

Genetic Polymorphism of Five STR Markers among Four Groups of Punjabi Population in North-West Punjab, India

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ABSTRACT Historically, Punjab has served a major passage way for human migration to Indian subcontinent and has influenced the genetic structure of extant populations in Punjab. Therefore, Punjabi population possesses an exclusive genetic profile primarily due to the many migratory events in this region which caused an extensive range of genetic diversity. Hence, the present study is an attempt to understand the effect of these influences on genetic differentiation, diversity and population structure of Punjab. Genetic polymorphism at five highly polymorphic short tandem repeat loci (STR) is studied in four endogamous population groups of Punjab, India. The studied groups included Jat Sikh, Majbi Sikh, Brahmin and Ramdasia to evaluate their significance in human identification and genetic study. All selected groups practice endogamy and a total of 358 individuals belonging to these four endogamous groups were studied for five highly polymorphic with greater power of exclusion STR loci: THO1, TPOX, D7S820, CSF1PO and vWA. The highest observed heterozygosity was found in Ramdasia population for almost all the markers except vWA which had highest observed heterozygosity among Majbi Sikh population group. In this study, the average sub-ethnic differentiation (F_{st}) among the four populations of north-west Punjab was 0.0821. The marker with the highest contribution to interpopulation genetic difference was observed to be vWA.