SIMULTANEOUS SEQUENCING OF STR AND SNP MARKERS ON A SINGAPORE POPULATION USING THE ILLUMINA MiSeq FGx SYSTEM

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Next generation sequencing (NGS) is now being evaluated by forensic scientists worldwide due to its ability to allow sequencing of large numbers of amplicons in a single, targeted assay. NGS assays have been developed to target short tandem repeats (STRs) and single nucleotide polymorphisms (SNPs) to answer multiple forensic questions simultaneously. Sequencing of autosomal STRs such as those in the core US CODIS set and European Standard Set, as well as X and Y STRs, together with identity informative SNPs, permit a power of discrimination greater than any other currently available capillary electrophoresis (CE) methods. Sequencing of ancestry and phenotypic informative SNPs provides predictive investigative leads sought by law enforcement when direct matching to the national convicted offenders DNA database fails to identify a suspect.

We describe herein an evaluation of the Universal Forensic Panel by Illumina (provided as part of an early access program) a targeted amplicon panel which combine the above mentioned STR and SNP markers, on a Singapore population set. Whereas much work has already been done in the identification of genetic markers useful in ancestry and physical trait prediction in Caucasian populations, little has been done in appraising these markers in an Asian context. 350 DNA samples from the Chinese, Malay and Indian populations in Singapore have been sequenced using the Universal Forensic Panel on the Illumina MiSeq FGx. In addition to standard evaluations of reproducibility, sensitivity and concordance as compared to current CE methods, the ancestry and phenotypic markers on the panel have been evaluated for their ability to discriminate between individuals of the different racial groups and physical characteristics.