

Multiplex Typing of 74 Y-SNPs in Japanese using Liquid Bead Array technology

Masaki Hashiyada, Yukio Itakura, Masato Funayama

Analysis of single nucleotide polymorphism markers on the Y chromosome (Y-SNPs) could provide useful information in some forensic cases or paternal genetic relationships. However, comparing with STR, analyses of many SNPs loci were required to get information of individual identification because SNPs are biallelic loci. There are several different methods for analyzing SNPs. One of them is a liquid bead array system, which is rapid, cost-effective, high-throughput readout system performed on a flow cytometer, LuminexTM 100 (Luminex, Austin, USA). This system is capable of conducting multiplex analysis of up to 100 different tests in a single tube. In this study, 74 Y-SNPs loci were investigated in 199 unrelated Japanese male volunteers by the SignetTM Y-SNP Identification System MK2 (Marligen Biosciences, Ijamsville, USA). Genomic DNA was extracted buccal swab using QIAmp DNA Blood Mini Kit (QIAGEN, Hagen, Germany). PCR and Exonuclease I enzyme treatment were performed in accordance with manufacture's protocols. Collected LuminexTM data were analyzed by MasterPlex GT software (MiraiBaio, Alameda, USA). This Y-SNPs kit has 74 Y-SNP markers which are grouped into 10 multiplexes during amplification and labeling to determine the ethnic groups using the tree of human Y-chromosomal binary haplogroups, which was made by the Y Chromosome Consortium [1]. The first procedure is 'multiplex A-R' which has M9, M45, M89, M96, M122, M168, M175, M207 and M304 markers to define the major groupings of Y haplogroups. After that, the other multiplexes may be chosen based on the presence of particular 'Multiplex A-R' key SNPs because each group has several markers under their down stream. Of the 199 subjects, 16 haplogroups were found, where in which 80, 65 and 46 samples were classified to the major clades, 'Haplogroup CD', 'Haplogroup O1' and 'Haplogroup O2', respectively. Japanese samples using in this study were divided into halves, 'Haplogroup CD' which is different from the haplogroup distribution for other East Asian races and 'Haplogroup O' which is widely distributed over East Eurasia. Concerning a forensic identification, it is necessary to more detailed information. However, this result may be proposed to define the race by making consideration of the results of Y-STR and mtDNA at the same time. Reference: 1. The Y Chromosome Consortium. A Nomenclature System for the Tree of Human Y-Chromosomal Binary Haplogroups. *Genome Res.* 12 (2002):339-348.