

HUNGARIAN AND ROMANI POPULATION DATA BASED ON 11 Y-STR AND 49 Y-SNP MARKERS

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49 Y-chromosomal single nucleotide polymorphisms (SNPs) with TaqMan assay and 11 Y chromosomal STR loci were tested in independent Hungarian, Hungarian Romani, Tiszavasvári Romani and Slovakian Romani male samples. The Tiszavasvári and Slovakian Romani populations live in isolated Romani slums. The haplotype and haplogroup diversity values for the examined Hungarian population were 0.9967 and 0.8808, respectively, while in the Romani population the values appeared to be less, as expected. Some of the characteristic Romani haplotypes were present in the Hungarian population due to the incidence of Romanies in Hungary being high. According to the last census their presence in Hungary was 0.7%, but because they often deny their Romani origin their real presence is estimated at 3.5–10%. Genetic distances to 38 different populations were calculated based on haplogroup frequencies with AMOVA implemented in Arlequin2.0. Based on distances a phylogenetic tree was constructed with Neighbor-joining method using Phylip 3.66.