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RESEARCH PAPER

Genetic polymorphism and forensic application of 23 autosomal STR loci in the Han population of Panjin City, Liaoning Province, Northeastern China

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ABSTRACT

Background: Short tandem repeats (STRs) are consecutive repetition of a repeat motif and widely used in forensic medicine and human genetics because of their high polymorphism.

Subjects and methods: In the current study, 23 autosomal STR loci were genotyped from 1263 unrelated healthy individuals living in Panjin City, Liaoning Province, Northeastern China using the VeriFiler™ Express PCR Amplification Kit. The population comparison was performed between the Panjin Han population and the other relevant groups to further explore the structure of Panjin Han and its relationship with the other groups.

Results: The results found 316 alleles across the 23 STRs and the corresponding allelic frequencies ranged from 0.5198 to 0.0004. Except for D3S1358, TPOX, TH01, and D3S1358, all STR loci were highly polymorphic (PIC > 0.7), with the Penta E locus having the highest degree of polymorphism (0.9147). For population comparison, the exact test of population differentiation found that no significant difference was observed between the Panjin Han and the other Han populations, except for Guangdong Han and Jiangxi Han.

Conclusion: The Panjin Han population showed significant differences with the other ethnic groups in China (Bouyei, Dong, Hui, Miao, Tibetan, and Uygur) and the foreign ethnic groups.

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Han population; autosomal STR; population genetics; forensic medicine

1. Introduction

Short tandem repeats (STRs), also known as microsatellites, are consecutive repetition of a repeat motif with three to six base nucleotides (Rubab et al. 2020). The mean mutation rate of autosomal STRs is 1.8 10^3 for paternal origin and 0.3 10^3 for maternal origin (Hamester et al. 2019). On account of their high polymorphism and strong discrimination ability, they can be widely used in forensic medicine and human genetics (Zhu et al. 2015; Yao and Wang 2016). Due to their high mutation rate, they can provide more information for exploring the population genetic structure and revealing the evolutionary relationships between different populations (Chen et al. 2017; Guo 2017; He et al. 2017). In forensic medicine, STRs have high discrimination ability due to their variable repeat counts among different individuals. Thus, they can be utilised in personal identification and paternity testing (Adnan et al. 2016, 2018; Zhan et al. 2018).

Panjin City, part of Liaoning Province, is located in Northeast China and the centre of the Liaohe Delta. Its land area is 4103 km^2 with a warm temperate continental semi-humid monsoon climate. It is bordered by Anshan City in the east and northeast, Yingkou City in the southeast across the Daliao River, Jinzhou City in the west and northwest, and Liaodong Bay in the Bohai Sea in the south. Panjin had a population of over 1.44 million in 2019 (www.stats.gov.cn). Han is the most dominant ethnic group of Panjin city followed by other minority groups such as Manchu, Koreans, Mongolians, Hui, and Xibe.

In the current study, we used the VeriFiler™ Express PCR Amplification Kit (Lu et al. 2017) to explore the genetic characteristics of 1263 Han individuals from Panjin City, Northeastern China. Additionally, in order to understand the genetics and structural background of the Panjin Han population, we compared our population with other reference populations. Population comparisons including Reynold's genetic distance, neighbor-joining tree, and multi-dimensional scaling (MDS) analysis were carried out between the Panjin Han population and different ethnic groups to better understand the genetic background and structure of the Panjin Han population.

2. Subjects and methods

2.1. Ethical compliance

This study was approved by the ethical review board of Shenyang Medical College, Shenyang, Liaoning Province,

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People's Republic of China, and in accordance with the standards of the Declaration of Helsinki (SYMC-20211015–15). All participants gave their informed consent either orally and with thumb prints (in case they could not write) or in writing after the study aims and procedures were carefully explained to them.

2.2. Study population

Blood samples were collected using the FTA cards from 1263 unrelated healthy individuals living in Panjin City, Liaoning Province, Northeastern China (Figure 1).

2.3. DNA extraction, PCR amplification, and genotyping

Genomic DNA was extracted from FTA cards using Chelex-100 method (Walsh et al. 1991). A total of 23 autosomal STR loci (D3S1358, vWA, D16S539, CSF1PO,TPOX, D8S1179, D21S11, D18S51, Penta E, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, D6S1043, D10S1248, D1S1656, D12S391, D2S1338, and Penta D) were amplified simultaneously using the VeriFiler™ Express PCR Amplification Kit (ThermoFisher SCIENTIFIC, MA, USA). The 23 autosomal STR loci satisfied the requirements of the Chinese National autosomal DNA database as well as expanded Combined DNA Index System (Green et al. 2021). Multiplex amplification was conducted on a ProFlex™ PCR thermal cycler (ThermoFisher SCIENTIFIC), following the manufacturer's recommendations. Separation and detection were performed using the Applied Biosystems™ 3500 Genetic Analyser (ThermoFisher SCIENTIFIC). Internal controls (H_2O as a negative control and 9947 A DNA as a positive control) were genotyped along with each batch of samples to ensure that the results were reproducible and accurate. The raw data was analysed using GeneMapper ID-X v1.2 software (ThermoFisher SCIENTIFIC).

2.4. Statistical and phylogenetic analysis

The allele frequencies of samples, exact tests of Hardy-Weinberg equilibrium (HWE), and pair linkage disequilibrium (LD) tests were calculated with the PowerMarker v3.25 (Liu and Muse 2005). The values for matching probability (MP), power of discrimination (PD), polymorphism information content (PIC), power of exclusion (PE), typical paternity index (TPI), gene diversity (GD), and heterozygosity (He) were calculated using the PowerStats software v1.2 (Promega, Madison, WI, USA) (Tereba 1999), which was modified from Silva, et al. in order to support and manage the large number of samples (Cabezas Silva et al. 2016). Reynold's genetic distance, based on allele frequencies across the 15 autosomal loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, and FGA) shared by the included compared populations, and exact test p values were generated using PowerMarker v3.25. Nei's standard genetic distance between populations was calculated using the allele frequencies by Phylip 3.69 package (Felsenstein 2009) and visualised by MEGA v7.0.26 software (Kumar et al. 2016). Finally, MDS analyses on the basis of Reynold's genetic

Figure 1. In this study, Panjin City was the area of sample collection (Map from Wikipedia, https://en.wikipedia.org/wiki/).

distance matrix were performed using SPSS 26.0 software (IBM Corp., Armonk, NY).

3. Results and discussions

3.1. Allele frequencies and forensic parameters of the 23 autosomal STR loci

The allele frequencies for the 23 autosomal STRs from 1263 Panjin Han individuals are listed in Supplementary Table S1. A total of 316 alleles were observed with the allele frequencies ranging from 0.5198 (TPOX) to 0.0004 (D3S1358, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, Penta E, D2S441, D19S433, FGA, D5S818, D7S820, D6S1043, D1S1656, D12S391, D2S1338, and Penta D). Forensic efficiency and statistical parameters across the 23 STR loci are shown in Table 1. A high degree of genetic variation was observed by all STR loci in the Panjin Han population. The values of MP, PD, and PE ranged from 0.2042 (TPOX) to 0.0122 (Penta E), 0.9878 (Penta E) to 0.7958 (TPOX), and 0.9147 (Penta E) to 0.5647 (TPOX), respectively. The ranges of GD and He spanned from 0.9204 (Penta E) to 0.6246 (TPOX) and from 0.9074 (Penta E) to 0.6358 (TPOX), respectively. Except for D3S1358 (0.6770), TPOX (0.5647), TH01 (0.5960), and D3S1358 (0.6770), all STR loci were highly polymorphic (PIC > 0.7), with the Penta E locus having the highest degree of polymorphism (0.9147).

3.2. Hardy-Weinberg equilibrium (HWE)

Initially nineteen loci were in HWE, with D8S1197, TH01, D12S391, and Penta D not in HWE ($p < 0.05$). However, when

Table 1. Forensic efficiency and statistical parameters of 23 autosomal STR loci in the Panjin Han population (n ¼ 1263).

Loci	MP	PD	PIC	PE	TPI	GD	He	p
D3S1358	0.1248	0.8752	0.6770	0.4933	1.9253	0.7247	0.7403	0.9242
vWA	0.0701	0.9299	0.7707	0.6088	2.5671	0.8007	0.8052	1.0000
D16S539	0.0784	0.9216	0.7560	0.5737	2.3389	0.7883	0.7862	0.8352
CSF1PO	0.1136	0.8864	0.6902	0.4801	1.8683	0.7332	0.7324	1.0000
TPOX	0.2042	0.7958	0.5647	0.3360	1.3728	0.6246	0.6358	0.2510
D8S1179	0.0437	0.9563	0.8246	0.6738	3.1108	0.8438	0.8393	0.0231
D21S11	0.0607	0.9393	0.7831	0.6043	2.5361	0.8071	0.8029	0.4350
D18S51	0.0402	0.9598	0.8346	0.7239	3.6930	0.8513	0.8646	0.9122
Penta E	0.0122	0.9878	0.9147	0.8105	5.3974	0.9204	0.9074	0.7972
D2S441	0.0911	0.9089	0.7277	0.5327	2.1120	0.7625	0.7633	0.0948
D19S433	0.0573	0.9427	0.7934	0.6677	3.0507	0.8168	0.8361	0.3633
TH01	0.1743	0.8257	0.5960	0.3403	1.3849	0.6459	0.6390	0.0143
FGA	0.0379	0.9621	0.8355	0.6862	3.2385	0.8517	0.8456	0.6974
D22S1045	0.0960	0.9040	0.7282	0.5637	2.2798	0.7678	0.7807	0.2382
D5S818	0.0881	0.9119	0.7373	0.5453	2.1776	0.7718	0.7704	0.1081
D13S317	0.0687	0.9313	0.7743	0.6147	2.6095	0.8032	0.8084	0.9508
D7S820	0.0793	0.9207	0.7491	0.5411	2.1553	0.7814	0.7680	0.8775
D6S1043	0.0303	0.9697	0.8590	0.7318	3.8042	0.8725	0.8686	0.2802
D10S1248	0.1062	0.8938	0.7019	0.4947	1.9312	0.7416	0.7411	0.8362
D1S1656	0.0546	0.9454	0.7942	0.6073	2.5567	0.8155	0.8044	0.8285
D12S391	0.0474	0.9526	0.8178	0.6924	3.3063	0.8376	0.8488	0.0112
D2S1338	0.0361	0.9639	0.8450	0.7081	3.4890	0.8604	0.8567	0.2923
Penta D	0.0574	0.9426	0.7967	0.6312	2.7338	0.8198	0.8171	0.0343
D3S1358	0.1248	0.8752	0.6770	0.4933	1.9253	0.7803	0.7953	0.9242

Note. MP: matching probability; PD: power of discrimination; PIC: polymorphism information content; PE: power of exclusion; TPI: typical paternity index; GD: gene diversity; He: expected heterozygosity; p: probability values of exact tests for Hardy-Weinberg equilibrium (HWE).

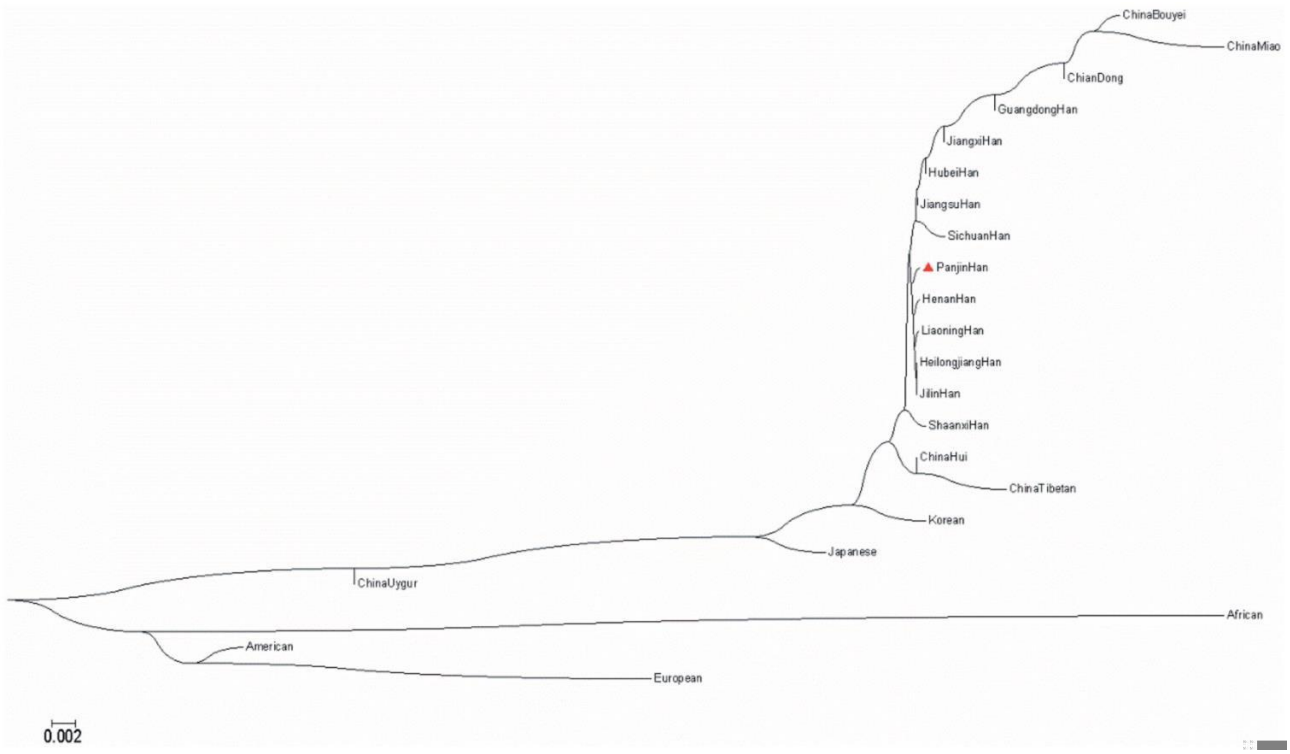

Figure 2. Neighbor-joining phylogenetic tree based on the allele frequencies of 15 shared STRs between the Panjin Han and the other 21 populations.

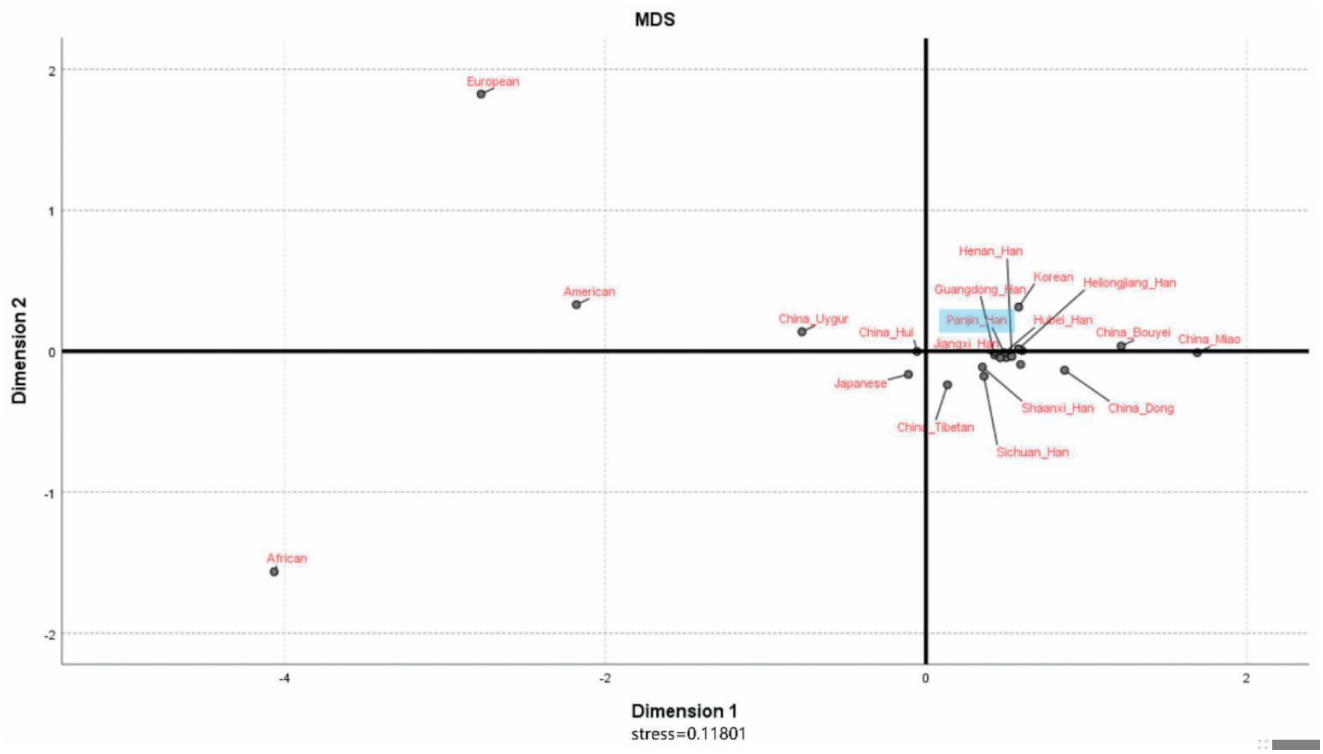

Figure 3. MDS plot based on the Reynold's genetic distance between the Panjin Han and the other 21 populations.

a sequential Bonferroni's correction was applied, all 23 loci were found to be in Hardly-Weinberg equilibrium (Table 1).

3.3. Linkage equilibrium (LE)

Linkage disequilibrium (LD) indicates the association between qualitative random variables corresponding to alleles at different STRs. Measuring the levels of linkage disequilibrium is important for gene mapping and it helps in the understanding of genome structure. Exact tests for LE between 253 pairs showed that the values of only 23 pairs were below 0.05 and thus displaying LD (Supplementary Table S2). When sequential Bonferroni's correction was applied, there were no pairs of loci displaying LD.

3.4. Population comparison with the other populations

In order to study the genetic structure of the Panjin Han population and its relationship with the other populations, the Reynold's genetic distance was calculated based on the allele frequencies across the 15 autosomal loci shared by the 21 included compared populations (Tie et al. 2006; Zuniga et al. 2006; Yan et al. 2007; Montelius et al. 2008; Wu et al. 2008; Gomes et al. 2009; Deng et al. 2011; Yoo et al. 2011; Chen et al. 2012; Tong et al. 2013; Zhang et al. 2015; Zhang 2015a, 2015b; Xiao et al. 2016; Yao, Wang, et al. 2016; Yao, Xing, et al. 2016; Hongdan et al. 2017; Li et al. 2017; Xu, Feng, et al. 2017; Xu, Xu, et al. 2017; He et al. 2018). The results showed that the Panjin Han had the nearest genetic distance with Liaoning Han (0.000289), followed by Heilongjiang Han (0.000325), Jilin Han (0.000325), Jiangsu Han (0.000377), Henan Han (0.000417), Hubei Han (0.000546), Jiangxi Han (0.000713), Shaanxi Han (0.000958), Sichuan Han (0.000966), China Hui (0.000989), Guangdong Han (0.002234), China Tibetans (0.003198), Koreans (0.003261), China Dong (0.003851), China Bouyei (0.005347), Japanese (0.005528), China Miao (0.007613), China Uygur (0.008692), Americans (0.024125), Europeans (0.033369), and Africans (0.042489) (Table 2). The exact test of population differentiation found that no significant difference was observed between the Panjin Han and the other Han populations, except for Guangdong Han ($p < 0.0001$) and Jiangxi Han ($p \approx 0.0190$). Moreover, the Panjin Han population was significantly different to the other ethnic groups in China (Bouyei, Dong, Hui, Miao, Tibetan, and Uygur) and the foreign ethnic groups (Japanese, Korean, African, American, and European). The phylogenetic neighbor-joining (N-J) tree was generated to reflect the historical and geographical background of the compared populations (Figure 2). The N-J tree exhibited significant differences between the Han population and the other minority groups. We also observed variations between Han populations from north to south, which was intricately sub-structured and clustered into three subgroups (northern Han, central Han and southern Han) in the previous study (Xu et al. 2009). Clearly, the Panjin Han population belongs to the northern Han subgroup, which also includes Heilongjiang, Jilin, Liaoning, Henan, and Hubei Han populations. These northern Han populations were also distributed in the close clusters in our N-J tree. In addition, the analysis of population differentiation found that The Panjin Han had major differences with the other Chinese minority ethnic populations and the foreign ethnic groups, which was also simultaneously mirrored in the N-J tree. The MDS plot was generated using the Reynold's genetic distance among the 22 compared populations (Figure 3). The Panjin Han and other Han groups were gathered together. The Chinese ethnic minorities, Korean and Japanese populations were scattered around the periphery. Additionally, the distribution of African, American, and European populations was more discrete. The location of the compared populations in the MDS plot was consistent with the results in the N-J tree. Geographically, Panjin city is located in Liaoning Province. The Liaoning Han integrated gradually with natives, such as Manchu, following geographical migration (Yao, Wang, et al. 2016). Consequently, the Liaoning Han population has its own unique genetic characteristics that are different from Han populations from other provinces. Similarly, the Panjin Han population belongs to the northern Han with its own unique structure characteristics.

4. Conclusions

In summary, 23 autosomal STR loci were genotyped in 1263 Panjin Han individuals using the VeriFiler™ Express PCR Amplification Kit. Population comparison was performed between the Panjin Han population and the other relevant groups to further explore the structure of Panjin Han and its relationship with the other groups. The results showed that the Panjin Han belong to the subgroup of northern Han and have major differences with the other Chinese minority ethnic populations and the foreign ethnic groups.

Author contributions

Hongbo Wang and Jun Yao developed the idea. Hongbo Wang analysed the results and wrote the manuscript. Bao-jie Wang and Cairui Xin conducted the experiment. All authors reviewed the manuscript.

Disclosure statement

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References

Adnan A, Rakha A, Noor A, VAN Oven M, Ralf A, Kayser M. 2018. Population data of 17 Y-STRs (Yfiler) from Punjabis and Kashmiris of Pakistan. Int J Legal Med. 132(1):137–138.

Adnan A, Ralf A, Rakha A, Kousouri N, Kayser M. 2016. Improving empirical evidence on differentiating closely related men with RM Y-STRs: a comprehensive pedigree study from Pakistan. Forensic Sci Int Genet. 25:45–51.

Cabezas Silva R, Ribeiro T, Lucas I, Porto MJ, Costa Santos J, Dario P. 2016. Analysis of 17 STR data on 5362 southern Portuguese individuals-an update on reference database. Forensic Sci Int Genet. 21: e10–e12.

Chen JG, Pu HW, Chen Y, Chen HJ, Ma R, Xie ST, Zhang LP. 2012. Population genetic data of 15 autosomal STR loci in Uygur ethnic group of China. Forensic Sci Int Genet. 6(6):e178–e179.

Chen L, Duan L, Yuan L, Shen Z, He W, Zhai D, Huang Y, Xu B. 2017. Genetic polymorphisms of 19 autosomal STR loci in the China Burmese immigrants. Forensic Sci Int Genet. 31:e46–e47.

Deng YJ, Zhu BF, Shen CM, Wang HD, Huang JF, Li YZ, Qin HX, et al. 2011. Genetic polymorphism analysis of 15 STR loci in Chinese Hui ethnic group residing in Qinghai province of China. Mol Biol Rep. 38(4):2315–2322.

Felsenstein J. 2009. PHYLIP (phylogeny inference package) version 3.69. Seattle: University of Washington.

Gomes V, Sanchez-Diz P, Alves C, Gomes I, Amorim A, Carracedo A, Gusmao L. 2009. Population data defined by 15 autosomal STR loci in Karamoja population (Uganda) using AmpF/STR Identifiler kit. Forensic Sci Int Genet. 3(2):e55–e58.

Green R, Elliott JL, Norona W, Go F, Nguyen VT, Ge J, Short ML, et al. 2021. Developmental validation of VeriFiler Plus PCR Amplification Kit: A 6-dye multiplex assay designed for casework samples. Forensic Sci Int Genet. 53:102494.

Guo F. 2017. Genetic polymorphism of 17 autosomal STR loci in the Lahu ethnic minority from Yunnan Province, Southwest China. Forensic Sci Int Genet. 31:e52–e53.

Hamester FIR, DA Silva DS, Leboute APM, Motta CHA, Alho CS. 2019. Slippage mutation rates in 15 autosomal short tandem repeat loci for forensic purposes in a Southeastern Brazilian population. Electrophoresis. 40(21):2873–2876.

He GLin, Li Y, Zou X, Li P, Chen PYu, Song F, Gao T, et al. 2017. Forensic features and phylogenetic analyses of Sichuan Han population via 23 autosomal STR loci included in the Huaxia Platinum System. Int J Legal Med. 131(5):1243–1246.

He G, Wang M, Liu J, Hou Y, Wang Z. 2018. Forensic features and phylogenetic analyses of Sichuan Han population via 23 autosomal STR loci included in the Huaxia Platinum System. Int J Legal Med. 132(4): 1079–1082.

Hongdan W, Bing K, Ning S, Miao H, Bo Z, Yuxin G, Bofeng Z, et al. 2017. Evaluation of the genetic parameters and mutation analysis of 22 STR loci in the central Chinese Han population. Int J Legal Med. 131(1):103–105.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol Biol Evol. 33(7): 1870–1874.

Li XN, Zheng JL, Jun Y. 2017. Genetic polymorphisms of 15 autosomal STR loci in 3962 individuals from the Han population of Jiangxi, Southeast China. Forensic Sci Int Genet. 31:e57–e58.

Liu K, Muse SV. 2005. PowerMarker: an integrated analysis environment for genetic marker analysis. Bioinformatics. 21(9):2128–2129.

Lu Y, Song P, Huang JC, Wu X. 2017. Genetic polymorphisms of 20 autosomal STR loci in 5141 individuals from the Han population of Xiamen, Southeast China. Forensic Sci Int Genet. 29:e31–e32.

Montelius K, Karlsson AO, Holmlund G. 2008. STR data for the AmpFlSTR Identifiler loci from Swedish population in comparison to European, as well as with non-European population. Forensic Sci Int Genet. 2(3): e49–e52.

Rubab A, Shafique M, Javed F, Saleem S, Zahra FT, Mcnevin D, Shahid AA. 2020. Population genetic portrait of Pakistani Lahore-Christians based on 32 STR loci. Sci Rep. 10(1):18960.

Tereba A. 1999. Tools for analysis of population statistics. Profiles in DNA. 3:14–16.

Tie J, Wang X, Oxida S. 2006. Genetic polymorphisms of 15 STR loci in a Japanese population. J Forensic Sci. 51(1):188–189.

Tong D, Chen Y, Ou X, Chen W, Liu S, Zhang Y, Sun H. 2013. Polymorphism analysis and evaluation of 19 STR loci in the Han population of Southern China. Ann Hum Biol. 40(2):191–196.

Walsh PS, Metzger DA, Higuchi R. 1991. Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. Biotechniques. 10:506–513.

Wu YM, Zhang XN, Zhou Y, Chen ZY, Wang XB. 2008. Genetic polymorphisms of 15 STR loci in Chinese Han population living in Xi'an city of Shaanxi Province. Forensic Sci Int Genet. 2(2):e15-8–e18.

Xiao C, Zhang W, Wei T, Pan C, Huang D. 2016. Population data of 21 autosomal STR loci in Chinese Han population from Hubei province in Central China. Forensic Sci Int Genet. 20:e13–e14.

Xu S, Yin X, Li S, Jin W, Lou H, Yang L, Gong X, et al. 2009. Genomic dissection of population substructure of Han Chinese and its implication in association studies. Am J Hum Genet. 85(6):762–774.

Xu XM, Feng Z, Yao J. 2017. Population data of 15 autosomal STR loci in Chinese Han population from Jilin Province, Northeast China. Forensic Sci Int Genet. 27:187–188.

Xu XM, Xu ZH, Wang DW, Yao J. 2017. Population data of 18 autosomal STR loci in the Chinese Han population from Heilongjiang Province, Northeast China. Forensic Sci Int Genet. 29:e33–e34.

Yan J, Shen C, Li Y, Yu X, Xiong X, Mu H, Huang Y, et al. 2007. Genetic analysis of 15 STR loci on Chinese Tibetan in Qinghai Province. Forensic Sci Int. 169(1):e3–e6.

Yao J, Wang BJ. 2016. Genetic variation of 25 Y-chromosomal and 15 autosomal STR loci in the Han Chinese population of Liaoning Province, Northeast China. PLoS One. 11(8):e0160415.

Yao J, Wang LM, Gui J, Xing JX, Xuan JF, Wang BJ. 2016. Population data of 15 autosomal STR loci in Chinese Han population from Liaoning Province, Northeast China. Forensic Sci Int Genet. 23:e20–e21.

Yao J, Xing JX, Xuan JF, Wang BJ. 2016. Population data of 15 autosomal STR loci in Chinese Han population from Jiangsu Province, Eastern China. Forensic Sci Int Genet. 24:112–113.

Yoo SY, Cho NS, Park MJ, Seong KM, Hwang JH, Song SB, Han MS, et al. 2011. A large population genetic study of 15 autosomal short tandem repeat loci for establishment of Korean DNA profile database. Mol Cells. 32(1):15–19.

Zhan X, Adnan A, Zhou Y, Khan A, Kasim K, Mcnevin D. 2018. Forensic characterization of 15 autosomal STRs in four populations from Xinjiang, China, and genetic relationships with neighboring populations. Sci Rep. 8(1):4673.

Zhang L. 2015a. Population data for 15 autosomal STR loci in the Bouyei ethnic minority from Guizhou Province, Southwest China. Forensic Sci Int Genet. 17:108–109.

Zhang L. 2015b. Population data for 15 autosomal STR loci in the Dong ethnic minority from Guizhou Province, Southwest China. Forensic Sci Int Genet. 16:237–238.

Zhang L, Zhao Y, Guo F, Liu Y, Wang B. 2015. Population data for 15 autosomal STR loci in the Miao ethnic minority from Guizhou Province, Southwest China. Forensic Sci Int Genet. 16:e3–e4.

Zhu BF, Zhang YD, Shen CM, Du WA, Liu WJ, Meng HT, Wang HD, et al. 2015. Developmental validation of the AGCU 21þ1 STR kit: a novel multiplex assay for forensic application. Electrophoresis. 36(2): 271–276.

Zuniga J, Ilzarbe M, Acunha-Alonzo V, Rosetti F, Herbert Z, Romero V, Almeciga I, et al. 2006. Allele frequencies for 15 autosomal STR loci and admixture estimates in Puerto Rican Americans. Forensic Sci Int. 164(2-3):266–270.