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Overview of the Genetic STR Clustering among Worldwide Human Populations

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ABSTRACT Although DNA genetic markers, including Y-chromosomal short tandem repeats (Y-STRs), are widely used in the analysis of population data, autosomal short tandem repeats (STRs) have a wide role in the investigation of human migration patterns throughout the history, genealogical research, and population genetics. In this review, allele frequencies of 13 autosomal STR loci (D3S1358, TH01, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, CSF1PO, vWA, D8S1179, TPOX, and FGA) have been reviewed in 64 different worldwide populations. Allele frequency data for 13 STR loci was collected from previously published scientific papers in the journal databases for each studied population and molecular genetic diversity among the 64 sample populations was compared. Further, a worldwide phylogenetic tree and genetic distance values were created using POPTREE2 software and UPGMA method. Results confirmed that the differences among local sub-populations are much smaller than the differences among geographically separated populations. The obtained results, as the researchers had expected, were in the compliance with previously published papers with the difference that the researchers used data on populations from all over the world and thus created a more detailed phylogenetic tree. In that way, the authors offer an insight into the global phylogenetic tree created on the basis of STR allele frequencies for the first time. The goal of this manuscript is to prove the usefulness of these 13 STR markers within the analysis of the genetic distance and its correlation with "geographically-based genetic clustering" among the worldwide populations.