

POWER OF SINGLE NUCLEOTIDE POLYMORPHISMS IN FORENSIC IDENTIFICATION

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Single nucleotide polymorphisms(SNPs) are typically biallelic loci that segregate in a Mendelian fashion and are the most common type of genetic variation in humans. Recently, the interest in scoring SNPs for a multitude of different applications has increased dramatically. Furthermore, advance of SNP chips allow researchers to examine genetic variation in much greater detail. In forensic application, Short Tandem Repeats(STRs) are the most commonly used form of genetic information and are widely accepted. But advances in SNPs have raised the potential that these markers could replace the forensically established STRs.

In this study, we conducted the simulation studies allowing to estimate how many SNPs are needed if these markers were used instead of STRs in the criminal case and paternity investigation. We used two different simulation methods. In the first method, we calculated the cumulative mean exclusion chance(CMEC) and the cumulative power of discrimination(CPD) for SNPs with various allele frequencies and for STRs with various allele numbers and compared the number of SNPs with that of STRs. The second method is to estimate the number of loci needed for obtaining paternity index or identity index of 1000 in SNPs and STRs, respectively. Our simulation result will provide statistical guidelines when the SNPs are used instead of STRs in the criminal cases and paternity testing.