Genetic diversity and phylogenetic analysis of Chinese Han and Li ethnic populations from Hainan Island by 30 autosomal insertion/deletion polymorphisms

Jing Liu*, Ziwei Ye*, Zheng Wang, Xing Zou, Guanglin He, Mengge Wang, Shouyu Wang and Yiping Hou

Institute of Forensic Medicine, West China School of Basic Medical Sciences & Forensic Medicine, Sichuan University, Chengdu, China

ABSTRACT

With the characteristics of low mutation rate, length variation and short amplicon size, insertion/deletion polymorphisms (InDels) have the advantages of both short tandem repeats (STRs) and single nucleotide polymorphisms (SNPs). Herein, people of two ethnicities from Hainan Island were genotyped for the first time using the Investigator DIPplex kit. We investigated the forensic parameters of the 30 InDels and the phylogenetic relationships among different populations. The accumulated powers of discrimination and powers of exclusion were 0.999 999 999 9646 and 0.9897 in the Hainan Han population and 0.999 999 999 9292 and 0.9861 in the Hainan Li population, respectively. Additionally, population comparisons among geographically, ethnically and linguistically diverse populations via cluster heatmap, multidimensional scaling, principal component analysis, phylogenetic tree and STRUCTURE analyses demonstrated that the Hainan Han population had genetic similarities to the other Han, She and Tujia populations, while the Hainan Li population had close genetic relationships to the Zhuang and Miao groups; both populations had a high degree of genetic differentiation from most Turkic-speaking populations. Aforementioned results suggested that the 30 autosomal InDels are highly polymorphic and informative, which are suitable for human identification and population genetics.

KEYPOINTS

- Four hundred and forty-five Chinese individuals from two ethnicities (Hainan Han and Hainan Li) were firstly analyzed by 30 autosomal InDels included in the Investigator DIPplex panel.
- Forensic parameters of the 30 InDels in the two populations showed high polymorphism and universality for human identification purposes.
- The Investigator DIPplex panel had a certain capacity of differentiating intercontinental populations and different language populations.

Introduction

Insertion/deletion polymorphisms (InDels), also known as DIPs, are abundant in the human genome and usually appear biallelic feature, which have attracted the interests of forensic researchers and population geneticists recently [1–3]. With the characteristics of low mutation rate, small amplicon size, length variation as well as absence of stutter peaks and so on, InDels combine the advantages of both short tandem repeats (STRs) and single nucleotide polymorphisms (SNPs) markers and are gradually becoming a promising approach in forensic applications (especially for degraded DNA and mixed stain identification), population substructure analysis and biogeographic ancestry inference [2,4–6]. The Investigator DIPplex kit (Qiagen, Valenci, CA, USA), which contains 30 biallelic autosomal InDels and amelogenin, has been validated and studied in some populations to evaluate its efficacy in forensic applications [7–12]. However, the genetic polymorphisms and forensic parameters of the 30 InDels in the Hainan Han and Hainan Li populations remain unknown.

Hainan Island, the second largest island in China, is located at the southernmost tip of China, facing the Mainland to the north across the Qiongzhou
Strait (https://en.wikipedia.org/wiki/Hainan). Based on the 2010 National Population Census (http://www.stats.gov.cn/tjsj/pcsj/rkpc/6rp/indexch.htm), Han (84%) and Li (15%) are the dominant ethnicities of Hainan Island and account for 99% of the island’s population. At the time of the Song dynasty (A.D. 960–1279), large numbers of Han people from the Mainland arrived and settled on Hainan Island. However, according to the literature and archaeological studies, scholars believe that the Li people are the original inhabitants of Hainan Island and represent descendants of the ancient Yue tribe, who settled on the island between 7000–27000 years ago [13,14]. They have their own language, Hlai, which is a sub-branch of the Tai-Kadai language family [15]. The special geographic location, population characteristic and history of Hainan Island provide precious resources to conduct genetic-related analysis.

In the present study, we firstly genotyped Han and Li ethnicities from Hainan Island using the Investigator DIPplex kit and evaluated the forensic efficiency of this panel in the aforementioned two populations. Then, we performed population comparisons and genetic structure analysis between the two investigated groups and other previously studied populations based on 30 autosomal InDels. The details of the relevant populations are displayed in Supplementary Table S1.

Materials and methods

Sample collection and DNA isolation

A total of 445 blood samples were collected from unrelated individuals (238 Han and 207 Li people) living on Hainan Island with written informed consent. The collection of blood samples was approved by the Ethics Committee of Sichuan University. All participants declared that their ancestors have lived on this island for at least three generations. Genomic DNA was isolated utilizing the PureLink Genomic DNA Mini Kit (Thermo Fisher Scientific, Carlsbad, CA, USA) and quantified using the Nanodrop-2000C (Thermo Fisher Scientific) following the manufacturer’s recommendations. Then, DNA samples were normalized to 1.0 ng/μL and stored at −20°C until amplification.

PCR amplification and InDel genotyping

The 30 InDels and amelogenin included in the Investigator DIPplex kit were coamplified on a ProFlex 96-well PCR System (Thermo Fisher Scientific) according to the manufacturer’s protocol. Subsequently, PCR products were separated and detected using the Applied Biosystems 3130 Genetic Analyzer (Thermo Fisher Scientific). Allele allocation was carried out using GeneMapper ID-X v1.5 software. Control DNA 9948 (Qiagen) and ddH2O were used as positive and negative controls for each batch of genotyping. Our laboratory has been accredited by the China National Accreditation Service (CNAS) for Conformity Assessment and ISO 17025. The experimental methods and procedures of this study were conducted according to the approved guidelines of Institute of Forensic Medicine, Sichuan University.

Statistical analysis

Allele frequencies and forensic parameters, including observed heterozygosity ($H_o$), expected heterozygosity ($H_e$), matching probability (PM), power of discrimination (PD), probability of exclusion (PE) and typical paternal index (TPI), as well as the Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium (LD) tests were assessed using the online tool of STRAF [16]. Subsequently, the population relationships between the two studied groups and other previously studied populations were investigated. The heatmaps of allele frequencies and Net’s standard genetic distances ($R_{st}$) were produced with an online tool Morpheus (https://software.broadinstitute.org/morpheus/). $R_{st}$ was calculated based on allele frequencies using the PHYLIP 3.695 package. The $R_{st}$ matrix was then used to implement a multidimensional scaling (MDS) plot via the SPSS software (IBM SPSS, version 19.0; IBM Corp., Armonk, NY, USA) and construct the neighbour-joining (NJ) tree via the MEGA v7.0 software [17]. Allele frequency-based principal component analysis (PCA) was carried out using MVSP v3.22 software [18]. Population structure analysis was performed using STRUCTURE v.2.3.4 software with K values spanned from 2 to 7 [19]. Besides, Structure Harvester was used to infer the optimal K value, CLUMPP v.1.1.2 (Rosenberg Lab, Dallas, TX, USA) and Distruct v.1.1 (Rosenberg Lab) were employed to visualize the population genetic structures.

Results and discussion

Allele frequency and forensic parameter analysis

Supplementary Table S2 presents the genotype data of the 30 InDels in the Hainan Han and Hainan Li populations. No significant deviation from HWE was observed in either population after applying the Bonferroni correction ($P < 0.0017$) (Supplementary Table S3). LD test were performed using a shuffling test for all of the locus by locus pairwise combinations. No significant LD was found in either group, with the exception of HLD93–HLD97 in Hainan Han people after applying the Bonferroni correction ($P < 0.0001$) (Supplementary Tables S4–S5). The observed significance may represent substructure
association, which may be caused by the sample size or genetic admixture [20]. The allele frequencies and forensic parameters of the 30 InDels are shown in Supplementary Table S3 and Figure 1. The frequencies of deletion allele varied from 0.0714 to 0.9034 in Hainan Han people and from 0.0749 to 0.9541 in Hainan Li people. The \( H_o \) ranged from 0.1092 to 0.5756 in Hainan Han people and from 0.0725 to 0.5942 in Hainan Li people. In both populations, HLD88 possessed the largest PD and the values were 0.6361 (Hainan Han) and 0.6423 (Hainan Li), HLD93 had the highest PE, and the values were 0.2627 (Hainan Han) and 0.2840 (Hainan Li). The combined powers of discrimination and exclusion were 0.999 999 999 9646 and 0.9897 in Hainan Han people and 0.999 999 999 9292 and 0.9861 in Hainan Li people. These results suggested that this panel was effective for personal identification but not sufficiently powerful to perform a paternity test in the two groups.

**Genetic differentiation along continental divisions**

To gain an overview of the genetic similarities and differences between our studied populations and 56 global populations (East Asian [8–12,21–35], West Asian [36,37], European [33,37–42], American [43–45], African [23,46]), we conducted population comparisons along continental divisions through a series of analyses. In the cluster heatmap (Supplementary Figure S1), the HLD101, HLD114, HLD39, HLD48 and HLD111 loci showed high deletion frequencies in most East Asian populations, while the HLD118, HLD99, HLD64 and HLD81 loci showed low deletion frequencies in these groups. Moreover, three African populations (Xhosa, Zulu and Nigeria groups) displayed high deletion frequencies at the HLD06, HLD124, HLD77, HLD125, HLD58, HLD40 and HLD45 loci and low deletion frequencies at the HLD101, HLD114, HLD128, HLD131, HLD39 and HLD70 loci. In brief, there were significant differences in allele frequency distribution between populations from different continents (especially between East Asian and African populations).

As shown in Supplementary Table S6 and Supplementary Figure S2, the Hainan Han population had the closest relationship with the Shanghai Han population (\( R_{st} = 0.0024 \)), while the Hainan Li population had the smallest \( R_{st} \) with the Vietnam group (\( R_{st} = 0.0040 \)). Both showed the highest \( R_{st} \) with the African Nigeria population, and the values were 0.1878 (Hainan Han) and 0.2059 (Hainan Li), respectively. As demonstrated in Supplementary Figure S3(A), our studied populations and most East Asian populations were located at the right part of the y-axis, West Asian and European populations were distributed in the second quadrant, and most American and African populations were scattered in the third quadrant. A PCA plot (Supplementary Figure S3(B)) showed that the population distribution pattern was similar to the MDS, and the top two components could explain 74.01% of the total variance (PC1: 55.85% and PC2: 18.16%). Our studied populations and the East Asian populations were separated from other continental populations and had the greatest genetic differences from the three African populations (Xhosa, Zulu and Nigeria groups). Furthermore, the six Xinjiang minorities were situated between the other East Asian and European populations, in accordance with our previous study [47]. As shown in the NJ cladogram (Supplementary Figure S3(C)), three main branches were observed. The lower branch included Brazil and four African populations, the middle one contained six American groups, and the upper one was split into two subclades. Our studied populations and the East Asian populations clustered in the upper subclade, while the lower subclade consisted of the West Asian, European, Afrikaner and Southern Brazil populations. To sum up, the results of MDS, PCA and phylogenetic tree were consistent with each other.

Figure 1. Forensic statistical parameters from 30 InDels in the (A) Hainan Han (n = 238) and (B) Hainan Li (n = 207) populations. Del: deletion; In: insertion; \( H_o \): observed heterozygosity; \( H_e \): expected heterozygosity; PM: matching probability; PD: power of discrimination; PE: probability of exclusion; TPI: typical paternity index.
**Genetic differentiation along ethnic and linguistic divisions**

For the purpose of obtaining a clearer insight into Chinese population relationships, we performed various analyses among our studied populations and 28 Chinese populations [8–12,21,22,24–33]. Supplementary Figure S4 presents the cluster heatmap of deletion allele frequencies among the 30 populations, and three primary clusters (I, II and III) were easily distinguished. Cluster I was divided into two subclusters (IA and IB); the IA subcluster included five Tibetan groups, and the IB subcluster consisted of the Han, Bai, Tujia, Hui, Xibe, Dongxiang, She, Salar and Liangshan Yi populations. Cluster II contained the Hainan Li, Gaoshan, Zhuang, Miao, Dong and Yunnan Yi populations. In cluster III, there were six Xinjiang minorities. The Hainan Han population had a similar frequency pattern to the other Han, Hui and Tujia populations, while the Hainan Li population had a similar frequency pattern to the Gaoshan, Zhuang and Miao populations.

As shown in Supplementary Table S6 and Supplementary Figure S5, the Hainan Han population had relatively small $R_{st}$ with the other Han, Hui and Tujia populations, while the Hainan Li population had genetic affinities with the Zhuang, Dong and Gaoshan populations. Both had distant genetic relationships with the six Xinjiang groups. In Figure 2, different coloured fonts represent different language families. The MDS plot (Figure 2A) showed that all of the Turkic-speaking populations were distributed in the second quadrant, and all of the Tibeto-Burman-speaking populations (except the Bai group) were scattered below the $x$-axis. The Hainan Han population clustered with the Tujia, Bai, She (Hmong-Mien-speaking population) and Sinitic-speaking populations, while the Hainan Li population had close genetic relationships with the Zhuang (Tai-Kadai-speaking population) and Miao (Hmong-Mien-speaking population) groups. In our PCA plot (Figure 2B), the first two components accounted for 61.98% of the total variance. Most Turkic-speaking populations were distributed in the fourth quadrant,

![Figure 2. Genetic differentiation along ethnic and linguistic divisions.](image)

(A) The multidimensional scaling (MDS) plot was drawn based on pairwise $R_{st}$ values. (B) The principal component analysis (PCA) plot was performed based on allele frequencies of 30 InDels. (C) The phylogenetic tree was constructed based on pairwise $R_{st}$ values with the NJ method. Different coloured fonts represent different language families (Green: Sinitic; Dark blue: Tibeto-Burman; Pink: Tungusic; Orange: Mongolic; Red purple: Tai-Kadai; Yellow: Hmong-Mien; Light blue: Turkic).
and most Tibeto-Burman-speaking populations were situated above the x-axis. The Hainan Han population had genetic similarities to the She, Tujia, Bai, Yunnan Yi and Sinitic-speaking populations, while the Hainan Li population had genetic affinities with two Tai-Kadai-speaking populations (Zhuang and Dong groups) and the Miao group. In the NJ tree (Figure 2C), three clades were observed: a Turkic-speaking and Mongolic-speaking clade, a Tibeto-Burman-speaking clade (excluding the Yi and Tujia groups), and a clade containing our studied populations and other linguistic groups. The Hainan Han population clustered with the She people and then with three additional Han populations. The Hainan Li population first grouped with the Yunnan Yi, Miao and Dong groups and then with the Zhuang people. In short, we verified the genetic similarities among the same language families through multiple analyses and observed close genetic relationships between the Tai-Kadai-speaking and Hmong-Mien-speaking populations.

**Population structure analysis**

Structure analysis among four continental populations [9–12, 22–27, 29–32, 38, 45] is displayed in Figure 3. At K = 3, the genetic makeup showed a clear distinction between the East Asian populations and the populations from the other three continents. Our studied populations shared a resemblance to the East Asian groups, apart from the three Turkic-speaking populations. At K > 3, no further substructure was distinguished with the exception of the Xinjiang Hui population, which may be caused by the complex history of that group.

**Conclusion**

We firstly reported a batch of genotype data of 30 InDels included in the Investigator DIPplex kit in the Hainan Han and Hainan Li groups and evaluated the forensic application ability of this panel in the two populations. Furthermore, population comparisons along geographical, ethnical and linguistic divisions through multiple analyses manifested that the 30-InDels panel had a certain intercontinental differentiation ability (especially between the East Asian and African populations) and could also distinguish different language populations to a certain extent (especially for most Turkic-speaking populations). For our investigated populations, the Hainan Han population had close relationships to the other Han, She and Tujia populations, and the Hainan Li population had genetic affinities with the Zhuang and Miao minorities.

**Authors’ contributions**

Jing Liu and Ziwei Ye wrote the manuscript; Guanglin He, Mengge Wang and Shouyu Wang collected the

![Figure 3.](image-url) Structure clustering analysis was performed based on genotypes of 30 InDels among 30 populations, assuming K = 2–7.
samples; Jing Liu and Xing Zou conducted the experiment; Jing Liu and Xing Zou analyzed the results; Zheng Wang and Yiping Hou conceived the experiment. All authors approved the final text.

Compliance with ethical standards
This study was approved by the Ethics Committee of the Sichuan University (Approval Number: K2015008). Blood samples were collected from participants with written informed consent.

Disclosure statement
No conflict of interest was declared by the authors.

Funding
This work was supported by the National Natural Science Foundation of China [grant numbers 81571854 and 81871532], the Open Project of Key Laboratory of Forensic Genetics in Ministry of Public Security [grant number 2017FGKFKT01] and the Fundamental Research Funds for the Central University [grant number Y201651].

ORCID
Guanglin He http://orcid.org/0000-0002-6614-5267

References
[1] Pereira R, Phillips C, Alves C, et al. A new multiplex for human identification using insertion/deletion polymorphisms. Electrophoresis. 2009;30: 3682–3690.
[2] Santos NP, Ribeiro-Rodrigues EM, Ribeiro-Dos-Santos AK, et al. Assessing individual interethnic admixture and population substructure using a 48-insertion-deletion (INSEL) ancestry-informative marker (AIM) panel. Hum Mutat. 2010;31: 184–190.
[3] Montgomery SB, Goode DL, Kvikstad E, et al. The origin, evolution, and functional impact of short insertion-deletion variants identified in 179 human genomes. Genome Res. 2013;23:749–761.
[4] Romanini C, Catelli ML, Borosky A, et al. Typing short amplicon binary polymorphisms: supplementary SNP and Indel genetic information in the analysis of highly degraded skeletal remains. Forensic Sci Int Genet. 2012;6:469–476.
[5] Oldoni F, Castella V, Grosjean F, et al. Sensitive DIP-STR markers for the analysis of unbalanced mixtures from “touch DNA samples”. Forensic Sci Int Genet. 2017;28:111–117.
[6] Romanini C, Romero M, Salado Puerto M, et al. Ancestry informative markers: inference of ancestry in aged bone samples using an autosomal AIM-Indel multiplex. Forensic Sci Int Genet. 2015; 16:58–63.
[7] LaRue BL, Ge J, King JL, et al. A validation study of the Qiagen Investigator DIPplex® kit; an INDEL-based assay for human identification. Int J Legal Med. 2012;126:533–540.
[8] Wei YL, Qin CJ, Dong H, et al. A validation study of a multiplex INDEL assay for forensic use in four Chinese populations. Forensic Sci Int Genet. 2014;9:e22–e25.
[9] Shen C, Zhu B, Yao T, et al. A 30-InDel assay for genetic variation and population structure analysis of Chinese Tujia Group. Sci Rep. 2016;6:36842.
[10] Zhu B, Lan Q, Guo Y, et al. Population genetic diversity and clustering analysis for Chinese Dongxiang group with 30 autosomal InDel loci simultaneously analyzed. Front Genet. 2018;9:279.
[11] Kong T, Chen Y, Guo Y, et al. Autosomal InDel polymorphisms for population genetic structure and differentiation analysis of Chinese Kazakh ethnic group. Oncotarget. 2017;8:56651–56658.
[12] Meng HT, Zhang YD, Shen CM, et al. Genetic polymorphism analyses of 30 InDels in Chinese Xibe ethnic group and its population genetic differentiations with other groups. Sci Rep. 2015;5: 8260.
[13] Peng MS, He JD, Liu HX, et al. Tracing the legacy of the early Hainan Islanders—a perspective from mitochondrial DNA. BMC Evol Biol. 2011;11:46.
[14] Li D, Li H, Ou C, et al. Paternal genetic structure of Hainan aborigines isolated at the entrance to East Asia. PLoS One. 2008;3:e2168.
[15] Li D, Sun Y, Lu Y, et al. Genetic origin of Kaidi-speaking Gelong people on Hainan Island viewed from Y chromosomes. J Hum Genet. 2010;55: 462–468.
[16] Gouy A, Zieger M. STRAF—A convenient online tool for STR data evaluation in forensic genetics. Forensic Sci Int Genet. 2017;30:148–151.
[17] Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Mol Biol Evol. 2016;33: 1870–1874.
[18] Kovach WL. MVSP—A multivariate statistical package for Windows, ver. 3.1. Pentraeth (Wales): Kovach Computing Services, 2007.
[19] Evanno G, Regnaut S, Goudet J. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Mol Ecol. 2005;14:2611–2620.
[20] Pritchard JK, Donnelly P. Case-control studies of association in structured or admixed populations. Theor Popul Biol. 2001;60:227–237.
[21] Li Z, Xu J, Chen P, et al. Forensic efficiency and genetic divergence of 30 autosomal InDels in Chinese Han population from Jiangsu province. Forensic Sci Int Genet. 2018;37:e17–e19.
[22] Xie T, Guo Y, Chen L, et al. A set of autosomal multiple InDel markers for forensic application and population genetic analysis in the Chinese Xinjiang Hui group. Forensic Sci Int Genet. 2018; 35:1–8.
[23] Du W, Peng Z, Feng C, et al. Forensic efficiency and genetic variation of 30 InDels in Vietnamese and Nigerian populations. Oncotarget. 2017;8: 88934–88940.
[24] Yang CH, Yin CY, Shen CM, et al. Genetic variation and forensic efficiency of autosomal insertion/deletion polymorphisms in Chinese Bai ethnic group: phylogenetic analysis to other populations. Oncotarget. 2017;8:39582–39591.
[25] Wang Z, Zhang S, Zhao S, et al. Population genetics of 30 insertion–deletion polymorphisms in two Chinese populations using Qiagen Investigator© DIPplex kit. Forensic Sci Int Genet. 2014;11: e12–e14.

[26] Wang L, Lv M, Zaumsegel D, et al. A comparative study of insertion/deletion polymorphisms applied among Southwest, South and Northwest Chinese populations using Investigator© DIPplex. Forensic Sci Int Genet. 2016;21:10–14.

[27] Guo Y, Shen C, Meng H, et al. Population differentiation and phylogenetic analysis of Tibet and Qinghai Tibetan groups based on 30 InDel loci. DNA Cell Biol. 2016;35:787–794.

[28] Jian H, Wang L, Wang H, et al. Population genetic analysis of 30 insertion-deletion (INDEL) loci in a Qinghai Tibetan group using the Investigator DIPplex Kit. Int J Legal Med. 2019;133:1039–1041.

[29] Ma R, Shen C, Wei Y, et al. Genetic differentiation and forensic efficiency evaluation for Chinese Salar ethnic minority based on a 5-dye multiplex insertion and deletion panel. Gene. 2018;660:41–50.

[30] Zhang YD, Shen CM, Jin R, et al. Forensic evaluation and population genetic study of 30 insertion/deletion polymorphisms in a Chinese Yi group. Electrophoresis. 2015;36:1196–1201.

[31] Mei T, Shen CM, Liu YS, et al. Population genetic structure analysis and forensic evaluation of Xinjiang Uigur ethnic group on genomic deletion and insertion polymorphisms. SpringerPlus. 2016; 5:1087.

[32] Guo Y, Chen C, Jin X, et al. Autosomal DIPs for population genetic structure and differentiation analyses of Chinese Xinjiang Kyrgyz ethnic group. Sci Rep. 2018;8:11054.

[33] Pepinski W, Abreu-Gl wowacka M, Koralewska-Kordel M, et al. Population genetics of 30 INDELS in populations of Poland and Taiwan. Mol Biol Rep. 2013;40:4333–4338.

[34] Kim EH, Lee HY, Yang IS, et al. Population data for 30 insertion-deletion markers in a Korean population. Int J Legal Med. 2014;128:51–52.

[35] Seong KM, Park JH, Hyun YS, et al. Population genetics of insertion-deletion polymorphisms in South Koreans using Investigator DIPplex kit. Forensic Sci Int Genet. 2014;8:80–83.

[36] Poulsen L, Farzad MS, Borsting C, et al. Population and forensic data for three sets of forensic genetic markers in four ethnic groups from Iran: Persians, Lurs, Kurds and Azeris. Forensic Sci Int Genet. 2015;17:43–46.

[37] Tomas C, Poulsen L, Drobnic K, et al. Thirty autosomal insertion–deletion polymorphisms analyzed using the Investigator© DIPplex Kit in populations from Iraq, Lithuania, Slovenia, and Turkey. Forensic Sci Int Genet. 2016;25:142–144.

[38] Friis SL, Borsting C, Rockenbauer E, et al. Typing of 30 insertion/deletions in Danes using the first commercial indel kit—Mentype© DIPplex. Forensic Sci Int Genet. 2012;6:e72–e74.

[39] Zidkova A, Horinek A, Kebdrlova V, et al. Application of the new insertion–deletion polymorphism kit for forensic identification and parentage testing on the Czech population. Int J Legal Med. 2013;127:7–10.

[40] Martin P, Garcia O, Heinrichs B, et al. Population genetic data of 30 autosomal indels in Central Spain and the Basque Country populations. Forensic Sci Int Genet. 2013;7:e27–e30.

[41] Neuvonen AM, Palo JU, Hedman M, et al. Discrimination power of Investigator DIPplex loci in Finnish and Somali populations. Forensic Sci Int Genet. 2012;6:e99–e102.

[42] Carvalho A, Pinheiro MF. Population data of 30 insertion/deletion polymorphisms from a sample taken in the North of Portugal. Int J Legal Med. 2013;127:65–67.

[43] Ferreira Palha TJB, Ribeiro Rodrigues EM, Cavalcante GC, et al. Population genetic analysis of insertion–deletion polymorphisms in a Brazilian population using the Investigator DIPplex kit. Forensic Sci Int Genet. 2015;19:10–14.

[44] Torres SR, Uehara CJ, Sutter-Latorre AF, et al. Population genetic data and forensic parameters of 30 autosomal InDel markers in Santa Catarina State population, Southern Brazil. Mol Biol Rep. 2014;41:5429–5433.

[45] Martinez-Cortés G, García-Aceves M, Favera-Mendoza AF, et al. Forensic parameters of the Investigator DIPplex kit (Qiagen) in six Mexican populations. Int J Legal Med. 2016;130:683–685.

[46] Hefke G, Davison S, D’Amato ME. Forensic performance of Investigator DIPplex indels genotyping kit in native, immigrant, and admixed populations in South Africa. Electrophoresis. 2015; 36:3018–3025.

[47] Liu J, Wang Z, He G, et al. Massively parallel sequencing of 124 SNPs included in the precision ID identity panel in three East Asian minority ethnicities. Forensic Sci Int Genet. 2018;35:141–148.