

Population Data for 17 Y-STRs in Samples from Southeastern Anatolia Region of Turkey

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ABSTRACT In this study, Y chromosome short tandem repeats (Y-STR) haplotype data were obtained for 86 individuals from the Southeastern Anatolia region of Turkey. Allele frequencies were determined for 17 Y-STRs and haplotypes were obtained. The highest gene diversity was observed at DYS385 (0.95) while the lowest was at DYS437 (0.44). A total of 79 different haplotypes were identified, of which 74 were unique. The haplotype diversity for all loci and discrimination capacity were calculated as 0.9959 ± 0.0029 and 0.92, respectively. Haplotype data for different neighbouring populations obtained from Y-Chromosome Haplotype Reference Database (YHRD) were used for comparison. The result of the Analysis of Molecular Variance (AMOVA) indicated that there is no significant genetic distance between Southeastern Anatolia population and neighbouring populations at all. Armenian, Rasht (Iran-Gilaki) and Izeh (Iran-Bakhtiari) populations were found to be closest to our population, while Syria and Iraq populations were more distant.