

Genetic Polymorphisms of 11 Y-Short Tandem Repeat loci in Singapore populations

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Human chromosome Y-specific Short Tandem Repeats (Y-STRs) loci are useful markers in paternity testing, forensic analysis, genealogical and evolutionary studies. Population database for Y-STR is necessary for matching probability calculation in forensic analysis. In this study, 11 Y-STR loci (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS437, DYS438 and DYS439) were analysed in the three main ethnic groups in Singapore, namely 210 Chinese, 186 Malay and 183 Indian. Y-STR locus diversity ranges from 0.359 to 0.965. DYS385 showed the highest diversity in all three populations (0.955, 0.965 & 0.946 for Chinese, Malay & Indian). DYS391 was the lowest in Chinese (0.362) and Indian (0.402), while DYS437 the lowest in Malay (0.359). A total of 534 haplotypes were found in all three ethnic groups, consisting 191 haplotypes in Chinese, 175 in Malay and 174 in Indian, with 6 haplotypes shared between 2 groups of the populations. Unique haplotype in Chinese, Malay & Indian numbered 178, 165 and 167 respectively. The Chinese group has a common haplotype with a frequency of 2.4%. Haplotype diversity of the 11 Y-STRs was calculated to be 0.9987, 0.9993 and 0.9993, while discrimination capacity 90.95%, 94.09% and 95.08% for Chinese, Malay and Indian respectively. Two microvariant alleles for DYS391 and DYS385 were observed. A locus duplication at DYS385 and a deletion at DYS392 were also noted in this database. Preliminary genetic distance analysis between two populations indicated Chinese-Malay are the most related, while Chinese-Indian are the furthest apart genetically. Subgroup within the Chinese population that consists of males with the same surname generally showed lower genetic heterogeneity compared to the random Chinese population. To our knowledge, this study represents the most comprehensive report of Y-STR haplotype distribution in Singapore to date.