

ANALYSIS OF Y-CHROMOSOMAL HAPLOTYPE DIVERSITY IN SINGAPORE

Qing Wei CHEANG, Jia Hao NG, Sarah SAMYNATHAN, Nurul IMAN, Christopher Kiu Choong SYN

DNA Database Laboratory, Biology Division, Health Sciences Authority

The analysis of Y-chromosomal short tandem repeats (Y-STRs) is an important tool in criminal investigations. It has the ability to 1) detect male perpetrators, particularly in sexual assault cases, where there is an excess of female DNA; and 2) identify the paternal lineage of the male perpetrator and provide investigative (familial) leads. Y-STR analysis is also useful in population studies; it would, therefore, be informative to investigate the occurrences of the Y-STR haplotypes in the Singapore population. Singapore is a Southeast Asian island country whose citizenry is primarily comprised of three main ethnic groups: Chinese, Malay and Indian. There is also a large fluctuating population of transient migrant workers, many of whom are from Asian countries, making up over 20% of the total population. The present study to analyse the Y-chromosomal genetic diversity in Singapore was initiated in June 2018, and will seek to profile over 150,000 haplotypes. To-date, some 15,000 haplotypes have been typed using the 25-marker YFiler Plus (YFP; Thermo Fisher Scientific) System. Haplotype-based parameters were calculated and the increased information for forensic casework from the YFP panel were compared to the YFiler, PPY12, SWGDAM and minimal haplotype panels. We observed a significant number of null, duplicate, intermediate and off-ladder alleles and highlight two new microdeletions observed in our study.