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Genetic diversity and haplotype structure of 27 Y-STR loci in a Yanbian Korean population from Jilin Province, Northeast China

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ABSTRACT

In this study, 27 Y-STRs were analyzed in 347 male individuals from the Yanbian Korean population. Haplotype diversity (HD) and discrimination capacity (DC) values were calculated. Pairwise R_{st} values were evaluated in AMOVA analysis and visualized through multidimensional scaling (MDS). Yfiler Plus system indicated higher Discrimination Power (DP), HD and DC which is 0.9969, 0.9998 and 0.9769. There is no significant genetic distance between Yanbian Koreans and South Koreans, however, there is a great distance from Chinese Han population. The present results may provide useful information for paternal lineages in forensic cases and increase our understanding of the genetic relationships between Yanbian Korean and other groups.

1. Introduction

Yanbian is an Autonomous Prefecture in northeastern Jilin Province, People's Republic of China, just north of the border with North Korea. Yanbian is surrounded by Heilongjiang (north), Baishan City and Jilin City (west), North Hamgyong Province of North Korea (south), and PrimorskyKrai of Russia (east) (Fig. S1). Yanbian is designated as an autonomous prefecture due to the large number of ethnic Koreans living in the region. In total, 35.45% of the Yanbian population belongs to a minority group, of which the Korean ethnic group is the largest (91.54%), followed by the Manchu group (7.11%) (according to the 2010 census).

Blood samples were collected from 347 unrelated Yanbian Korean individuals were collected with informed consent. They were healthy unrelated individuals and were randomly chosen among Yanbian Korean population. It is ensured that their ancestors had lived in the region for three generations at least. The blood samples of every participant in Yanbian were obtained respectively by standard procedures.

2. DNA extraction and PCR

FTA cards were used to save as samples. Without DNA extraction, Polymerase chain reaction (PCR) was directly performed by the Yfiler Plus PCR Amplification Kit (Applied biosystems, USA) in the GeneAmp PCR 9700 system (Applied biosystems, USA). The multiplex system was combined with 17 Yfiler loci, 7 rapidly mutating Y-STRs (DYS576, DYS627, DYS570, DYS518, DYS449, DYF387S1a/b) and 3 new Y-STRs (DYS460, DYS481, and DYS533) [1,2].

3. Typing

Then amplification products were separated by capillary electrophoresis on the ABI 3500 Genetic Analyzer (Applied biosystems, USA). The male control DNA 007 and ddH_2O were employed as positive and negative controls respectively. Raw data was analyzed by GeneMapper ID-X (Applied biosystems, USA) for genotype assignment. Allele designations were based on comparisons with allelic ladder provided with kit.

Abbreviations: HD, haplotype diversity; DC, discrimination capacity; MDS, multidimensional scaling; DP, discrimination power; NDH, number of different haplotypes; FUH, fraction of unique haplotypes; UH, unique haplotypes; NJ, neighbour-joining; AMOVA, analysis of molecular variance; MHT, minimal haplotype

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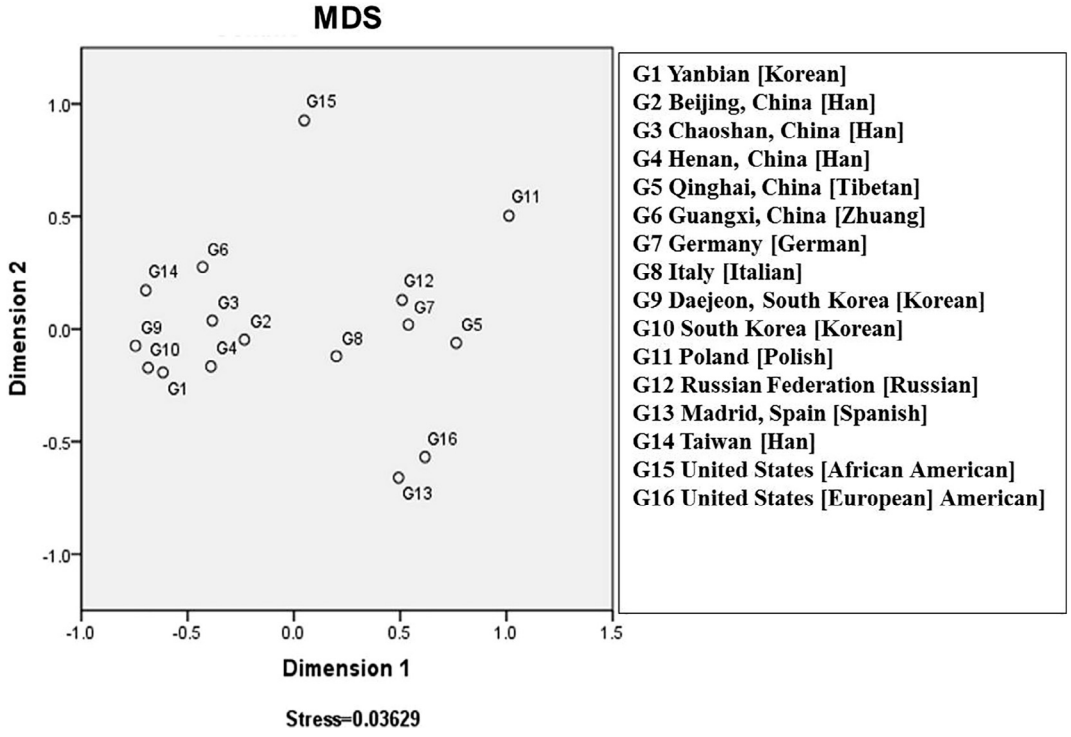

Fig. 1. MDS plot based on pairwise R_{st} values using the Yfiler Plus system for 16 populations.

4. Quality control

All experimental procedures were operated exactly according to kit controls and laboratory internal standards. The nomenclature of different alleles was strictly based on the updated recommendations of DNA commission of the International Society of Forensic Genetics (ISFG). Haplotype data were submitted to the Y-Chromosome Haplotype Reference Database. An accession number YA004289 has been received. This paper follows the guidelines for publication of population data proposed by the journal [3,4].

5. Data analysis

Alleles frequencies and haplotype diversities were directly estimated by genetic counting. Haplotype diversities (HD) were calculated according to the formula by Nei [5]. Discrimination Power (DP) and Discrimination capacity (DC) are represented as a ratio of the number of different haplotypes (NDH) to the total sample size. The fraction of unique haplotypes (FUH) was calculated as the proportion of unique haplotypes (UH) in the database. Genetic distances (R_{st}), which were ascertained at a significance level of 0.05 using 10,000 permutations, were measured by analysis of molecular variance (AMOVA) in YHRD database (http://www.yhrd.org). To illustrate the relationship between populations, a multidimensional scaling (MDS) plot was performed from pairwise R_{st} values using SPSS statistics version 22. A Neighbour-Joining (NJ) tree was built by MEGA software version 4.1 based on R_{st} values. However, all samples carrying null alleles were excluded from the analysis.

6. Results and discussion

The frequencies of different alleles, gene or haplotype diversity, discrimination capacity, match probability and discrimination power were directly calculated by Excel, which appended on Supplementary materials. Haplotype statistics was separated into four composition modes, including minimal haplotype (MHT), Power Plex Y12 haplotype (PPY12), Yfiler haplotype and Yfiler Plus haplotype, shown in Fig. S2. Genetic distances (R_{st}) which implied population genetic comparison were measured by analysis of molecular variance (AMOVA) and visualized in a MDS plot in YHRD database (http://www.yhrd.org).

As is shown in Table S1, a total of 51 alleles were observed and gene diversity for each locus ranged from 0.3080 of DYS391 to 0.8606 of DYS518, while two muti-copy loci haplotypes were detected highly haplotype diversity values with 0.9641 for DYS385a/b and 0.9402 for DYF387S1 respectively (Table S2). A total of 339 distinct were found from 347 unrelated Yanbian Korean individuals, listed in Table S3, of which 332 were unique, 6 were shared by two individuals and 1 was shared by 3 individuals. Obviously, Yfiler Plus system indicated higher DP, HD and DC which is 0.9969, 0.9998 and 0.9769 than the other combinations (Fig. S2).

The present data of Pairwise R_{st} values in Table S4 compared Yanbian Korean population with 15 other reference populations, based on haplotype database. There is no significant genetic distance between Yanbian Koreans and South Koreans ($P > 0.005$) [6,7]. While the MDS plot (Fig. 1) revealed that Yanbian Korean population clustered with South Koreans ($R_{st} = 0.0002$) and Daejeon Koreans ($R_{st} = -0.0012$), which was close to Han population cluster [8,9]. According to Neighbor-Joining tree (Fig. S3), Zhuang from Guangxi and Tibetan from Qinghai were divided from Chinese Groups [10,11]. In European analysis, an East-West branch separated clearly. Meanwhile, European American belonged to European cluster but African American population was separated by itself because of original geographic distributions [12–15].

In conclusion, our results showed that these data in Chinese Yanbian Korean could be useful for forensic genetic science, especially in paternity and genealogical study.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.legalmed.2018.11.010.

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