## G39 Application of Single Nucleotide Polymorphisms (SNPs) to Forensic Casework in Malaysia

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After attending this presentation, attendees will learn another reliable SNPs panel developed from the SNP*for*ID markers that can be applied for population study or forensic human identification. Data obtained showed the SNP markers and platform chosen are informative and suitable to be used in forensic casework, where samples with minute amount of DNA input (as low as 30 picogram) can be detected.

This presentation will impact the forensic science community by introducing reliable and sensitive SNaPshot assays in order to genotype the population or to be used in human identification. Data obtained from the study will provide knowledge about the allele frequencies distribution in three major ethnic groups in Malaysia (Malay, Chinese, and Indian).

The analysis of degraded DNA can be problematic. Recent advances in the identification and analysis of single nucleotide polymorphisms (SNPs) have demonstrated the advantage of these markers over short tandem repeats (STRs) in that they only require small amplicons. However, before applying to casework, it is important to develop allele frequency databases from relevant populations. The purpose of this phase of the study is to characterize three Malaysian major ethnic groups: Malay, Chinese, and Indian, using 52 autosomal SNP markers that have been identified in the SNP*for*ID project.

*Sanchez et. al*., 2006 reported a multiplex of 52 SNP markers in one PCR reaction with two single base reaction (SBE) in the detection of SNPs using capillary electrophoresis (CE). The amplicons for PCR ranged from 59 bp to 115 bp. Whilst for SBE reactions ranged from 16 nt to 92 nt. In their study, full complete profile was obtained from 500 pg DNA input. The study was carried out on three major populations: African, Asian, and European.

As in this study, a total of 150 Malaysian samples (50 samples from each ethnic group) were genotyped. In order to genotype the population samples reliably and robustly, four sets of 13-plex SNPs were developed. Sensitivity and reproducibility studies demonstrated that the assays were highly sensitive, requiring as little as 30 pg of DNA. Full, complete, and clear profiles were generated. Data were collected and evaluated statistically for forensic usefulness.

Across the three ethnic groups, few significant departures from HWE were observed in Malay, Chinese, and Indian ethnic groups. At marker rs2107612, no heterozygosity was observed at all in Malay group (Ho=0) but the Indian group showed higher heterozygosities (above 80%). Whereas, for marker rs1413212, Malay group showed higher heterozygosities (above 80%) compared to Chinese or Indian groups. Major departure from HWE also was observed in both Chinese and Indian ethnic groups at rs1528460 marker.

The combined mean match probabilities for the 52 SNPs of Malay, Chinese, and Indian are $2.1974^{e-18}$, $6.0042^{e-18}$ and $1.1756^{e-18}$, corresponding to a combined power of discrimination of >99.99999999%, respectively. Paired $F_{st}$ values obtained in the study showed, as expected, that Malay group is closely related to the Chinese population, with the Indian population being more distant.

**SNPs Marker, Malaysian Population, SNP for ID**

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