

DNA PROFILING OF CHINESE POPULATION IN HONG KONG

Frederick C. Leung and Charis M.N. Chan

Department of Zoology, University of Hong Kong, Hong Kong, SAR, China.



Chinese populations are usually underrepresented in genetic study of worldwide populations. Our objective is to construct a DNA population database starting with the Chinese population in Hong Kong. We are in the process of constructing a DNA population database that consists of DNA profiles of Chinese population in Hong Kong using the Promega *GenePrint*[®] PowerPlex[™] 1.2 kit. The *GenePrint*[®] PowerPlex[™] 1.2 is the newly released personal identification kit from Promega, and it allows the simultaneous single-tube amplification and two-color detection of eight polymorphic short tandem repeat (STR) loci. They are: D5S818, D13S317, D7S820, D16S539, vWA, TH01, TPOX, and CSF1PO. In addition, Amelogenin primers provide the PCR products for the sex determination. In addition, population statistics are obligatory for the calculation of matching probability in forensic examination and power of exclusion in paternity testing. We have collected 300 random adult consent samples, and finished analyzing 150 samples. Genomic DNA was extracted with the Wizard[®] Genomic DNA purification kit and the DNA concentration was quantified fluorometrically. DNA profile of individual sample was generated following the DNA amplification protocols exactly listed in the Promega *GenePrint*[®] PowerPlex[™] 1.2 Technical Manual using the Perkin-Elmer Thermal Cycler Model 480. Amplified PCR fragments were detected using the ABI[™] PRISM[®] 310 Genetic Analyzer, and we followed the exact protocols as listed in the manual for sample preparation and including the fluorescent ladder as an internal lane standard. The observed heterozygosities for D5S818, D13S317, D7S820, D16S539, vWA, TH01, TPOX, and CSF1PO were 77.20%, 81.20%, 75.30%, 79.40%, 80.60%, 72.90%, 65.30%, 72.80%. We noticed a high number of +1 and -1 bp amplified PCR products, and further examinations are needed to determine whether they are PCR artifacts. Another noticeable feature is the allele frequency for TH01, 9 and 9.3, which is 43.2% vs. 3.2%, respectively. The data presented here can be used in human identity testing to estimate the frequency of a multiple STR locus DNA profile in the Hong Kong Chinese population. (Supported in part by Promega and University of Hong Kong)

