

SEQUENCE DIVERSITY WITHIN STR LOCI IN SINGAPORE POPULATION SAMPLES

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Massively Parallel Sequencing (MPS) has facilitated the detection and classification of intra-allelic sequence variants within the repeat regions of the short tandem repeats (STRs) used for human identification. The additional allelic diversity contributed by the sequence variants over traditional length-based genotyping is likely to improve discriminatory power. The aim of this study was to identify and characterize the sequence variants within the repeat regions of STRs covered by Illumina's ForenSeq DNA Signature Prep Kit in population samples in Singapore. 200 each of Chinese, Malay and Indian samples were genotyped to build a reference database of such variants in Singapore. Sequencing was performed on the MiSeq FGx, while analysis was performed within the ForenSeq Universal Analysis Software (UAS) and using in-house developed Excel workbooks. The results of the study will be presented herein. The additional allelic diversity, heterozygosity and discriminatory power contributed by the sequence variants will also be reported.