VALIDATING SNP PANEL FOR FORENSIC HUMAN IDENTIFICATION PURPOSES IN INDIAN POPULATIONS

Anujit Sarkar and Madhusudan R. Nandineni, Centre for DNA Fingerprinting and Diagnostics (CDFD)

Forensic human identification (HID) process currently relies on determining the repeat length polymorphisms of a set of ~20 highly informative short tandem repeats (STRs) distributed on the autosomes. Although efficient, robust and sensitive, at times the current approach fails to amplify the target STRs while encountering challenging forensic samples subjected to extensive DNA degradation. Single nucleotide polymorphisms (SNPs) have been proposed as an alternative in such instances as they rely on a much reduced amplicon size (within 100 bp) as compared to the STRs whose amplicon length can be upto 450 bp. Several SNP-based panels were proposed for worldwide populations but similar studies for Indian populations have not yet been undertaken. The present study aims to design and validate a SNP-based panel for Indian populations for HID. A bioinformatic approach involving stringent filters was employed to shortlist a panel of 275 SNPs from various publically available SNP databases and genotyped them in 460 unrelated adult volunteers from various locations in India using *GoldenGate*® Genotyping Assay (Illumina, Inc, USA). 2-4 distantly located SNPs (> 20 Mb apart) on each autosome with heterozygosity ≥ 0.4 and F_{ST} ≤ 0.02 were further shortlisted to empanel 70 SNPs for HID. Random match probability (RMP) and other forensic parameters for these 70 SNPs in the Indian populations tested were much higher than those derived from the currently employed STR-based chemistries. Comparisons with a previously published panel showed that the current panel had much higher efficiency and better suited for HID applications in Indian populations. The results from these studies would be discussed during the presentation.