

Y-CHROMOSOME MULTIPLEXES AND THEIR POTENTIAL FOR THE DNA PROFILING OF KOREANS

Dong-Jik Shin¹, Han-Jun Jin¹, Kyoung-Don Kwak¹, Jeon-Won Choi¹, Myun-Soo Han², Sang-Kyu Choi², Wook Kim¹

¹*Department of Biology, Dankook University, Cheonan, Korea*

²*DNA Analysis Section, National Institute of Scientific Investigation, Seoul, Korea*



We have developed four multiplex genotyping systems (GeneKin[®] Y-STR multiplexes) using silver staining with allelic ladders for ten Y-chromosome STR markers (DYS19, DYS385, DYS388, DYS389I/II, DYS390, DYS391, DYS392, DYS393, and DXYS156Y), with a view towards the application of rapid and simple genotyping assay methods for DNA profiling. The GeneKin[®] Y-STR multiplexes developed have followed the published nomenclature and ISFG guidelines for STR analysis. Allele and haplotype frequencies at these Y-STRs loci were analyzed by PCR amplification using the GeneKin[®] Y-STR multiplexes, followed by denaturing polyacrylamide gel electrophoresis in 316 unrelated males in the Korean population. A total of 295 different haplotypes were found, 279 of them being unique. Gene diversity ranged from 0.4026 at DYS391 to 0.9606 at DYS385. The haplotype diversity value (which is the same as the discrimination index) calculated from all ten loci combined was 0.9995, which is informative. Our results revealed that a set of ten Y-STRs could discriminate between most of the male individuals in the Korean population (discrimination capacity: 93.35%). The Y-STR multiplexes thus provide useful information for forensic analysis and paternity tests, and can also be of great benefit for providing information not normally available from autosomal DNA systems.