POPULATION GENETIC ANALYSIS ON THE THIRTEEN CODIS CORE STR LOCI IN THREE HUNGARIAN POPULATIONS

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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. Due to their relatively high proportion (approx. 6%) among the Hungarian inhabitants the Romanies (Gypsies) represent one of the most relevant groups of the Hungarian population. Previous studies have shown that population analyses in the Hungarian Romanies can be of great importance from the viewpoint of the examination of population differentiation. This study provides additional population genetic data of Hungarian populations on the thirteen CODIS core STR loci (D3S1358, vWA, FGA, D8S1170, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1po, and D16S539). Allele frequency and profile databases were generated for three Hungarian population samples. Blood samples were collected from 223 individuals living in Budapest (Central Hungary), from 206 Romanies living in Baranya county (southwestern Hungary) and from 116 Romanies living in Hajdu-Bihar and Szabolcs-Szatmar-Bereg counties (eastern Hungary). In this study the Budapest sample was used as a reference group for the missed 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 Ampf*l*STR Profiler Plus™ and COfiler™ PCR kits (PE Biosystems). ABI Prism® 310/377 instruments (PE Biosystems) were used for genotyping.

Altogether four departures from Hardy-Weinberg equilibrium were observed at the loci D3S1358, D7S820, D8S1179, and D13S317 in the Romany population databases. Comparing the allele frequency values by G-statistic, calculating the FST indices and with the pairwise comparisons of interpopulation molecular variance, the three Hungarian populations could be distinguished using data of thirteen STR loci. Interpopulation differences were also evaluated computing the differences between the respective log likelihood ratio estimates of each multilocus profile from the databases to be compared. The effect of incorporating coancestry and inbreeding coefficients (FST and FIS indices) in the match probability calculations will also be discussed.

In conclusion, Hungarian population databases have been established for the thirteen CODIS core STR loci. Our results suggest that the possibility of population differentiation should be taken into account on the calculation of match probabilities in Hungarian forensic cases.