



ABSTRACT

A short tandem repeat is a microsatellite, consisting of a unit of two to seven nucleotide core sequence repeated up to several hundred times in a row on the DNA strand. STR analysis is a tool in forensic analysis that investigates specific STR loci found on the genomic DNA. The polymorphic nature of the STR regions that are analyzed for forensic testing greatly enhances the power of discrimination between the DNA profiles of different individuals. Forensic science exploits the population's variability in STR lengths, enabling scientists to distinguish one DNA sample from another. This property is used in criminal cases as well as parentage and sibship analyses. This study was aimed to calculate the allelic frequency distribution of selected STR loci, parentage determination and sibship analysis in a selected sample of 125 individuals from the Pakistani population.

Buccal swab samples from 125 related and unrelated individuals were subjected to DNA extraction and amplification using AmpF λ STR identifier plus kit that were subsequently genotyped using capillary electrophoresis. 15 STR markers D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA along with additional amelogenin for gender discrimination were analyzed in this study. Allelic frequency distribution and degree of homozygosity or heterozygosity were calculated for the aforementioned 15 loci in the sample population, using gene counting method.

Paternity index, combined paternity index and probability of paternity were calculated by applying statistical tools for the 62 trios tested in this study. The values of Max CPI, Min CPI and Probability of Paternity were observed to be 3014935823, 94498 and 0.9999999425599 respectively to set the ranges. Although single step mutations were observed in few individuals, however parentage was significantly established in all the families tested in this study.

Statistical sibship analysis was performed on the same 62 trios which were subjected to parentage analysis. 80% of the cases showed LH of FS > LH of HS > LH of UR. The max and min values of likelihood ratios for FS vs UR were calculated for both true sibs and unrelated



individuals to determine the ranges. In approximately 90% of the trios in which parentage was significantly established, offspring could not be excluded as being the biological brother or sister of each other.