Int J Legal Med (2005) 119: 306–309
DOI 10.1007/s00414-005-0549-5

SHORT COMMUNICATION

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Y-chromosomal STR haplotypes in Chinese Uigur ethnic group

Received: 4 August 2004 / Accepted: 8 April 2005 / Published online: 18 June 2005
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Abstract We have already coamplified minimal haplotypes (DYS19, D.YS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385I/II), two additional loci, namely, DYS438, DYS439, and Amelogenin, in a single PCR using the Y-PLEX 12 kit. We investigated 107 unrelated male individuals from the Uigur ethnic group and studied the allelic frequency distribution and haplotype diversity of 11 Y-chromosomal STRs. A number of 43 alleles (nine STR loci) and 27 phenotypes (including DYS385) were detected, with frequencies ranging from 0.0092 to 0.6296. A total of 103 haplotypes were identified, among which 99 were individual-specific and four haplotypes were found twice. The haplotype diversity for these 12 Y-STR loci was 0.9993.

Keywords Y-chromosomal STR haplotypes · Chinese Uigur ethnic group · Y-PLEX 12 kit

Introduction

Researches in Y-chromosomal genetic markers, assay, and forensic applications and population genetic studies have seen tremendous growth in recent years [1–4]. Genetic markers of Y chromosome were inherited by the patrilineal and haploid methods. The anthropologist studied human migration and evolution by comparing the genetic distance and by clustering among different populations using Y-STR loci. Y-STR loci have been recognized as very useful tools because of some specific properties compared with autosomal STR loci [5, 6]. They can be used to analyze mixed stains in sexual assault cases, especially analysis of azoospermia semen samples from vasectomized men. We analyzed 11 Y-STR loci of 107 unrelated Uigur male individuals. Research results will be based on forensic applications and population genetics in the future and enriched Chinese genetic informational resources.

Material and methods

DNA samples

The blood samples were obtained from 107 unrelated healthy male individuals of Chinese Uigur ethnic group living in Yili Uigur Ethnic Autonomous Region, Xingjiang province of China. The ethnic group is a member of a mainly agricultural Turkic people inhabiting the Xinjiang region in China and believes Islam. It has national characters and languages that affiliated the Altai phylum and Tuiki branch.

PCR amplification and typing

Whole blood samples were obtained by venipuncture and collected into EDTA tubes. Genomic DNA was extracted using the Chelex-100 protocol as described by Walsh et al. [7]. PCR for 11 Y-chromosomal STRs was performed in fluorescence-based multiplex reaction using Y-PLEX 12 kit (Reliagene Technologies Inc., New Orleans, LA). Thermal cycling was conducted using the following conditions: 95°C for 10 min; 30 cycles of 94°C for 60 s, 58°C for 60 s, 70°C for 60 s; and a final extension of 60°C for 60 min. Detection and genotyping of all PCR products were sep-

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Table 1 Y chromosome haplotypes were observed in Chinese Uigur ethnic population (*n*=107)

Sample	Pop.	n	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	DYS385
CU12	U	1	14	13	31	23	10	10	12	10	12	14,20
CU22	U	1	14	14	32	23	9	10	13	9	11	12,15
CU40	U	1	14	14	32	23	9	10	13	9	11	12,16
CU62	U	1	14	14	29	23	11	10	13	10	11	14,18
CU1	U	1	14	14	29	23	10	10	14	11	12	13,13
CU18	U	1	16	14	30	22	9	11	13	11	10	11,12
CU50	U	1	15	13	30	22	10	11	14	11	12	13,15
CU32	U	1	13	12	28	23	10	11	11	11	12	14,16
CU42	U	1	15	13	29	23	10	11	12	9	12	13,16
CU64	U	1	14	13	31	23	10	11	12	9	11	13,14
CU3	U	1	14	13	29	23	10	11	13	10	11	10,13
CU19	U	1	13	14	31	23	11	11	13	11	12	14,15
CU75	U	1	15	13	28	23	10	11	14	10	11	11,13
CU70	U	2	14	13	29	24	10	11	12	10	11	13,16
CU85	U		14	13	29	24	10	11	12	10	11	13,16
CU100	U	1	15	13	29	24	9	11	13	11	11	12,15
CU51	U	1	15	13	28	24	10	11	13	10	13	11,13
CU33	U	1	14	13	29	24	10	11	13	11	11	11,14
CU41	U	1	15	13	29	24	10	11	13	11	12	12,13
CU20	U	1	17	13	30	24	10	11	13	11	10	13,13
CU2	U	1	16	13	31	24	10	11	13	11	11	11,15
CU95	U	1	15	13	31	24	11	11	13	11	10	14,14
CU63	U	1	16	14	31	24	9	11	13	10	11	12,12
CU86	U	1	13	14	30	24	10	11	13	10	10	14,20
CU102	U	1	16	13	28	25	10	11	13	10	10	12,13
CU93	U	1	15	13	29	25	10	11	13	10	10	12,13
CU71	U	1	16	13	29	25	10	11	13	10	10	12,12
CU43	U	1	16	13	29	25	10	11	13	10	10	13,13
CU53	U	2	16	13	29	25	10	11	13	10	10	12,13
CU88	U		16	13	29	25	10	11	13	10	10	12,13
CU76	U	1	16	13	29	25	10	11	13	11	10	13,14
CU35	U	1	16	13	29	25	10	11	13	11	11	13,13
CU52	U	1	16	13	30	25	10	11	13	11	10	13,14
CU21	U	1	16	13	31	25	10	11	13	11	10	10,13
CU4	U	1	16	13	30	25	11	11	13	12	10	11,14
CU67	U	1	16	13	31	25	11	11	13	11	10	11,14
CU44	U	1	15	14	31	25	11	11	13	11	10	11,15
CU98	U	1	16	14	31	25	11	11	13	10	10	11,14
CU34	U	1	14	13	31	25	9	11	14	10	11	12,16
CU87	U	1	17	13	29	25	10	11	14	10	10	11,12
CU78	U	1	14	13	30	22	10	12	12	10	11	14,19
CU13	U	1	15	12	29	23	9	12	12	10	11	13,13
CU5	U	1	14	12	28	23	10	12	12	11	12	13,19
CU23	U	1	15	12	29	23	10	12	12	10	12	13,18
CU84	U	1	13	13	29	23	10	12	12	9	11	13,17
CU94	U	1	15	13	29	23	10	12	12	9	12	13,14
CU45	U	1	14	13	31	23	10	12	12	9	11	13,14
CU69	U	1	14	13	29	23	11	12	12	11	11	11,14
CU74	U	1	13	14	31	23	10	12	13	11	12	13,13
CU25	U	1	14	14	31	23	10	12	13	11	11	13,13
CU10	U	1	14	12	28	23	10	12	14	10	11	13,14
CU54	U	1	17	12	28	24	11	12	12	10	11	12,17
CU31	U	1	14	13	29	24	10	12	12	9	11	13,14
CU66	U	1	14	13	29	24	10	12	12	10	11	13,16

Table 1 (continued)

Sample	Pop.	n	DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	DYS385
CU73	U	1	15	13	30	24	10	12	12	11	11	13,18
CU77	U	1	15	14	31	24	9	12	12	10	12	12,14
CU68	U	1	14	12	28	24	10	12	15	9	12	13,17
CU36	U	1	15	13	29	25	10	12	12	10	12	12,13
CU89	U	1	14	13	29	25	11	12	12	10	11	13,16
CU24	U	1	16	13	30	22	10	13	12	10	11	11,20
CU7	U	1	15	12	28	22	9	13	13	10	12	12,24
CU30	U	1	13	14	31	22	10	13	13	12	12	13,16
CU59	U	1	17	12	28	23	10	13	12	10	11	13,13
CU16	U	1	15	12	29	23	10	13	12	10	12	13,18
CU105	U	1	15	12	29	23	11	13	12	10	11	11,14
CU83	U	1	15	13	29	23	11	13	12	10	11	12,14
CU26	U	2	14	14	32	23	9	13	13	9	11	12,15
CU103	U		14	14	32	23	9	13	13	9	11	12,15
CU107	U	1	15	14	30	23	10	13	13	13	12	10,13
CU37	U	1	16	14	31	23	10	13	13	11	12	11,13
CU97	U	1	14	14	32	23	10	13	13	10	12	14,16
CU101	U	1	13	14	31	23	11	13	13	11	12	14,15
CU39	U	1	15	13	29	24	10	13	12	10	11	13,14
CU91	U	1	13	13	30	24	10	13	12	12	12	12,14
CU79	U	1	14	13	29	24	11	13	12	12	14	11,14
CU6	U	1	15	11	29	24	11	13	13	10	11	12,14
CU99	U	1	16	12	29	24	10	13	13	11	11	11,13
CU82	U	1	15	13	29	24	10	13	13	11	11	13,14
CU14	U	1	14	13	29	24	11	13	13	12	13	11,14
CU92	U	1	15	13	31	24	11	13	13	10	13	14,15
CU106	U	1	16	14	31	24	10	13	13	11	12	11,13
CU27	U	1	15	12	29	24	10	13	14	11	11	13,16
CU96	U	1	16	14	31	24	10	13	14	11	11	11,13
CU55	U	1	15	14	30	24	11	13	15	10	11	10,14
CU72	U	1	13	12	29	25	11	13	12	10	11	12,17
CU58	U	1	16	14	31	25	9	13	12	10	10	13,15
CU65	U	1	13	12	28	25	10	13	13	10	13	12,13
CU104	U	1	17	13	31	25	10	13	13	11	11	13,14
CU17	U	2	16	13	31	25	11	13	13	11	11	11,14
CU28	U		16	13	31	25	11	13	13	11	11	11,14
CU48	U	1	14	14	31	25	9	13	13	10	11	12,12
CU9	U	1	15	13	29	21	10	14	12	10	12	11,13
CU80	U	1	13	14	31	22	9	14	14	11	12	12,14
CU57	U	1	14	14	30	22	10	14	14	10	10	11,12
CU29	U	1	14	14	31	23	10	14	11	10	12	12,16
CU38	U	1	13	14	30	23	9	14	13	12	12	12,15
CU47	U	1	14	12	28	24	10	14	12	11	12	13,18
CU96	U	1	14	12	28	24	10	14	12	11	12	13,20
CU61	U	1	14	13	29	24	10	14	14	11	10	11,14
CU49	U	1	13	13	30	22	11	15	13	12	12	14,16
CU81	U	1	15	12	29	22	9	15	14	10	11	13,15
CU71	U	1	15	12	29	22	10	15	14	10	12	12,13
CU15	U	1	15	14	32	23	10	15	11	10	12	12,13
CU56	U	1	14	13	29	23	10	15	13	10	11	13,13
CU60	U	1	13	13	31	23	10	15	14	11	12	13,15
CU46	U	1	15	13	29	23	11	15	14	10	11	14,20
CU8	U	1	15	12	30	24	10	15	14	11	11	12,13
GD			0.7569	0.6182	0.7316	0.7268	0.5325	0.7658	0.6419	0.6466	0.6698	0.9498
AN			5	4	5	5	3	6	5	5	5	27

GD: gene diversity of STR loci; AN: observed allelic number of STR loci

CU=Chinese Uigur population; U=Uigur ethnic group arated using capillary electrophoresis on an ABI3100 DNA genetic analyzer (Applied Biosystem) and Y12-Typer3100*v* 2.0 macros (Reliagene) together with the allelic ladders provided by the kit.

Statistical analysis

Allele frequencies were calculated by gene-counting method. Haplotypes and gene diversities were estimated according to Nei [8]. The relationship of different populations was estimated by the method of Bonferroni's correction in ANOVA, which is a multiple-comparison method used when several independent statistical tests are being performed simultaneously.

Results and discussion

Most of the members of the Chinese Uigur ethnic group live in Xinjiang Uigur Autonomous Region, northwest China. This region borders three Central Asian states; thus, they have many ethnical and linguistical common backgrounds. Chinese Uigur has a religion of Islam, its own language and characters were based on Arabic. According to the fifth population survey China, the population of Uigur in this region is 8,345,622 (45.21% of total). There has never been any report about Y-chromosomal STR haplotypes in Chinese Uigur ethnic group until now.

Haplotype results were obtained for the 11 loci selected by the Scientific Working Group on DNA analysis methods (SWGDAM) for forensic DNA analysis. Haplotypes and gene diversity of 11 Y-STRs in Uigur ethnic group are shown in Table 1, which was designed according to Kyoung et al. [4]. A total of 103 haplotypes were identified, among which 99 were individual-specific and four haplotypes were found twice. The haplotype diversity for 11 Y-STR loci was 0.9993. DYS385 locus showed the highest gene diversity (0.9498), but DYS391 locus was the lowest (0.5325). A number of 43 alleles (nine Y-STR loci) and 27 phenotypes (including DYS385) were observed in 11 Y-STR loci, with frequencies ranging from 0.0092 to 0.6296. The allele 10 of DYS391 locus had the highest frequency (0.6296). The four most frequent haplotypes H14 (14–13–29–24–10–11–12–13,16–10–11), H28 (16–13–29–25–10–11–13–12,13–10–10), H65 (14–14–32–23–9–13–13–12,15–9–11), and H86 (16–13–31–25–11–13–13–11,14–11–11) of this population were found in eight individuals (7.48%). We have searched these four most frequent haplotypes in the YHRD database (http://www.yhrd.org) and found that H14 was matched with the most frequent haplotypes of central Anatolia population of Turkey (0.89%). By the statistical method of Bonferroni's correction in ANOVA of SPSS, we have compared the data in the present study with other reported results [9–14] and found that there were significant differences between Uigur and Han populations (p=0.047) [9], between Uigur and Spain populations (p=0.017) [11], and between Uigur and Korean populations (p=0.006) [12]. Thus, the results in the present study are valuable to establish Y-STR database in Uigur ethnic group for forensic statistical calculations, which can enrich our ethnical informational resources. Y-STR haplotypes of other Chinese ethnic groups are being investigated in process. Chinese population genetics study will be carried out in the future.

Data of Y-chromosomal STR haplotypes in Chinese Uigur ethnic group are submitted to the YHRD database at http://www.yhrd.org and are in process.

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