GENETIC POLYMORPHISM AND HAPLOTYPE ANALYSIS OF MENTYPE® ARGUS X-8 STR LOCI IN KOREANS

Eun Jin Lim[1], Jeong Eun Sim[1], Hwan Young Lee[1], Myung Jin Park[1], Na Young Kim[1], Hyung-Joon Ahn[2], Woo Ick Yang[1] and Kyoung-Jin Shin[1]

[1]Department of Forensic Medicine and Brain Korea 21 Project for Medical Science, Yonsei University College of Medicine, Seoul, Korea

[2]Department of Oral Medicine, Yonsei University College of Dentistry, Seoul, Korea

One of the main aims of forensic X-chromosomal STR analysis is to solve kinship constellations by the reconstruction of family trees using chromosome X haplotyping. For this application of tightly linked STR clusters, 4 X-STR duos in linkage group 1-4 (DXS10135-DXS8378, DXS7132-DXS10074, HPRTB-DXS10101 and DXS10134-DXS7423) were investigated in 450 unrelated Koreans (300 males and 150 females) using Mentype® Argus X-8 kit. Forensic efficiency parameters for these eight X-STR markers indicated that they are highly informative for forensic application in Koreans. No significant deviation was observed from Hardy–Weinberg equilibrium for all eight markers, and no evidence of linkage disequilibrium was detected in any pairs of these markers. During analysis, triallelic pattern was observed once at DXS10135 (24-26-28), and 11 off-ladder alleles were observed in 15 samples: four samples at DXS7132 (allele 10 and 18), one sample at DXS8378 (allele 7), two samples at DXS10074 (allele 17.3), three samples at DXS10134 (allele 30, 34.2 and 37.1) and five samples at DXS10135 (allele 21.3, 22.2, 29.2 and 37). These are characterized by cloning and sequencing analysis. In addition, haplotype analysis for 4 X-STR duos was carried out in 300 males, which showed a total of 38–58 haplotypes for each linkage duo. However, to verify the usefulness of these haplotypes in reconstruction of family trees, the accurate recombination frequency between these linked markers should be determined before introducing them into the forensic practice.