



# Population genetics of 25 Y-STR loci in Chinese Han population from Liaoning Province, Northeast China

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## ABSTRACT

In this study, we investigated the genetic characteristics of 25 Y-chromosomal short tandem repeat loci in 305 unrelated Chinese Han male individuals from Liaoning Province, using AmpFISTR® Yfiler® Plus amplification kit. A total of 293 different haplotypes were observed at the 25 Y-STR loci; among them, 281 were unique and 12 were occurred twice. The overall haplotype diversity was 0.9997 and the discrimination capacity was 0.9607. The gene diversity values ranged from 0.4525 (DYS391) to 0.9617 (DYS385). Population relationships between our data and other published populations were measured by *Rst* and visualized in two multi-dimensional scaling plots. The results showed that the 25 Y-STR loci in Liaoning Han population are valuable for forensic application and human genetics.

## 1. Introduction

The analysis of Y-chromosomal short tandem repeat (Y-STR) has been widely used in forensic investigation and paternity testing, mainly due to its male-specific characteristic and paternal genetic model [1,2]. It can provide more information for identifying a male component in sexual assaults, where the very low amount of male DNA is mixed with the high amount of female DNA [3]. Additionally, Y-STR is also a useful tool for inferring genetic genealogy revolution [4] and ancient human migration trajectories and timing [5].

AmpFISTR® Yfiler® Plus amplification kit (Thermo Fisher Scientific, Waltham, MA, USA) can co-amplify 25 Y-STR loci with the six dye, including seven rapidly mutating loci [6]. It is meaningful to expand available population information on forensic medicine and human genetic diversity. Thus, we used the Yfiler® Plus kit to investigate the genetic characteristics of Han population from Liaoning Province, Northeast China. In addition, in order to better understand the genetic background of the Liaoning Han population, we compared our data with other ethnic groups.

## 2. Methods

### 2.1. Study population

Blood stained filter papers were collected from 305 unrelated healthy male individuals living in Liaoning Province, Northeast China

after providing written informed consent to participate in the study. Samples were obtained and analyzed after the approval of the Ethics Committee of China Medical University.

### 2.2. Data extraction, PCR amplification and genotyping

Genomic DNA was extracted using Chelex-100 [7]. Twenty-five Y-STR loci were amplified simultaneously using AmpFISTR® Yfiler® Plus amplification kit (Thermo Fisher Scientific) in a GeneAmp® PCR 9700 (Life Technologies, CA, USA) thermal cycler, according to the manufacturer's recommendations. Separation and detection were performed using an Applied Biosystems™ 3500 Series Genetic Analyzer (Life Technologies). Raw data was analyzed using GeneMapper ID v4.1 software (Life Technologies). The control DNA 007 was genotyped as standard reference in each batch of genotyping. We strictly followed the recommendations of the DNA Commission of the International Society of Forensic Genetics (ISFG) on the analysis of Y-STRs [8].

### 2.3. Analysis of the data

The allele frequencies and gene diversity were calculated using PowerMarker v3.25 [9]. The haplotype frequencies, random match probability (sum of squares) and haplotype diversity were calculated using the Arelequin Software v3.5 [10]. The discrimination capacity (DC) was determined as the proportion of different haplotypes in the sample. Genetic distance (*Rst* statistics) between our data and other

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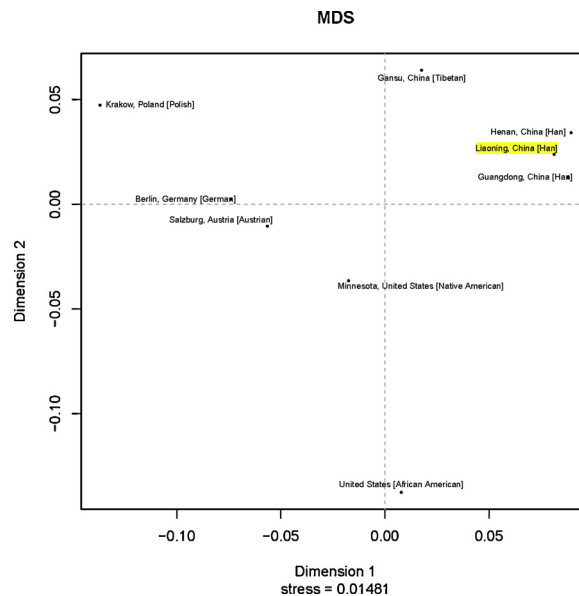
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**Table 1**  
Rst values of pairwise comparisons between populations.

Population	Liaoning, China [Han]	Salzburg, Austria [Austrian]	Guangdong, China [Han]	Henan, China [Han]	Gansu, China [Tibetan]	Berlin, Germany [German]	Krakow, Poland [Polish]	United States [African American]	Minnesota, United States [Native American]
Liaoning, China [Han]	-	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Salzburg, Austria [Austrian]	0.1331	-	0.0000	0.0000	0.0000	0.0041	0.0000	0.0000	0.0003
Guangdong, China [Han]	0.0121	0.1429	-	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Henan, China [Han]	0.0119	0.1472	0.0225	-	0.0000	0.0000	0.0000	0.0000	0.0000
Gansu, China [Tibetan]	0.0759	0.1191	0.0913	0.0838	-	0.0000	0.0000	0.0000	0.0000
Berlin, Germany [German]	0.1514	0.0155	0.1658	0.1659	0.1135	-	0.0000	0.0000	0.0000
Krakow, Poland [Polish]	0.2189	0.1221	0.2313	0.2200	0.1504	0.0574	-	0.0000	0.0000
United States [African American]	0.1800	0.1458	0.1732	0.2023	0.1549	0.1678	0.2121	-	0.0000
Minnesota, United States [Native American]	0.1136	0.0399	0.1144	0.1352	0.1264	0.0712	0.2077	0.1412	-

Above diagonal: P values. Below diagonal: Rst values.



**Fig. 1.** MDS plot based on Rst between Liaoning Han population and 8 reference populations in the YHRD database (Liaoning Han population marked with yellow) (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article).

published groups was measured by analysis of molecular variance (AMOVA) and was visualized in two multi-dimensional scaling (MDS) plots of Rst using YHRD online tools (<http://www.yhrd.org/Analyse/AMOVA>).

**3. Results and discussion**

A total of 293 different haplotypes were found from 305 unrelated individuals, of which 281 were unique and 12 were shared in two individuals. Null alleles were observed in nine individuals at DYS448 and one individual at DYS385, respectively. The haplotype frequencies rendered a high diversity value (0.9997 ± 0.0003). Likewise, a high random match probability (0.0035) was determined with DC of 0.9607. The gene diversity values of 25 loci ranged from 0.4525 (DYS391) to 0.9617 (DYS385). Our haplotype data were compared with the eight populations submitted to the YHRD database (Release 51) including Austrian (YP000352), Guangdong Chinese Han [11], Henan Chinese Han (YP000938), Gansu Chinese Tibetan (YP001032), German [12], Polish [13], African American [14,15], Native American (YP001068). Rst Values for genetic distance showed that haplotypes of Liaoning Han population had significant differences from those of the other eight populations (all p values < 0.01, Table 1). As shown in the MDS plot (Fig. 1), there were minor differences compared to Henan Chinese Han, Guangdong Chinese Han and Gansu Chinese Han, but major differences with respect to the populations from Austrian, German, Polish, Native American and African American. The populations' distribution in the MDS plot corresponded with their ethno-geographic origins.

In summary, 25 Y-STR loci allelic frequencies, haplotype distribution of Liaoning Han population were reported and its genetic characteristics were compared with those of the other published populations. The data provide a reference for Y-STR database of Liaoning Province and might be valuable for human genetics.

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## Declaration of Competing Interest

None.

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