

FOR THE RECORD

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Allele Frequency Distribution at Seven Y-Chromosomal STR Loci Among Five Ethnic Groups from Northwest China

POPULATION: Chinese Ethnic group Dongxiang, Bao'an, Hui and Yugu and Han Chinese in Gansu province (NW China), $N = 403$.

KEYWORDS: forensic science, DNA typing, population genetics, Y chromosome, short tandem repeat, Chinese ethnic group, allele frequency, DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385

We have analyzed the distribution of allele frequencies at seven Y-chromosomal short tandem repeat (STR) loci (DYS19, DYS389I/II, DYS390, DYS391, DYS392, DYS393 and DYS385) among five anthropologically distinct ethnic groups of China, namely, Dongxiang, Bao'an, Hui, Yugu, and Han. In this study, 403 unrelated male subjects from five areas that belong to Gansu province (NW China) and scattered along the old "silk road" were investigated. 133 Dongxiang individuals from Dongxiang county, 78 Bao'an individuals from Bao'an county, 56 Yugu males from the Sunan county, 66 Hui males from the Linxia city and 70 Han males from the Tianshui area. Both Bao'an and Dongxiang are Mongolian-speaking, Yugu ethnic group speak Mongolian, while the Hui is Chinese-speaking but some of Arabic and Farsi remained (1).

Genomic DNA was extracted from EDTA Blood using a standard method of Phenol-chloroform-isoamyl alcohol extraction (2). Blood samples from 403 unrelated healthy males were collected from randomly selected individuals in each ethnic group. All subjects were resident in their own hometown, respectively, and whose last three generations was endogamy.

The amplification was carried out in a Perkin-Elmer 2400 Thermo Cycle, each locus was amplified individually except for DYS389 I/II and DYS385. The primer sequences and cycling conditions for DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393 are described in Kayser et al. (3) and for DYS385 in Schneider et al. (4).

Detection of the amplified products was carried out by electrophoresis on a 6% denaturing polyacrylamide gel containing 8 M urea, in $1 \times$ TBE buffer, for 2.5 h at a constant 50 W, with

a separation distance of 40 cm. Bands were visualized by silver staining (5). Allele designations were based on comparison with the self-constructed allelic ladders obtained by the mixture of previously sequenced samples for the most common alleles. Allele nomenclature follows Kayser et al. (3) and de Knijff et al. (6).

Access to Data—Via electronic mail from communicating author, An Lizhe, e-mail: mailto:yyj229@263.net

Allele frequencies and gene diversities were calculated by using the software ARLEQUIN ver.2000.

Y-STR allele distribution and frequencies and gene diversity for seven STR locus in five populations were seen in Table 1. Allele distribution and frequencies and gene diversity value at the locus DYS385 in the Yugu, Hui, Han, Dongxiang and Bao'an ethnic groups were shown in Table 2.

Among all the 403 samples, a total number of 346 different haplotypes were observed, 308 of them being unique, while the others were shared by 2 or 3 individuals: 27 haplotypes were observed twice, 11 occurred 3 times, 1 occurred 4 times, 1 occurred 6 times. The haplotype 16-12-28-24-10-10-14-16/18, which is the most frequent in our samples, was shared by 6 individuals. In the 133 Dongxiang samples, there are 110 different haplotypes were observed, while in Bao'ans, we found 68 different haplotypes among 78 samples, We also found 59 different haplotypes among 66 Hui samples, 52 different haplotypes among 56 yugu samples, and 66 different haplotypes among 70 Han male samples.

Gene diversity ranged from 0.331 at DYS391 (Yugu) to 0.952 at DYS385 (Han). The overall discrimination capacity of the eight loci haplotypes analysed was 82.7% (Dongxiang), 87.18% (Bao'an), 89.39% (Hui), 92.86% (Yugu), and 94.29% (Han), respectively. The haplotype diversity value calculated from all eight-loci combined was 0.981 (Bao'an), 0.989 (Dongxiang), 0.978 (Yugu), 0.980 (Hui) and 0.983 (Han), respectively, which is informative.

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TABLE 1—Y-STR allele distribution and frequencies (%) for microsatellites DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392 and DYS393 in the Dongxiang, Bao'an, Yugu, Han and Hui populations (h^a : Gene diversity value).

Locus	Allele (Repeat)	Frequency					
		Dongxiang	Bao'an	Yugu	Hui	Han	
DYS19	12	1.50	0.0	0.0	0.0	0.0	
	13	6.02	1.28	0.0	9.10	0.0	
	14	25.56	16.67	3.60	28.8	17.1	
	15	35.34	19.23	41.00	31.8	35.7	
	16	30.08	48.72	37.5	27.3	35.7	
	17	1.50	12.82	14.3	3.00	10.0	
	18	0.0	1.28	3.60	0.0	1.4	
	h^a	0.719	0.681	0.67	0.732	0.705	
DYS389I	9	0.0	0.0	1.8	0.0	0.0	
	10	0.0	0.0	44.6	12.1	21.4	
	11	7.52	15.38	26.8	34.9	17.1	
	12	31.58	47.44	23.2	30.3	34.3	
	13	42.86	17.95	3.6	19.7	17.1	
	14	15.79	16.67	0.0	3.0	10.0	
	15	2.26	2.56	0.0	0.0	0.0	
h^a	0.686	0.691	0.674	0.731	0.768		
DYS389II	25	0.0	3.85	0.0	0.0	0.0	
	26	0.0	0.0	0.0	0.0	0.0	
	27	0.0	20.51	0.0	19.7	28.6	
	28	32.33	41.03	39.3	43.9	21.4	
	29	54.14	30.77	48.2	27.3	51.4	
	30	13.53	3.85	7.1	9.1	20.0	
	31	0.0	0.0	5.4	0.0	2.9	
	32	0.0	0.0	0.0	0.0	1.4	
	h^a	0.584	0.692	0.605	0.686	0.648	
	DYS390	21	1.5	2.56	12.5	4.6	1.4
		22	5.26	3.85	23.2	9.1	30.0
		23	12.78	8.97	19.6	31.8	28.6
24		37.59	25.64	26.8	45.5	21.4	
25		30.08	21.79	7.1	7.6	12.9	
26		12.03	33.33	7.1	3.6	1.5	
27		0.0	3.85	3.6	1.5	1.4	
h^a		0.734	0.764	0.808	0.676	0.764	
DYS391	9	16.54	1.28	14.3	48.5	18.6	
	10	50.38	65.38	80.4	43.9	60.0	
	11	29.32	33.33	5.4	4.6	20.0	
	12	3.76	0.0	0.0	1.5	1.4	
h^a	0.631	0.461	0.331	0.555	0.565		
DYS392	10	0.0	0.0	1.8	0.0	0.0	
	11	2.26	5.13	16.1	9.1	7.1	
	12	1.5	10.26	7.1	15.2	17.1	
	13	16.54	23.08	33.9	33.3	22.9	
	14	55.64	48.72	17.9	22.7	28.6	
	15	14.29	7.69	16.1	10.6	15.7	
	16	9.77	5.13	7.1	9.1	8.6	
h^a	0.632	0.690	0.791	0.787	0.799		
DYS393	11	0.0	2.56	0.0	0.0	0.0	
	12	0.0	8.97	0.0	3	1.4	
	13	27.82	35.9	48.2	33.3	55.7	
	14	43.61	33.33	33.9	42.4	21.4	
	15	23.31	17.95	17.9	16.7	14.3	
	16	5.26	1.29	0.0	4.6	7.1	
h^a	0.675	0.719	0.621	0.678	0.618		

Our results revealed that a set of eight Y-STRs can discriminate between most of the male individuals in the Northwest Chinese population. The Y-STR polymorphism in the Northwest Chinese population with an mean haplotype diversity of 0.983 and a mean discrimination capacity of 88.56% will be very useful for testing paternal lineages.

TABLE 2—Allele distribution and frequencies (%) and gene diversity (h^a) value at the Y-chromosome STR locus DYS385 in the Dongxiang, Bao'an, Yugu, Hui and Han ethnic groups.

Allele	Dongxiang	Bao'an	Yugu	Han	Hui
10-15	0.0	1.28	0.0	0.0	0.0
11-16	0.0	1.28	0.0	0.0	0.0
12-20	0.0	1.28	0.0	0.0	0.0
13-13	0.0	1.28	0.0	0.0	0.0
13-14	0.0	1.28	0.0	2.9	0.0
13-16	0.75	1.28	0.0	2.9	0.0
14-14	0.75	1.28	0.0	1.4	0.0
14-15	1.5	0.0	1.8	4.3	0.0
14-16	3.76	0.0	0.0	5.7	0.0
14-17	6.77	3.85	0.0	2.9	0.0
14-18	0.0	1.28	0.0	2.9	0.0
14-19	0.75	6.41	0.0	5.7	0.0
14-20	0.0	0.0	0.0	1.4	0.0
15-15	2.26	0.0	1.8	1.4	1.5
15-16	4.51	1.28	1.8	4.3	1.5
15-17	5.26	1.28	1.8	1.4	1.5
15-18	1.5	1.28	5.4	2.9	6.1
15-19	0.75	2.56	8.9	8.6	1.5
15-20	3.01	3.85	1.8	2.9	0.0
15-21	0.75	5.13	0.0	0.0	0.0
16-16	2.26	0.0	1.8	1.4	1.5
16-17	17.29	1.28	5.4	7.1	10.6
16-18	15.79	5.13	7.1	8.6	7.6
16-19	6.02	17.95	12.5	4.3	6.1
16-20	5.26	11.54	1.8	1.4	3.0
16-21	0.75	1.28	3.6	1.4	1.5
16-22	0.0	1.28	0.0	0.0	0.0
17-17	2.26	3.85	5.4	0.0	3.0
17-18	2.26	1.28	5.4	0.0	6.0
17-19	3.01	3.85	12.5	4.3	15.2
17-20	4.51	2.56	8.9	5.7	21.2
17-21	1.5	3.85	1.8	1.4	1.5
17-22	2.26	0.0	0.0	0.0	0.0
18-18	0.75	2.56	0.0	2.9	0.0
18-19	0.75	3.85	0.0	4.3	1.5
18-20	0.75	0.0	8.9	1.4	3.0
18-21	2.26	1.28	1.8	2.9	3.0
19-19	0.0	1.28	0.0	1.4	0.0
19-20	0.0	2.56	0.0	0.0	0.0
19-21	0.0	0.0	0.0	0.0	3.0
h^a	0.92	0.932	0.924	0.952	0.898

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