

Reconstructing recent human phylogenies with forensic STR loci: A statistical approach

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Background: Forensic STR loci are effective for the purpose of individual identification, and other forensic applications. Most of these markers have high allelic variability and mutation rate because of which they have limited use in the phylogenetic reconstruction. In the present study, we have carried out a meta-analysis to explore the possibility of using only five STR loci (TPOX, FES, vWA, F13A and Tho1) to carry out phylogenetic assessment based on the allele frequency profile of 20 world population and north Indian Hindus analyzed in the present study.

Results: Phylogenetic analysis based on two different approaches – genetic distance and maximum likelihood along with statistical bootstrapping procedure involving 1000 replicates was carried out. The ensuing tree topologies and PC plots were further compared with those obtained in earlier phylogenetic investigations. The compiled database of 21 populations got segregated and finely resolved into three basal clusters with very high bootstrap values corresponding to three geo-ethnic groups of African, Orientals, and Caucasians. Along with it we studied the mt DNA and also the Y-STR,s and confirmed the above findings

Conclusion: Based on this study we conclude that if appropriate and logistic statistical approaches are followed then even lesser number of forensic STR loci is powerful enough to reconstruct the recent human phylogenies despite of their relatively high mutation rates.

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