A new 19 X-STR multiplex PCR system was developed, however its applicability in forensic purpose still need some supports. In this study, 932 unrelated individuals from four ethnic groups (i.e., Han, Tibet, Uighur and Hui) in China were successfully genotyped using a new multiplex PCR system. Our results revealed that significant linkage disequilibrium was found between markers DXS10103 and DXS10101 in all four ethnic groups; DXS10159 and DXS10162, DXS6809 and DXS6789, HPTRB and DXS10101 in Tibet; DXS10074 and DXS10075 in Uighur. The combined powers of discrimination in males and females were calculated according to haplotype frequencies from allele distributions rather than haplotype count in the relevant population and high in four ethnic groups. Moreover cumulative powers of discrimination of the tested X-STR loci were 1.000 000 000 000 000 and 0.999 999 997 940 in females and males, respectively. All 19 X-STR loci are highly polymorphic. Highest values of Reynolds genetic distances was observed at Tibet-Uighur pairwise when analyzed with 19 X-STRs. This study is the extensive report on variations of X-STR markers in minor populations from China and the comprehensive analysis of diversity of these 19 X STR in four ethnic groups in China.

Keywords: X chromosomal short tandem repeats (STRs); Forensic genetics; linkage disequilibrium (LDE)