## MULTIPLEXING OF Y-CHROMOSOME STRS AND POPULATION STUDY FOR THE DNA PROFILING IN KOREANS

<u>Wook Kim</u><sup>1</sup>, Dong-Jik Shin<sup>1</sup>, Jung-Min Kim<sup>1</sup>, Han-Jun Jin<sup>1</sup>, Kyoung-Don Kwak<sup>1</sup>, Myun-Soo Han<sup>2</sup>, and Sang-Kyu Choi<sup>2</sup>

<sup>1</sup>Department of Biology, Dankook University, Cheoman, Korea

<sup>2</sup>DNA Analysis Section, National Institute of Scientific Investigation, Seoul, Korea

We have developed three multiplex genotyping systems with allelic ladders of nine Y-chromosome STR markers (DYS19, DYS388, DYS389l/II, DYS390, DYS391, DYS392, DYS393, and DXYS156Y), with a view towards the application of rapid and simple genotyping assay methods for the DNA profiling. Allele and haplotype frequencies at these Y-STRs loci were analyzed by PCR amplification using the triplex kits, followed by denaturing polyacrylamide get electrophoresis in 232 unrelated males in the Korean population. A total of 210 different haploytpes were found, 194 of them being unique. Gene diversity varied from 0.4130 at DYS 391 to 0.7648 at DYS389II. The haplotype diversity value (which is the same as the discrimination index) calculated from all nine loci combined was 0.9989, which is informative. Our results revealed that a set of nine Y-STRs can discriminate between most of the male individuals in the Korean population (discrimination capacity 90.25%). These multiplex systems thus provide useful information for forensic analysis and paternity tests, and can also be of great benefit for providing information not normally available from autosomes.