



# Genetic diversity and haplotype analysis of Guizhou Miao identified with 19 X-chromosomal short tandem repeats

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## Abstract

We analyzed Chinese Miao population samples ( $n = 268$ ) from Guizhou province, Southwest China, with 19 X-chromosomal short tandem repeats (STRs) included in the AGCU X19 amplification kit. The combined PE is 0.999999922 and the combined PDs in males and females are 0.9999999999999999994 and 0.999999999998, respectively. The mean paternity exclusion change values are larger than 0.99999996. The HDs in seven linkage groups vary from 0.9324 to 0.9968. Subsequently, comparison among different Chinese populations shows that the substructures of Chinese were significantly influenced by ethno-linguistic rather than geographical boundaries, including most prominently Turkic-speaking and Tibeto-Burman-speaking populations.

**Keywords** X-chromosomal STRs · Miao population · Population genetics · Haplotype diversity

X-chromosomal short tandem repeats (STRs) with the advantages of both autosomal and uni-parental biomarkers have been widely used in the forensic deficiency cases and other complex kinship identification [1]. Chinese Miao (also called Hmong) is the fourth largest minority ethnic group officially

recognized by the government of the People's Republic of China. The population size of Chinese Miao is approximately 12 million over the world and around 9 million in China. Chinese Miao live primarily in remote Southwest China's mountains, in the provinces of Guizhou, Yunnan, Sichuan, Hubei, Hunan, Guangxi, Guangdong, and Hainan. The Miao language belongs to the Hmong-Mien linguistic family. Historically, contemporary Miao is the descendants of the Jiuli tribe led by Chiyou and has experienced five large-scale migrations. Archeological evidence from the Daxi Culture (5300–6000 years ago) led to the hypothesis that Miao was the first people to settle in present-day China. The language formations and changes of present-day Miao ethnicity have genetic assimilation of neighboring ethnically diverse populations [2].

Yanyan Han and Guanglin He contributed equally to this work.

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In the presented study, we used the AGCU X19 kit to genotype the 19 X-STRs belonging to seven linkage groups [3–5] (DXS10074-DXS10075-DXS10079-DXS7132, DXS101-DXS7424, DXS10101-DXS10103-HPRTB, DXS10134-DXS7423, DXS10135-DXS10148-DXS8378, DXS10159-DXS10162-DXS10164, and DXS6789-DXS6809) in 268 volunteers (117 females and 151 males) who self-identified themselves as Miaos and compared the genetic relationship with 12 reference populations. All peripheral blood samples reported were obtained from Zunyi City in Guizhou Province (Southwest China) under the protocols



and our focus population, the Guizhou Chinese Miao population. The Guizhou Chinese Miao is identified to be most close to the Sichuan Han population and then to Guanzhong Han population.

Our study provided the first batch of X-chromosomal STR data from Miao ethnicity, thus enriches the Chinese ethnic genetic information. The 19 X-STRs and seven linkage groups are informative and powerful markers to distinguish individuals and complex testing kinship. Comprehensive population comparisons on the genetic variations of 19X-STRs through the MDS, PCA and N-J tree indicate that as a representative Hmong-Miao-speaking population the Guizhou Miao has a close genetic relationship with surrounding Sinitic-speaking populations, especially with Sichuan and Guanzhong Han populations. In a summary, genetic differentiations exist among linguistic diverse populations and genetic affinity exists among populations within the same language family.

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### Compliance with ethical standards

This study had been approved by the institutional review boards at Zunyi Medical University. Informed consent was obtained from volunteers before sample collection.

**Competing interests** The authors declare that they have no competing interests.

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