Abstract 74

GENETIC VARIATION OF 18 Y-CHROMOSOMAL STR LOCI IN THE SLOVAK POPULATION

Krzysztof Rębała[1], Daniela Siváková[2], Zuzana Džupinková[3] and Zofia Szczerkowska[1]
[1]Department of Forensic Medicine, Medical University, Gdansk, Poland
[2]Department of Anthropology, Comenius University, Bratislava, Slovakia
[3]Department of Experimental and Applied Genetics, Institute of Preventive and Clinical Medicine, Slovak Medical University, Bratislava, Slovakia

Human Y-chromosomal short tandem repeat (Y-STR) loci have been widely applied in forensics, kinship investigation, genealogy and evolutionary studies. In order to establish the usefulness and informative power of Y-STR haplotypes in the Slovak male lineage identification, 18 Y-linked microsatellite loci (DYS19, DYS388, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS426, DYS437, DYS438, DYS439, DYS460, GATA H4.1, DYS385 a/b, and YCAII a/b) were genotyped in a population sample of randomly selected, unrelated Slovak males by means of a multiplex (octadecaplex) PCR reaction and capillary electrophoresis. Allele and haplotype frequencies, respective diversity values and potential of the markers for resolution of similar haplotypes were estimated. Among 164 unrelated Slovak males, 155 different haplotypes were identified. The most frequent haplotypes were shared by 3 individuals (1.8%), 5 haplotypes were seen twice, while 148 haplotypes were individual-specific. The calculated gene diversity ranged from 0.379 to 0.830 for DYS393 and DYS385, respectively, while the haplotype diversity for all 18 Y-STR loci was 0.9992. The two-locus systems DYS385 and DYS389 had the greatest potential to discriminate similar haplotypes, whereas elimination of DYS426 and DYS438 appeared not to have any impact on the haplotype discrimination power. Our results demonstrate the usefulness of the analysed Y-STR loci and the studied multiplex PCR system in forensic practice in Slovakia.