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Population genetic analysis in Hungarian populations using the Powerplex™ 16 system

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With the advent of STR profiling it has become possible for forensic scientists to rapidly gain a reliable impression of the scale of population genetic effects caused by several factors such as inbreeding and substructuring. Previous studies have shown that population analyses in Hungarian populations can be of great importance from the viewpoint of the examination of population differentiation. This study provides additional population genetic data of the Hungarian population on the 13 CODIS core STR loci and the two penta STRs (Penta D, Penta E). Allele frequency and profile databases were generated for four population samples, which had been collected from 223 individuals living in the Budapest area (Central Hungary), from 206 Romanies living in Baranya county (southwestern Hungary), from 116 Romanies living in Hajdú–Bihar and Szabolcs–Szatmár–Bereg counties (eastern Hungary) and from 178 Ashkenazims living in Budapest. In the study, the Budapest area sample was used as a reference group for the mixed character of the Hungarian population, because the sample was collected in a blood bank irrespective of ethnic background.

Amplification was performed using the GenePrint® PowerPlex™ 16 System (Promega) and the ABI Prism™ 310/377 instruments (Applied Biosystems) were used for genotyping.

At the locus FGA, one type of intermediate-sized alleles were detected in three samples of the eastern Hungarian Romany population. According to sequence results, the presence of an additional T in the 5′ flanking region leads to an intermediate allele 24.1. The presence of the variant allele in three independent samples with the little evidence for

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association of alleles between the STR systems indicates possible sampling error or inbreeding in this population.

Comparing the allele frequency values by *G*-statistic, calculating the F_{ST} indices and with the pairwise comparisons of interpopulation molecular variance (AMOVA), the four Hungarian populations could be distinguished using data of 15 STR loci.

The results suggest that the population structure may have an effect on the interpretation of forensic DNA evidence in Hungary.