Y-STR HAPLOTYPES IN SOUTH KOREAN POPULATION GROUPS AND APPLICATION IN CRIME CASES

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Y chromosome short tandem repeat (Y-STR) analysis has become an important tool for forensic genetics, patrilineage tracking and human population history. Close paternal relatives have very similar Y-STR haplotypes because of co-segregate surname ancestry. In societies, patrilineal surnames and Y-STR haplotypes are expected to be correlated. The population genetic data of the Y-STR haplotypes of 1021 unrelated males having 72 South Korean surnames was analyzed to evaluate their usefulness for South Korean forensic science. Haplotypes and allele frequencies of 17 Y-STR loci were obtained by using the AmpF*l*STR® Yfiler® kit (Applied Biosystems, FosterCity, CA). A total of 938 haplotypes were observed in the 1021 individuals studied, of which 885 were unique. The overall haplotype diversity (*HD*) for the 17 Y-STR loci was 0.9998, and the discrimination capacity (*DC*) was 0.9187. For the 10 most common surname subpopulations of South Korea, the discrimination capacity (*DC*) index ranged from 0.9651 to 1.0000. High haplotype diversity indicates that Y-STR haplotypes are very heterogeneous within each surname. In several crime cases, we applied an analysis method for predicting the surname of origin for forensic purposes. Our experiences show that Y-STR haplotypes database searching and surname analysis is a very useful method to estimate a real criminal in South Korea.