GENETIC POLYMORPHISM OF TWENTY-THREE Y - STR LOCI IN HAN POPULATION IN TIANJIN

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To investigate the haplotype distribution of 23 Y-STR loci in 233 unrelated males in Tianjin Han nationality, and to explore forensic medicine applications. Methods Twenty-three Y-STR loci were genotyped by using PowerPlex® Y23 System and ABI-3500xL genetic analyzer. The gene diversity was calculated by counting the haploid genotype frequency of each locus. Results A total of 233 haplotypes were detected by 23 Y-STR loci. The genetic diversity value ranged from 0.3517 to 0.8918, and the cumulative genetic diversity (TGD) was 0.999920234. Conclusion Twenty-three Y loci in Tianjin Han population were polymorphic, and have important application value to individual identification and paternity testing in forensic science filed.

1 Materials and Methods

1.1 Materials

Blood samples were collected from two hundred and thirty- three irrelevant male individuals in Tianjin Han nationality when dealing with daily cases.

1.2 Instruments and Reagents

AB-9700 PCR Thermal Cycler (ABI Corporation, USA); PowerPlex®Y23 System (Promega Corporation, USA); ABI-3500xl Genetic Analyzer (ABI Corporation, USA), WEN ILS500 (Promega Corporation, USA).

1.3 Methods

Blood samples collected on FTA card were directly amplified using Powerplex Y23 System. The PCR reaction volume was 10μl. All the operating procedures were completed according to product manual from PCR amplification to data analysis.

1.4 Statistical Analysis

PX (haploid frequency) = n/N. The value of PX means the frequency of the haploid X. The value of n represents the number haploid X was observed, and the value of N was the number of the population.

GD (gene diversity)= $N(1-\sum Pi2)/(N-1)$. The value of Pi represents haplotype frequency, and the value of N was the number of the population.

2 Results and Discussion

2.1 Results

Two hundred and thirty-three haplotypes were detected through using the kit PowerPlex® Y23 System to analyze two hundred and thirty-three irrelevant males selected randomly from Tianjin Han population (Fig1, Fig.2). The genetic diversity value ranged from 0.3517 to 0.8918, and the cumulative genetic diversity (TGD) was 0.999920234.

Fig.1 Allele frequencies and gene diversity of 23 Y-STR loci detected in 233 irrelevant males from Tianjin Han population

DYS576（ GD=0.7934）			DYS389 I（ GD=0.6325）			DYS448（ GD=0.6919）		
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency
13	1	0.0043	11	2	0.0086	16	2	0.0086
14	1	0.0043	12	117	0.5021	17	2	0.0086
15	7	0.0300	13	68	0.2918	18	28	0.1202
16	21	0.0901	14	42	0.1803	19	111	0.4764
17	41	0.1760	15	4	0.0172	20	51	0.2189
18	69	0.2961				21	34	0.1459
19	61	0.2618				22	5	0.0215
20	27	0.1159						
21	4	0.0172						
22	1	0.0043						

DYS389 II （ GD=0.7521）			DYS19 （ GD= 0.7099）			DYS391（ GD=0.3517）		
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency
26	1	0.0043	13	13	0.0558	6	2	0.0086
27	16	0.0687	14	50	0.2146	9	11	0.0472
28	85	0.3648	15	99	0.4249	10	184	0.7897
29	58	0.2489	16	57	0.2446	11	36	0.1545
30	49	0.2103	17	14	0.0601			
31	19	0.0815						
32	5	0.0215						

DYS481 （ GD= 0.8056）			DYS549 （ GD= 0.6191）			DYS533（ GD=0.5828）		
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency
19	1	0.0043	11	15	0.0644	9	2	0.0086
20	3	0.0129	12	122	0.5236	10	8	0.0343
21	9	0.0386	13	72	0.3090	11	124	0.5322
22	42	0.1803	14	23	0.0987	12	85	0.3648
23	58	0.2489	15	1	0.0043	13	10	0.0429
24	65	0.2790				14	4	0.0172

25	29	0.1245						
26	21	0.0901						
27	2	0.0086						
28	3	0.0129						
DYS438 （ GD=0.3908）			DYS437 （ GD=0.4982）			DYS570 （ GD=0.8184）		
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency
9	3	0.0129	13	2	0.0086	13	1	0.0043
10	177	0.7597	14	140	0.6009	14	2	0.0086
11	41	0.1760	15	88	0.3777	15	15	0.0644
12	12	0.0515	16	3	0.0129	16	33	0.1416
						17	50	0.2146
						18	61	0.2618
						19	48	0.2060
						20	12	0.0515
						21	7	0.0300
						22	3	0.0129
						23	1	0.0043
DYS635 （ GD=0.7834）			DYS390 （ GD= 0.6888）			DYS439 （ GD= 0.6676）		
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency
18	1	0.0043	20	1	0.0043	9	1	0.0043
19	28	0.1202	21	4	0.0172	10	16	0.0687
20	53	0.2275	22	15	0.0644	11	97	0.4163
21	78	0.3348	23	99	0.4249	12	88	0.3777
22	41	0.1760	24	76	0.3262	13	28	0.1202
23	23	0.0987	25	35	0.1502	14	3	0.0129
24	7	0.0300	26	3	0.0129			
25	2	0.0086						
DYS392 （ GD=0.7879）			DYS643 （ GD=0.7119）			DYS393 （ GD= 0.6480）		
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency
10	4	0.0172	8	13	0.0558	9	1	0.0043

11	36	0.1545	9	22	0.0944	12	116	0.4979
12	41	0.1760	10	70	0.3004	13	67	0.2876
13	71	0.3047	11	97	0.4163	14	32	0.1373
14	57	0.2446	12	29	0.1245	15	17	0.0730
15	20	0.0858	13	2	0.0086			
16	4	0.0172						

DYS458 （ GD=0.8042）			DYS385-a（ GD=0.7442）			DYS385-b （ GD=0.8918）		
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency
14	2	0.0086	10	1	0.0043	11	5	0.0215
15	32	0.1373	11	53	0.2275	12	20	0.0858
16	56	0.2403	12	91	0.3906	13	20	0.0858
17	52	0.2232	13	47	0.2017	14	11	0.0472
18	55	0.2361	14	25	0.1073	15	5	0.0215
19	30	0.1288	15	11	0.0472	16	28	0.1202
20	5	0.0215	16	4	0.0172	17	29	0.1245
23	1	0.0043	17	1	0.0043	18	40	0.1717
						19	32	0.1373
						20	28	0.1202
						21	7	0.0300
						22	5	0.0215
						23	1	0.0043
						24	2	0.0086

DYS456 （ GD= 0.6393）			YGATAH4（ GD= 0.5913）			
Number of alleles	n	Allele frequency	Number of alleles	n	Allele frequency	Number of alleles
12	1	0.0043	9	1	0.0043	
13	7	0.0300	10	15	0.0644	
14	40	0.1717	11	76	0.3262	
15	126	0.5408	12	127	0.5451	
16	46	0.1974	13	14	0.0601	
17	9	0.0386				
18	3	0.0129				
19	1	0.0043				

2.2 Discussion

Y-STR analysis technology is very commonly used in forensic science filed. There are many reports about Y-STR loci distribution at home and abroad. The recurrence probability of haplotypes detected by five or six Y-STR loci is a little higher. This situation appeared occasionally to twelve Y-STR loci. The same haplotype was not found in this study using PowerPlex Y23 System including twenty-three Y-STR loci. However, for male individuals from the same parent line, the haplotypes of Y-STR loci were consistent, as gene information of Y-STR loci has the characteristic of paternal inheritance. Therefore, individual identification was not assured only by Y-STR testing. Y-STR testing can be used as an effective complement to the autosomal STR testing, which has important application value in the suspect familial identification, paternity testing, the male component detecting from mixed samples, and the judgment of multiple mixed male samples.

In this study, the polymorphism of locus DYS391 in twenty-three Y-STR loci was the lowest, and the GD value was 0.3517, which was in conformity with other domestic reports of DYS391 diversity. Except for locus DYS391, DYS438 and DYS437, the other 20 loci had a GD value greater than 0.5. These loci had great value, as the loci polymorphism is well distributed, in individual identification and paternity testing in forensic science field.