

# Forensic characteristics and phylogenetic analyses of the Chinese Yi population via 19 X-chromosomal STR loci

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Received: 4 January 2017 / Accepted: 14 February 2017 / Published online: 28 February 2017  
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**Abstract** The demographic characteristics and genetic polymorphism data of 56 Chinese nationalities or 31 administrative divisions in Chinese mainland have repeatedly been the genetic research hotspots. While most genetic studies focused on some particular Chinese populations based on autosomal or Y-chromosomal genetic markers, the forensic characteristics and phylogenetic analyses of the seventh largest Chinese population (Yi ethnicity) on the X-chromosomal genetic markers are scarce. Here, allele frequencies and forensic statistical parameters for 19 X-chromosomal short tandem repeat loci (DXS7424-DXS101, DXS6789-DXS6809, DXS7423-DXS10134, DXS10103-HPRTB-DXS10101, DXS10159-DXS10162-DXS10164, DXS10148-DXS10135-DXS8378, and DXS7132-DXS10079-DXS10074-DXS10075) of 331 Chinese Yi individuals were

obtained. All 19 X-chromosomal short tandem repeat (STR) loci in females were consistent with the Hardy-Weinberg equilibrium test. A total of 214 alleles were identified with the corresponding allele frequencies spanned from 0.0019 to 0.6106. The combined PE, PDF, and PDM were 0.9999999214, 0.999999999999999993, and 0.999999999998, respectively. The high combined MEC<sub>Krüger</sub>, MEC<sub>Kishida</sub>, MEC<sub>Desmarais</sub>, and MEC<sub>Desmarais Duo</sub> were achieved as 0.9999999617638, 0.999999999971, 0.999999999971, and 0.9999999931538, respectively. The findings suggested that the panel of 19 X-STR loci is highly polymorphic and informative in the Yi ethnic population and can be considered to be a powerful tool in forensic complex kinship identification. Population differentiation analyses among 12 populations indicated that significant differences in genetic structure were observed in between the Yi ethnicity and the Chinese Uyghur as well as Kazakh, and genetic homogeneity existed in similar ethno-origin or geographic origin populations.

GuangLin He and Ye Li contributed equally to these studies.

**Electronic supplementary material** The online version of this article (doi:10.1007/s00414-017-1563-0) contains supplementary material, which is available to authorized users.

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**Keywords** X-chromosomal STR · Phylogenetic analyses · Forensic science · Genetic polymorphisms · Yi ethnicity

Autosomal short tandem repeats (STRs), as a common genetic marker in forensic practice, had limitation in addressing deficiency paternity cases [1]. Recently, X-chromosomal short tandem repeats played an important complementary role in forensic parentage test and personal identification, especially in the complicated kinship [1, 2]. In the past decades, several mature multiplex amplification systems including the Mentype® Argus X-UL, Mentype® Argus X-8, Investigator Argus X-12, and X-Decaplex (In-house Kit) PCR amplification kits (Table S1) had been applied in forensic application and explored the population data in different ethnicity groups. The AGCU X19 commercial kit is a new amplification system



Population genetic relationships between the Chinese Yi ethnic group and the five Han Chinese groups [5, 10, 12–14] as well as six different minority ethnic groups [3, 4, 11, 15–17] (Fig. S1) are investigated in the present study. The  $F_{st}$  and the corresponding  $p$  value are listed in Table S5. Along ethnic divisions, significant genetic differences between the Chinese Yi and the Uyghur as well as Kazakh ethnic group were identified at four and three loci, respectively. Along Han Chinese populations, no significant genetic differences were observed with the Chinese Yi ethnic group except the Guangdong Han at one locus.

Inter-population genetic variability was further analyzed by phylogenetic analyses. Genetic distances among 12 populations are presented in Table S6. The smallest and largest Nei's standard distances between the Chinese Yi and the reference populations were identified were 0.0038 (Chinese Yi and Henan Han) and 0.0348 (Chinese Yi and Xinjiang Uyghur). A neighboring-joining tree (N-J tree) derived from the Nei's genetic distance is displayed in Fig. S2. Twelve Chinese populations were clustered into two branches. Two Chinese minority populations (Uyghurs and Kazakhs) residing in Xinjiang formed one branch. Additional ten populations were grouped closely. Our studied population and the branch consisting of most Han Chinese populations clustered first and then with the branch comprising three populations living in Guangdong provinces. Population comparisons and phylogenetic analyses indicated that significant differences with the Chinese Yi ethnic group were identified with the Chinese Uyghur and Kazakh, and genetic homogeneity was observed in similar ethno-origin or geography close populations.

In summary, our study presents the first batch of genetic polymorphism data on X-chromosome in the Chinese Yi ethnicity group and enriched Chinese minority ethnic population reference databases. Nineteen X-STR loci included in AGCU X19 amplification system showed highly polymorphic and informative in the Yi ethnicity and can be used as a potential tool in forensic complex kinship identification and population genetic study. Inter-population comparisons and phylogenetic analyses revealed that the Chinese Yi group had close genetic distance with most Han Chinese populations and kept far from Uyghurs and Kazakhs. Besides, our findings indicated that geographic close population possessed the genetic homogeneity in X-chromosome.

**Acknowledgements** The study was supported by the Sichuan Science and Technology Support Program (2014SZ0012).

**Compliance with ethical standards** Our study design was subject to approval by the Ethics Committee of the Institute of Forensic Medicine, Sichuan University, China. Informed consents were achieved before sample collection.

**Conflict of interests** None.

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