

Full Length Research Paper

Genetic polymorphisms of 17 Y-chromosome STRs in Han population from Henan province of China

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Haplotypes and allele frequencies of 17 Y-short tandem repeats (STRs) included in the PowerPlex1 Y systems kit (DYS19, DYS389 I, DYS389 II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS438, DYS439, DYS437, DYS448, DYS456, DYS458, DYS635 and Y GATA H4) were examined in a population sample of 276 unrelated Han male living in Henan province. A total of 272 haplotypes were observed in the 276 individuals studied, of which 268 were unique and four were found in two individuals. The gene diversity values ranged from 0.5019 (DYS391) to 0.9579 (DYS385a, b). The overall haplotype diversity for the 17 Y-STR loci was 0.9998.

Key words: Y-chromosomal short tandem repeats (STRs), haplotype, genetic polymorphisms, Chinese Han population

INTRODUCTION

The Y- short tandem repeat (STR) markers from the male specific region of the Y chromosome have become an important tool in the study of human evolution, forensics and population genetics. The peculiar characteristics of the Y-chromosome markers such as paternal inheritance and haploidy make it possible to infer about population histories of paternal lineages and the contribution of these lineages to the gene pool of the extant populations. Although, there is some controversy whether Y-STR can define the population source of individuals and groups, because of a high mutation rate and the occurrence of homoplasmy, which allow haplotypes to be shared by identity by state (IBS) without being identical by descent, several studies have demonstrated the utility of these markers to trace the history of populations and to assign individuals within populations.

An intrinsic limitation of Y-STRs compared with autosomal STRs is the reduced power of discrimination due to a lack of recombination throughout most of the Y-chromosome 1. To increase the power of discrimination of current single amplification Y-STR, multiplexed systems have been developed, a 17 plex Y-STR system that includes the European minimal haplotype and SWGDAM markers and six additional highly polymorphic Y-STR markers (DYS437, DYS448, DYS456, DYS458, DYS635 and Y GATA H4).

Empirically, the Y-STR markers of commercial multiplex assays have become widely used by the forensic community and therefore, population data of these loci are of high interest for forensic purposes. Here, we present a population study that has been carried out on northern Chinese individuals using a version of the recent commercially released AmpFISTR[®] Yfiler[™] polymerase chain reaction (PCR) amplification kit containing 17 Y-STR loci.

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Abbreviations: AMOVA, Analysis of molecular variance; STR, short tandem repeat; PCR, polymerase chain reaction; IBS, identity by state; ISFG, International Society of Forensic Genetics; GD, gene diversity; HD, haplotype diversity.

MATERIALS AND METHODS

Population

The blood stained samples were obtained from 276 unrelated healthy male individuals.

Table 1. Observed allele/genotype frequencies of the 17 Y-STR loci in Han population living in Henan Province of China.

DYS19		DYS389I		DYS389II		DYS390		DYS391		DYS392		DYS393	
A	F	A	F	A	F	A	F	A	F	A	F	A	F
12	0.0145	11	0.0254	24	0.0145	21	0.0399	6	0.0254	10	0.0290	11	0.0145
13	0.0399	12	0.4819	25	0.0109	22	0.0761	9	0.0435	11	0.0290	12	0.4928
14	0.3043	13	0.2391	26	0.0181	23	0.3732	10	0.6522	12	0.1884	13	0.2899
15	0.4275	14	0.2101	27	0.1377	24	0.3225	11	0.2645	13	0.3007	14	0.1449
16	0.1449	15	0.0435	28	0.2826	25	0.1884	12	0.0145	14	0.3442	15	0.0435
17	0.0399	GD	0.6639	29	0.3080	26		GD	0.5019	15	0.0652	16	0.0145
18	0.0290			30	0.1957	GD	0.7139			16	0.0435	GD	0.6498
GD	0.6994			31	0.0326					GD	0.7478		
				GD	0.7663								

DYS438		DYS439		DYS437		DYS448		DYS456		DYS458		DYS635	
A	F	A	F	A	F	A	F	A	F	A	F	A	F
7	0.0181	10	0.0399	13	0.0471	16	0.0145	13	0.0435	14	0.0145	19	0.1812
8	0.0181	11	0.3768	14	0.5833	17	0.0507	14	0.2246	15	0.2935	20	0.3804
9	0.0580	12	0.3587	15	0.3370	18	0.2572	15	0.4746	16	0.1123	21	0.1812
10	0.5906	13	0.1993	16	0.0217	19	0.3152	16	0.1775	17	0.2572	22	0.1341
11	0.1486	14	0.0254	17	0.0109	20	0.1884	17	0.0616	18	0.2101	23	0.0833
12	0.1486	GD	0.6875	GD	0.5434	21	0.1486	18	0.0181	19	0.0725	24	0.0399
13	0.0181					22	0.0254	GD	0.6868	20	0.0290	GD	0.7631
GD	0.6027					GD	0.7735			21	0.0109		
										GD	0.7845		

DNA extraction and PCR

Genomic DNA was extracted from bloodstains using the Chelex-100 protocol as described by Walsh et al. (1991). Amplification of the 17 Y-STR loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385a/b, DYS438, DYS439, DYS437, DYS448, DYS456, DYS458, DYS635 and Y GATA H4) was performed using AmpFISTR[®] Yfiler[™] PCR amplification kit in a thermocycler GeneAmp PCR system 9700 (Applied Biosystems), following the manufacturer's recommendations.

Typing

Detection and genotyping of all PCR products were accomplished using ABI 3100 DNA genetic analyzer (Applied Biosystems, Foster City, CA, USA). The results were analyzed by GeneScan 1 analysis 3.7 software (Applied Biosystems) and allele designations were carried out based on comparison with allelic ladder included in the PowerPlex1 Y Systems with PowerTyper Y Macro Software (Promega). Alleles were designated according to the International Society of Forensic Genetics (ISFG) guidelines for forensic STR analysis (Gusmao et al., 2006).

Analysis of data

Allele frequencies for each locus were calculated by direct counting method. The gene diversity (GD) was calculated as:

$$GD = (1 - \sum p_i^2) / (n - 1)$$

Where n represents the sample size and p_i is the allele frequency.

Haplotype diversity (HD) was calculated with the same equation using haplotype frequencies rather than allele frequencies. A comparative analysis between these haplotype data and previously published data was carried out by means of molecular variance (AMOVA) test implemented in the Arlequin software, Version 3.1 (Excoffier et al., 2005).

Quality control

The laboratory internal control standards and kit controls were employed. The data have been submitted to the YHRD for quality checks in advance of publication and received the following accession numbers: Henan/Xinxiang, China (Han), and YA003639. The populations earlier cited can be searched at www.yhrd.org by contributor, accession number or by population name.

RESULTS AND DISCUSSION

In this population, the average gene diversity (GD) of the 16 Y-STR was 0.6966, DYS391 is one of the least polymorphic with a GD value of 0.5019 (Table 1). The most polymorphic marker in this study was the multi-copy loci DYS385a/b with a GD value of 0.9579 (Table 1).

A total of 272 different haplotypes were found from 276 unrelated individuals, of which 268 were unique and 4 were found in 2 individuals (Table 2). The overall haplotype diversity for the 17 Y-STR loci was 0.9998. These values are higher than the values for the Han and

Table 2. Y-STR haplotypes in 276 unrelated male individuals of Han population living in Henan Province of China

Haplotype	N	DYS 19	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 385	DYS 438	DYS 439	DYS 437	DYS 448	DYS 456	DYS 458	DYS 635	YGATA H4
H1	1	12	13	28	22	10	14	12	13,17	11	12	15	18	14	18	19	12
H2	1	12	13	28	23	10	13	13	13,20	12	14	14	18	14	15	20	12
H3	1	12	13	29	23	12	11	14	15,21	10	12	15	18	15	18	23	10
H4	1	12	14	27	22	10	13	12	14,18	10	12	15	18	16	18	19	12
H5	1	13	12	27	23	10	14	13	13,19	10	12	15	20	15	19	20	10
H6	1	13	12	28	23	10	12	14	14,17	10	12	15	16	15	17	19	10
H7	1	13	12	28	23	10	13	13	13,14	10	11	15	18	16	16	19	12
H8	1	13	12	29	23	10	12	13	13,18	8	12	15	21	18	19	20	12
H9	1	13	12	29	24	10	13	14	15,16	10	11	15	18	14	16	20	12
H10	1	13	12	29	24	10	14	14	12,16	10	12	14	18	17	15	21	12
H11	1	13	12	30	24	10	14	13	13,18	10	12	15	19	15	19	21	10
H12	1	13	13	28	21	11	12	12	13,17	10	12	15	18	15	18	21	12
H13	1	13	13	28	24	10	12	14	13,17	12	12	15	17	16	18	19	12
H14	1	13	14	28	24	10	14	16	13,14	11	12	15	16	15	17	19	10
H15	1	13	14	30	23	6	13	13	13,21	11	11	15	22	16	16	21	12
H16	1	14	11	26	24	10	12	12	12,17	8	11	14	21	14	15	24	11
H17	1	14	11	28	24	10	14	12	14,16	12	11	13	20	15	20	22	12
H18	1	14	12	26	23	11	14	12	15,19	10	12	15	21	15	16	22	12
H19	1	14	12	27	24	10	13	13	13,20	10	12	15	19	15	15	24	11
H20	1	14	12	27	24	11	13	12	14,21	12	11	15	19	14	18	23	12
H21	1	14	12	27	25	10	14	12	14,17	11	11	15	18	15	17	19	11
H22	1	14	12	27	25	10	14	14	12,13	12	11	13	21	14	15	22	12
H23	1	14	12	27	25	10	14	14	12,17	10	11	15	17	14	17	20	13
H24	1	14	12	27	25	11	13	13	13,20	10	11	14	18	14	15	21	12
H25	1	14	12	27	25	11	14	14	13,14	10	11	14	18	14	15	19	12
H26	1	14	12	28	23	10	12	12	13,14	12	14	14	21	16	15	20	12
H27	1	14	12	28	23	10	13	13	12,16	10	12	15	19	17	15	20	11
H28	1	14	12	28	24	10	13	14	18,18	10	12	15	19	14	15	20	12
H29	1	14	12	28	24	11	12	12	12,17	12	10	15	18	15	18	20	12
H30	1	14	12	28	25	10	13	12	14,16	10	12	15	20	16	15	24	11
H31	1	14	12	28	25	10	13	12	14,18	11	12	15	19	15	15	22	12
H32	1	14	12	28	25	10	13	13	13,14	10	12	15	21	14	15	20	11
H33	1	14	12	28	25	10	14	12	12,16	10	12	14	21	14	15	20	11
H34	1	14	12	29	22	10	12	12	12,19	10	11	14	21	17	15	22	12
H35	1	14	12	29	23	9	14	12	14,15	10	12	14	20	15	18	20	11
H36	1	14	12	29	23	10	12	12	13,16	10	11	14	21	15	15	20	12
H37	1	14	12	29	23	11	14	13	13,14	12	11	14	18	17	15	19	12
H38	1	14	12	29	24	6	14	14	13,18	10	11	15	20	15	17	20	13
H39	1	14	12	29	24	10	12	12	13,21	12	11	13	20	15	17	22	12
H40	1	14	12	29	24	10	12	14	15,18	11	11	14	21	14	15	20	12
H41	1	14	12	29	24	10	13	13	13,14	10	12	15	19	15	15	19	12

Table 2. Continue.

H42	1	14	12	29	24	10	14	12	12,16	10	12	14	20	15	15	22	12
H43	1	14	12	29	24	11	13	13	13,17	10	11	14	18	15	15	23	12
H44	1	14	12	29	25	10	13	12	12,17	9	13	14	17	17	18	19	12
H45	1	14	12	29	25	10	13	12	14,18	12	12	15	19	15	15	22	11
H46	1	14	12	29	25	10	13	13	15,19	11	12	15	19	16	15	23	12
H47	1	14	12	29	25	10	15	12	13,14	10	12	15	21	15	16	22	12
H48	1	14	12	29	25	11	12	12	13,14	10	11	15	18	15	18	23	12
H49	1	14	12	29	25	11	13	12	15,16	8	11	15	19	14	15	20	13
H50	1	14	12	30	22	10	13	12	15,19	10	13	14	17	15	18	20	12
H51	2	14	12	30	23	10	14	12	13,14	10	12	15	19	14	15	20	11
H52	1	14	12	30	23	10	15	12	12,19	11	11	14	21	17	15	20	12
H53	1	14	12	30	23	11	14	13	13,16	11	11	14	17	15	15	20	12
H54	1	14	12	30	24	10	15	14	13,21	12	12	15	21	15	16	20	12
H55	1	14	12	30	25	10	11	12	12,16	9	12	15	21	13	16	22	11
H56	1	14	12	30	25	10	15	12	12,16	10	12	15	19	15	16	22	12
H57	1	14	12	30	25	11	13	13	12,15	10	11	15	19	14	19	19	12
H58	1	14	12	31	22	10	14	13	13,13	12	11	13	20	15	18	22	12
H59	1	14	13	27	21	10	13	13	13,14	10	13	14	17	15	18	20	9
H60	1	14	13	27	24	11	14	15	16,20	11	11	14	18	15	15	20	13
H61	1	14	13	27	25	10	14	12	16,17	10	14	13	20	15	20	19	12
H62	1	14	13	28	22	11	14	12	13,19	10	12	14	19	15	17	19	11
H63	1	14	13	28	24	6	14	14	13,14	10	11	15	20	13	17	23	11
H64	1	14	13	29	23	10	15	14	12,14	10	12	15	21	15	16	22	12
H65	1	14	13	29	23	11	13	11	15,22	10	11	15	19	15	15	22	13
H66	1	14	13	30	22	11	13	12	15,17	12	13	14	19	15	18	20	11
H67	1	14	13	30	23	11	12	12	13,15	11	10	15	18	15	18	20	13
H68	1	14	13	30	23	11	14	12	12,19	10	11	14	18	15	15	20	13
H69	1	14	13	30	23	11	15	14	12,16	10	12	15	21	15	16	22	12
H70	1	14	13	30	25	10	14	12	12,17	10	11	15	18	16	17	21	13
H71	1	14	14	27	24	11	14	12	15,16	10	10	15	18	15	18	19	12
H72	1	14	14	28	23	10	13	13	13,19	12	12	15	19	15	15	20	11
H73	1	14	14	28	23	10	13	14	13,17	12	13	14	17	16	18	21	12
H74	1	14	14	28	23	11	14	12	13,19	10	11	14	21	16	15	20	13
H75	1	14	14	28	24	10	13	13	12,19	10	12	15	21	17	15	24	11
H76	1	14	14	29	22	10	14	13	14,18	11	11	14	18	14	15	20	12
H77	1	14	14	29	23	10	12	12	13,17	10	12	14	20	15	20	21	11
H78	2	14	14	29	23	10	12	12	13,17	10	12	15	19	15	15	20	12
H79	1	14	14	29	24	10	12	12	12,16	11	12	14	20	14	15	19	11
H80	1	14	14	29	24	10	13	12	12,17	10	13	14	17	15	18	20	12
H81	1	14	14	29	24	11	13	12	13,20	10	11	14	18	15	15	19	11
H82	1	14	14	29	24	11	14	14	13,21	10	11	15	19	17	17	23	12
H83	1	14	14	29	24	11	14	14	14,17	11	11	14	18	15	15	20	12
H84	1	14	14	29	24	12	13	14	12,13	9	13	14	19	16	18	20	12

Table 2. Continue.

H85	1	14	14	29	25	11	13	12	13,14	10	11	14	17	13	15	19	12
H86	1	14	14	30	23	11	14	12	14,19	8	11	14	18	15	15	24	13
H87	1	14	14	30	24	11	13	15	15,17	10	11	15	20	14	15	22	12
H88	1	14	14	30	24	11	14	15	15,18	10	11	14	18	15	15	19	12
H89	1	14	14	30	25	11	13	13	12,20	10	11	15	19	15	19	23	12
H90	1	14	14	31	23	10	14	12	14,15	12	14	13	20	16	15	21	11
H91	1	14	15	24	24	10	14	13	13,13	10	14	13	20	14	17	21	12
H92	1	14	15	27	24	10	11	13	15,18	10	12	15	21	15	16	22	12
H93	1	14	15	28	23	11	15	12	14,19	12	11	15	18	15	18	23	12
H94	1	14	15	29	22	12	13	12	14,20	10	13	14	18	17	18	21	12
H95	1	14	15	29	25	10	14	14	14,18	10	12	14	20	16	20	19	11
H96	1	14	15	30	23	11	16	13	13,16	10	11	15	19	18	19	22	12
H97	1	14	15	30	24	11	14	12	12,19	10	11	14	18	15	15	21	13
H98	1	15	11	24	22	10	14	12	14,17	9	12	14	21	14	16	20	14
H99	1	15	11	28	23	11	12	12	14,16	10	12	15	20	15	17	19	12
H100	1	15	11	30	24	10	14	12	15,19	11	11	14	18	15	15	22	11
H101	1	15	12	25	23	10	14	12	14,16	10	11	15	19	15	18	19	13
H102	1	15	12	25	24	11	14	12	13,14	7	11	14	17	15	21	22	10
H103	1	15	12	26	25	9	13	11	13,14	10	11	14	18	14	17	22	11
H104	1	15	12	27	23	10	12	12	12,19	12	11	14	20	13	18	21	11
H105	2	15	12	27	23	10	12	12	13,14	10	11	14	18	15	15	22	12
H106	1	15	12	27	23	10	12	12	13,14	10	11	15	19	14	18	20	11
H107	1	15	12	27	23	10	14	14	12,13	10	12	14	21	15	16	20	12
H108	1	15	12	27	23	11	14	13	13,20	10	11	14	21	15	17	19	12
H109	1	15	12	27	24	10	15	12	14,17	12	13	14	18	15	17	20	11
H110	1	15	12	27	24	11	14	12	12,16	11	11	14	18	13	15	20	11
H111	1	15	12	27	25	11	12	15	13,14	12	11	14	19	14	20	24	12
H112	1	15	12	27	25	11	13	12	12,16	11	10	15	19	13	17	21	12
H113	1	15	12	27	25	11	13	13	14,18	11	13	14	21	14	18	20	12
H114	1	15	12	28	21	10	14	16	14,18	10	12	15	20	14	17	20	12
H115	1	15	12	28	21	11	14	13	13,14	10	12	15	19	13	17	23	12
H116	1	15	12	28	23	10	12	12	14,18	10	12	15	17	15	18	22	12
H117	1	15	12	28	23	10	13	13	16,19	10	11	14	18	14	15	20	11
H118	1	15	12	28	23	10	14	12	13,19	10	11	14	18	16	17	20	11
H119	1	15	12	28	23	10	14	13	13,17	10	11	14	19	16	17	23	12
H120	1	15	12	28	23	10	15	12	12,19	12	11	14	20	15	20	21	11
H121	1	15	12	28	23	10	16	14	12,17	11	12	14	21	15	16	20	12
H122	1	15	12	28	24	9	14	12	14,18	9	12	14	19	15	18	24	12
H123	1	15	12	28	24	10	12	12	12,17	11	13	15	19	15	18	20	13
H124	1	15	12	28	24	10	12	14	12,17	10	12	14	18	15	17	21	11
H125	1	15	12	28	24	10	12	14	12,17	10	12	14	18	16	15	21	13
H126	1	15	12	28	24	10	12	14	12,17	10	12	15	17	15	18	22	12
H127	1	15	12	28	24	11	13	12	12,15	12	13	14	21	14	14	20	12

Table 2. Continue.

H128	1	15	12	28	24	11	14	13	12,20	10	12	14	19	14	18	20	11
H129	1	15	12	28	25	10	10	12	12,19	13	13	14	20	15	15	19	12
H130	1	15	12	28	25	10	14	12	13,14	10	12	15	20	13	19	20	11
H131	1	15	12	28	25	10	14	14	12,16	10	13	14	20	15	15	20	12
H132	1	15	12	28	25	10	14	14	13,14	10	13	14	20	15	15	20	12
H133	1	15	12	28	25	11	14	12	14,17	10	11	14	21	15	15	20	12
H134	1	15	12	29	22	10	13	14	12,19	11	11	15	18	14	16	21	12
H135	1	15	12	29	23	6	14	13	14,21	11	11	15	19	14	16	21	12
H136	1	15	12	29	23	9	16	13	13,21	10	12	14	21	15	16	20	14
H137	1	15	12	29	23	10	12	12	14,20	10	12	15	16	15	17	20	10
H138	1	15	12	29	23	10	13	12	13,18	10	11	14	18	15	15	24	12
H139	1	15	12	29	23	10	13	16	12,18	10	11	14	19	15	17	20	12
H140	1	15	12	29	23	10	14	13	13,20	10	12	15	20	16	18	22	12
H141	1	15	12	29	23	11	13	12	17,18	10	12	15	18	14	18	20	10
H142	1	15	12	29	24	10	12	12	14,19	10	11	14	21	16	15	20	12
H143	1	15	12	29	24	10	12	15	13,13	10	14	14	19	16	15	22	12
H144	1	15	12	29	24	10	14	12	14,20	10	11	14	20	15	15	22	13
H145	1	15	12	29	24	10	14	13	12,20	10	13	14	18	14	21	19	12
H146	1	15	12	29	24	11	13	14	12,15	10	12	14	22	14	18	23	12
H147	1	15	12	29	24	11	14	13	13,16	10	13	14	21	15	18	19	12
H148	1	15	12	29	25	10	13	12	13,14	9	12	15	17	15	18	22	11
H149	1	15	12	30	21	10	12	12	13,14	10	11	14	18	15	15	22	12
H150	1	15	12	30	23	10	15	14	14,15	10	11	14	20	15	17	20	12
H151	1	15	12	30	23	11	14	12	13,18	10	12	14	18	15	18	19	11
H152	1	15	12	30	24	10	14	15	12,19	12	12	15	18	13	18	19	12
H153	1	15	12	30	24	10	15	12	14,20	12	13	14	22	15	18	21	11
H154	1	15	12	30	24	10	15	12	15,16	10	13	14	22	14	14	20	11
H155	1	15	12	30	25	10	14	12	14,19	10	10	15	19	14	18	19	12
H156	1	15	12	30	25	10	14	12	15,16	11	13	14	20	14	17	21	12
H157	1	15	12	31	23	9	14	12	13,21	9	12	14	19	15	19	21	12
H158	1	15	12	31	23	10	14	12	12,15	11	12	14	18	16	15	19	14
H159	1	15	12	31	25	10	13	12	12,16	10	12	14	18	15	17	21	12
H160	1	15	13	24	21	10	12	12	14,20	11	12	15	19	18	17	21	10
H161	1	15	13	25	22	12	12	12	12,17	12	12	15	18	15	17	19	10
H162	1	15	13	26	23	11	10	14	16,17	10	12	14	19	15	18	23	11
H163	1	15	13	27	23	10	12	15	12,13	10	11	14	19	14	18	20	12
H164	1	15	13	27	25	10	15	13	13,14	10	11	14	20	15	20	19	11
H165	1	15	13	28	21	10	12	12	12,13	12	14	14	18	15	15	21	12
H166	1	15	13	28	23	9	16	15	13,18	10	12	14	19	16	17	20	14
H167	1	15	13	28	23	10	13	13	12,21	10	12	14	21	15	16	20	12
H168	1	15	13	28	23	10	14	14	12,18	10	12	14	18	18	15	19	12
H169	1	15	13	28	23	10	16	13	13,21	12	11	14	19	16	17	23	12
H170	1	15	13	28	23	10	16	13	14,22	10	12	14	21	15	16	20	14

Table 2. Continue.

H171	1	15	13	28	24	10	13	12	15,20	11	11	15	18	15	16	21	11
H172	1	15	13	28	24	10	14	12	16,20	10	13	14	19	15	17	19	11
H173	1	15	13	28	24	11	13	13	12,13	7	11	14	21	16	17	20	12
H174	1	15	13	28	25	10	13	13	13,14	11	11	14	19	14	17	19	12
H175	1	15	13	29	21	10	13	13	13,20	10	12	14	18	15	17	21	12
H176	1	15	13	29	21	10	13	13	15,19	12	11	14	19	14	17	21	12
H177	1	15	13	29	22	10	10	13	15,19	13	13	14	20	16	17	19	10
H178	1	15	13	29	22	10	14	12	13,17	13	12	14	19	15	18	20	12
H179	1	15	13	29	22	10	14	13	12,13	10	12	15	18	15	18	20	12
H180	1	15	13	29	22	11	13	12	13,14,18	10	11	14	18	15	18	20	11
H181	1	15	13	29	23	10	10	12	13,20	12	13	14	19	15	14	20	12
H182	1	15	13	29	23	10	14	12	14,17	11	12	14	18	15	15	20	12
H183	1	15	13	29	23	10	14	13	12,17	10	11	15	19	15	18	19	13
H184	1	15	13	29	23	10	15	13	14,18	7	13	14	19	17	17	20	12
H185	1	15	13	29	23	10	16	13	12,17	10	12	14	21	14	16	20	14
H186	1	15	13	29	23	11	13	14	12,19	10	11	15	19	17	17	21	11
H187	1	15	13	29	23	11	14	12	14,20	10	11	14	21	16	18	20	12
H188	1	15	13	29	24	10	14	11	16,20	10	11	15	19	15	18	20	13
H189	1	15	13	30	23	10	13	13	12,18	9	11	14	19	16	17	19	12
H190	1	15	13	31	21	10	10	12	14,17	13	13	14	20	15	15	23	12
H191	1	15	14	27	23	10	14	12	13,14	10	10	15	19	16	18	20	11
H192	1	15	14	27	23	10	14	13	12,16	10	12	15	21	16	17	20	12
H193	1	15	14	27	23	10	15	12	12,19	12	13	14	19	16	17	20	11
H194	1	15	14	27	24	10	14	15	15,18	12	12	15	20	15	18	21	12
H195	1	15	14	28	23	11	13	13	12,18	10	13	14	21	16	14	22	11
H196	1	15	14	28	23	11	13	13	13,16	10	13	14	21	16	17	22	12
H197	1	15	14	28	24	9	15	14	13,19	10	11	14	19	15	15	20	11
H198	1	15	14	28	24	10	12	13	13,17	10	11	17	19	15	17	20	12
H199	1	15	14	28	24	10	14	13	12,13	11	12	14	19	15	17	22	14
H200	1	15	14	28	25	6	12	12	12,19	12	11	14	19	14	17	20	12
H201	1	15	14	29	23	10	13	13	12,19	9	13	14	22	14	17	20	11
H202	1	15	14	29	23	11	10	14	12,15	10	12	14	18	15	18	21	11
H203	1	15	14	29	23	11	14	13	12,16	10	12	15	17	17	18	21	11
H204	1	15	14	29	24	10	14	15	13,14	10	12	14	19	14	19	20	12
H205	1	15	14	29	25	9	15	14	12,16	12	11	14	20	14	20	20	11
H206	1	15	14	30	23	10	13	12	14,20	7	11	14	18	16	17	20	11
H207	1	15	14	30	23	11	14	13	12,18	7	11	14	21	16	18	20	12
H208	1	15	14	30	24	9	13	12	12,15	13	13	14	20	15	21	23	12
H209	1	15	14	30	24	10	12	12	12,17	10	13	14	19	16	19	20	12
H210	1	15	14	30	24	10	12	12	12,17	10	13	14	20	14	17	20	11
H211	1	15	14	30	25	11	10	12	13,20	10	12	14	21	13	18	23	12
H212	1	15	15	28	23	9	14	12	15,16	10	13	14	20	15	18	20	10
H213	1	15	15	29	24	11	13	13	14,15	10	13	14	21	17	17	21	12

Table 2. Continue.

H214	1	15	15	30	22	10	14	12	13,16	10	12	14	19	17	15	20	12
H215	1	16	12	27	23	6	12	13	12,16	12	11	17	19	16	17	22	13
H216	1	16	12	27	24	10	13	13	17,18	9	12	14	18	14	17	21	10
H217	1	16	12	28	22	11	11	12	14,16	10	11	14	19	15	18	23	11
H218	1	16	12	28	23	10	14	12	12,13	10	12	16	18	16	17	21	12
H219	1	16	12	28	23	11	12	13	18,19	10	12	15	19	14	18	22	12
H220	1	16	12	28	24	10	10	14	14,19	10	12	15	20	14	19	19	10
H221	1	16	12	28	25	10	15	12	13,16	12	13	14	19	15	19	19	14
H222	1	16	12	29	24	10	13	12	13,14	10	13	13	18	13	15	20	12
H223	1	16	12	29	24	10	14	15	14,19	8	12	16	19	14	17	22	12
H224	1	16	12	29	24	11	13	12	14,15	10	11	14	19	15	18	21	11
H225	1	16	12	29	25	10	14	14	13,14	10	12	14	18	14	15	21	12
H226	1	16	12	30	23	11	11	12	14,17	10	11	14	19	16	19	22	11
H227	1	16	12	30	24	10	12	11	12,13	10	13	13	19	15	15	21	13
H228	1	16	12	30	25	10	13	12	13,13	9	13	13	18	16	15	21	12
H229	1	16	12	30	25	10	14	13	13,13	10	12	16	20	14	17	20	12
H230	1	16	13	27	22	10	12	12	13,19	11	12	15	19	14	17	19	10
H231	1	16	13	27	24	9	13	13	13,15	10	11	14	20	15	17	24	11
H232	1	16	13	27	24	11	11	13	12,14	10	11	14	19	15	15	21	11
H233	1	16	13	28	23	10	13	13	14,17	11	12	14	18	14	17	19	12
H234	1	16	13	28	24	10	13	13	12,14	12	11	14	19	15	17	21	11
H235	1	16	13	28	25	10	13	13	14,17	10	11	14	20	16	17	21	10
H236	1	16	13	28	25	11	14	12	13,14	10	11	14	19	14	15	23	11
H237	1	16	13	29	21	10	13	12	14,16	12	13	13	18	16	15	21	12
H238	1	16	13	29	22	10	13	13	13,22	10	12	16	18	15	17	21	12
H239	1	16	13	29	23	10	14	13	14,18	10	12	16	19	15	17	20	12
H240	1	16	13	30	23	10	14	12	14,18	10	12	14	18	14	15	21	12
H241	1	16	13	30	24	10	13	13	15,17	10	10	14	20	15	19	19	11
H242	1	16	13	30	24	10	14	12	12,21	11	12	14	18	15	17	21	12
H243	1	16	13	31	24	9	13	12	13,20	10	11	14	20	16	19	23	11
H244	1	16	14	26	25	10	13	13	14,18	9	13	13	22	14	15	19	12
H245	1	16	14	27	24	11	14	12	13,18	9	11	14	18	16	15	24	10
H246	1	16	14	28	23	10	13	12	14,15	10	10	14	20	16	17	20	11
H247	1	16	14	28	25	10	14	12	18,18	10	12	16	19	13	17	21	12
H248	1	16	14	29	23	6	12	12	13,14	12	11	17	20	17	15	20	12
H249	2	16	14	29	23	10	13	13	12,20	9	11	15	18	15	16	20	12
H250	1	16	14	29	24	10	13	14	14,18	11	10	14	20	15	15	19	11
H251	1	16	14	30	23	11	11	12	13,16	10	11	14	19	16	18	19	11
H252	1	16	14	30	25	10	13	12	13,14	11	13	13	18	14	15	20	12
H253	1	16	15	29	22	11	11	12	12,18	10	11	14	19	17	19	23	12
H254	1	17	11	28	23	10	12	12	15,19	12	13	14	19	15	17	20	11
H255	1	17	12	27	25	10	12	13	12,17	10	13	14	19	15	17	19	12
H256	1	17	12	29	24	11	12	12	13,14	12	11	15	19	17	19	21	12

Table 2. Continue.

H257	1	17	12	29	24	11	14	12	13,21	10	10	15	19	18	19	20	11
H258	1	17	12	30	24	11	13	16	13,20	9	10	15	19	15	19	23	11
H259	1	17	12	30	25	10	12	13	14,16	10	13	14	19	14	17	21	12
H260	1	17	12	31	23	10	12	13	14,20	10	13	14	19	15	17	20	11
H261	1	17	13	28	24	10	12	13	13,15	12	13	14	22	15	17	21	11
H262	1	17	14	28	23	11	13	14	13,18	10	11	15	21	16	17	23	11
H263	1	17	14	30	24	11	13	13	12,17	10	11	15	19	16	19	20	11
H264	1	17	15	28	23	10	14	15	13,19	10	13	14	19	14	17	19	12
H265	1	18	11	24	24	10	16	12	13,13	11	13	14	16	15	16	24	11
H266	1	18	12	28	23	10	16	12	13,14	10	13	14	20	15	16	20	12
H267	1	18	12	30	23	10	13	12	12,17	11	13	14	20	16	16	20	11
H268	1	18	12	31	24	10	16	12	13,19	11	13	14	20	14	16	20	11
H269	1	18	13	28	24	10	16	13	15,20	11	13	14	20	15	16	19	11
H270	1	18	13	30	23	10	12	12	15,20	11	13	14	20	15	16	20	12
H271	1	18	13	30	23	10	14	12	13,19	11	13	14	20	16	16	20	12
H272	1	18	14	29	24	10	16	12	13,20	11	13	14	20	16	16	19	11

Table 3. R_{st} analysis of the Han population sample residing in the Henan province of China compared with other populations in different ethnics or areas.

Population	R_{st}	Reference
Han population in Shandong	0.14123	Yan et al. (2007)
Taiwan population	0.01710	Huang et al. (2007)
Hui population	0.10001	Hua et al. (2008)
Chinese Tibetan population	0.30626	Bofeng et al. (2008)
Han population in Chaoshan	0.00869	Haijun et al. (2008)
Han population in Sichuan	0.01336	Meisen (2008)
Chinese population in Hong Kong	0.01216	Yeung et al. (2006)
Korean population	0.93945	Zhang et al. (2007)
Han population in northeast China	0.02589	Yang et al. (2009)
Naxi population	0.10317	Xin et al. (2008)
Tujia population	0.21049	Meisen et al. (2008)
Han population in Liaoning	0.04675	Wang et al. (2006)
Mongol population	0.14029	Zhu et al. (2005)

other population of China. These results indicate a high potential for differentiating between male individuals.

The most common haplotypes of this population were H51, H78, H105 and H249, which were shared by 0.7353% of the sample, respectively. We found no matches of these four frequent haplotypes of the whole population in the database of YHRD (<http://www.yhrd.org>) (last update 12/02/2011).

Upon analysis of the 11 Y-STR loci, the most frequent haplotypes in our population (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS438 and DYS439) were H78, H105 and H124 (1.103%),

respectively. In searching the Y-STR haplotype reference database, this haplotype had 0 matches in worldwide population sample of 57313 haplotypes.

Our present haplotype data were compared with the previously published data available by means of analysis of molecular variance (AMOVA) based on pairwise R_{st} comparisons in samples from Han population residing in the Shandong province of China (Yan et al., 2007), from Chinese population in Taiwan (Huang et al., 2007), from Chinese Hui population (Hua et al., 2008), and Tibetan living in Qinghai province of China (Bofeng et al., 2008). Our present data were compared with previously published

data available for the same set of Y-STR loci in samples from Chaoshan Han Chinese in southeast China (Meisen et al., 2009), Sichuan Han Chinese in southeast China (Haijun et al., 2008), the Chinese population in Hong Kong (Yeung et al., 2006), the Chinese Korean ethnic group (Zhang et al., 2007), the Han population residing in northeast China (Yang et al., 2009), the Chinese Naxi ethnic group (Xin et al., 2008), the Chinese Tujia ethnic group (Meisen et al., 2008), the Liaoning Han Chinese in northeast China (Wang et al., 2006), and from Chinese Mongol ethnic group (Zhu et al., 2005) and the results are presented in Table 3. Pairwise analysis confirmed that, our population is more similar with the Chaoshan Han population, the result is same with that of Zhang (Tian-Xiao et al., 2009) and more close to Sichuan Han Chinese Hong Kong and Taiwan populations, being more distant from Korean ethnic group.

These results indicated that, the 17 Y-STRs can be used to define highly discriminative haplotypes, providing a powerful tool in forensic body identification especially the male lineage.

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