generations lived in Neimengu, north China. Mongol is 1 of 56 nations living in China. The population of Mongol in China is 4.807 million. Most of them live in Inner Mongolia Autonomous Region, and few lived in northeast and northwest China. Mongol is speaking Mongolian. In 1206, a leader of a Mongolia group, named Tiemuzhen, established the Mongol empire. From then on, Mongol had become an independent ethnic group.

DNA extraction: Genomic DNA was extracted from EDTA whole blood by Chelex-100 protocol [1].

PCR: PCR amplifications were performed using primer sequences based on GeneBank information (http://www.gdb.org) and literature [2]. PCR was performed using Gene® Amp PCR sys9600 Thermal Cycler (Applied Biosystems Division/Perkin-Elmer, Foster City, CA).

Gene typing: PCR products were separated in 8% denaturing PAGE gel containing 7 M urea and DNA fragments were visualized by silver staining. Gene typing was done by home-made reference allelic ladders.

Results: All data are shown in Tables 1 and 2.

Data analysis: The allele frequencies data were analyzed based on the Hard–Weinberg probability test. Polymorphism information content (PIC), average power of discrimination in female (PD^F) and in male (PD^M) [3,6], and the heterozygosity value (H) [4,5]. The statistical analysis indicated no significant deviation from Hard–Weinberg equilibrium.

* Corresponding author. Tel.: +86 29 82655474; fax: +86 29 82655113.
E-mail address: Shbinlee@mail.xjtu.edu.cn (S. Li).

0379-0738/$ – see front matter © 2005 Elsevier Ireland Ltd. All rights reserved.
doi:10.1016/j.forsciint.2005.04.027

Table 1
Allele frequencies for X-chromosomal STRs loci in the population of Mongol (north China)

Allele	DXS7133		DXS6799		DXS8378		DXS7423	
	Female	Male	Female	Male	Female	Male	Female	Male
8			–	0.0326				
9	0.6792	0.6848	0.0189	0.0435	0.0189	0.0326		
10	0.2075	0.2065	0.1321	0.1630	0.6226	0.5435		
11	0.0566	0.1087	0.6604	0.5435	0.2264	0.2609		
12	0.0566	–	0.1887	0.1739	0.1132	0.1413	0.0370	–
13			–	0.0435	0.0189	0.0217	–	–
14							0.1667	0.3370
15							0.6667	0.6304
16							0.0926	0.0326
17							0.0370	–

	DXS6804		HPRTB		DXS7424		DXS7132	
	Female	Male	Female	Male	Female	Male	Female	Male
9	–	0.0109	0.0200	–				
10	–	0.0217	0.0600	0.0870				
11	0.1509	0.1957	0.1600	0.0978				
12	0.1887	0.1957	0.2200	0.2826	–	0.0213	0.0189	0.0745
13	0.3962	0.3696	0.2200	0.3043	–	–	0.2642	0.2128
14	0.1509	0.1196	0.2800	0.1739	0.0588	0.0213	0.3585	0.3936
15	0.1132	0.0761	0.0400	0.0435	0.2157	0.0213	0.2642	0.2340
16	–	0.0109	–	0.0109	0.0588	0.2553	0.0755	0.0851
17					0.3922	0.3936	0.0189	–
18					0.1765	0.2447		
19					0.0784	0.0319		
20					0.0196	0.0106		

	DXS6789		DXS101	
	Female	Male	Female	Male
14			0.0192	–
15			–	–
16	0.1132	0.1000	–	–
17	0.2453	0.1889	–	–
18	0.0189	0.0222	–	0.0109
19	–	–	–	–
20	0.0377	0.1000	–	–
21	0.3208	0.1778	0.0577	0.0652
22	0.1509	0.2000	0.1731	0.0978
23	0.1132	0.1889	0.3269	0.2609
24	–	0.0222	0.1538	0.1304
25			0.1154	0.2609
26			0.0769	0.1196
27			0.0577	0.0217
28			0.0192	0.0217
29			–	0.0109

Access to the data: The complete data are available to any interested researchers via e-mail of author (liuqing7510@sohu.com).

Other remarks: This study proved that allele distribution of 10 X-chromosome STRs loci was equal polymorphism in Mongol ethnic group of China, as in other population [2]. The data of 10 X-chromosome STRs in Mongol ethnic group of China is according to Hard–Weinberg equilibrium. We have only performed eight STR loci population comparison analysis because the fact that population data on these new X-STRs are scarce. The population data are cited from the previous reports of Korean, German, Italy, Spain and Chinese Han populations with one-way ANOVA [7–15]. The allele frequencies for each X-STR marker were calculated for females and males separately in five populations. There was no