POLYMORPHISM OF SEVENTEEN STRS OF THE MULTIPLEX ANALYSIS SYSTEM IN JAPANESE POPULATION

M. Hashiyada[1], Y. Itakura[2], T. Nagashima[2] and M. Nata[1]
[1]*Tohoku University Graduate School of Medicine, Japan*
[2]*NTT Data Technology Corporation, Japan*

➤◁

Short tandem repeat (STR) analysis is a useful tool in forensic sciences to get information of individual identification. Recently, several STR loci can be amplified in one tube using multiplex PCR STR kit, which are commercially available.

We investigated 17 STR loci in 520 unrelated Japanese volunteers by PowerPlex® 16 System (Promega, USA) and the AmpF/STR® Identifiler® (Applied Biosystems, USA). Genomic DNA was extracted from buccal swab using SDS-Proteinase K and Chelex® 100 treatment followed by the phenol/chloroform extraction. PCR was performed in accordance with manufacture's protocols. Electrophoresis was carried out on an ABI PRISM® 310 Genetic Analyzer and the alleles were determined by GeneScan® 2.0.2 software (Applied Biosystems, USA).

The statistical data of 17 analysed STRs, excluding Amelogenin locus, showed a relatively high rate, and no significant deviation from Hardy-Weinberg Equilibrium was detected. In 17 STRs, the 'Penta E' loci was found to be a most highly polymorphic locus. The matching probability of this system showed in 1 in 6.81×10^{19} and the power of exclusion was 0.99999988 in Japanese population. Our results suggest that this system provides powerful discrimination.

Then, we applied this data to not only forensic cases, but also information security system such as biometoric personal authentication.