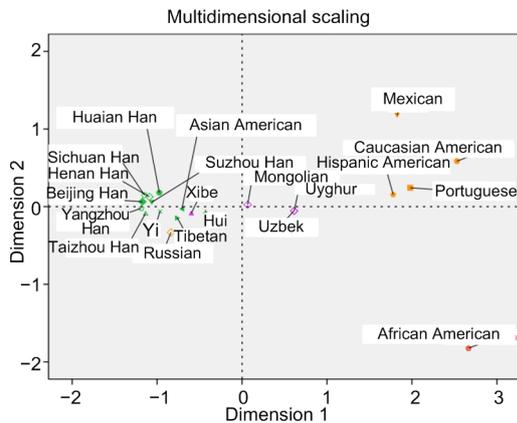


**Fig. 1 Heatmap of the genetic distances ( $D_A$ ) among 21 populations**

Different colors indicate different levels of  $D_A$  values: cyan for low values, pink for intermediate values, and green for large values



**Fig. 2 Multidimensional scaling analysis between the Mongolian group and other compared populations**

Based on the 15 shared STR data, we found that close relationships existed between the Mongolian group and the Uyghur, Xibe, and other Chinese populations. According to Chinese historical records, the Donghu, a nomadic group living in eastern Mongolian and northeast Chinese regions, might be proto-Mongols of the present Mongolian group. In the 13th century, Genghis Khan unified an army of Mongolian tribes, and he along with his Mongolian soldiers expanded westward and soon occupied almost all Eurasian regions. After the fall of the Mongolian empire,

these dispersed Mongolian individuals were gradually assimilated by the surrounding people and became a part of the Uyghur, Xibe, and other tribes (<https://en.wikipedia.org/wiki/Mongols>). Findley (2005) suggested that the modern Uyghurs probably possessed admixture genetic information of Mongolian and Caucasian people, resulting in close genetic relationships between the Mongolian and Uyghur groups. Another study also revealed that the Xibe had an intimate relationship with the Mongolian group. For instance, the phylogenetic tree constructed using 17 Y-STR loci haplotypes showed the Xibe forming a branch with the Mongolian group firstly, followed by other populations (Zheng et al., 2009). More importantly, the Xibe people are descendants of the ancient Xianbei tribes, who are a branch of the ancient Donghu group (Wu, 2002). Thus, the common ancestral origins of the Mongolian and Xibe groups likely contributed to their close ties.

In brief, allele frequencies and forensic statistical parameters were obtained for 19 autosomal STRs in the Xinjiang Mongolian group, and these results laid the foundation for the STR database spanning different Chinese ethnic groups. The cumulative DP and PE values indicated that the multiplex STR system exhibited exceedingly high values for forensic applications in the Xinjiang Mongolian group. Moreover, the results of genetic distances and MDS analysis between the studied Mongolian group and other reference populations revealed that the Mongolian group had close genetic relationships with the Uyghur, Xibe, and other Chinese populations.

**Contributors**

Bo-feng ZHU and Jian-gang CHEN designed this research. Yuan-yuan WEI wrote the main manuscript. Jian-gang CHEN collected samples. Yuan-yuan WEI, Wei CUI, and Chong CHEN performed experiment. Xiao-ye JIN and Qiong LAN conducted statistical analysis. Ting-ting KONG and Yu-xin GUO revised the manuscript.

**Compliance with ethics guidelines**

Yuan-yuan WEI, Xiao-ye JIN, Qiong LAN, Wei CUI, Chong CHEN, Ting-ting KONG, Yu-xin GUO, Jian-gang CHEN, and Bo-feng ZHU declare that they have no conflicts of interest.

All procedures followed were in accordance with the ethical standards of the responsible committee on human experimentation (institutional and national) and with the Helsinki Declaration of 1975, as revised in 2008 (5). Informed

