Forensic Science International: Genetics 19 (2015) 250–251

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

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Genetic analysis of 17 Y-STR loci in Han, Dong, Miao and Tujia populations from Hunan province, central-southern China

Dear Editor,

Hunan province locates in the south-central part of China (Fig. S1). According to the census in 2000, the population of Hunan reaches to 64,400,700, consisting of 41 ethnic groups. Among them, Han is the largest group (89.79%), and then follows by Tujia, Miao and Dong etc.

In this study, a total of 458 male individuals were collected from Hunan province, including 201Hans (Hunan, China [Han]), 80 Dongs (Hunan, China [Dong]), 87 Miaos (Hunan, China [Miao]) and 90 Tujias (Hunan, China [Tujia]). Peripheral blood samples were collected from these individuals after acquiring their informed consent. Genomic DNA was extracted using Gentra Puregene Blood Kit (QIAGEN). Polymerase chain reaction (PCR) was performed using the AmpFlSTR Yfiler^{TM} PCR Amplification kit (Life technologies) in the GeneAmp PCR System 9700 (Life technologies) according to the manufacturer's instruction. PCR products were separated by capillary electrophoresis in ABI PRISM 3130xL Genetic Analyzer (Life Technologies). The GeneMapper ID software v3.2 (Life technologies) was employed for genotype assignment. DNA typing and assignment of nomenclature were based on the ISFG recommendations [1,2].

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. The haplotype frequencies were estimated using direct counting method. Haplotype diversity were calculated as described by Nei [3]. Pairwise Rst was estimated between populations of the present study and other reports involving Chinese populations using Arlequin v3.5 [4], and was visualized by multidimensional scaling plot (MDS) using 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.

A total of 190 different haplotypes were observed among the individuals of Hunan, China [Han], of which 181 were unique, 7 were shared in two individuals and 2 were shared in three individuals. A total of 74 different haplotypes were observed among Hunan, China [Dong], of which 69 were unique, 4 were shared in two individuals and 1 were shared in three individuals. A total of 79 different haplotypes were observed among Hunan, China [Miao], of which 73 were unique, 5 were shared in two individuals and 1 were shared in four individuals. A total of 79 different haplotypes were observed among Hunan, China [Tujia], of which 75 were unique, 2, 1 and 1 were shared in three, four and five individuals, respectively. The haplotype diversities of four populations reach to 0.9994, 0.9978, 0.9971 and 0.9945, respectively.

Pairwise Rst was estimated between populations of the present study and other reports involving Chinese populations based on 17 Y-STR loci. The samples of six Chinese Han (Nanyang, China [Han] [5], Luzhou, China [Han] [6], Mudanjiang, China [Han] [7], Shanxi, China [Han] [8], Zhejiang, China [Han] [9] and Henan, China [Han] [10]) and eight ethnic populations (Guangxi, China [Zhuang] [11], Lassa, China [Tibetan] [12], Qinghai, China [Tibetan] [13], Xinjiang, China [Kazakh] [14], Xinjiang, China [Uyghur] [14], Liaoning, China [Manchu] [15], Taiwan, China [Paiwan] [16] and Chongqing, China [Tujia] [17]) were obtained from earlier reports, and a total of 8900 reference samples were analyzed. Table S2 showed that Han, Dong, Miao and Tujia in Hunan province had significant differences between each other after Bonferroni correction ($p > 0.05/153 = 0.000327$), suggesting limited gene flows occurred between these populations. Moreover, Dong and Miao showed significant differences between all populations of earlier reports, respectively, and Tujia in the present study had no significant differences between that of Chongqing ($Rst = 0.02204$, $p = 0.00069$), indicating substantial homogeneity of two populations. Five comparison between Hunan Han and Chinese populations examined in previous investigations showed no significant differences, including Nanyang, China [Han] ($Rst = 0.0013$, $p = 0.18850$), Mudanjiang, China [Han] ($Rst = 0.00423$, $p = 0.01228$), Henan, China [Han] ($Rst = 0.00683$, $p = 0.00089$), Liaoning, China [Manchu] ($Rst = 0.00683$, $p = 0.00599$) and Chongqing, China [Tujia] ($Rst = 0.0035$, $p = 0.08108$). The same conclusion could be observed in Fig. S2.

In conclusion, we report 17 Y-STR loci's allelic frequencies, haplotype distributions and forensic parameters of four populations in Hunan 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: Hunan, China [Han], $n = 201$, YA004052; Hunan, China [Dong], $n = 80$, YA004051; Hunan, China [Miao], $n = 87$, YA004050; and Hunan, China [Tujia], $n = 90$, YA004049.

This study was supported by grants from the National Science Foundation of China (31401060), National Science Foundation of China (31271338), Project of Chinese Ministry of Education (113022A) and National High Technology Research and Development Program (2012AA021802).

The study follows the new guidelines for publication of population data requested by the journal [18,19].

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.fsigen.2015.07.007.

http://dx.doi.org/10.1016/j.fsigen.2015.07.007

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Received 14 April 2015
Received in revised form 24 June 2015
Accepted 11 July 2015