Genetic analysis of 17 Y-STR loci in Han and Korea populations from Jilin

Province, Northeast China

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Abstract

In this study, 17 Y chromosomal short tandem repeats (Y-STRs) were analyzed in 302 male individuals from the Chinese Han and Korean populations of Jilin Province. The haplotype diversities of two populations reached 0.99969 and 0.99874, respectively. The Jilin Han and Korean populations differed from each other significantly. The Jilin Han population showed no significant difference from almost any other Han population, but it did show significant differences from most other Chinese ethnic populations. The haplotype frequencies in the Jilin Korean population studied here showed significant differences from all reference populations in earlier reports. These data provide a reference for the Y-STR database in Jilin Province, and they may be valuable for population genetic analysis.

1. Introduction

Jilin Province is located in northeastern China (Fig. S1). According to the 2000 census, at which point the population of Jilin had reached to 26,802,191 and contained 44 ethnic groups. Among them, Han were the most numerous (90.85%), followed by Chinese Koreans (4.27%), Manchus (3.71%), Mongolians (0.64%), and Hui (0.47%).

The composition of Jilin population has been profoundly changed by population migrations. In particular, the Qing government began to open this area in 1860,

enabling a large number of Han Chinese migrants to enter. They came primarily came from Shandong Province in eastern China. Koreans also migrated into Jilin during the same period, coming mainly from what is now northern Korea and most of them live in the Yanbian Korean Autonomous Prefecture.

2. Materials and methods

2.1. Samples and experiments

A total of 302 male individuals were collected from Jilin Province, including 196 Hans (Jilin, China [Han]) and 106 Koreans (Jilin, China [Korean]). All individuals provided informed consent, and then peripheral blood samples were collected. Genomic DNA was extracted using Gentra Puregene Blood Kit (Qiagen). Polymerase chain reaction (PCR) was performed using the AmpFISTR Yfiler™ PCR Amplification Kit (Thermo Fisher Scientific Company, Carlsbad, CA, U.S.) in the GeneAmp PCR System 9700 (Thermo Fisher Scientific Company) according to the manufacturer's instructions. A total of 17 Y-STRs were analyzed, including DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, YGATAH4, and DYS385a/b. PCR products were separated by capillary electrophoresis in ABI PRISM 3130xL Genetic Analyzer (Thermo Fisher Scientific Company). The GeneMapper ID software v3.2 (Thermo Fisher Scientific Company) was used for genotype assignment. DNA typing and assignment of nomenclature was based on the ISFG recommendations [1].

2.2. Statistical analyses

The haplotype frequencies were estimated using direct counting. Haplotype diversity

was calculated as described by Nei [2]. The algorithm is $HD = (n/n - 1)(1 - \sum p_i^2)$, where n is the sample size and p_i is the frequency of the i th haplotype. Pairwise R_{st} was estimated between populations of the present study and other reports involving Chinese populations using Arlequin v3.5 [3]. Results were visualized using multidimensional scaling plot (MDS) with R v3.1.2 (<http://www.r-project.org>). DYS385 a/b was excluded from the analysis, and DYS389B was obtained by subtracting the allele of DYS389I from that of DYS389II.

3. Results and discussion

3.1 Haplotype distributions

A total of 190 different haplotypes were observed among the individuals in the Han population of the present study, of which 184 were unique and 6 were shared in two individuals. A total of 100 different haplotypes were observed among Koreans, of which 95 were unique, 4 were shared by two individuals, and 1 was shared by three individuals. The haplotype diversities of Han and Korean were 0.99969 and 0.99874, respectively.

3.2 Genetic distance and population comparison

Pairwise R_{st} was estimated between populations in the present study and other reports involving Chinese populations based on 17 Y-STR loci. Overall, the haplotype frequency data of 26 Chinese populations were obtained from earlier reports [4–21], which included 14 Han [5–14] and 12 Chinese ethnic populations [6, 14–21], and a total of 8,784 reference samples were analyzed. As shown in Table S2, Han and Korean populations in Jilin Province showed significant differences after Bonferroni

correction ($p > 0.05/378 = 0.0001323$). No significant differences were observed between Jilin Han and the other Han populations in earlier reports, except Zhejiang, China [Han] [5] and Luzhou, China [Han] [9]. The results showed that most of Han populations in the present study had substantial homogeneity based on 17 Y-STRs, and significant differences in haplotype frequencies were observed between the Han populations of and Jilin and Zhejiang and between that of Jilin and Luzhou. These differences are probably attributable to different sampling locations. Results showed that Jilin Han differed significantly from most Chinese ethnic populations. Among them, Jilin Han showed significant differences from all the Chinese ethnic populations in southern China, including Hunan [Dong] [6], Hunan [Miao] [6], Hunan [Tujia] [6], Guangxi [Zhuang] [14], and Taiwan [Paiwan] [21]. Jilin Han also showed significant differences from some Chinese ethnic populations from northern China, including Lassa [Tibetan] [17], Qinghai [Tibetan] [18], Xinjiang [Kazakh] [19], and Xinjiang [Uyghur] [19]. The results suggested that Jilin Han had population structure and history different from these populations. In addition, the haplotype frequencies of Jilin Koreans in the present study showed significant differences from all reference populations in earlier reports, indicating a distant genetic relationship between Jilin Korean and the other populations in this study. The details are shown in Table S2, and the same conclusions are given in Figure S2.

4. Conclusions

In conclusion, we report the haplotype frequency and forensic parameters based on 17 Y-STR loci of Han and Korean populations in Jilin Province. We believe the data is

valuable for both forensics and population genetics.

Our data has been submitted to YHRD, and received the accession number: Jilin, China [Han], n=196, YA004124, and Jilin, China [Korean], n=106, YA004126.

The study follows the new guidelines for publication of population data requested by the journal [22, 23].

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