SHORT TANDEM REPEATS VERSUS SINGLE NUCLEOTIDE POLYMORPHISMS: A COMPARATIVE STUDY OF UTILITY FOR HUMAN IDENTIFICATION

Ranajit Chakraborty[1], Marek Kimmel[2], David N. Stivers[1], and Bruce Budowle[3]

[1] *Human Genetics Center, University of Texas School of Public Health, Houston, Texas*
[2] *Department of Statistics, Rice University, Houston, Texas*
[3] *Forensic Science Research and Training Center, Federal Bureau of Investigation, Quantico, Virginia*

With more than 15 short tandem repeat (STR) loci currently validated for forensic analysis for the purpose of human identification, the discriminating power of forensic DNA analysis has reached a satisfactory level for most forensic case scenarios. However, miniaturization and automation of DNA technology prompted the need of consideration of the newly discovered single nucleotide polymorphism (SNP) sites in the form of 'DNA chips' for forensic analyses. This investigation considers the theoretical issues related to the comparative efficiencies of STR versus SNP loci for various scenarios of forensic analyses. First, we show that the expected effect of population substructure on the statistical strength of DNA evidence is greater for SNP loci as compared to that of STR loci. Second, we argue that because of the lower discriminatory power of individual SNP loci, a far larger number of SNP loci would be needed to attain an equivalent power of the current battery of STR markers for forensic analysis. Third, because of the bi-allelic nature of the SNPs, interpretation of mixture analysis based on SNPs is likely to be more difficult as compared to that based on the STR loci. Based on these considerations, we recommend that, once validated for forensic applications, the SNP-based DNA chips may be used as a supplementary battery of forensic markers, and the technology of STR typing should be retained as the primary set of markers for forensic DNA analyses. However, mitochondrial DNA and Y-chromosome-based DNA chips may be used in addition to STR-typing to help in determining the possible number of contributors in mixtures of DNA samples. The theories used in these arguments are illustrated with empirical data from the current battery of STR markers. (Research supported by US Public Health Service Research grants and grants from the US National Institute of Justice).